Statistics 501
Introduction to Nonparametrics & Log-Linear Models

Paul Rosenbaum, 473 Jon Huntsman Hall, 8-3120
rosenbaum@wharton.upenn.edu Office Hours Tuesdays 1:30-2:30.

BASIC STATISTICS REVIEW

NONPARAMETRICS

Paired Data

Two-Sample Data

Anova

Correlation/Regression

Extending Methods

LOG-LINEAR MODELS FOR DISCRETE DATA

Contingency Tables

Markov Chains

Square Tables

Incomplete Tables

Logit Models

Conditional Logit Models

Ordinal Logit Models

Latent Variables

Some abstracts

PRACTICE EXAMS

Old Exams (There are no 2009 and 2016 exams)

Get Course Data in an R workspace

http://www-stat.wharton.upenn.edu/~rosenbap/index.html

The one file for R is Rst501.RData It contains several data sets. Go back to the web page to get the latest version of this file.

Get R for Free: http://www.r-project.org/

Statistics Department

http://www-stat.wharton.upenn.edu/ (Note: "www-" not "www.")

Paul Rosenbaum's Home Page

http://www-stat.wharton.upenn.edu/~rosenbap/index.html

Course Materials: Hollander and Wolfe: *Nonparametric Statistical Methods* and Fienberg: *Analysis of Cross-Classified Categorical Data*. Optional additions are: Maindonald and Braun *Data Analysis and Graphics Using R* or Dalgaard *Introductory Statistics with R*. The recommended new (2014) third edition of *Nonparametric Statistical Methods* now uses R (the second edition did not), and there is an R package for the book, NSM3, freely available from cran, and described in the R Program Index at the back of the textbook. An optional alternative to Fienberg's book is Alan Agresti's *An Introduction to Categorical Data Analysis*. An optional additional book is *Nonparametric Statistical Methods Using R* by John Kloke and Joe McKean, Chapman and Hall, 2015.

Common Questions

How do I get R for Free?
http://www.r-project.org/

Where is the R workspace for the course?
http://www-stat.wharton.upenn.edu/~rosenbap/index.html

The R workspace I just downloaded doesn't have the new object I need.
Sometimes, when you download a file, your web browser things you have it already, and opens the old version on your computer instead of the new version on the web. You may need to clear your web browsers cache.

I don't want to buy an R book – I want a free introduction.
Go to http://www.r-project.org/, click manuals, and take:
An Introduction to R
(The R books you buy teach more)

I use a MAC and I can't open the R workspace from your web page.
Right-click on the workspace on your webpage and select "Save file/link as" and save the file onto the computer.

I want to know many R tricks.
cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf
(search for this at http://www.r-project.org/)

Statistics Department Courses (times, rooms)
http://www.upenn.edu/registrar/

Final Exams (dates, rules)
http://www.upenn.edu/registrar/

When does the the course start?
When does it end? Holidays?
http://www.upenn.edu/almanac/3yearcal.html

Does anybody have any record of this?
http://www.upenn.edu/registrar/

Grades/Cheating/Class Attendance

There is a take-home mid-term covering nonparametrics and a final covering categorical data. The final may be in-class or take-home. In either case, both exams are open-book, open-notebook. Take-home exams must be your own work, with no communication with other people. **If you communicate with anyone in any way about the midterm or the final, then you have cheated on exam.** Cheating on an exam is the single stupidest thing a PhD student at Penn can do.

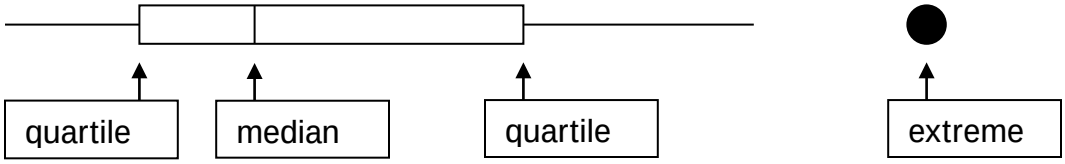
Copies of old midterms and finals are at the end of this bulk pack. You should do several of each for practice, ideally working on old exams all semester long as topics are covered. In working on old practice exams, you may work with other students. The exams involve working with data, and understanding statistical methods requires using them with data. If you want to learn the material in the course, do lots of practice exams.

You are expected to attend class. It is no problem at all if you miss one or two classes because of illness or family issues or transportation problems or a conference or job talk or a search for inner peace or whatever. If you miss a substantial number of classes, much more than one or two classes, then your grade in the class will be substantially reduced regardless of exam performance, and I may contact your departmental advisor to discuss your situation.

Review of Basic Statistics – Some Statistics

- The review of basic statistics is a quick review of ideas from your first course in statistics.
- n measurements: $X_1, X_2, ..., X_n$
- **mean** (or average): $\overline{X} = \frac{\sum_{i=1}^{n} X_i}{n} = \frac{X_1 + X_2 + ... + X_n}{n}$
- **order statistics** (or data sorted from smallest to largest): Sort $X_1, X_2, ..., X_n$ placing the smallest first, the largest last, and write $X_{(1)} \le X_{(2)} \le ... \le X_{(n)}$, so the smallest value is the first order statistic, $X_{(1)}$, and the largest is the nth order statistic, $X_{(n)}$. If there are n=4 observations, with values $X_1 = 5, X_2 = 4, X_3 = 9, X_4 = 5$, then the n=4 order statistics are $X_{(1)} = 4, X_{(2)} = 5, X_{(3)} = 5, X_{(4)} = 9$.
- **median** (or middle value): If n is odd, the median is the middle order statistic – e.g., $X_{(3)}$ if n=5. If n is even, there is no middle order statistic, and the median is the average of the two order statistics closest to the middle – e.g., $\frac{X_{(2)} + X_{(3)}}{2}$ if n=4. Depth of median is $\frac{n+1}{2}$ where a "half" tells you to average two order statistics – for n=5, $\frac{n+1}{2} = \frac{5+1}{2} = 3$, so the median is $X_{(3)}$, but for n=4, $\frac{n+1}{2} = \frac{4+1}{2} = 2.5$, so the median is $\frac{X_{(2)} + X_{(3)}}{2}$. The median cuts the data in half – half above, half below.
- **quartiles**: Cut the data in quarters – a quarter above the upper quartile, a quarter below the lower quartile, a quarter between the lower quartile and the median, a quarter between the median and the upper quartile. The **interquartile range** is the upper quartile minus the lower quartile.

- **boxplot**: Plots median and quartiles as a box, calls attention to extreme observations.



- **sample standard deviation**: square root of the typical squared deviation from the mean, sorta,

$$s = \sqrt{\frac{(X_1 - \overline{X})^2 + (X_2 - \overline{X})^2 + \ldots + (X_n - \overline{X})^2}{n-1}}$$

  however, you don't have to remember this ugly formula.
- **location**: if I add a constant to every data value, a measure of location goes up by the addition of that constant.
- **scale**: if I multiply every data value by a constant, a measure of scale is multiplied by that constant, but a measure of scale does not change when I add a constant to every data value.

Check your understanding: What happens to the mean if I drag the biggest data value to infinity? What happens to the median? To a quartile? To the interquartile range? To the standard deviation? Which of the following are measures of location, of scale or neither: median, quartile, interquartile range, mean, standard deviation? In a boxplot, what would it mean if the median is closer to the lower quartile than to the upper quartile?

Topic: Review of Basic Statistics – Probability

- **probability space**: the set of everything that can happen, Ω. Flip two coins, dime and quarter, and the sample space is Ω = {HH, HT, TH, TT} where HT means "head on dime, tail on quarter", etc.
- **probability**: each element of the sample space has a probability attached, where each probability is between 0 and 1 and the total probability over the sample space is 1. If I flip two fair coins: prob(HH) = prob(HT) = prob(TH) = prob(TT) = ¼.
- **random variable**: a rule **X** that assigns a number to each element of a sample space. Flip to coins, and the number of heads is a random variable: it assigns the number **X**=2 to HH, the number **X**=1 to both HT and TH, and the number **X**=0 to TT.
- **distribution of a random variable**: The chance the random variable **X** takes on each possible value, x, written prob(**X**=x). Example: flip two fair coins, and let **X** be the number of heads; then prob(**X**=2) = ¼, prob(**X**=1) = ½, prob(**X**=0) = ¼.
- **cumulative distribution of a random variable**: The chance the random variable **X** is less than or equal to each possible value, x, written prob(**X** $\leq$ x). Example: flip two fair coins, and let **X** be the number of heads; then prob(**X** $\leq$ 0) = ¼, prob(**X** $\leq$ 1) = ¾, prob(**X** $\leq$ 2) = 1. Tables at the back of statistics books are often cumulative distributions.
- **independence of random variables**: Captures the idea that two random variables are unrelated, that neither predicts the other. The formal definition which follows is not intuitive – you get to like it by trying many intuitive examples, like unrelated coins and taped coins, and finding the definition always works. Two random variables, **X** and **Y**, are independent if the chance that simultaneously **X**=x and **Y**=y can be found by multiplying the separate probabilities

  prob(**X**=x and **Y**=y) = prob(**X**=x) prob(**Y**=y) for every choice of x,y**.**

Check your understanding: Can you tell exactly what happened in the sample space from the value of a random variable? Pick one: Always, sometimes, never. For people, do you think **X**=height and **Y**=weight are independent? For undergraduates, might **X**=age and **Y**=gender (1=female, 2=male) be independent? If I flip two fair coins, a dime and a quarter, so that prob(HH) = prob(HT) = prob(TH) = prob(TT) = ¼, then is it true or false that getting a head on the dime is independent of getting a head on the quarter?

Topic: Review of Basics – Expectation and Variance

- **Expectation**: The expectation of a random variable **X** is the sum of its possible values weighted by their probabilities,

$$E(\mathbf{X}) = \sum_x x \cdot prob(\mathbf{X} = x)$$

- **Example**: I flip two fair coins, getting **X**=0 heads with probability ¼, **X**=1 head with probability ½, and **X**=2 heads with probability ¼; then the expected number of heads is $E(\mathbf{X}) = 0 \cdot \frac{1}{4} + 1 \cdot \frac{1}{2} + 2 \cdot \frac{1}{4} = 1$, so I expect 1 head when I flip two fair coins. Might actually get 0 heads, might get 2 heads, but 1 head is what is typical, or expected, on average.
- **Variance and Standard Deviation**: The standard deviation of a random variable **X** measures how far **X** typically is from its expectation $E(\mathbf{X})$. Being too high is as bad as being too low – we care about errors, and don't care about their signs. So we look at the squared difference between **X** and $E(\mathbf{X})$, namely $\mathbf{D} = \{\mathbf{X} - E(\mathbf{X})\}^2$, which is, itself, a random variable. The variance of **X** is the expected value of **D** and the standard deviation is the square root of the variance, $\text{var}(\mathbf{X}) = E(\mathbf{D})$ and $st.dev.(\mathbf{X}) = \sqrt{\text{var}(\mathbf{X})}$.
- **Example**: I independently flip two fair coins, getting **X**=0 heads with probability ¼, **X**=1 head with probability ½, and **X**=2 heads with probability ¼. Then $E(\mathbf{X})$=1, as noted above. So $\mathbf{D} = \{\mathbf{X} - E(\mathbf{X})\}^2$ takes the value **D** =

$(0-1)^2 = 1$ with probability ¼, the value **D** = $(1-1)^2 = 0$ with probability ½, and the value **D** = $(2-1)^2 = 1$ with probability ¼. The variance of **X** is the expected value of **D** namely: var(**X**) = $E(\mathbf{D}) = 1 \cdot \frac{1}{4} + 0 \cdot \frac{1}{2} + 1 \cdot \frac{1}{4} = \frac{1}{2}$. So the standard deviaiton is $st.dev.(\mathbf{X}) = \sqrt{\text{var}(\mathbf{X})} = \sqrt{\frac{1}{2}} = 0.707$. So when I flip two fair coins, I expect one head, but often I get 0 or 2 heads instead, and the typical deviation from what I expect is 0.707 heads. This 0.707 reflects the fact that I get exactly what I expect, namely 1 head, half the time, but I get 1 more than I expect a quarter of the time, and one less than I expect a quarter of the time.

Check your understanding: If a random variance has zero variance, how often does it differ from its expectation? Consider the height **X** of male adults in the US. What is a reasonable number for *E*(**X**)? Pick one: 4 feet, 5'9", 7 feet. What is a reasonable number for *st.dev.*(**X**)? Pick one: 1 inch, 4 inches, 3 feet. If I independently flip three fair coins, what is the expected number of heads? What is the standard deviation?

Topic: Review of Basics – Normal Distribution

- **Continuous random variable**: A continuous random variable can take values with any number of decimals, like 1.2361248912. Weight measured perfectly, with all the decimals and no rounding, is a continuous random variable. Because it can take so many different values, each value winds up having probability zero. If I ask you to guess someone's weight, not approximately to the nearest millionth of a gram, but rather exactly to all the decimals, there is no way you can guess correctly – each value with all the decimals has probability zero. But for an interval, say the nearest kilogram,

there is a nonzero chance you can guess correctly. This idea is captured in by the density function.

- **Density Functions**: A density function defines probability for a continuous random variable. It attaches zero probability to every number, but positive probability to ranges (e.g., nearest kilogram). The probability that the random variable **X** takes values between 3.9 and 6.2 is the area under the density function between 3.9 and 6.2. The total area under the density function is 1.
- **Normal density**: The Normal density is the familiar "bell shaped curve".

The standard Normal distribution has expectation zero, variance 1, standard deviation 1 = $\sqrt{1}$. About 2/3 of the area under the Normal density is between –1 and 1, so the probability that a standard Normal random variable takes values between –1 and 1 is about 2/3. About 95% of the area under the Normal density is between –2 and 2, so the probability that a standard Normal random variable takes values between –2 and 2 is about .95. (To be more precise, there is a 95% chance that a standard Normal random variable will be between –1.96 and 1.96.) If **X** is a standard Normal random variable, and μ and $\sigma > 0$ are two numbers, then $\mathbf{Y} = \mu + \sigma\mathbf{X}$ has the Normal distribution with expectation μ, variance σ^2 and standard deviation σ, which we write N(μ, σ^2). For example, $\mathbf{Y} = 3 + 2\mathbf{X}$ has expectation 3, variance 4, standard deviation 2, and is N(3,4).

- **Normal Plot**: To check whether or not data, $X_1, \ldots, X_n$ look like they came from a Normal distribution, we do a Normal plot. We get the order statistics – just the data sorted into order – or $X_{(1)} \le X_{(2)} \le \ldots \le X_{(n)}$ and plot this ordered data against what ordered data from a standard Normal distribution should look like. The computer takes care of the details. A straight line in a

Normal plot means the data look Normal. A straight line with a couple of strange points off the lines suggests a Normal with a couple of strange points (called outliers). Outliers are extremely rare if the data are truly Normal, but real data often exhibit outliers. A curve suggest data that are not Normal. Real data wiggle, so nothing is ever perfectly straight. In time, you develop an eye for Normal plots, and can distinguish wiggles from data that are not Normal.

Topic: Review of Basics – Confidence Intervals

- Let $X_1, \ldots, X_n$ be n independent observations from a Normal distribution with expectation μ and variance σ^2. A compact way of writing this is to say $X_1, \ldots, X_n$ are iid from N(μ, σ^2). Here, iid means independent and identically distributed, that is, unrelated to each other and all having the same distribution.
- How do we know $X_1, \ldots, X_n$ are iid from N(μ, σ^2)? We don't! But we check as best we can. We do a boxplot to check on the shape of the distribution. We do a Normal plot to see if the distribution looks Normal. Checking independence is harder, and we don't do it as well as we would like. We do look to see if measurements from related people look more similar than measurements from unrelated people. This would indicate a violation of independence. We do look to see if measurements taken close together in time are more similar than measurements taken far apart in time. This would indicate a violation of independence. Remember that statistical methods come with a warrantee of good performance if certain assumptions are true, assumptions like $X_1, \ldots, X_n$ are iid from N(μ, σ^2). We check the assumptions to make sure we get the promised good performance of statistical methods. Using statistical methods when the assumptions are not

true is like putting your CD player in washing machine – it voids the warrantee.

- To begin again, having checked every way we can, finding no problems, assume $X_1, \ldots, X_n$ are iid from N(μ, σ^2). We want to estimate the expectation μ. We want an interval that in most studies winds up covering the true value of μ. Typically we want an interval that covers μ in 95% of studies, or a **95% confidence interval**. Notice that the promise is about what happens in most studies, not what happened in the current study. If you use the interval in thousands of unrelated studies, it covers μ in 95% of these studies and misses in 5%. You cannot tell from your data whether this current study is one of the 95% or one of the 5%. All you can say is the interval usually works, so I have confidence in it.
- If $X_1, \ldots, X_n$ are iid from N(μ, σ^2), then the confidence interval uses the sample mean, $\overline{X}$, the sample standard deviation, *s*, the sample size, *n*, and a critical value obtained from the t-distribution with *n-1* degrees of freedom, namely the value, $t_{0.025}$, such that the chance a random variable with a t-distribution is above $t_{0.025}$ is 0.025. If *n* is not very small, say n>10, then $t_{0.025}$ is near 2. The 95% confidence interval is:

$$\overline{X} \pm (\text{allowance for error}) \quad = \quad \overline{X} \pm \frac{t_{0.025} \cdot s}{\sqrt{n}}$$

Topic: Review of Basics – Hypothesis Tests

- **Null Hypothesis**: Let $X_1, \ldots, X_n$ be n independent observations from a Normal distribution with expectation μ and variance σ^2. We have a particular value of μ in mind, say μ_0, and we want to ask if the data contradict this value. It means something special to us if μ_0 is the correct value – perhaps it means the treatment has no effect, so the treatment should be discarded. We wish to test the null hypothesis, $H_0: \mu = \mu_0$. Is the null hypothesis plausible? Or do the data force us to abandon the null hypothesis?
- **Logic of Hypothesis Tests**: A hypothesis test has a long-winded logic, but not an unreasonable one. We say: Suppose, just for the sake of argument, not because we believe it, that the null hypothesis is true. As is always true when we suppose something for the sake of argument, what we mean is: Let's suppose it and see if what follows logically from supposing it is believable. If not, we doubt our supposition. So suppose μ_0 is the true value after all. Is the data we got, namely $X_1, \ldots, X_n$, the sort of data you would usually see if the null hypothesis were true? If it is, if $X_1, \ldots, X_n$ are a common sort of data when the null hypothesis is true, then the null hypothesis looks sorta ok, and we *accept* it. Otherwise, if there is no way in the world you'd ever see data anything remotely like our data, $X_1, \ldots, X_n$, if the null hypothesis is true, then we can't really believe the null hypothesis having seen $X_1, \ldots, X_n$, and we *reject* it. So the basic question is: Is data like the data we got commonly seen when the null hypothesis is true? If not, the null hypothesis has gotta go.
- **P-values or significance levels**: We measure whether the data are commonly seen when the null hypothesis is true using something called the

P-value or significance level. Supposing the null hypothesis to be true, the P-value is the chance of data at least as inconsistent with the null hypothesis as the observed data. If the P-value is ½, then half the time you get data as or more inconsistent with the null hypothesis as the observed data – it happens half the time by chance – so there is no reason to doubt the null hypothesis. But if the P-value is 0.000001, then data like ours, or data more extreme than ours, would happen only one time in a million by chance if the null hypothesis were true, so you gotta being having some doubts about this null hypothesis.

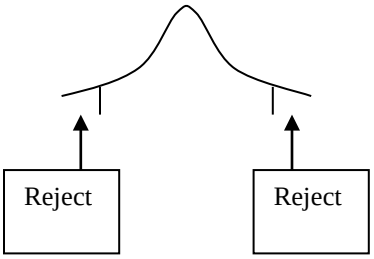
- **The magic 0.05 level:** A convention is that we "reject" the null hypothesis when the P-value is less than 0.05, and in this case we say we are testing at **level** 0.05. Scientific journals and law courts often take this convention seriously. It is, however, only a convention. In particular, sensible people realize that a P-value of 0.049 is not very different from a P-value of 0.051, and both are very different from P-values of 0.00001 and 0.3. It is best to report the P-value itself, rather than just saying the null hypothesis was rejected or accepted.
- **Example**: You are playing 5-card stud poker and the dealer sits down and gets 3 royal straight flushes in a row, winning each time. The null hypothesis is that this is a fair poker game and the dealer is not cheating. Now, there are or 2,598,960 five-card stud poker hands, and 4 of these are royal straight flushes, so the chance of a royal straight flush in a fair game is $\frac{4}{2{,}598{,}960} = 0.000001539$. In a fair game, the chance of three royal straight flushes in a row is 0.000001539x0.000001539x0.000001539 = 3.6×10^{-18}. (Why do we multiply probabilities here?) Assuming the null hypothesis, for the sake of argument, that is assuming he is not cheating, the chance he will get three royal straight flushes in a row is very, very small – that is the P-value or significance level. The data we see is highly improbable if the null hypothesis were true, so we doubt it is true. Either the dealer got very, very lucky, or he cheated. This is the logic of all hypothesis tests.

- **One sample t-test**: Let $X_1, \ldots, X_n$ be n independent observations from a Normal distribution with expectation μ and variance σ^2. We wish to test the null hypothesis, $H_0: \mu = \mu_0$. We do this using the one-sample t-test:

$$t = \frac{\sqrt{n}\left(\overline{X} - \mu_0\right)}{s}$$

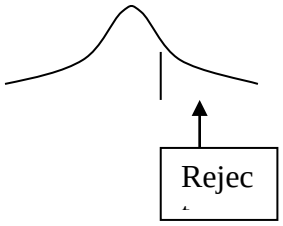
  looking this up in tables of the t-distribution with *n-1* degrees of freedom to get the P-value.

- **One-sided vs Two-sided tests**: In a two-sided test, we don't care whether $\overline{X}$ is bigger than or smaller than μ_0, so we reject at the 5% level when |t| is one of the 5% largest values of |t|. This means we reject for 2.5% of t's that are very positive and 2.5% of t's that are very negative:



In a two sided test we reject when t is big positive or big negative. If we reject when the P-value is less than 0.05, then each tail has probability 0.025.

In a one sided test, we do care, and only want to reject when $\overline{X}$ is on one particular side of μ_0, say when $\overline{X}$ is bigger than μ_0, so we reject at the 5% level when t is one of the 5% largest values of t. This means we reject for the 5% of t's that are very positive:



In a one sided test we reject on just one side, say big positive. If we reject when the P-value is less than 0.05, the tail on the right has probability 0.05.

- **Should I do a one-sided or a two-sided test**: Scientists mostly report two-sided tests.

Some Aspects of Nonparametrics in R

Script is my commentary to you. **Bold Courier is what I type in R.** Regular Courier is what R answered.

What is R?

R is a close relative of Splus, but R is available for free. You can download R from http://cran.r-project.org/ . *R is very powerful and is a favorite (if not the favorite) of statisticians; however, it is not easy to use. It is command driven, not menu driven. You can add things to R that R doesn't yet know how to do by writing a little program. R gives you fine control over graphics. Most people need a book to help them, and so Mainland & Braun's book, Data Analysis and Graphics Using R, Cambridge University Press, 2003, is in the book store as an OPTIONAL book.*

This is the cadmium example, paired data, Wilcoxon's signed rank test.

First, enter the data.

```
> cadmium<-c(30,35,353,106,-63,20,52,9966,106,24146,51,106896)
```

This command asks for Wilcoxon's signed rank test with the confidence interval and the Hodges-Lehmann estimate.

```
> wilcox.test(cadmium,conf.int=T)

        Wilcoxon signed rank test with continuity correction

data:  cadmium
V = 72, p-value = 0.01076
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
    35.00005 12249.49999
sample estimates:
(pseudo)median
      191.4999

Warning messages:
1: cannot compute exact p-value with ties in:
wilcox.test.default(cadmium, conf.int = T)
2: cannot compute exact confidence interval with ties in:
wilcox.test.default(cadmium, conf.int = T)
```

You can teach R new tricks. This is a little program to compute Walsh averages. You enter the program. Then R knows how to do it. You can skip this page if you don't want R to do new tricks.

```
> walsh<-function(data)
      {
      w <- outer(data, data, "+")/2.
      n <- length(data)
      w <- w[outer(1.:n, 1.:n, "<=")]
      sort(w)
   }
```

Now we try the program on the cadmium data. It returns all the Walsh averages.

```
> walsh(cadmium)
 [1]    -63.0    -21.5    -16.5    -14.0     -6.0     -5.5     20.0
21.5     21.5     25.0     27.5     30.0     32.5     35.0     35.5
36.0     40.5
[18]     41.0     43.0     43.5     51.0     51.5     52.0     63.0
63.0     68.0     68.0     70.5     70.5     78.5     78.5     79.0
79.0    106.0
[35]    106.0    106.0    145.0    186.5    191.5    194.0    202.0
202.5    229.5    229.5    353.0   4951.5   4993.0   4998.0   5000.5
5008.5   5009.0
[52]   5036.0   5036.0   5159.5   9966.0  12041.5  12083.0  12088.0
12090.5  12098.5  12099.0  12126.0  12126.0  12249.5  17056.0  24146.0
53416.5  53458.0
[69]  53463.0  53465.5  53473.5  53474.0  53501.0  53501.0  53624.5
58431.0  65521.0 106896.0
```

The Hodges-Lehmann estimate is the median of the Walsh averages. This agrees with what wilcox.test just told us.

```
> median(walsh(cadmium))
[1] 192.75
```

This does the Wilcoxon rank sum test with confidence interval and Hodges-Lehmann estimate.

First we enter the PTT times.

```
> pttRecan<-c(41,86,90,74,146,57,62,78,55,105,46,94,26,101,72,119,88)
> pttControl<-c(34,23,36,25,35,24,87,48)
```

Then we compare the two groups.

```
> wilcox.test(pttRecan,pttControl,conf.int=T)

        Wilcoxon rank sum test

data:  pttRecan and pttControl
W = 120, p-value = 0.00147
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
 18 63
sample estimates:
difference in location
                    40
```

Instead, we can take square roots first.

```
> wilcox.test(sqrt(pttRecan),sqrt(pttControl),conf.int=T)

        Wilcoxon rank sum test

data:  sqrt(pttRecan) and sqrt(pttControl)
W = 120, p-value = 0.00147
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
 1.416198 4.218924
sample estimates:
difference in location
              2.769265
```

This is the program that does both Wilcoxon tests.

help(wilcox.test)

```
wilcox.test              package:stats              R Documentation
Wilcoxon Rank Sum and Signed Rank Tests

Description:
     Performs one and two sample Wilcoxon tests on vectors of data; the
     latter is also known as 'Mann-Whitney' test.
Usage:

     wilcox.test(x, ...)

     ## Default S3 method:
     wilcox.test(x, y = NULL,
                 alternative = c("two.sided", "less", "greater"),
                 mu = 0, paired = FALSE, exact = NULL, correct = TRUE,
                 conf.int = FALSE, conf.level = 0.95, ...)

     ## S3 method for class 'formula':
     wilcox.test(formula, data, subset, na.action, ...)

Arguments:

       x: numeric vector of data values.  Non-finite (e.g. infinite or
          missing) values will be omitted.

       y: an optional numeric vector of data values.

alternative: a character string specifying the alternative hypothesis,
          must be one of '"two.sided"' (default), '"greater"' or
          '"less"'.  You can specify just the initial letter.

      mu: a number specifying an optional location parameter.

  paired: a logical indicating whether you want a paired test.

   exact: a logical indicating whether an exact p-value should be
          computed.

 correct: a logical indicating whether to apply continuity correction
          in the normal approximation for the p-value.

conf.int: a logical indicating whether a confidence interval should be
          computed.

conf.level: confidence level of the interval.

 formula: a formula of the form 'lhs ~ rhs' where 'lhs' is a numeric
          variable giving the data values and 'rhs' a factor with two
          levels giving the corresponding groups.

    data: an optional data frame containing the variables in the model
          formula.

  subset: an optional vector specifying a subset of observations to be
          used.
```

na.action: a function which indicates what should happen when the data
          contain 'NA's. Defaults to 'getOption("na.action")'.

     ...: further arguments to be passed to or from methods.

Details:

     The formula interface is only applicable for the 2-sample tests.

     If only 'x' is given, or if both 'x' and 'y' are given and
     'paired' is 'TRUE', a Wilcoxon signed rank test of the null that
     the distribution of 'x' (in the one sample case) or of 'x-y' (in
     the paired two sample case) is symmetric about 'mu' is performed.

     Otherwise, if both 'x' and 'y' are given and 'paired' is 'FALSE',
     a Wilcoxon rank sum test (equivalent to the Mann-Whitney test: see
     the Note) is carried out. In this case, the null hypothesis is
     that the location of the distributions of 'x' and 'y' differ by
     'mu'.

     By default (if 'exact' is not specified), an exact p-value is
     computed if the samples contain less than 50 finite values and
     there are no ties. Otherwise, a normal approximation is used.

     Optionally (if argument 'conf.int' is true), a nonparametric
     confidence interval and an estimator for the pseudomedian
     (one-sample case) or for the difference of the location parameters
     'x-y' is computed. (The pseudomedian of a distribution F is the
     median of the distribution of (u+v)/2, where u and v are
     independent, each with distribution F. If F is symmetric, then
     the pseudomedian and median coincide. See Hollander & Wolfe
     (1973), page 34.) If exact p-values are available, an exact
     confidence interval is obtained by the algorithm described in
     Bauer (1972), and the Hodges-Lehmann estimator is employed.
     Otherwise, the returned confidence interval and point estimate are
     based on normal approximations.

Value:

     A list with class '"htest"' containing the following components:

statistic: the value of the test statistic with a name describing it.

parameter: the parameter(s) for the exact distribution of the test
          statistic.

 p.value: the p-value for the test.

null.value: the location parameter 'mu'.

alternative: a character string describing the alternative hypothesis.

  method: the type of test applied.

data.name: a character string giving the names of the data.

conf.int: a confidence interval for the location parameter. (Only
          present if argument 'conf.int = TRUE'.)

estimate: an estimate of the location parameter. (Only present if
          argument 'conf.int = TRUE'.)

Note:

The literature is not unanimous about the definitions of the Wilcoxon rank sum and Mann-Whitney tests. The two most common definitions correspond to the sum of the ranks of the first sample with the minimum value subtracted or not: R subtracts and S-PLUS does not, giving a value which is larger by m(m+1)/2 for a first sample of size m. (It seems Wilcoxon's original paper used the unadjusted sum of the ranks but subsequent tables subtracted the minimum.)

R's value can also be computed as the number of all pairs '(x[i], y[j])' for which 'y[j]' is not greater than 'x[i]', the most common definition of the Mann-Whitney test.

References:

Myles Hollander & Douglas A. Wolfe (1999)Or second edition (1999).
David F. Bauer (1972), Constructing confidence sets using rank statistics. _Journal of the American Statistical Association_ *67*, 687-690.

See Also:

'psignrank', 'pwilcox'.

'kruskal.test' for testing homogeneity in location parameters in the case of two or more samples; 't.test' for a parametric alternative under normality assumptions.

Examples:

```
## One-sample test.
## Hollander & Wolfe (1973), 29f.
## Hamilton depression scale factor measurements in 9 patients with
##  mixed anxiety and depression, taken at the first (x) and second
##  (y) visit after initiation of a therapy (administration of a
##  tranquilizer).
x <- c(1.83,  0.50,  1.62,  2.48, 1.68, 1.88, 1.55, 3.06, 1.30)
y <- c(0.878, 0.647, 0.598, 2.05, 1.06, 1.29, 1.06, 3.14, 1.29)
wilcox.test(x, y, paired = TRUE, alternative = "greater")
wilcox.test(y - x, alternative = "less")    # The same.
wilcox.test(y - x, alternative = "less",
            exact = FALSE, correct = FALSE) # H&W large sample
                                            # approximation

## Two-sample test.
## Hollander & Wolfe (1973), 69f.
## Permeability constants of the human chorioamnion (a placental
##  membrane) at term (x) and between 12 to 26 weeks gestational
##  age (y).  The alternative of interest is greater permeability
##  of the human chorioamnion for the term pregnancy.
x <- c(0.80, 0.83, 1.89, 1.04, 1.45, 1.38, 1.91, 1.64, 0.73, 1.46)
y <- c(1.15, 0.88, 0.90, 0.74, 1.21)
wilcox.test(x, y, alternative = "g")        # greater
wilcox.test(x, y, alternative = "greater",
            exact = FALSE, correct = FALSE) # H&W large sample
                                            # approximation

wilcox.test(rnorm(10), rnorm(10, 2), conf.int = TRUE)

## Formula interface.
boxplot(Ozone ~ Month, data = airquality)
wilcox.test(Ozone ~ Month, data = airquality,
            subset = Month %in% c(5, 8))
```

You can get information about other nonparametric procedures.

```
help(kruskal.test)

help(friedman.test)

help(cor.test)

help(cor)
```

Binomial in R

Binomial probabilities

Chance of 2 heads in 3 independent trial with probability 1/3 of a head:

```
> dbinom(2,3,1/3)
[1] 0.2222222
```

Numbers from 0 to 3

```
> 0:3
[1] 0 1 2 3
```

Chances of 0, 1, 2 or 3 heads in 3 independent trials with probability 1/3 of a head

```
> dbinom(0:3,3,1/3)
[1] 0.29629630 0.44444444 0.22222222 0.03703704
```

Cumulative probabilities: chance of 1 or fewer heads in 3 independent trials with probability 1/3 of a head

```
> pbinom(1,3,1/3)
[1] 0.7407407
```

Compare with dbinom result above:

```
> 0.29629630+0.44444444
[1] 0.7407407
```

Probability of 24 or fewer heads in 50 trials with probability 1/3 of a head:

```
> pbinom(24,50,1/3)
[1] 0.9891733
```

Probability of 25 or more heads in 50 trials with probability 1/3 of a head:

```
> 1-pbinom(24,50,1/3)
[1] 0.01082668
```

So of course

```
> 0.01082668+0.9891733
[1] 1
```

One sided test and confidence interval

```
> binom.test(25,50,p=1/3,alternative="greater")

        Exact binomial test

data:  25 and 50
number of successes = 25, number of trials = 50, p-
value = 0.01083
alternative hypothesis: true probability of success
is greater than 0.3333333
95 percent confidence interval:
 0.3762459 1.0000000
sample estimates:
probability of success
                  0.5
```

Two sided test and confidence interval

```
> binom.test(25,50,p=1/3)

        Exact binomial test

data:  25 and 50
number of successes = 25, number of trials = 50, p-
value = 0.01586
alternative hypothesis: true probability of success
is not equal to 0.3333333
95 percent confidence interval:
 0.355273 0.644727
sample estimates:
probability of success
                  0.5
```

Get help

```
> help(rbinom)
```

or

```
> help(binom.test)
```

Looking at Densities
Sampling from Distributions
In R

This creates equally spaced numbers between -5 and 5. They will be plotting positions.

```
> space<-(-500):500/100
```

dnorm(x) gives you the Normal density function, rnorm(n) gives you n random draws from the Normal, pnorm gives you the Normal cumulative distribution, qnorm gives you the Normal quantiles. The same idea works for the Cauchy distribution (eg rcauchy(n)) or the logistic distribution (eg rlogis(n)).

```
> pnorm(-1.96)
[1] 0.02499790

> pnorm(1.96)
[1] 0.9750021

> qnorm(.025)
[1] -1.959964

> rnorm(5)
[1]  0.9154958  0.5835557  0.3850987 -1.1506946
     0.5503568
```

This sets you up to do a 2x2 four panel plot

```
> par(mfrow=c(2,2))

> plot(space,dnorm(space))
> plot(space,dcauchy(space))
> plot(space,dlogis(space))
> boxplot(rnorm(500),rlogis(500),rcauchy(500))
```

Bloodbags Data

```
> bloodbags2
   id acdA  acd   dif
1   1 63.0 58.5   4.5
2   2 48.4 82.6 -34.2
3   3 58.2 50.8   7.4
4   4 29.3 16.7  12.6
5   5 47.0 49.5  -2.5
6   6 27.7 26.0   1.7
7   7 22.3 56.3 -34.0
8   8 43.0 35.7   7.3
9   9 53.3 37.9  15.4
10 10 49.5 53.3  -3.8
11 11 41.1 38.2   2.9
12 12 32.9 37.1  -4.2
```

If you attach the data, then you can refer to variables by their names. Remember to detach when done.

```
> attach(bloodbags2)
```

Plot data!

```
> par(mfrow=c(1,2))
> boxplot(dif,ylim=c(-40,20))
> qqnorm(dif,ylim=c(-40,20))
```

Data do not look Normal in Normal plot, and Shapiro-Wilk test confirms this.

```
> shapiro.test(dif)
        Shapiro-Wilk normality test
data:  dif
W = 0.8054, p-value = 0.01079
```

Wilcoxon signed rank test, with Hodges-Lehmann point estimate and confidence interval using Walsh averages.

```
> wilcox.test(dif,conf.int=T)
        Wilcoxon signed rank test
data:  dif
V = 44, p-value = 0.7334
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
 -14.85   7.35
sample estimates:
(pseudo)median
         1.575
> detach(bloodbags2)
```

Sign Test Procedures in R

```
> attach(cadmium)
> dif
30     35    353    106    -63     20     52   9966    106  24146
51 106896
```

The sign test uses just the signs, not the ranks.

```
> 1*(dif<0)
0 0 0 0 1 0 0 0 0 0 0 0
```

There was 1 negative differences in 12 pairs.

```
> sum(1*(dif<0))
[1] 1
```

Compare to the binomial with 12 trials, 1 tail, probability of head ½: One sided p-value

```
> pbinom(1,12,1/2)
[1] 0.003173828
```

Usual two sided p-value

```
> 2*pbinom(1,12,1/2)
[1] 0.006347656
```

Because the distribution is very long tailed, the sign test is better than the signed rank for these data. This is the binomial for n=12:

```
> rbind(0:12,round(pbinom(0:12,12,.5),3))
     [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8]  [,9] [,10]  [,11] [,12] [,13]
[1,]    0 1.000 2.000 3.000 4.000 5.000 6.000 7.000 8.000 9.000 10.000    11    12
[2,]    0 0.003 0.019 0.073 0.194 0.387 0.613 0.806 0.927 0.981  0.997     1     1
```

Two of the sorted observations (order statistics) form the confidence interval for the population median

```
> sort(dif)
 [1]    -63     20     30     35     51     52    106    106    353
9966  24146 106896
```

At the 0.025 level, you can reject for a sign statistic of 2, but not 3,

```
> pbinom(3,12,1/2)
[1] 0.07299805
> pbinom(2,12,1/2)
[1] 0.01928711
```

So, it is #3 and #10 that form the confidence interval:

```
> sort(dif)[c(3,10)]
[1]   30 9966
> sum(1*(dif-30.001)<0)
[1] 3
> sum(1*(dif-29.9999)<0)
[1] 2

> 2*pbinom(sum(1*(dif-29.9999)<0),12,1/2)
[1] 0.03857422
> 2*pbinom(sum(1*(dif-30.001)<0),12,1/2)
[1] 0.1459961
```

Rank Sum & Transformations

Model $Y = 2^{\square\square\square}$, $X = 2^{\square}$, or $Y = (2^{\square})(2^{\square}) = (2^{\square})X$,

so $\log_2(Y) = \square\square\square$, $\log_2(X) = \square$

```
> wilcox.test(log2(pttRecan),log2(pttControl),conf.int=T)

        Wilcoxon rank sum test

data:  log2(pttRecan) and log2(pttControl)
W = 120, p-value = 0.00147
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
 0.5849625 1.6415460
sample estimates:
difference in location
              1.172577
```

Transform back to estimate multiplier $2^{\square}$

```
> 2^0.5849625
[1] 1.5

> 2^1.6415460
[1] 3.12

> 2^1.172577
[1] 2.25414
```

95% Confidence interval for multiplier $2^{\square}$ is [1.5, 3.12] and point estimate is 2.25.

Two Sample Comparisons in Stata

(Commands are in **bold**)

```
. kwallis PTT, by( Recanal)

Test: Equality of populations (Kruskal-Wallis test)

 Recanal          _Obs   _RankSum
       0             8      52.00
       1            17     273.00

chi-squared =     9.176 with 1 d.f.
probability =     0.0025

chi-squared with ties =     9.176 with 1 d.f.
probability =     0.0025


. generate rt = sqrt(PTT)

. generate lg2Ptt =ln( PTT)/0.693147

. npshift PTT, by(Recanal)  Bad idea!  Not a shift!

Hodges-Lehmann Estimates of Shift Parameters
------------------------------------------------------------------
Point Estimate of Shift : Theta = Pop_2 - Pop_1 = 40
95% Confidence Interval for Theta:         [17       ,       64]
------------------------------------------------------------------


. npshift  rt, by(Recanal)  Better idea.  Hard to interpret!

Hodges-Lehmann Estimates of Shift Parameters
------------------------------------------------------------------
Point Estimate of Shift : Theta = Pop_2 - Pop_1 = 2.769265
95% Confidence Interval for Theta:         [1.403124 , 4.246951]
------------------------------------------------------------------

. npshift lg2Ptt, by(Recanal) Best idea.  Correct, interpretable.

Hodges-Lehmann Estimates of Shift Parameters
------------------------------------------------------------------
Point Estimate of Shift : Theta = Pop_2 - Pop_1 = 1.172577
95% Confidence Interval for Theta:         [.4518747 , 1.646364]
------------------------------------------------------------------
```

$$2^{1.1726} = 2.25$$

$$2^{.4519} = 1.37 \qquad 2^{1.6464} = 3.13$$

Ansari Bradley Test

```
> help(ansari.test)
```

Example from book, page 147. Two methods of determining level of iron in serum. True level was 105m grams/100ml. Which is more accurate? (Data in R help)

```
> ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,101,
96, 97, 102, 107, 113, 116, 113, 110, 98)
> jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105,
104,100, 96, 108, 103, 104, 114, 114, 113, 108, 106, 99)
>      ansari.test(ramsay, jung.parekh)

        Ansari-Bradley test

data:  ramsay and jung.parekh
AB = 185.5, p-value = 0.1815
alternative hypothesis: true ratio of scales is not equal to 1

> ansari.test(pttControl,pttRecan)

        Ansari-Bradley test

data:  pttControl and pttRecan
AB = 42, p-value = 0.182
alternative hypothesis: true ratio of scales is not equal to 1

>ansari.test(pttControl-median(pttControl),pttRecan-
median(pttRecan))

        Ansari-Bradley test

data:  pttControl - median(pttControl) and pttRecan -
median(pttRecan)
AB = 68, p-value = 0.1205
alternative hypothesis: true ratio of scales is not equal to 1
```

Kolmogorov-Smirnov Test in R

Tests whether distributions differ in any way.
Mostly useful if you are not looking for a change in level or dispersion.

Two simulated data sets

```
> one<-rexp(1000)-1
> two<-1-rexp(1000)
```

Similar means and variances (would be the same if n were very large)

```
> mean(one)
[1] 0.01345924
> mean(two)
[1] -0.0345239
> sd(one)
[1] 0.9891292
> sd(two)
[1] 1.047116
```

Yet they look very different!

```
> boxplot(one,two)
```

The K-S test compares the empirical cumulative distributions:

```
> par(mfrow=c(1,2))
> plot(ecdf(one),ylab="Proportion <= x",main="one")
> plot(ecdf(two),ylab="Proportion <= x",main="two")
```

Very small p-value - distributions clearly different!

```
> ks.test(one,two)

        Two-sample Kolmogorov-Smirnov test

data:  one and two
D = 0.272, p-value < 2.2e-16
alternative hypothesis: two.sided
```

Ideas from Chapter 5 of Hollander et al.
Using Their R-package NSM3

Lepage in NSM3

```
> pLepage(pttRecan,pttControl,method="Asymptotic")
Number of X values:  17 Number of Y values:  8
Lepage D  Statistic:  11.1479
Asymptotic  upper-tail probability:  0.0038
```

Kolmogorov-Smirnov

```
> pKolSmirn(pttRecan,pttControl)
Number of X values:  17 Number of Y values:  8
Kolmogorov-Smirnov J  Statistic:  0.6985
Exact  upper-tail probability:  0.0052

> ks.test(pttRecan,pttControl)

        Two-sample Kolmogorov-Smirnov test

data:  pttRecan and pttControl
D = 0.6985, p-value = 0.005231
alternative hypothesis: two-sided
```

Confidence band

```
cbind(ecdf.ks.CI(meyerdif)$lower,ecdf.ks.CI(meyerdif)$upper
,sort(unique(meyerdif)))

Quantile
qKolSmirnLSA(.05)
```

Kruskal Wallis Test in R

Data from: Morton, D., Saah, A., Silberg, S., Owens, W., Roberts, M., and Saah, M. (1982) Lead absorption in children of employees in a lead-related industry. *American Journal of Epidemiology*, **115**, 549-555.

```
> lead
   control exposed  level  hyg
1       13      14   high good
2       16      13   high good
3       11      25   high good
4       18      41   high  mod
5       24      18   high  mod
6        7      49   high  mod
7       16      38   high poor
8       18      23   high poor
9       19      37   high poor
10      15      62   high poor
11      18      24   high poor
12       9      45   high poor
13      14      39   high poor
14      18      48   high poor
15      19      44   high poor
16      19      35   high poor
17      11      43   high poor
18      18      34   high poor
19      13      73   high poor
20      22      39 medium good
21      NA      29 medium  mod
22      16      31 medium poor
23      25      34 medium poor
24      16      20 medium poor
25      21      22 medium poor
26      12      35 medium poor
27      16      16    low  mod
28      11      36    low poor
29      10      23    low poor
30      19      21    low poor
31      10      17    low poor
32      13      27    low poor
33      24      15    low poor
34      13      10    low poor

-- level and hyg are factors.  Type: help(factor)
```

Type: help(kruskal.test)

First we do the test by level.

```
> kruskal.test(exposed~level,data=lead)

        Kruskal-Wallis rank sum test

data:  exposed by level
Kruskal-Wallis chi-squared = 8.5172, df = 2, p-value =
0.01414
```

Now we do the test by hyg for kids with level=high..

```
>kruskal.test(exposed~hyg,subset=(level=="high"),data=lead)

        Kruskal-Wallis rank sum test

data:  exposed by hyg
Kruskal-Wallis chi-squared = 5.5611, df = 2, p-value =
0.062
```

Now we do the test by level for kids with hyg=poor.

```
>kruskal.test(exposed~level,subset=(hyg=="poor"),data=lead)

        Kruskal-Wallis rank sum test

data:  exposed by level
Kruskal-Wallis chi-squared = 12.5104, df = 2, p-value =
0.001920
```

Jonckheere-Terpstra Test in R (almost)

You can get R to do most of the work in the Jonckheere-Terpstra test, but you have to do some by hand.

```
> high<-lead$exposed[lead$level=="high"]
> medium<-lead$exposed[lead$level=="medium"]
> low<-lead$exposed[lead$level=="low"]

> high
[1]14 13 25 41 18 49 38 23 37 62 24 45 39 48 44 35 43 34 73
> medium
[1] 39 29 31 34 20 22 35
> low
[1] 16 36 23 21 17 27 15 10
```

You do 3 wilcox.test commands, and add them up. Order matters in the command! Not wilcox.test(low,medium)!

```
> wilcox.test(medium,low)

        Wilcoxon rank sum test

data:  medium and low
W = 45, p-value = 0.05408
alternative hypothesis: true mu is not equal to 0

> wilcox.test(high,low)

        Wilcoxon rank sum test with continuity correction

data:  high and low
W = 125.5, p-value = 0.00926
alternative hypothesis: true mu is not equal to 0

> wilcox.test(high,medium)

        Wilcoxon rank sum test with continuity correction

data:  high and medium
W = 90.5, p-value = 0.1741
alternative hypothesis: true mu is not equal to 0
```

J = 45 + 125.5 + 90.5 = 261

Compute J in expression (6.17) on page 203 in H&W*

Kruskal-Wallis Test in R

Lead Data.

```
> lead[1:3,]
  control exposed level  hyg
1      13      14  high good
2      16      13  high good
3      11      25  high good
```

Kruskal Wallis test of no difference

```
> kruskal.test(exposed~level)

        Kruskal-Wallis rank sum test

data:  exposed by level
Kruskal-Wallis chi-squared = 8.5172, df = 2, p-value = 0.01414
```

To do multiple comparisons, get Mann-Whitney statistic from Wilcox.test and convert to Wilcoxon statistic

```
> wilcox.test(exposed[level=="high"],exposed[level=="low"])

        Wilcoxon rank sum test with continuity correction

data:  exposed[level == "high"] and exposed[level == "low"]
W = 125.5, p-value = 0.00926
alternative hypothesis: true mu is not equal to 0

Warning message:
cannot compute exact p-value with ties in:
wilcox.test.default(exposed[level == "high"], exposed[level ==
> 125.5+((19+1)*19/2)
[1] 315.5       This is one rank sum

> wilcox.test(exposed[level=="high"],exposed[level=="medium")

        Wilcoxon rank sum test with continuity correction

data:  exposed[level == "high"] and exposed[level == "medium"]
W = 90.5, p-value = 0.1741
alternative hypothesis: true mu is not equal to 0

Warning message:
cannot compute exact p-value with ties in:
wilcox.test.default(exposed[level == "high"], exposed[level ==
> 90.5+((19+1)*19/2)
[1] 280.5    This is one rank sum
> wilcox.test(exposed[level == "medium"],exposed[level == "low"])

        Wilcoxon rank sum test
data:  exposed[level == "medium"] and exposed[level == "low"]
W = 45, p-value = 0.05408
alternative hypothesis: true mu is not equal to 0

> 45+((7+1)*7/2)
[1] 73    This is one rank sum
```

Jonckheere/Terpstra Test for Ordered Alternatives (6.2)

```
Illustrates the use of NSM3 R-package from Hollander/Wolfe/
> library(NSM3)
> help(pJCK)
> head(lead)
  control exposed level  hyg    both
1      13      14  high good high.ok
2      16      13  high good high.ok
3      11      25  high good high.ok
4      18      41  high  mod high.ok
5      24      18  high  mod high.ok
6       7      49  high  mod high.ok
> attach(lead)
Does father’s exposure predict the child’s blood lead
level?
> pJCK(exposed,g=as.integer(level),method="Asymptotic")
Ties are present, so p-values are based on conditional null
distribution.
Group sizes:  8 7 19
Jonckheere-Terpstra J*  Statistic:  3.0078
Asymptotic  upper-tail probability:  0.0013

> kruskal.test(exposed~level)
        Kruskal-Wallis rank sum test
data:  exposed by level
Kruskal-Wallis chi-squared = 8.5172, df = 2, p-value =
0.01414

For father’s with high exposure, does father’s hygiene
predict the child’s blood lead level?
>
pJCK(exposed[level=="high"],g=as.integer(hyg[level=="high"]
),
    method="Asymptotic")
Group sizes:  3 3 13
Jonckheere-Terpstra J*  Statistic:  1.9347
Asymptotic  upper-tail probability:  0.0265
>
kruskal.test(exposed[level=="high"]~as.integer(hyg[level=="
high"]))
        Kruskal-Wallis rank sum test
data:  exposed[level == "high"] by as.integer(hyg[level ==
"high"])
Kruskal-Wallis chi-squared = 5.5611, df = 2, p-value =
0.062
```

Multiple Comparisons

```
> help(pairwise.wilcox.test)
```

Bonferroni

Bonferroni inequality says Pr(A or B) <= Pr(A)+Pr(B), or more generally, the

Bonferroni inequality says Pr(A_1 or A_2 or … or A_L) <= Pr(A_1)+ Pr(A_2)+…+ Pr(A_L).

Know that if H_0 is true, Pr(p-value<0.05)<=0.05. More generally, Pr(p-value<=□)<=□, for all 0<□<1.

If we have L hypotheses, H_{01},… H_{0L} with p-values p_1,…,p_L and we reject H_{0k} when p_k<=0.05/L, then the chance that we falsely reject any H_{0k} is <=0.05.

Pick one hypothesis. If H_{0k} is false, then we cannot falsely reject it, so the chance that we falsely reject it is zero. If H_{0k} is true, we falsely reject it when p_k<=0.05/L, which happens with probability <=0.05/L.

Then the chance that we falsely reject any H_{0k} is
Pr(Falsely reject H_{01} or …or Falsely reject H_{0L}) <=
Pr(Falsely reject H_{01})+…+Pr(Falsely reject H_{0L})<= 0.05/L+…+0.05/L = 0.05.

Because 0.0093 < 0.05/3 = 0.016667, we reject it by the Bonferroni method.

```
>
pairwise.wilcox.test(exposed,level,p.adjust.method="bonferroni")
        Pairwise comparisons using Wilcoxon rank sum test
data:  exposed and level
       low   medium
medium 0.162 -
high   0.028 0.522

P value adjustment method: bonferroni
```

Holm

Order p-values, smallest to largest, $p_{(1)}<\ldots<p_{(L)}$
$P_{(1)} = 0.0093$, $P_{(2)} = 0.0541$, $P_{(3)} = 0.1741$.

If $P_{(1)} <= 0.05/L = 0.01667$, then I can safely reject the corresponding hypothesis by Bonferroni.

Holm's idea is that it is now safe to assume this hypothesis is false, and test the rest assuming there are only L-1 possible true hypotheses.

This means that $P_{(2)}$ is significant if less than $0.05/(L-1) = 0.05/(3-1) = 0.025$.

If we reject this hypothesis, we continue and compare $P_{(3)}$ to $0.05/(L-2)$, etc.

Holm showed that the chance that we falsely reject any true hypothesis among the L hypotheses by this method is at most 0.05.

Notice that it gets easier to reject hypotheses as more hypotheses are rejected.

Notice that you must stop at the first j such that $P_{(j)} > 0.05/(L-j+1)$. You cannot skip forward.

```
> pairwise.wilcox.test(lead$exposed,lead$level)
        Pairwise comparisons using Wilcoxon rank sum test
data:  lead$exposed and lead$level
       low   medium
medium 0.108 -
high   0.028 0.174
P value adjustment method: holm
```


Holm, S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, 6, 65-70.

Wright, S. P. (1992). Adjusted P-values for simultaneous inference. *Biometrics*, 48, 1005-1013.

Rapid Eye Movement Example

```
> rapideye
  eyetrack fixation
1    980.8     4.85
2    926.4     4.41
3    892.9     3.80
4    870.2     4.53
5    854.6     4.33
6    777.2     3.81
7    772.6     3.97
8    702.4     3.68
9    561.7     3.43
> plot(rapideye$eyetrack,rapideye$fixation)
> cor.test(rapideye$eyetrack,rapideye$fixation,method="kendall")

        Kendall's rank correlation tau


data:  rapideye$eyetrack and rapideye$fixation
T = 30, p-value = 0.01267
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.6666667
```

```
> round(theil(rapideye$eyetrack,rapideye$fixation),5)
 [1] -0.03478 -0.03216 -0.01384 -0.00214 -0.00141 -0.00009  0.00063  0.00111
 [9]  0.00112  0.00174  0.00176  0.00178  0.00256  0.00269  0.00286  0.00289
[17]  0.00307  0.00326  0.00339  0.00357  0.00402  0.00412  0.00413  0.00420
[25]  0.00423  0.00427  0.00439  0.00507  0.00511  0.00574  0.00672  0.00774
[33]  0.00809  0.01195  0.01282  0.01821
>  median(theil(rapideye$eyetrack,rapideye$fixation))
[1] 0.003323571
```

Hoeffding's Test of Independence in R

Hollander and Wolfe (1999) Section 8.6

It's not in "standard R". So you search:

```
> help.search("hoeff")
```

And you find it.

```
> help(hoeffd,pack=Hmisc)
```

```
hhoeffd                 package:Hmisc                 R Documentation
Matrix of Hoeffding's D Statistics
Description:
     Computes a matrix of Hoeffding's (1948) 'D' statistics for all
     possible pairs of columns of a matrix.  'D' is a measure of the
     distance between 'F(x,y)' and 'G(x)H(y)', where 'F(x,y)' is the
     joint CDF of 'X' and 'Y', and 'G' and 'H' are marginal CDFs.
     Missing values are deleted in pairs rather than deleting all rows
     of 'x' having any missing variables. The 'D' statistic is robust
     against a wide variety of alternatives to independence, such as
     non-monotonic relationships. The larger the value of 'D', the more
     dependent are 'X' and 'Y' (for many types of dependencies).  'D'
     used here is 30 times Hoeffding's original 'D', and ranges from
     -0.5 to 1.0 if there are no ties in the data. 'print.hoeffd'
     prints the information derived by 'hoeffd'.  The higher the value
     of 'D', the more dependent are 'x' and 'y'  ...
```

Go to "Packages" menu, "Load Package" option, and pick "Hmisc"

Then it's yours. This is the example from the book:

```
> eg8.5
     collagen proline
[1,]      7.1     2.8
[2,]      7.1     2.9
[3,]      7.2     2.8
[4,]      8.3     2.6
[5,]      9.4     3.5
[6,]     10.5     4.6
[7,]     11.4     5.0


> hoeffd(eg8.5)
D
     [,1] [,2]
[1,] 1.00 0.19
[2,] 0.19 1.00

n= 7

P
     [,1]   [,2]
[1,]        0.0215
[2,] 0.0215
```

30 times the books answer is 0.19. The large sample p-value is given, close to the book's large sample value.

Bootstrap Confidence Interval for Kendall's Correlation

(Hollander and Wolfe 1999 section 8.4)

The original data.

```
> rapideye
  eyetrack fixation
1    980.8     4.85
2    926.4     4.41
3    892.9     3.80
4    870.2     4.53
5    854.6     4.33
6    777.2     3.81
7    772.6     3.97
8    702.4     3.68
9    561.7     3.43
```

Kendall's correlation for the original data

```
> cor.test(rapideye$eyetrack,rapideye$fixation,method="kendall")
        Kendall's rank correlation tau
data:  rapideye$eyetrack and rapideye$fixation
T = 30, p-value = 0.01267
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.6666667
```

A bootstrap sample is a sample of size n=9 WITH REPLACEMENT from the n=9 observations

```
> j<-sample(1:9,9,replace=T)
> j
[1] 2 1 9 9 3 9 4 4 9

> rapideye[j,]
    eyetrack fixation
2      926.4     4.41
1      980.8     4.85
9      561.7     3.43
9.1    561.7     3.43
3      892.9     3.80
9.2    561.7     3.43
4      870.2     4.53
4.1    870.2     4.53
9.3    561.7     3.43
```

Kendall's correlation for the first bootstrap sample

```
> cor.test(rapideye$eyetrack[j],rapideye$fixation[j],method="kendall")

        Kendall's rank correlation tau

data:  rapideye$eyetrack[j] and rapideye$fixation[j]
z = 2.7179, p-value = 0.00657
alternative hypothesis: true tau is not equal to 0
sample estimates:
     tau
0.724138
```

Little function bootkendall computes B bootstrap samples Kendall's tau's, sorts them, and gives the lower and upper 2.5% as the confidence interval.

```
> bootkendall
function(Z,B){
        tauhat<-rep(NA,B)
        n<-dim(Z)[1]
        for (i in 1:B){
           j<-sample(1:n,n,replace=T)
            tauhat[i]<cor.test(Z[j,1],Z[j,2],method="kendall")$estimate
                }
        tauhat<-sort(tauhat)
        k<-floor(B*0.025)
        c(tauhat[k],tauhat[B+1-k])
        }
```

Let's try it.

```
> bootkendall(rapideye,1000)
[1] 0.03225806 1.00000000
There were 50 or more warnings (use warnings() to see the first 50)
```

Because they are samples, you get different answers each time. Need to set B large!

```
> bootkendall(rapideye,1000)
[1] 0.1724138 1.0000000

> bootkendall(rapideye,5000)
[1] 0.125 1.000
There were 50 or more warnings (use warnings() to see the first 50)

> bootkendall(rapideye,5000)
[1] 0.1111111 1.0000000
There were 50 or more warnings (use warnings() to see the first 50)
```

Nonparametric Rank Based Multiple Regression (Section 9.6 in H&W)

```
> Fuel[1:3,]
  id state fuel tax  lic   inc  road
1  1    ME  541   9 52.5 3.571 1.976
2  2    NH  524   9 57.2 4.092 1.250
3  3    VT  561   9 58.0 3.865 1.586
You must install the Rfit package using the packages menu.
> library(Rfit)
> help(rfit)
> attach(Fuel)
```

Fitting a model

```
> out<-rfit(fuel~tax+lic)
> summary(out)
Call:  rfit.default(formula = fuel ~ tax + lic)
Coefficients:
    Estimate Std. Error t.value   p.value
    130.4176   181.9920  0.7166   0.47740
tax -29.8342    12.8729 -2.3176   0.02519 *
lic  11.7820     2.2064  5.3398 3.116e-06 ***
Multiple R-squared (Robust): 0.4534957
Reduction in Dispersion Test: 18.67077 p-value: 0
```

Residuals from this fit

```
> res<-as.vector(out$residual)
> res
 [1]   60.53645424  -11.83879810   15.73562704 …
```

Least squares minimizes the sum of the squares of the residuals. In contrast, rfit minimizes a rank based measure of the dispersion of the residuals due to Jaeckel (1972).

```
> outlm<-lm(fuel~tax+lic)
> reslm<-outlm$residual
```

So reslm has the least squares residuals.

```
> JaeckelD(res)
[1] 3313.408
> JaeckelD(reslm)
[1] 3322.443
> sum(res^2)
[1] 262540
> sum(reslm^2)
[1] 260834
```

So sum(reslm^2) < sum(res^2) but JaeckelD(res) < JaeckelD(reslm).

```
> Fuel2<-cbind(Fuel,res,reslm)
> Fuel2[39:41,]
   id state fuel tax  lic   inc  road       res    reslm
39 39    ID  648 8.5 66.3 3.635 3.274  -9.97179 -18.0659
40 40    WY  968 7.0 67.2 4.345 3.905 254.67321 242.5577
41 41    CO  587 7.0 62.6 4.449 4.639 -72.12974 -80.8739
```
Least squares made the residual for WY smaller but the residuals for ID and CO larger than did rfit.

Testing whether several regression coefficients are zero

```
> help(drop.test)
```
drop.test is the analog to the general linear hypothesis F-test asking whether additional terms in a full model (fitF) are needed or whether a reduced model (fitR) is plausible.

```
> out<-rfit(fuel~tax+lic)
> out2<-rfit(fuel~tax+lic+inc+road)

> JaeckelD(out$residual)
[1] 3313.408
> JaeckelD(out2$residual)
[1] 2700.551
```
So of course, the full model (out2) fits better than the reduced model (out), but could the improvement just be chance?

```
> drop.test(fitF=out2,fitR=out)
Drop in Dispersion Test
F-Statistic     p-value
 1.0191e+01  2.3847e-04
```
So the improvement in fit from inc and road is not plausibly due to chance.

Hettmansperger, T.P. and McKean J.W. (2011), *Robust Nonparametric Statistical Methods, 2nd ed.*, New York: Chapman-Hall.

Hettmansperger, T.P. and McKean J.W. (1977) A robust alternative based on ranks to least squares in analyzing linear models. Technonmetrics, 19, 275-284. In JSTOR on the library web-page.

Jaeckel, L. A. (1972). Estimating regression coefficients by minimizing the dispersion of residuals. *Annals of Mathematical Statistics*, 43, 1449 - 1458. In JSTOR on the library web-page.

Robust Regression in R

Robust and nonparametric regression are not quite as standardized as most topics in Hollander and Wolfe. In part, there are many competing proposals, and the dust has not settled to yield one conventional proposal.

The more commonly used procedure is m-estimation. It is available in R, Splus, SAS and Stata.

In R, you need the MASS package, which may be available with your version of R, or can be obtained from the usual location http://www.r-project.org/

Once you have the MASS package, type:

```
>library(MASS)
```

to make its features available. The specific routine you want is rlm (for robust linear model) so type

```
>help(rlm)
```

to obtain documentation.

The first five rows of the fuel data (from stat 500) are:

```
> dim(fuel)
[1] 48  7

> fuel[1:5,]
  id state fuel tax  lic   inc  road
1  1    ME  541 9.0 52.5 3.571 1.976
2  2    NH  524 9.0 57.2 4.092 1.250
3  3    VT  561 9.0 58.0 3.865 1.586
4  4    MA  414 7.5 52.9 4.870 2.351
5  5    RI  410 8.0 54.4 4.399 0.431
```

The call for a robust regression is

```
> rlm(fuel~tax+lic,fuel)
```

but that generates only a little output, so instead type

```
> summary(rlm(fuel~tax+lic,fuel))

Call: rlm(formula = fuel ~ tax + lic, data = fuel)
Residuals:
      Min        1Q    Median        3Q       Max
-122.3625  -54.8412    0.5224   47.3381  256.4014

Coefficients:
            Value    Std. Error t value
(Intercept) 143.1360 165.7618     0.8635
tax         -30.4104  11.7694    -2.5838
lic          11.6270   2.0173     5.7636

Residual standard error: 81.85 on 45 degrees of freedom

Correlation of Coefficients:
    (Intercept) tax
tax -0.7444
lic -0.8509      0.2880
```

You interpret this much as you do a least squares regression. However, outliers get gradually down-weighted, rather than tested-and-deleted.

```
> w<-rlm(fuel~tax+lic,fuel)$w
> resid<-rlm(fuel~tax+lic,fuel)$resid
```

Look at Wyoming on the next page: without rejecting it as an outlier, it got down-weighted to have weight w=.43 compared to 1 for most observations.

```
> cbind(fuel,w,resid)
   id state fuel   tax  lic   inc   road         w        resid
1   1    ME  541  9.00 52.5 3.571  1.976 1.0000000   61.1391882
2   2    NH  524  9.00 57.2 4.092  1.250 1.0000000  -10.5077687
3   3    VT  561  9.00 58.0 3.865  1.586 1.0000000   17.1906216
4   4    MA  414  7.50 52.9 4.870  2.351 0.9480140 -116.1271732
5   5    RI  410  8.00 54.4 4.399  0.431 0.8997146 -122.3625059
6   6    CN  457 10.00 57.1 5.342  1.333 1.0000000  -45.9346965
7   7    NY  344  8.00 45.1 5.319 11.868 1.0000000  -80.2312932
8   8    NJ  467  8.00 55.3 5.126  2.138 1.0000000  -75.8268168
9   9    PA  464  8.00 52.9 4.447  8.577 1.0000000  -50.9219877
10 10    OH  498  7.00 55.2 4.512  8.507 1.0000000  -74.0744866
11 11    IN  580  8.00 53.0 4.391  5.939 1.0000000   63.9153111
12 12    IL  471  7.50 52.5 5.126 14.186 1.0000000  -54.4763684
13 13    MI  525  7.00 57.4 4.817  6.930 1.0000000  -72.6539132
14 14    WI  508  7.00 54.5 4.207  6.580 1.0000000  -55.9355781
15 15    MN  566  7.00 60.8 4.332  8.159 1.0000000  -71.1857544
16 16    IA  635  7.00 58.6 4.318 10.340 1.0000000   23.3936723
17 17    MO  603  7.00 57.2 4.206  8.508 1.0000000    7.6714892
18 18    ND  714  7.00 54.0 3.718  4.725 0.7063010  155.8779280
19 19    SD  865  7.00 72.4 4.716  5.915 1.0000000   92.9409052
20 20    NE  640  8.50 67.7 4.341  6.010 1.0000000  -31.7965814
21 21    KS  649  7.00 66.3 4.593  7.834 1.0000000  -52.1343210
22 22    DE  540  8.00 60.2 4.983  0.602 1.0000000  -59.7991761
23 23    MD  464  9.00 51.1 4.897  2.449 1.0000000    0.4170051
24 24    VA  547  9.00 51.7 4.258  4.686 1.0000000   76.4407979
25 25    WV  460  8.50 55.1 4.574  2.619 1.0000000  -65.2962288
26 26    NC  566  9.00 54.4 3.721  4.746 1.0000000   64.0478652
27 27    SC  577  8.00 54.8 3.448  5.399 1.0000000   39.9866893
28 28    GA  631  7.50 57.9 3.846  9.061 1.0000000   42.7377662
29 29    FA  574  8.00 56.3 4.188  5.975 1.0000000   19.5461711
30 30    KY  534  9.00 49.3 3.601  4.650 1.0000000   91.3456269
31 31    TN  571  7.00 51.8 3.640  6.905 1.0000000   38.4573546
32 32    AL  554  7.00 51.3 3.333  6.594 1.0000000   27.2708606
33 33    MS  577  8.00 57.8 3.063  6.524 1.0000000    5.1056530
34 34    AR  628  7.50 54.7 3.357  4.121 1.0000000   76.9442050
35 35    LA  487  8.00 48.7 3.528  3.495 1.0000000   20.9114632
36 36    OK  644  6.58 62.9 3.802  7.834 1.0000000  -30.3748357
37 37    TX  640  5.00 56.6 4.045 17.782 1.0000000   -9.1730456
38 38    MT  704  7.00 58.6 3.897  6.385 1.0000000   92.3936723
39 39    ID  648  8.50 66.3 3.635  3.274 1.0000000   -7.5187644
40 40    WY  968  7.00 67.2 4.345  3.905 0.4293990  256.4013681
41 41    CO  587  7.00 62.6 4.449  4.639 1.0000000  -71.1143762
42 42    NM  699  7.00 56.3 3.656  3.985 0.9646353  114.1358001
43 43    AZ  632  7.00 60.3 4.300  3.635 1.0000000    0.6277517
44 44    UT  591  7.00 50.8 3.745  2.611 1.0000000   70.0843667
45 45    NV  782  6.00 67.2 5.215  2.302 1.0000000   39.9909971
46 46    WN  510  9.00 57.1 4.476  3.942 1.0000000  -23.3450675
47 47    OR  610  7.00 62.3 4.296  4.083 1.0000000  -44.6262726
48 48    CA  524  7.00 59.3 5.002  9.794 1.0000000  -95.7452362
```

The ideas in section 9.6 of Hollander and Wolfe are now available in R.

```
Install the Rreg package.  Then load it.
> library(Rreg)
> help(rfit)
> help(drop.test)

rfit fits a multiple regression by ranks, whereas drop.test
is used to test that a subset of regression coefficients
have values zero.

> attach(Fuel)
> Fuel[1:3,]
  id state fuel tax  lic   inc  road
1  1    ME  541   9 52.5 3.571 1.976
2  2    NH  524   9 57.2 4.092 1.250
3  3    VT  561   9 58.0 3.865 1.586

Syntax is similar to linear models, lm, in Stat 500.
> rfit(fuel~tax+lic)
Call:
rfit.default(formula = fuel ~ tax + lic)

Coefficients:
                tax       lic
135.91506 -30.22136  11.73888
> summary(rfit(fuel~tax+lic))
Call:
rfit.default(formula = fuel ~ tax + lic)

Coefficients:
    Estimate Std. Error t.value   p.value
     135.915    182.842  0.7433   0.46122
tax  -30.221     12.935 -2.3364   0.02409 *
lic   11.739      2.217  5.2948 3.621e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
’ 1

Multiple R-squared (Robust): 0.4523139
Reduction in Dispersion Test: 18.58193 p-value: 0

> rfit(fuel~tax+lic)$residual[1:5]
[1]   60.78579  -11.38696   16.22193 -116.24181 -122.73945
> rfit(fuel~tax+lic)$fit[1:5]
[1] 480.2142 535.3870 544.7781 530.2418 532.7395
```

```
> modf<-rfit(fuel~tax+lic+road)
> modr<-rfit(fuel~tax)
> drop.test(modf,modr)

Test whether lic and road have zero coefficients in the
model with predictors tax, lic, road.

Drop in Dispersion Test
F-Statistic     p-value
 1.2385e+01  5.4084e-05
```

For mor info, go o to the Journal of Statistical Software

Authors:	Jeff T. Terpstra and Joseph W. McKean
Title:	**Rank-Based Analysis of Linear Models Using R**
Reference:	Volume 14, 2005, Issue 7
Acquire:	paper [1816] browse files [749]
Dates:	*submitted*: 2004-04-06 *accepted*: 2005-07-01

which is at:

http://www.jstatsoft.org/index.php?vol=14
with documentation
http://www.jstatsoft.org/v14/i07/v14i07.pdf

Log-Linear Models in R

Script is my commentary to you. **Bold Courier is what I type in R.** Regular Courier is what R answered.

What is R?

R is a close relative of Splus, but R is available for free. You can download R from http://cran.r-project.org/ . *R is very powerful and is a favorite (if not the favorite) of statisticians; however, it is not easy to use. It is command driven, not menu driven. You can add things to R that R doesn't yet know how to do by writing a little program. R gives you fine control over graphics. Most people need a book to help them, and so Mainland & Braun's book, Data Analysis and Graphics Using R, Cambridge University Press, 2003, is in the book store as an OPTIONAL book.*

Who should use R?

If statistics and computers terrify you, stay away from R. On the other hand, if you want a very powerful package for free, one you won't outgrow, then R worth a try. For some people, getting stuck is a minor challenge, like a cross-word puzzle; people like that like R. For other people, getting stuck is an ulcer; people like that hate R. If you find you need lots of help to install R or make R work, then R isn't for you.

This is the crabmeat-potato salad data. R is case-sensitive, so crabpot.tab is an object, a table, but Crabpot.tab is an error.

```
> crabpot.tab
, , Illness = Ill

      Crabmeat
Potato  CM NoCM
  PS   120   22
  NoPS   4    0

, , Illness = NotIll

      Crabmeat
Potato  CM NoCM
  PS    80   24
  NoPS  31   23
```

This is the way you fit the potato-crabmeat = c(1,2) margin and the potato-illness =c(1,3) margin. Because I did not request any options, all I got back were the likelihood ratio chi square ($lrt), the Pearson chi square ($pearson) and the degrees of freedom ($df). Note carefully the placement of the (); they matter. The form is always loglin(name-of-your-table, list(c(first margin),c(second margin),...,(last margin)), XXXXX) where XXXXX are requests for optional output.

```
>loglin(crabpot.tab,list(c(1,2),c(1,3)))
2 iterations: deviation 0
$lrt
[1] 6.481655

$pearson
[1] 5.094513

$df
[1] 2

$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"

$margin[[2]]
[1] "Potato"  "Illness"
```

This is the way you fit the potato-crabmeat = c(1,2) margin and the potato-illness =c(1,3) margin and the crabmeat-illness margin =c(2,3). Because I did not request any options, all I got back were the likelihood ratio chi square ($lrt), the Pearson chi square ($pearson) and the degrees of freedom ($df).

```
> loglin(crabpot.tab,list(c(1,2),c(1,3),c(2,3)))
4 iterations: deviation 0.07563798
$lrt
[1] 2.742749

$pearson
[1] 1.702133

$df
[1] 1

$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"

$margin[[2]]
[1] "Potato"  "Illness"

$margin[[3]]
[1] "Crabmeat" "Illness"
```

This is the same fit, with the potato-crabmeat = c(1,2) margin and the potato-illness =c(1,3) margin and the crabmeat-illness margin =c(2,3). Here, I requested optional output, fit=T. That gives the fitted values.

```
> loglin(crabpot.tab,list(c(1,2),c(1,3),c(2,3)),fit=T)
4 iterations: deviation 0.07563798
$lrt
[1] 2.742749

$pearson
[1] 1.702133

$df
[1] 1

$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"

$margin[[2]]
[1] "Potato"  "Illness"

$margin[[3]]
[1] "Crabmeat" "Illness"


$fit
, , Illness = Ill

      Crabmeat
Potato         CM       NoCM
  PS   121.084527  20.916258
  NoPS   2.915473   1.083742

, , Illness = NotIll

      Crabmeat
Potato         CM       NoCM
  PS    78.922805  25.071857
  NoPS  32.077195  21.928143
```

This is the same fit, with the potato-crabmeat = c(1,2) margin and the potato-illness =c(1,3) margin and the crabmeat-illness margin =c(2,3). Here, I requested optional output, param=T. That gives parameter estimates.

```
> loglin(crabpot.tab,list(c(1,2),c(1,3),c(2,3)),param=T)
4 iterations: deviation 0.07563798
$lrt
[1] 2.742749

$pearson
[1] 1.702133

$df
[1] 1

$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"

$margin[[2]]
[1] "Potato"  "Illness"

$margin[[3]]
[1] "Crabmeat" "Illness"

$param
$param$"(Intercept)"
[1] 2.8917

$param$Potato
       PS      NoPS
 0.965108 -0.965108

$param$Crabmeat
        CM       NoCM
 0.5340841 -0.5340841

$param$Illness
       Ill     NotIll
-0.6448331  0.6448331

$param$Potato.Crabmeat
      Crabmeat
Potato         CM       NoCM
  PS    0.1915874 -0.1915874
  NoPS -0.1915874  0.1915874

$param$Potato.Illness
      Illness
Potato       Ill    NotIll
  PS    0.706533 -0.706533
  NoPS -0.706533  0.706533

$param$Crabmeat.Illness
        Illness
Crabmeat        Ill     NotIll
    CM    0.1523095 -0.1523095
    NoCM -0.1523095  0.1523095
```

```
> names(dimnames(crabpot.tab))
[1] "Potato"   "Crabmeat" "Illness"
```

You can refer to the margins of a table by name rather than by number.

```
>loglin(crabpot.tab,list(c("Potato","Crabmeat"),c("Potato","Illness")))
2 iterations: deviation 0
$lrt
[1] 6.481655

$pearson
[1] 5.094513

$df
[1] 2

$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"

$margin[[2]]
[1] "Potato"  "Illness"
```

There are several ways to enter a contingency table in R. This is one way. Use the command "array". Do help(array) to learn how array works. Essentially, it is array(c(counts),c(dimensions-of-table),list(c(labels for dimension 1),...,c(labels for last dimension))). The example below is from the Srping 2005 final exam for Stat 501 in your bulk pack. I made up the name binge.tab, but you can make up any name you want. I said binge.tab <- something, which creates a new object called binge.tab, defined to be equal to something. The something is an array. The counts go down the first column, then down the second. The first variable is the one changing fastest, namely DrinkW. The third variable is the one changing slowest, namely CC. You have to be very, very, very careful to make sure that the order of the numbers agrees with the order of the variables.

```
>binge.tab<-array(c(1912,191,42,110,82,134,150,22,8,18,20,34),c(3,2,2),
dimnames=list(c("0 to 6","7 to 13","14+"), c("0 to 1","2+"),
c("No","Yes")))
```

Usually, you want to give names to the variables too, and this is how you do that.

```
> names(dimnames(binge.tab))<-c("DrinkW","BingeM","CC")
```

You have just created the following object.

```
> binge.tab
, , CC = No
         BingeM
DrinkW    0 to 1  2+
  0 to 6    1912 110
  7 to 13    191  82
  14+         42 134

, , CC = Yes
         BingeM
DrinkW    0 to 1 2+
  0 to 6     150 18
  7 to 13     22 20
  14+          8 34

> loglin(binge.tab,list(c(1,2),c(3)))
2 iterations: deviation 2.842171e-14
$lrt
[1] 44.75657

$pearson
[1] 53.30375

$df
[1] 5

$margin
$margin[[1]]
[1] "DrinkW" "BingeM"

$margin[[2]]
[1] "CC"
```

You can always ask for help. Type help(command-name). Sometimes, when you ask R for help, it helps you. Sometimes not. Life is like that. Or, at least, R is like that. This is what happens when you ask for help about loglin.

>help(loglin)

loglin package:stats R Documentation

Fitting Log-Linear Models

Description:

'loglin' is used to fit log-linear models to multidimensional contingency tables by Iterative Proportional Fitting.

Usage:

```
loglin(table, margin, start = rep(1, length(table)), fit = FALSE,
       eps = 0.1, iter = 20, param = FALSE, print = TRUE)
```

Arguments:

table: a contingency table to be fit, typically the output from 'table'.

margin: a list of vectors with the marginal totals to be fit.

(Hierarchical) log-linear models can be specified in terms of these marginal totals which give the "maximal" factor subsets contained in the model. For example, in a three-factor model, 'list(c(1, 2), c(1, 3))' specifies a model which contains parameters for the grand mean, each factor, and the 1-2 and 1-3 interactions, respectively (but no 2-3 or 1-2-3 interaction), i.e., a model where factors 2 and 3 are independent conditional on factor 1 (sometimes represented as '[12][13]').

The names of factors (i.e., 'names(dimnames(table))') may be used rather than numeric indices.

start: a starting estimate for the fitted table. This optional argument is important for incomplete tables with structural zeros in 'table' which should be preserved in the fit. In this case, the corresponding entries in 'start' should be zero and the others can be taken as one.

fit: a logical indicating whether the fitted values should be returned.

eps: maximum deviation allowed between observed and fitted margins.

iter: maximum number of iterations.

param: a logical indicating whether the parameter values should be returned.

print: a logical. If 'TRUE', the number of iterations and the final deviation are printed.

Details:

The Iterative Proportional Fitting algorithm as presented in Haberman (1972) is used for fitting the model. At most 'iter' iterations are performed, convergence is taken to occur when the maximum deviation between observed and fitted margins is less than 'eps'. All internal computations are done in double precision; there is no limit on the number of factors (the dimension of the table) in the model.

Assuming that there are no structural zeros, both the Likelihood Ratio Test and Pearson test statistics have an asymptotic chi-squared distribution with 'df' degrees of freedom.

Package 'MASS' contains 'loglm', a front-end to 'loglin' which allows the log-linear model to be specified and fitted in a formula-based manner similar to that of other fitting functions such as 'lm' or 'glm'.

Value:

A list with the following components.

lrt: the Likelihood Ratio Test statistic.

pearson: the Pearson test statistic (X-squared).

df: the degrees of freedom for the fitted model. There is no adjustment for structural zeros.

margin: list of the margins that were fit. Basically the same as the input 'margin', but with numbers replaced by names where possible.

fit: An array like 'table' containing the fitted values. Only returned if 'fit' is 'TRUE'.

param: A list containing the estimated parameters of the model. The "standard" constraints of zero marginal sums (e.g., zero row and column sums for a two factor parameter) are employed. Only returned if 'param' is 'TRUE'.

Author(s):

Kurt Hornik

References:

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) _The New S Language_. Wadsworth & Brooks/Cole.

Haberman, S. J. (1972) Log-linear fit for contingency tables-Algorithm AS51. _Applied Statistics_, *21*, 218-225.

Agresti, A. (1990) _Categorical data analysis_. New York: Wiley.

See Also:

'table'

Examples:

```
## Model of joint independence of sex from hair and eye color.
fm <- loglin(HairEyeColor, list(c(1, 2), c(1, 3), c(2, 3)))
fm
1 - pchisq(fm$lrt, fm$df)
## Model with no three-factor interactions fits well.
```

You can use array to enter a contingency table.

> **help(array)**

array package:base R Documentation

Multi-way Arrays

Description:

Creates or tests for arrays.

Usage:

```
array(data = NA, dim = length(data), dimnames = NULL)
as.array(x)
is.array(x)
```

Arguments:

data: a vector (including a list) giving data to fill the array.

dim: the dim attribute for the array to be created, that is a vector of length one or more giving the maximal indices in each dimension.

dimnames: the names for the dimensions. This is a list with one component for each dimension, either NULL or a character vector of the length given by 'dim' for that dimension. The list can be names, and the names will be used as names for the dimensions.

x: an R object.

Value:

'array' returns an array with the extents specified in 'dim' and naming information in 'dimnames'. The values in 'data' are taken to be those in the array with the leftmost subscript moving fastest. If there are too few elements in 'data' to fill the array, then the elements in 'data' are recycled. If 'data' has length zero, 'NA' of an appropriate type is used for atomic vectors ('0' for raw vectors) and 'NULL' for lists.

'as.array()' coerces its argument to be an array by attaching a 'dim' attribute to it. It also attaches 'dimnames' if 'x' has 'names'. The sole purpose of this is to make it possible to access the 'dim'[names] attribute at a later time.

'is.array' returns 'TRUE' or 'FALSE' depending on whether its argument is an array (i.e., has a 'dim' attribute) or not. It is generic: you can write methods to handle specific classes of objects, see InternalMethods.

References:

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) _The New S Language_. Wadsworth & Brooks/Cole.

See Also:

'aperm', 'matrix', 'dim', 'dimnames'.

Examples:

```
dim(as.array(letters))
array(1:3, c(2,4)) # recycle 1:3 "2 2/3 times"
#     [,1] [,2] [,3] [,4]
#[1,]    1    3    2    1
#[2,]    2    1    3    2
```

MODEL	INTERPRETATION
$u+u_{1(i)}+u_{2(j)}+u_{3(k)}$	Independence
$u+u_{1(i)}+u_{2(j)}+u_{3(k)}+u_{23(jk)}$	Variable 1 is independent of variables 2 and 3
$u+u_{1(i)}+u_{2(j)}+u_{3(k)}+u_{13(ik)}+u_{23(jk)}$	Variables 1 and 2 are conditionally independent given variable 3
$u+u_{1(i)}+u_{2(j)}+u_{3(k)}$ $u_{12(ij)}+u_{13(ik)}+u_{23(jk)}$	Constant association: The relationship between any two variables (say 1 and 2) is the same at each level of the third (say 3).
$u+u_{1(i)}+u_{2(j)}+u_{3(k)}$ $u_{12(ij)}+u_{13(ik)}+u_{23(jk)}+u_{123(ijk)}$	Saturated model: Fits any table.

Creating a Contingency Table in R from a Vector of Counts

This concerns the mechanics of creating a contingency table from a vector of counts. You use "array". The example is from the Spring 2008 Final. The counts are in d2. In array, you tell it the dimensions, here 2x3x2, and the dimnames, that is, the levels of the variables. As a second step, using "names(dimnames())" you tell it the names of the variables.

```
> help(array)
> d2
653 1516 4307 8963  331  884   27   78  176  592   53  136

> TurnCrash <- array(data=d2,
dim=c(2,3,2),dimnames=list(c("KSI","Other"),
c("Uncon","Sign","Signal"),c("A","B")))

> TurnCrash
, , A

      Uncon Sign Signal
KSI     653 4307    331
Other  1516 8963    884

, , B

      Uncon Sign Signal
KSI      27  176     53
Other    78  592    136

> names(dimnames(TurnCrash))<-c("Injury","Control","CrashType")
> TurnCrash
, , CrashType = A

       Control
Injury  Uncon Sign Signal
  KSI     653 4307    331
  Other  1516 8963    884

, , CrashType = B

       Control
Injury  Uncon Sign Signal
  KSI      27  176     53
  Other    78  592    136
```

2x2 Tables in R
(Many ways of doing one thing)

```
> sdsyaf
     SDS YAF
Auth  29  33
Dem  131  78
```

Who joins the SDS? Two binomials in the rows.

```
> 29/(29+33)
[1] 0.4677419
> 131/(131+78)
[1] 0.6267943
```

Compares SDS membership for Auth and Dem homes:

```
> prop.test(sdsyaf)
2-sample test for equality of proportions with continuity correction
data:  sdsyaf
X-squared = 4.3659, df = 1, p-value = 0.03666
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.309954304 -0.008150341
sample estimates:
   prop 1    prop 2
0.4677419 0.6267943
```

Who came from an authoritarian home? Two binomials in the columns.

```
> 29/(29+131)
[1] 0.18125
> 33/(33+78)
[1] 0.2972973
```

To interchange rows and columns, use transpose t(.)

```
> t(sdsyaf)
    Auth Dem
SDS   29 131
YAF   33  78
```

Compares SDS membership for Auth and Dem homes:

```
> prop.test(t(sdsyaf))
2-sample test for equality of proportions with continuity correction
data:  t(sdsyaf)
X-squared = 4.3659, df = 1, p-value = 0.03666
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.227565559 -0.004529036
sample estimates:
   prop 1    prop 2
0.1812500 0.2972973
```

2x2 Tables in R, Continued

```
> sum(sdsyaf)
[1] 271
```

Who done what? One multinomial.

```
> sdsyaf/271
           SDS       YAF
Auth 0.1070111 0.1217712
Dem  0.4833948 0.2878229

> chisq.test(sdsyaf)
        Pearson's Chi-squared test with Yates' continuity correction
data:  sdsyaf
X-squared = 4.3659, df = 1, p-value = 0.03666
```

Chi Square test compares observed and "expected" = fitted counts under independence

```
> chisq.test(sdsyaf)$expected
           SDS      YAF
Auth  36.60517 25.39483
Dem  123.39483 85.60517
```

Fitted counts have the same total as observed counts

```
> sum(chisq.test(sdsyaf)$expected)
[1] 271
```

But the sample proportions satisfy independence

```
> chisq.test(sdsyaf)$expected/271
           SDS        YAF
Auth 0.1350744 0.09370787
Dem  0.4553315 0.31588622
```

A key idea: the odds ratio

```
> sdsyaf
     SDS YAF
Auth  29  33
Dem  131  78
```

Kids from authoritarian homes are half as likely to join the SDS

```
> (29*78)/(131*33)
[1] 0.5232477
```

Kids from democratic homes are twice as likely to join the SDS

```
> (131*33)/(29*78)
[1] 1.911141

> fisher.test(sdsyaf)
        Fisher's Exact Test for Count Data
data:  sdsyaf
p-value = 0.02809
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.2833216 0.9659237
sample estimates:
odds ratio
 0.5245336
```

Loglinear Model for a 2x2 Table

(Big weapon, little target!)

x_{ij}

```
> sdsyaf
     SDS YAF
Auth  29  33
Dem  131  78
```

Independence model

```
> loglin(sdsyaf,list(1,2),fit=T,param=T)
2 iterations: deviation 0
$lrt
[1] 4.937627
```

The familiar chi square

```
$pearson
[1] 5.002007
```

Degrees of freedom

```
$df
[1] 1

$margin
$margin[[1]]
[1] 1

$margin[[2]]
[1] 2
```

Estimates of $m_{ij} = E(x_{ij})$

```
$fit
           SDS      YAF
Auth  36.60517 25.39483
Dem  123.39483 85.60517
```

Estimates of model parameters

$\log(m_{ij}) = u + u_{1(i)} + u_{2(j)}$

```
$param
$param$"(Intercept)"
[1] 4.024968

$param$"1"
      Auth        Dem
-0.6075999  0.6075999

$param$"2"
       SDS        YAF
 0.1828218 -0.1828218
```

Saturated model

```
> loglin(sdsyaf,list(c(1,2)),fit=T,param=T)
2 iterations: deviation 0
$lrt
[1] 0
```

The familiar chi square

```
$pearson
[1] 0

$df
[1] 0

$margin
$margin[[1]]
[1] 1 2
```

Estimates of $m_{ij} = E(x_{ij})$

```
$fit
     SDS YAF
Auth  29  33
Dem  131  78
```

Estimates of model parameters

$\log(m_{ij}) = u + u_{1(i)} + u_{2(j)} + u_{12(ij)}$

```
$param
$param$"(Intercept)"
[1] 4.023927

$param$"1"
      Auth        Dem
-0.5920257  0.5920257

$param$"2"
       SDS        YAF
 0.0973192 -0.0973192

$param$"1.2"
            SDS        YAF
Auth -0.1619251  0.1619251
Dem   0.1619251 -0.1619251
```

Hierarchical Models Preserve Marginal Totals

Our data

```
> crabpot.tab
, , Illness = Ill
      Crabmeat
Potato  CM NoCM
  PS   120   22
  NoPS   4    0
, , Illness = NotIll
      Crabmeat
Potato  CM NoCM
  PS    80   24
  NoPS  31   23
```

Fit independence of illness and save fitted counts in "fit"

```
> fit<-loglin(crabpot.tab,list(c(1,2),3),fit=T)$fit
2 iterations: deviation 2.842171e-14
```

Our fitted counts

```
> fit
, , Illness = Ill
      Crabmeat
Potato        CM      NoCM
  PS    96.05263  22.09211
  NoPS  16.80921  11.04605
, , Illness = NotIll
      Crabmeat
Potato        CM      NoCM
  PS   103.94737  23.90789
  NoPS  18.19079  11.95395
```

Margin from data

```
> apply(crabpot.tab,c(1,2),sum)
      Crabmeat
Potato  CM NoCM
  PS   200   46
  NoPS  35   23
```

Margin from fit — they are equal because 12 is in model

```
> apply(fit,c(1,2),sum)
      Crabmeat
Potato  CM NoCM
  PS   200   46
  NoPS  35   23
```

Margin from data

```
> apply(crabpot.tab,c(1,3),sum)
      Illness
Potato Ill NotIll
  PS   142    104
  NoPS   4     54
```

Margin from fit – they are unequal because 13 is not in model

```
> apply(fit,c(1,3),sum)
      Illness
Potato       Ill    NotIll
  PS   118.14474 127.85526
  NoPS  27.85526  30.14474
```

Breast Cancer Survival

Based on Morrison, et al. (1973) International Journal of Cancer, 11, 261-267.

```
> cancer.tab
, , Age = 50, Center = Boston
       appear
Surv3y  Benign Malignant
  Alive     24        15
  Dead       7        12

, , Age = 60, Center = Boston
       appear
Surv3y  Benign Malignant
  Alive     61        28
  Dead      22        11

, , Age = 70, Center = Boston
       appear
Surv3y  Benign Malignant
  Alive     27        16
  Dead      18        12

, , Age = 50, Center = Glamorgn
       appear
Surv3y  Benign Malignant
  Alive     21        24
  Dead       7        19

, , Age = 60, Center = Glamorgn
       appear
Surv3y  Benign Malignant
  Alive     43        37
  Dead      12        17

, , Age = 70, Center = Glamorgn
       appear
Surv3y  Benign Malignant
  Alive     12        16
  Dead       7         6

, , Age = 50, Center = Tokyo
       appear
Surv3y  Benign Malignant
  Alive     77        51
  Dead      10        13

, , Age = 60, Center = Tokyo
       appear
Surv3y  Benign Malignant
  Alive     51        38
  Dead      11        20

, , Age = 70, Center = Tokyo
       appear
Surv3y  Benign Malignant
  Alive      7         6
  Dead       3         3
```

```
> help(margin.table)
> margin.table(cancer.tab,margin=c(1,4))
       Center
Surv3y  Boston Glamorgn Tokyo
  Alive    171      153   230
  Dead      82       68    60

> loglin(cancer.tab,list(c(1,2,3),c(2,3,4)))
2 iterations: deviation 2.842171e-14
$lrt
[1] 16.46446

$pearson
[1] 16.30529

$df
[1] 12

$margin
$margin[[1]]
[1] "Surv3y" "appear" "Age"

$margin[[2]]
[1] "appear" "Age"    "Center"

> loglin(cancer.tab,list(c(1,2,3),c(2,3,4),c(1,4)))
4 iterations: deviation 0.04292951
$lrt
[1] 9.130212

$pearson
[1] 9.142773

$df
[1] 10

$margin
$margin[[1]]
[1] "Surv3y" "appear" "Age"

$margin[[2]]
[1] "appear" "Age"    "Center"

$margin[[3]]
[1] "Surv3y" "Center"


> 16.46446-9.130212
[1] 7.334248
> 12-10
[1] 2
> 1-pchisq(7.334248,2)
[1] 0.02554985
```

A 2^4 Table: How Are Symptoms Related?

A 2x2x2x2 table recording 4 psychiatric symptoms. Originally from Coppen, A (1966) The Mark-Nyman temperament scale: an English translation, British Journal of Medical Psychology, 33, 55-59; used as an example in Wermuth (1976) Model search in multiplicative models, Biometrics 32, 253-263.

```
> symptoms.tab
, , Stability = introvert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid           15            30
  hysteric         9            32
, , Stability = extrovert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid           23            22
  hysteric        14            16
, , Stability = introvert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid           25            22
  hysteric        46            27
, , Stability = extrovert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid           14             8
  hysteric        47            12
```

Independence is a poor fit

```
> loglin(symptoms.tab,list(1,2,3,4))
2 iterations: deviation 2.842171e-14
$lrt
[1] 68.89475
$df
[1] 11
```

Constant association is a plausible fit

```
>loglin(symptoms.tab,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)))
5 iterations: deviation 0.02118533
$lrt
[1] 8.476963
$df
[1] 5
> 1-pchisq(8.477,5)
[1] 0.131833
```

A 2^4 Table, Continued: Looking for a Simpler Model

Remove (3,4): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4)))$lrt,6)
4 iterations: deviation 0.02907685
[1] 0.0348279
```

Remove (2,4): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,2),c(1,3),c(1,4),c(2,3),c(3,4)))$lrt,6)
3 iterations: deviation 0.01097763
[1] 1.416786e-06
```

Remove (2,3): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,2),c(1,3),c(1,4),c(2,4),c(3,4)))$lrt,6)
3 iterations: deviation 0.05751916
[1] 0.001317691
```

Remove (1,4): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,2),c(1,3),c(2,3),c(2,4),c(3,4)))$lrt,6)
4 iterations: deviation 0.08614444
[1] 0.0007099575
```

Remove (1,3): fit is ok

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,2),c(1,4),c(2,3),c(2,4),c(3,4)))$lrt,6)
4 iterations: deviation 0.09620685
[1] 0.1892320
```

Remove (1,2): fit is ok

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)))$lrt,6)
5 iterations: deviation 0.01863555
[1] 0.1930569
```

Remove (1,2), (1,3): fit is ok

```
>  1-pchisq(loglin(symptoms.tab,list(c(1,4),c(2,3),c(2,4),c(3,4)))$lrt,7)
4 iterations: deviation 0.0846266
[1] 0.2505973
```

Remove (1,4): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(2,3),c(2,4),c(3,4)))$lrt,8)
4 iterations: deviation 0.0846266
[1] 0.0001212491
```

Remove (2,3): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,4),c(2,4),c(3,4)))$lrt,8)
2 iterations: deviation 2.842171e-14
[1] 0.004141092
```

Remove (2,4): fit is poor

```
>  1-pchisq(loglin(symptoms.tab,list(c(1,4),c(2,3),c(3,4)))$lrt,8)
2 iterations: deviation 1.421085e-14
[1] 2.626477e-06
```

Remove (3,4): fit is poor

```
> 1-pchisq(loglin(symptoms.tab,list(c(1,4),c(2,3),c(2,4)))$lrt,8)
2 iterations: deviation 2.842171e-14
[1] 0.0852286
```

See-Buy Data

```
> seebuy
, , 1st Buy = Buy1, 1st See = See1
        2nd See
2nd Buy  See2 NoSee2
  Buy2     83     35
  NoBuy2    8      7

, , 1st Buy = NoBuy1, 1st See = See1
        2nd See
2nd Buy  See2 NoSee2
  Buy2     22     11
  NoBuy2   68     28

, , 1st Buy = Buy1, 1st See = NoSee1
        2nd See
2nd Buy  See2 NoSee2
  Buy2     25     95
  NoBuy2   10     15

, , 1st Buy = NoBuy1, 1st See = NoSee1
        2nd See
2nd Buy  See2 NoSee2
  Buy2      8      6
  NoBuy2   32    493
```

Only saturated model fits:

```
> loglin(seebuy,list(c(1,2,3),c(1,2,4),c(1,3,4),c(2,3,4)))
9 iterations: deviation 0.06642452
$lrt
[1] 21.87360
$df
[1] 1
```

Didn't see, Didn't buy:

```
> or(seebuy[,,2,2])
[1] 20.54167
```

Saw, bought:

```
> or(seebuy[,,1,1])
[1] 2.075
```

Saw, didn't buy:

```
> or(seebuy[,,2,1])
[1] 0.8235294
```

Didn't see, bought:

```
> or(seebuy[,,1,2])
[1] 0.3947368
```

Log-Linear Models with Structural Zeros in R

To fit a log-linear model with structural zeros, you use the “start=” option in loglin:

```
loglin(table, margin, start = rep(1, length(table)), fit = FALSE,
        eps = 0.1, iter = 20, param = FALSE, print = TRUE)
```

```
start: a starting estimate for the fitted table.  This optional
       argument is important for incomplete tables with structural
       zeros in 'table' which should be preserved in the fit.  In
       this case, the corresponding entries in 'start' should be
       zero and the others can be taken as one.
```

This is from page I1, Table 5.2-3 “Classification of Purum Marriages,” from Bishop, Fienberg and Holland, *Discrete Multivariate Analysis*.

```
> Marriages
       Marrim Makan Parpa Thao Keyang
Marrim      0     5    17    0      6
Makan       5     0     0   16      2
Parpa       0     2     0   10     11
Thao       10     0     0    0      9
Keyang      6    20     8    0      1
```

Some of the zeros are “random” (meaning “didn’t happen”) and others are “structural” (meaning “can’t happen”). In the start table, you put a 0 for the structural zeros and a 1 for everything else, including the random zeros.

```
> MarriagesS
       Marrim Makan Parpa Thao Keyang
Marrim      0     1     1    0      1
Makan       1     0     1    1      1
Parpa       0     1     0    1      1
Thao        1     0     0    0      1
Keyang      1     1     1    1      1
```

This fits “quasi-independence:”

```
> loglin(Marriages,list(1,2),start=MarriagesS,fit=T)
5 iterations: deviation 0.09330366
$lrt
[1] 76.2508

$pearson
[1] 66.54045

$df
[1] 16

$margin
$margin[[1]]
[1] 1

$margin[[2]]
[1] 2


$fit
          Marrim     Makan     Parpa     Thao   Keyang
Marrim  0.000000 10.786776 10.682608 0.000000 6.548952
Makan   4.866051  0.000000  6.562317 7.543237 4.023015
Parpa   0.000000  8.382528  0.000000 9.542478 5.089266
Thao   10.383451  0.000000  0.000000 0.000000 8.584534
Keyang  5.750498  7.830696  7.755075 8.914285 4.754233
```

This fit satisfies quasi-independence, for intstance:

```
> mfit<-
loglin(Marriages,list(1,2),start=MarriagesS,fit=T)$fit
5 iterations: deviation 0.09330366
```

The odds ratio is 1 in any complete piece:

```
> mfit[2:3,4:5]
          Thao   Keyang
Makan 7.543237 4.023015
Parpa 9.542478 5.089266
> mfit[2,4]*mfit[3,5]/(mfit[3,4]*mfit[2,5])
[1] 1
```

Log-Linear and Logit Models for the Same Data

We look at this data set before: a 2x2x2x2 table recording 4 psychiatric symptoms. Originally from Coppen, A (1966) The Mark-Nyman temperament scale: an English translation, British Journal of Medical Psychology, 33, 55-59; used as an example in Wermuth (1976) Model search in multiplicative models, Biometrics 32, 253-263.

```
> symptoms.tab
, , Stability = introvert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid           15            30
  hysteric         9            32
, , Stability = extrovert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid           23            22
  hysteric        14            16
, , Stability = introvert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid           25            22
  hysteric        46            27
, , Stability = extrovert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid           14             8
  hysteric        47            12
```

If you recall, we came to like the model in which variable 1, Solidity was conditionally independent of variables 2 and 3, Validity and Stability, given variable 4, Depression:

```
>  1-pchisq(loglin(symptoms.tab,list(c(1,4),c(2,3),c(2,4),c(3,4)))$lrt,7)
4 iterations: deviation 0.0846266
[1] 0.2505973
```

This is an nice model in some ways, but not one that you could fit with a standard logit model. In a standard logit model, one of the variables is a binary "dependent variable" and the others are "independent variables." There are many kinds of logit models, but this is the typical kind. Let's take variable 4, Depression as the dependent variable, and predict it from the other symptoms. This means we only fit models which preserve the relationships among the independent variables, 1,2 and 3, and only model relationships that involve the dependent variable. This means we always include the c(1,2,3) term. This means we can't discover a simple relationship among the independent variables, because we have declared we are not interested in such things; we are only interested in predicting depression from other symptoms.

```
> loglin(symptoms.tab,list(c(1,2,3),c(1,4),c(2,4),c(3,4)))
5 iterations: deviation 0.03387941
$lrt                $df
[1] 7.762877         4
$margin[[1]]
[1] "Solidity"  "Validity"  "Stability"
$margin[[2]]
[1] "Solidity"   "Depression"
$margin[[3]]
[1] "Validity"   "Depression"
$margin[[4]]
[1] "Stability"  "Depression"
```

Log-Linear and Logit Models, Continued

For the logit model, we rearrange the data to look more like regression, with coded variables, etc.

```
> symptoms.X
  depressed notdepressed Solidity Validity Stability
1        15           25      0.5      0.5       0.5
2         9           46     -0.5      0.5       0.5
3        30           22      0.5     -0.5       0.5
4        32           27     -0.5     -0.5       0.5
5        23           14      0.5      0.5      -0.5
6        14           47     -0.5      0.5      -0.5
7        22            8      0.5     -0.5      -0.5
8        16           12     -0.5     -0.5      -0.5
> y<-as.matrix(symptoms.X[,1:2])
> y
  depressed notdepressed
1        15           25
2         9           46
3        30           22
4        32           27
5        23           14
6        14           47
7        22            8
8        16           12
> attach(symptoms.X)
```

The glm program fits many types of "generalized" linear models. If you say, "family=binomial" it fits a logit model.

```
> summary(glm(y~Solidity+Validity+Stability,family=binomial))
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -0.1197     0.1148  -1.043 0.296957
Solidity      0.8658     0.2276   3.804 0.000142 ***
Validity     -1.2212     0.2330  -5.242 1.59e-07 ***
Stability    -0.5246     0.2351  -2.231 0.025655 *
---
    Null deviance: 55.4057  on 7  degrees of freedom
Residual deviance:  7.7629  on 4  degrees of freedom
AIC: 48.304
Number of Fisher Scoring iterations: 3
```

Although it may not look like it, this is actually the "same" model. For instance, the likelihood ratio chi square from the log-linear model was

```
$lrt                $df
[1] 7.762877         4
```

which is the same as the "residual deviance" from the logit model

```
Residual deviance:  7.7629  on 4  degrees of freedom
```

Similarly, the "Null deviance" in the logit model is

```
    Null deviance: 55.4057  on 7  degrees of freedom
```

which is the same as the likelihood ratio chi square from the loglinear model which says Depression (#4) is independent of the other three variables, but the other three variables can have any relationship.

```
> loglin(symptoms.tab,list(c(1,2,3),4))
2 iterations: deviation 2.842171e-14
$lrt              $df
[1] 55.40572       7
```

Log-Linear and Logit Models, Fitted Values

They also give the same "fitted values" or fitted probabilities of degression:

```
> glm(y~Solidity+Validity+Stability,family=binomial)$fitted.values
     1      2      3      4      5      6      7      8
0.3636 0.1938 0.6595 0.4491 0.4912 0.2888 0.7660 0.5793
```

We can compute the same thing from the fitted counts for the log-linear model:

```
> 14.54564/(14.54564+ 25.45283)
[1] 0.3636549
> loglin(symptoms.tab,list(c(1,2,3),c(1,4),c(2,4),c(3,4)),fit=T)
, , Stability = introvert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid     14.54564      34.29702
  hysteric  10.66283      26.49452
, , Stability = extrovert, Depression = depressed
          Validity
Solidity   energetic psychasthenic
  rigid     18.17336      22.98440
  hysteric  17.62069      16.22155
, , Stability = introvert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid     25.45283      17.70196
  hysteric  44.34483      32.50037
, , Stability = extrovert, Depression = not depressed
          Validity
Solidity   energetic psychasthenic
  rigid     18.82339      7.021948
  hysteric  43.37632     11.778337
```

$$\log(m_{hijk}) = u + u_{R(h)} + u_{V(i)} + u_{S(j)} + u_{D(k)} + \ldots + u_{SD(jk)}$$

$$\log(m_{hij1}/m_{hij2}) = \log(m_{hij1}) - \log(m_{hij2}) = u_{D(1)} - u_{D(2)} + u_{RD(h1)} - u_{RD(h2)} + u_{VD(i1)} - u_{VD(i2)} + u_{SD(h1)} - u_{SD(j2)} = w + w_{R(h)} + w_{V(i)} + w_{S(j)}$$

Log-Linear and Logit Models, Model Parameters

They also give the "same" parameters. If you type:

```
> loglin(symptoms.tab,list(c(1,2,3),c(1,4),c(2,4),c(3,4)),param=T)
```

you get many parameters, including:

```
$param$Solidity.Depression
          Depression
Solidity    depressed not depressed
  rigid     0.2164241    -0.2164241
  hysteric -0.2164241     0.2164241

$param$Validity.Depression
              Depression
Validity         depressed not depressed
  energetic     -0.3052297     0.3052297
  psychasthenic  0.3052297    -0.3052297

$param$Stability.Depression
           Depression
Stability    depressed not depressed
  introvert -0.1310981     0.1310981
  extrovert  0.1310981    -0.1310981
```

whereas glm gives

```
> glm(y~Solidity+Validity+Stability,family=binomial)
Coefficients:
(Intercept)     Solidity     Validity    Stability
    -0.1197       0.8658      -1.2212      -0.5246
```

but they are the same once you multiply by 4:

```
> 4*0.2164241
[1] 0.8656964

> 4*-0.3052297
[1] -1.220919

> 4*-0.1310981
[1] -0.5243924
```

Fitting Logit Models

*The data are from DC*MADS which is study #2347 at http://www.icpsr.umich.edu/ available from the Penn Library web page. These are 986 babies born in Washington DC hospitals. From NIDA.* Abuse *The DCBaby data.frame includes a few incomplete cases excluded from DCBaby.complete*

```
> dim(DCBaby)
[1] 986   8
> dim(DCBaby.complete)
[1] 974   8
```

First two babies:

```
> DCBaby[1:2,]
  ID Bweight low15 low25 BWgroup cigs alcoh momage
1  1    2438     0     1       2    0     0     18
2  2    2296     0     1       2    0     0     18
```

Birth weight appears four ways, in grams (Bweight), as a binary variable <1500 grams or not, as a binary variable <2500 grams or not, and as an ordinal variable <1500 grams, 1500-2500 grams, ≥ 2500 grams as 3, 2 or 1. Notice that 3 is very under weight. Cigs = 1 if mom smoked during pregnancy, = 0 otherwise. Alcoh = 1 if mom drank alcohol during pregnancy, =0 otherwise. Here, use is "at least once a week". Momage is mom's age.

```
> attach(DCBaby.complete)
> table(factor(cigs),factor(alcoh))
      0   1
  0 615 104
  1 107 148
> or(table(factor(cigs),factor(alcoh)))
[1] 8.179367
```

Mom's who smoked were 8 times more likely to drink. Older moms smoked and drank somewhat more.

Fitting Logit Models, continued

Let's predict birthweight < 2500 grams using cigs, alcoh, momage:

```
> summary(glm(low25~cigs+alcoh+momage,family=binomial))
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.72283    0.34612  -2.088   0.0368 *
cigs         1.26114    0.17982   7.013 2.33e-12 ***
alcoh        0.17240    0.18710   0.921   0.3568
momage      -0.03030    0.01309  -2.315   0.0206 *
---
    Null deviance: 1103.1  on 973  degrees of freedom
Residual deviance: 1033.3  on 970  degrees of freedom
```

In sparse problems, like this one, you ***cannot*** *use G^2 to test goodness of fit, but you can compare models. Looks like cigs = 1 smoking is bad, z=7.0, p<0.0001. We can use the estimate of β_{cigs}, namely 1.26, to estimate how bad:*

```
> exp(1.26114)
[1] 3.529443
```

So we estimate that the odds of a small baby, <2500 grams, are 3.5 times greater for a mom who smokes. Might want a confidence interval. Build a confidence interval for β_{cigs}, then take antilogs. Confidence interval is estimate plus or minus 1.96 x std.error.

```
> exp(c(1.26114-1.96*0.17982,1.26114+1.96*0.17982))
[1] 2.481077 5.020790
```

So our point estimate is 3.5 times, but the 95% confidence interval is [2.5, 5.0] times greater risk of a small baby for smoking moms.

Let's add some interactions and see if they improve the fit.

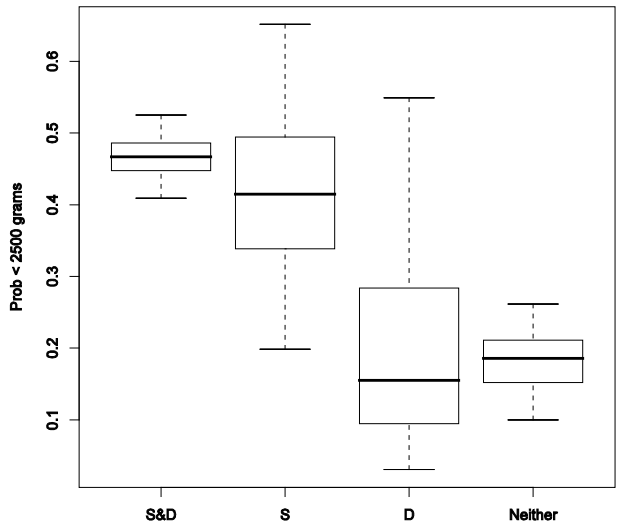
```
> glm(low25~cigs+alcoh+momage+cigs*alcoh+cigs*momage
        +alcoh*momage,family=binomial)
Coefficients:
 (Intercept)          cigs         alcoh        momage
    -0.47840      -2.13229       2.92436      -0.04002
 cigs:alcoh cigs:momage  alcoh:momage
     0.10041    0.12093      -0.10045
```

Does the new model fit significantly better than the simpler model? They are nested, so we use the change in G^2 = residual deviance to compare the models. Reduced model G^2 =1033.3 on 970 degrees of freedom, versus full model G^2 = 1018 on 967 because 3 parameters were added.

```
> 1033.3-1018
[1] 15.3
> 1-pchisq(15.3,3)
[1] 0.001577423
```

So the full model with interactions fits significantly better: The null hypothesis that the three interaction coefficients are all zero is rejected at the 0.0016 level. Look at fit:

```
> boxplot(p[cigs==1&alcoh==1],p[cigs==1&alcoh==0],
   p[cigs==0&alcoh==1],p[cigs==0&alcoh==0], ylab =
   "Prob < 2500 grams",names=c("S&D","S","D","Neither"))
```



Leukemia Logit

```
> boxplot(wbc)
> boxplot(log(wbc))

> summary(glm(year~ag10+log(wbc),family=binomial))
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   8.0964     4.0537   1.997   0.0458 *
ag10          2.5196     1.0907   2.310   0.0209 *
log(wbc)     -1.1088     0.4609  -2.405   0.0162 *
---
    Null deviance: 42.010  on 32  degrees of freedom
Residual deviance: 26.833  on 30  degrees of freedom
AIC: 32.833

>summary(glm(year~ag10+log(wbc)+ag10*log(wbc),family=binomial))
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    11.4603     8.9559   1.280    0.201
ag10           -2.0078    10.1840  -0.197    0.844
log(wbc)       -1.5039     1.0574  -1.422    0.155
ag10:log(wbc)   0.5181     1.1732   0.442    0.659
    Null deviance: 42.010  on 32  degrees of freedom
Residual deviance: 26.615  on 29  degrees of freedom
AIC: 34.615

Number of Fisher Scoring iterations: 6

> p<-glm(year~ag10+log(wbc),family=binomial)$fitted.values
> cbind(leukemia,round(p,3))

> summary(wbc)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    750    5300   10500   29170   32000  100000
> l<-8.096+2.520+(-1.109*log(5300))
> exp(l)/(1+exp(l))
[1] 0.7513476
> l<-8.096+2.520+(-1.109*log(32000))
>  exp(l)/(1+exp(l))
[1] 0.2914811
> l<-8.096+(-1.109*log(5300))
>  exp(l)/(1+exp(l))
[1] 0.1955744
> l<-8.096+(-1.109*log(32000))
> exp(l)/(1+exp(l))
[1] 0.03204012
```

McNemar Test via Conditional Logit Regression

```
> library(survival)
> sartwell[1:8,]
  pair thromb ocuse
1    1      0     1
2    1      1     1
3    2      0     1
4    2      1     1
5    3      0     1
6    3      1     1
7    4      0     1
8    4      1     1

> dim(sartwell)
[1] 350   3
> attach(sartwell)
> table(ocuse[thromb==1],ocuse[thromb==0])

     0  1
  0 95 13
  1 57 10

> pbinom(13,13+57,1/2)
[1] 5.144971e-08
> 2* pbinom(13,13+57,1/2)
[1] 1.028994e-07
> 57/13
[1] 4.384615

> clogit(ocuse~thromb+strata(pair),data=sartwell)
Call:
clogit(ocuse ~ thromb + strata(pair), data = sartwell)


       coef exp(coef) se(coef)    z       p
thromb 1.48      4.38    0.307 4.81 1.5e-06

Likelihood ratio test=29.9  on 1 df, p=4.67e-08  n= 350
```

Conditional Logit Regression

In this example, there are 59 matched sets, i=1,2,…,59, and each set contains 3 boys, j=1,2,3 who were matched on many variables. In each set, the first boy, boy j=1, joined a gang for the first time at age 14, while the other two boys had not yet joined gangs. (Look at newgang14, which is 1 for the joiner and 0 for the controls.) gang17 indicates whether the boy is in a gang at age 14. vio13 measures violence at age 13, iqC is a rough iq measure, and nbp13 is self-reported # of sexual partners at age 13.

Example adapted from Haviland, et al. (2007) Psychological Methods. Data from "Montréal Longitudinal Study of Boys," Tremblay, R. E., et al (1987), International Journal of Behavioral Development, 10, 467-484.

```
> dim(gangEG)
[1] 177   6

> gangEG[1:21,]
    mset newgang14 gang17 vio13 iqC nbp13
26   235         1      0     0  10     0
212  235         0     NA     1  11     0
298  235         0      0     0  10     0
274  236         1      0     0  11     0
166  236         0      0     0   8     0
304  236         0      0     0  10     0
280  237         1      1     1   7     0
16   237         0      0     1   9     0
487  237         0      0     1   9     0
285  238         1      0     0  11     0
52   238         0      0     0  11     0
275  238         0      0     1  10     0
311  239         1      0     1  11     0
114  239         0      0     1   9     0
362  239         0      0     1  10     0
355  240         1      0     0  11     0
95   240         0     NA     1  10     0
328  240         0      0     0  11     0
357  241         1      1     0   7    NA
218  241         0      0     0  12     0
461  241         0      1    NA   0    NA
```

Conditional Logit Regression, Continued

Will predict gang17 from other variables. Here, p_{ij}=Prob(gang17=1).

$$\log\{p_{ij}/(1-p_{ij})\} = \alpha_i + \beta_1 x_{ij} + \beta_2 w_{ij}$$

Notice that each matched set has its own parameter, α_i, so this model looks tiny, but it has 59+2 = 61 parameters. The conditional logit model eliminates 59 of the parameters by conditioning on the total number of boys in gangs at age 17 in each set, i=1,2,…,59, where that total can be 0, 1, 2, or 3. The model then just has the betas.

```
> library(survival)
> help(clogit)

> clogit(gang17~newgang14+iqC+strata(mset),data=gangEG)
Call:
clogit(gang17 ~ newgang14 + iqC + strata(mset), data =
gangEG)


            coef exp(coef) se(coef)     z    p
newgang14  0.562     1.755    0.522  1.08 0.28
iqC       -0.402     0.669    0.196 -2.05 0.04

Likelihood ratio test=6.65  on 2 df, p=0.0360  n=157 (20
observations deleted due to missing)

> clogit(gang17~newgang14+iqC+vio13+strata(mset),data=gangEG)
Call:
clogit(gang17 ~ newgang14 + iqC + vio13 + strata(mset),
data = gangEG)


            coef exp(coef) se(coef)     z     p
newgang14  0.702     2.017    0.577  1.22 0.220
iqC       -0.449     0.638    0.224 -2.01 0.045
vio13     -0.546     0.579    0.355 -1.54 0.120

Likelihood ratio test=8.47  on 3 df, p=0.0373  n=155 (22
observations deleted due to missing)
```

Proportional Odds Model for Ordinal Data

DCBaby contains data on 986 babies born in 8 Washington DC hospitals.

```
> dim(DCBaby)
[1] 986   8
```

This is data for baby 1 and baby 2:

```
> DCBaby[1:2,]
  ID Bweight low15 low25 BWgroup cigs alcoh momage
1  1    2438     0     1       2    0     0     18
2  2    2296     0     1       2    0     0     18
```

Birth weight appears four ways, in grams (Bweight), as a binary variable <1500 grams or not, as a binary variable <2500 grams or not, and as an ordinal variable <1500 grams, 1500-2500 grams, ≥ 2500 grams as 3, 2 or 1. Notice that 3 is very under weight, and 1 is much heavier.

```
> table(low15,low25)
     low25
low15   0   1
    0 734 195
    1   0  55

> table(low15,BWgroup)
     BWgroup
low15   1   2   3
    0 734 195   0
    1   0   0  55

> table(low25,BWgroup)
     BWgroup
low25   1   2   3
    0 734   0   0
    1   0 195  55
```

You need to get the polr program in the MASS library.

```
> library(MASS)
> help(polr)
```

To use polr, the outcome, here BWgroup, must be an ordered factor. If BWgroup were entered as 1, 2, 3, it becomes an ordered factor by setting BWgroup<- factor(BWgroup, ordered=T).

Proportional Odds Model for Ordinal Data, continued

Ordinal logit fits log{pr(Y ≤ j)/pr(Y>j)} = α_j – β x simultaneously for all j, whereas a binary logit regression of a similar sort fits log{pr(Y > j)/pr(Y≤j)} = α_j + β x for one j at a time. Notice that there are small changes in the model which mix the signs.

```
> glm(low15~cigs,family=binomial)
Coefficients:
(Intercept)         cigs
     -3.215        1.064

> glm(low25~cigs,family=binomial)

Coefficients:
(Intercept)         cigs
     -1.484        1.275

> polr(BWgroup~cigs)

Coefficients:
    cigs
1.252373

Intercepts:
     1|2      2|3
1.479582 3.311650
```

Notice that polr gave you one slope, two intercepts, whereas binary logit regression gave you two of each.

Let's get the "fitted values" from the ordinal logit model, and round them to 3 decimals.

```
> fit<-polr(BWgroup~cigs)$fitted.values

> fit<-round(fit,3)
```

Let's add the fitted values to the data set and print the first 7 babies.

```
> cbind(DCBaby[1:7,],fit[1:7,])
  ID Bweight low15 low25 BWgroup cigs alcoh momage     1    2     3
1  1    2438     0     1       2    0     0     18 0.815 0.15 0.035
2  2    2296     0     1       2    0     0     18 0.815 0.15 0.035
3  3    3020     0     0       1    0     0     30 0.815 0.15 0.035
4  4    2385     0     1       2    0     0     17 0.815 0.15 0.035
5  5    3016     0     0       1    0     1     35 0.815 0.15 0.035
6  6    4175     0     0       1    0     0     23 0.815 0.15 0.035
7  7    3725     0     0       1    1     1     27 0.557 0.33 0.113
```

Look at baby 6 and baby 7. Baby 6 had a mom who did not smoke. Baby 7 had a mom who smoked. So baby 7 had a much higher chance of being in

Latent Class Model

```
> army.tab

> dim(army)
[1] 1000    4

> army[1:2,]
  Well run Favorable Square Deal Enlisted
1        1         1           1        1
2        1         1           1        1

> summary(army)
    Well run       Favorable      Square Deal     Enlisted
 Min.   :0.000   Min.   :0.000   Min.   :0.0   Min.   :0.000
 1st Qu.:0.000   1st Qu.:0.000   1st Qu.:0.0   1st Qu.:0.000
 Median :1.000   Median :0.000   Median :0.0   Median :0.000
 Mean   :0.641   Mean   :0.374   Mean   :0.3   Mean   :0.254
 3rd Qu.:1.000   3rd Qu.:1.000   3rd Qu.:1.0   3rd Qu.:1.000
 Max.   :1.000   Max.   :1.000   Max.   :1.0   Max.   :1.000

> library(e1071)
Loading required package: class
> help(lca)

> lca(as.matrix(army),2,niter=100)
LCA-Result
----------

Datapoints: 1000
Classes:    2
Probability of classes
[1] 0.492 0.508
Itemprobabilities
     1    2    3    4
1 0.89 0.59 0.53 0.47
2 0.40 0.16 0.08 0.04
> summary(lca(as.matrix(army),2,niter=100))
LCA-Result
----------
Datapoints: 1000
Classes:    2

Goodness of fit statistics:
Number of parameters, estimated model: 9
Number of parameters, saturated model: 15
Log-Likelihood, estimated model:       -2348.906
Log-Likelihood, saturated model:       -2343.960

Information Criteria:

BIC, estimated model: 4759.982
BIC, saturated model: 4791.537

TestStatistics:
Likelihood ratio:   9.891697   p-val: 0.1292876
Pearson Chi^2:      9.04448   p-val: 0.171092
Degress of freedom: 6
```

Using glm for Poisson Regression

```
> crabpot.tab
, , Illness = Ill
      Crabmeat
Potato  CM NoCM
  PS   120   22
  NoPS   4    0
, , Illness = NotIll
      Crabmeat
Potato  CM NoCM
  PS    80   24
  NoPS  31   23

> loglin(crabpot.tab,list(c(1,2),c(1,3)))
2 iterations: deviation 0
$lrt
[1] 6.481655
$df
[1] 2
$margin
$margin[[1]]
[1] "Potato"   "Crabmeat"
$margin[[2]]
[1] "Potato"  "Illness"

> crabpot.X
  count ill potato crabmeat ip ic cp
1   120   1      1        1  1  1  1
2     4   1      0        1  0  1  0
3    22   1      1        0  1  0  0
4     0   1      0        0  0  0  0
5    80   0      1        1  0  0  1
6    31   0      0        1  0  0  0
7    24   0      1        0  0  0  0
8    23   0      0        0  0  0  0

> glm(count~ill+potato+crabmeat+ip+cp,family=poisson)
Coefficients:
(Intercept)          ill       potato     crabmeat           ip
cp
    3.06404     -2.60269     -0.09633      0.41985      2.91413
1.04982
Degrees of Freedom: 7 Total (i.e. Null);  2 Residual
Null Deviance:      295.3
Residual Deviance:    6.482        AIC: 54.81
```

Measuring Agreement Using Kappa

Flip a dime and a quarter and they agree with probability ½:

```
> ((1/2)^2)+((1/2)^2)
[1] 0.5

> dime<-sample(c("head","tail"),10000,replace=T)
> quarter<-sample(c("head","tail"),10000,replace=T)
> table(dime,quarter)
      quarter
dime   head tail
  head 2564 2467
  tail 2506 2463
> (2564+2463)/10000
[1] 0.5027
```

So agreeing half the time does not mean much.

Roll a red die and a blue die and record 1 or other. They agree with probability:

```
> ((1/6)^2)+((5/6)^2)
[1] 0.7222222
> red<-rbinom(10000,1,1/6)
> blue<-rbinom(10000,1,1/6)
> table(red,blue)
   blue
red    0    1
  0 6950 1327
  1 1428  295
> (295+6950)/10000
[1] 0.7245
```

So .72 agreement does not mean much, nor does the fact that dice agree more than coins – it is just luck.

Cohen's kappa asks about agreement above chance.

Cohen, J. (1960). A coefficient of agreement for nominal scales. Educational and Psychological Measurement, 20, 37-46.

Fleiss, J. L., et al. (2003) Statistical Methods for Rates and Proportions. NY: Wiley.

```
Find the expected counts under independence:
> chisq.test(table(red,blue))$expected
   blue
red        0         1
  0 6934.471 1342.5294
  1 1443.529  279.4706
> (6934.471+279.4706)/10000
[1] 0.7213942
So although we got 72% agreement, we also expected 72%
agreement by chance.

Kappa is the percent agreement in excess of change,
(actual – expected)/(1 – expected)
> (0.7245-0.7213942)/(1-0.7213942)
[1] 0.01114765
So it is just 1% better than expected by chance.

> library(irr)
> help(package=irr)

> kappa2(cbind(red,blue))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 10000
   Raters = 2
    Kappa = 0.0111
        z = 1.12
  p-value = 0.265

> kappa2(cbind(dime,quarter))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 10000
   Raters = 2
    Kappa = 0.00531
        z = 0.531
  p-value = 0.595
```

```
Erie County Ohio
> attach(erieAgree)
> kappa2(cbind(MayFrom,MayTo))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 445
   Raters = 2
    Kappa = 0.756
        z = 22.5
  p-value = 0

> kappa2(cbind(JuneFrom,JuneTo))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 445
   Raters = 2
    Kappa = 0.762
        z = 22.7
  p-value = 0

> kappa2(cbind(JulyFrom,JulyTo))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 445
   Raters = 2
    Kappa = 0.692
        z = 21.3
  p-value = 0

> kappa2(cbind(AugFrom,AugTo))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 445
   Raters = 2
    Kappa = 0.864
        z = 25.3
  p-value = 0

> kappa2(cbind(SeptFrom,SeptTo))
 Cohen's Kappa for 2 Raters (Weights: unweighted)
 Subjects = 445
   Raters = 2
    Kappa = 0.872

        z = 25.2
  p-value = 0
```

So people changed least in August and Sept, and most from July to August.

Is There a One-Dimensional Latent Variable?

If there is a one-dimensional latent variable positively related to all the variables, then the partial association between any two variables, say S and E, given the sum of all other variables, here WF12, is positive – that is, the odds ration is at least 1.

```
> table(S,E,WF12)
, , WF12 = 0
   E
S     0   1
  0 229  16
  1  25  10
, , WF12 = 1
   E
S     0   1
  0 251  53
  1  76  45
, , WF12 = 2
   E
S     0   1
  0  96  55
  1  69  75

> table(S,E,WF12)[,,1]
   E
S     0  1
  0 229 16
  1  25 10
> or(table(S,E,WF12)[,,1])
[1] 5.725
> table(S,E,WF12)[,,2]
   E
S     0  1
  0 251 53
  1  76 45
> or(table(S,E,WF12)[,,2])
[1] 2.804121
> table(S,E,WF12)[,,3]
   E
S    0  1
  0 96 55
  1 69 75
> or(table(S,E,WF12)[,,3])
[1] 1.897233

> mantelhaen.test(S,E,WF12)
        Mantel-Haenszel chi-squared test with continuity correction

data:  S and E and WF12
Mantel-Haenszel X-squared = 33.6202, df = 1, p-value = 6.7e-09
alternative hypothesis: true common odds ratio is not equal to 1
95 percent confidence interval:
 1.819444 3.404577
sample estimates:
common odds ratio
         2.488863
```

PROBLEM SET #1 STATISTICS 501 Spring 2019: DATA PAGE 1

Due at noon in class Tuesday 2 April 2019.

This is an exam. Do not discuss it with anyone.

We will examine use of e-cigarettes in the 2013-2104 National Health and Nutrition Examination Survey. The data are in an object Ecig501 in the course workspace. The variables in Ecig501 are:

SEQN = NHANES id number
female = 1 for female, 0 for male
age = age in years, 8-20
grp = A factor with four levels: None, Cigarettes, E-Cigarettes, Both. The factory describes tobacco use in the previous 5 days. None = no tobacco use. Cigarettes = cigarettes only. E-Cigarettes = E-cigarettes only. Both = both cigarettes and E-cigarettes. Some other cases were excluded.
Cigarettes5 = smoked cigarettes in the past 5 days, 1=yes.
Cigarettes5d = days smoked cigarettes in past 5 days,0-5.
Cigarettes5c = cigarettes per day in past 5 days, 0-40.
ecig5 = e-cigarettes in the past 5 days, 1=yes
ecig5d = days used e-cigarettes in the past 5 days, 0-5.
cotinine = blood cotinine level in ng/mL, a biomarker of tobacco exposure
lead = blood lead level in μg/dL
cadmium = blood cadmium level in μg/L
You should look at the data in various ways.

```
> table(grp)
> table(grp,cigarettes5)
> table(grp,ecig5)
> boxplot(cadmium~grp)
> boxplot(cotinine~grp)
> table(ecigd,grp)
> table(cigarettes5d,grp)
```

Create the factor nocig and look at it in various ways. Use nocig to answer the questions in part 1. That part compares E-cigarettes alone to not smoking, or groups 3 and 1. Make sure you create nocig correctly or you will get many things wrong.

```
> nocig<-factor(as.integer(grp),levels=c(3,1),labels=c("E-only","None"))
> table(nocig)
> summary(nocig)
> table(nocig,grp)
        grp
nocig    None Cigarettes E-Cigarettes Both
  E-only    0          0           34    0
  None   1946          0            0    0
```

PROBLEM SET #1 STATISTICS 501 Spring 2019: DATA PAGE 2

This is an exam. Do not discuss it with anyone.

Due at noon in class Tuesday 2 April 2019

```
> boxplot(cadmium~nocig)
```

Smoking cigarettes is believed to increase lead and cadmium levels in the blood? What about e-cigarettes? Are they harmless? Are they better than cigarettes?

The function IQR computes the inter-quartile range, which is the length of the box in the boxplot.

```
> help(IQR)
```

You can do things faster with tapply, but you don't have to use tapply.

```
> help(tapply)
```

y_{ij} = cadmium level for individual i in group j, where the four groups are defined by grp, j=1 for none, j=2 for cigarettes only, j=3 for e-cigarettes only, and j=4 for both.

Model 1: $y_{ij} = \theta + \omega_j + \zeta_{ij}$ where the ζ_{ij} are independent and identically distributed.

Model 2: $\log(y_{ij}) = \mu + \tau_j + \varepsilon_{ij}$ where the ε_{ij} are independent and identically distributed.

Question 3 asks you to focus on the 34 people who used E-cigarettes but did not smoke cigarettes. It asks whether there is a relationship between the number of days using E-cigarettes and cadmium levels.

```
> justEcig<-grp=="E-Cigarettes"
> table(justEcig)
> table(ecigd[justEcig])
> w<-cadmium[justEcig]
> x<-ecigd[justEcig]
> plox(x,w)
```

So w_k is the cadmium level and x_k is days using E-cigarettes, k=1,2,…,34.

Model 3: The (x_k,w_k) are 34 independent and independent and identically distributed observations.

Hypothesis I: In model 3, x and w are independent.

Model 4: $w_k = \alpha + \beta x_k + \xi_k$ where the ξ_k are independent from the same distribution, independent of x_k.

Hypothesis S: H0: $\beta = .5$

This is an exam. Do not discuss the exam with anyone. If you discuss the exam, you have cheated on an exam. The single dumbest thing a PhD student at Penn can do is cheat on an exam.

Name (**Last**, First):_____ ID# _____

PROBLEM SET #1 STATISTICS 501 Spring 2019: ANSWER PAGE 1

This is an exam. Do not discuss it. Due 2 April, noon.

Part 1. Compare cadmium levels in the four groups defined by grp.	Fill in or **circle** the correct answer.
1.1 Give the interquartile ranges for cadmium y_{ij} and log(cadmium) or $\log(y_{ij})$ by grp. For the four groups, in each column, give the ratio of the largest of the 4 interquartile ranges to the smallest, separately for y_{ij} and $\log(y_{ij})$.	

	y_{ij}	$\log(y_{ij})$
None		
Cigarettes		
E-Cigarettes		
Both		
Ratio max/min		

1.2 The calculation in 1.1 is relevant to Wilcoxon's rank sum confidence interval for shift in the distributions between two groups.	CIRCLE ONE TRUE FALSE
1.3 Test H_0:$\tau_1=\tau_2=\tau_3=\tau_4$ in Model 2 using the Kruskal-Wallis test. Give the value of the test statistic, its degrees of freedom, its P-value and state whether H_0 is plausible under Model 2.	Value:_____ DF:_____ P-value_____ H_0 is: (CIRCLE ONE) PLAUSIBLE NOT PLAUSIBLE
1.4 To test H_0:$\tau_1=\tau_2=\tau_3=\tau_4$ against an ordered alternative, you should examine the boxplots of $\log(y_{ij})$ to determine the correct order.	CIRCLE ONE TRUE FALSE
1.5 In Model 2, use Wilcoxon's two-sample rank test to compare the four groups in all 6 possible pairs, correcting for multiple testing using **Holm's method**. Give the adjusted, 2-sided P-value.	

grp	grp	P-value
None	Cigarettes	
None	E-Cigarettes	
None	Both	
Cigarettes	E-Cigarettes	
Cigarettes	Both	
E-Cigarettes	Both	

1.6 Because you did six 2-sided tests in question 1.5, the probability that you falsely rejected at least one true null hypothesis is at most:	If you reject when the P-value in 1.5 is ≤ 0.05, the chance of $\geq$false rejection is at most: (circle one) 0.05 6×0.05 2×6×0.05
1.7 Unlike Holm, Shaffer's method would not control the familywise error rate in Model 2.	CIRCLE ONE TRUE FALSE

Name (**Last**, First):_____ ID# _____

PROBLEM SET #1 STATISTICS 501 Spring 2019: ANSWER PAGE 2

This is an exam. Do not discuss it. Due 2 April, noon..

Part 2. Compare cadmium levels among nonsmokers and people who only smoke E-cigarettes using **nocig** on the data page.	Fill in or **circle** the correct answer.
2.1 Use Wilcoxon' two-sample rank sum in Model 2 to produce a 95% confidence interval (CI) a Hodges-Lehmann (HL) point estimate for $\tau_3 - \tau_1$.	(E-cigarettes only – None) 95% CI: [_____, _____] HL point estimate: _____
2.2 Use the result in 2.1 to given a confidence interval and point estimate for the multiplicative effect, $\exp(\tau_3)/\exp(\tau_1)$.	95% CI: [_____, _____] HL point estimate: _____
2.3 What is the value of the Mann-Whitney U-statistic as reported by R for comparison in 2.1? Use it to give an estimate of Prob(Y>X), for the cadmium levels of E-cigarettes only, Y, versus None, X. (R gives half credit for ties – do that in your estimate of Prob(Y>X).)	Mann-Whitney U: _____ Estimate of Prob(Y>X):_____

Part 3. **For just the 34 individuals who use just E-cigarettes**, justEcig==TRUE), examine the relationship between days of use of ecigarettes and cadmium levels (ecigd[justEcig] and cadmium[justEcig]).	Fill in or **circle** the correct answer.
3.1 Use Kendall's correction in Model 3 to test Hypothesis I. Give Kendall's correlation and the two-sided P-value. Is it plausible that days of use is independent of cadmium levels?	Kendall's correlation:_____ P-value:_____ Hypothesis I is: circle one PLAUSIBLE NOT PLAUSIBLE
3.2 Convert Kendall's correlation to an estimate of the probability of concordance. What would the probability of concordance be if the two variables were independent?	Estimate of the Probability of concordance: _____ Value when Independent: _____
3.3 Give the 95% confidence interval for Kendall's correlation using the large sample method (i.e., not the bootstrap method).	95% CI: [_____, _____]
3.4 If model 4 were true, then model 3 would be true, but converse need not hold.	CIRCLE ONE TRUE FALSE
3.5 Use Kendall's correlation to test Hypothesis S in model 4.	2-sided P-value:_____

ANSWERS PROBLEM SET #1 STATISTICS 501 Spring 2019: 1

Part 1. Compare cadmium levels in the four groups defined by grp.	Fill in or **circle** the correct answer.
1.1 Give the interquartile ranges for cadmium y_{ij} and log(cadmium) or $\log(y_{ij})$ by grp. For the four groups, in each column, give the ratio of the largest of the 4 interquartile ranges to the smallest, separately for y_{ij} and $\log(y_{ij})$. You can estimate the magnitude of a shift only if two distributions are related by a shift. If the two distributions have unequal dispersions, then they are not related by a shift. Looking at the boxplots and IQRs is a check for shift.	

	y_{ij}	$\log(y_{ij})$
None	0.22	.865
Cigarettes	0.80	.943
E-Cigarettes	0.47	1.171
Both	1.12	1.290
Ratio max/min	1.12/.22 =5.1	1.29/.865 =1.49

1.2 The calculation in 1.1 is relevant to Wilcoxon's rank sum **confidence interval for shift** in the distributions between two groups.	CIRCLE ONE (TRUE) FALSE A shift is more plausible for $\log(y_{ij})$, so you build a confidence interval on the log scale.
1.3 Test $H_0: \tau_1=\tau_2=\tau_3=\tau_4$ in Model 2 using the Kruskal-Wallis test. Give the value of the test statistic, its degrees of freedom, its P-value and state whether H_0 is plausible under Model 2.	Value: 688.34 DF: 3 P-value $<2.2\times10^{-16}$ H_0 is: (CIRCLE ONE) PLAUSIBLE (NOT PLAUSIBLE)
1.4 To test $H_0: \tau_1=\tau_2=\tau_3=\tau_4$ against an ordered alternative, you should examine the boxplots of $\log(y_{ij})$ to determine the correct order.	CIRCLE ONE TRUE (FALSE) No, no, no, no, no. The test for an ordered alternative presumes there is only one alternative that makes sense.

1.5 In Model 2, use Wilcoxon's two-sample rank test to compare the four groups in all 6 possible pairs, correcting for multiple testing using **Holm's method.** Give the adjusted, 2-sided P-value.			
	grp	grp	P-value
	None	Cigarettes	$<2.2\times10^{-16}$
	None	E-Cigarettes	9.3×10^{-5}
	None	Both	1.4×10^{-12}
	Cigarettes	E-Cigarettes	2.7×10^{-5}
	Cigarettes	Both	0.72
	E-Cigarettes	Both	0.011

1.6 Because you did six 2-sided tests in question 1.5, the probability that you falsely rejected at least one true null hypothesis is at most:	If you reject when the P-value in 1.5 is ≤0.05, the chance of ≥false rejection is at most: (circle one) Holm strongly controls the familywise error rate! (0.05) 6×0.05 2×6×0.05
1.7 Unlike Holm, Shaffer's method would not control the familywise error rate in Model 2.	CIRCLE ONE They both control the familywise error rate. TRUE (FALSE)

ANSWERS: PROBLEM SET #1 STATISTICS 501 Spring 2019: 2

Part 2. Compare cadmium levels among nonsmokers and people who only smoke E-cigarettes using **nocig** on the data page.	Fill in or **circle** the correct answer.
2.1 Use Wilcoxon' two-sample rank sum in Model 2 to produce a 95% confidence interval (CI) a Hodges-Lehmann (HL) point estimate for $\tau_3 - \tau_1$.	(E-cigarettes only – None) 95% CI: [0.312, .829] HL point estimate: 0.571
2.2 Use the result in 2.1 to given a confidence interval and point estimate for the multiplicative effect, $\exp(\tau_3)/\exp(\tau_1)$.	95% CI: [1.37, 2.29] HL point estimate: 1.77
2.3 What is the value of the Mann-Whitney U-statistic as reported by R for comparison in 2.1? Use it to give an estimate of Prob(Y>X), for the cadmium levels of E-cigarettes only, Y, versus None, X. (R gives half credit for ties – do that in your estimate of Prob(Y>X).)	Mann-Whitney U: 46842 Estimate of Prob(Y>X): 46842/(34*1946)=0.7079681 When you compare an e-cigarette smoker to a nonsmoker, we estimate that 71% of the time, the e-smoker will have more cadmium in his blood. Does it matter whether you take logs here?

Part 3. For just the 34 individuals who use just E-cigarettes, examine the relationship between days of use of ecigarettes and cadmium levels.	Fill in or **circle** the correct answer.
3.1 Use Kendall's correction in Model 3 to test Hypothesis I. Give Kendall's correlation and the two-sided P-value. Is it plausible that days of use is independent of cadmium levels?	Kendall's correlation: 0.446 P-value: 0.001055 Hypothesis I is: circle one PLAUSIBLE NOT PLAUSIBLE
3.2 Convert Kendall's correlation to an estimate of the probability of concordance. What would the probability of concordance be if the two variables were independent?	Estimate of the Probability of concordance: 0.723 Value when Independent: 0.5 = 1/2
3.3 Give the 95% confidence interval for Kendall's correlation using the large sample method (i.e., not the bootstrap method).	95% CI: [0.249, 0.643] You could transform this interval to an interval for the probability of concordance in 3.2.
3.4 If model 4 were true, then model 3 would be true, but converse need not hold.	TRUE FALSE Model 4 says the relationship is linear, but model 3 does not require this. Suppose model 4 is true for w_k; then model 4 would not be true if w_k were replaced by $\log(w_k)$ – it would not be linear for $\log(w_k)$ -- but model 3 would still be true.
3.5 Use Kendall's correlation to test Hypothesis S in model 4.	2-sided P-value: 2.067×10^{-7}

Spring 2019 Problem Set 1
DOING THE PROBLEM SET IN R

```
attach(Ecig501)
# Part 1
boxplot(cadmium~grp)
boxplot(log(cadmium)~grp)
#1.1
tapply(cadmium,grp,IQR)
tapply(log(cadmium),grp,IQR)
#1.3.
lcad<-log(cadmium)
kruskal.test(lcad~grp)
#1.5.
pairwise.wilcox.test(lcad,grp) # Defaults to Holm's method.

#2.1
nocig<-factor(as.integer(grp),levels=c(3,1),labels=c("E-
only","None"))
boxplot(cadmium~nocig)
boxplot(lcad~nocig)
wilcox.test(lcad~nocig,conf.int=TRUE)

#2.2
exp(c(0.3123426, 0.8293356))
exp(0.5705218)

#2.3
wilcox.test(log(cadmium)~nocig)
46842/(34*1946)

#3.1
justEcig<-grp=="E-Cigarettes"
plot(ecigd[justEcig],log(cadmium[justEcig]))
lines(lowess(ecigd[justEcig],log(cadmium[justEcig]),delta=.
2),col="blue")
cor.test(cadmium[justEcig],ecigd[justEcig],method="kendall"
)
#3.2
(1+0.4460715)/2
#3.3
kendall.ci(cadmium[justEcig],ecigd[justEcig])
#3.5
cor.test(cadmium[justEcig]-
.5*ecigd[justEcig],ecigd[justEcig],method="kendall")

detach(Ecig501)
```

PROBLEM SET #2 STATISTICS 501 SPRING 2019: DATA PAGE 1

Due at noon on Wednesday 8 May 2019, 11:00am, my office 473 JMHH.

This is an exam. Do not discuss it with anyone.

The data are from a study of the association between diabetes mellitus and exposure to arsenic in drinking water in Bangladesh. The data collapse a table from Rahman, et al. (1998) "Diabetes mellitus associated with arsenic exposure in Bangladesh," *American Journal of Epidemiology* 148, 198-203. The paper is available from the library web-page, but there is no need to consult the paper unless you want to. The study compare 163 individuals exposed to arsenic to 854 unexposed individuals. The data are in an object **Rahman1998** on the course workspace. You must download it again. The data are below.

```
> Rahman1998
, , B = <=22, A = 30-44
          E
C          Arsenic No Arsenic
  Diabetes       2          2
  Healthy      105         60

, , B = >22, A = 30-44
          E
C          Arsenic No Arsenic
  Diabetes      10          1
  Healthy      217         14

, , B = <=22, A = 45-59
          E
C          Arsenic No Arsenic
  Diabetes       2         11
  Healthy      110         33
, , B = >22, A = 45-59
          E
C          Arsenic No Arsenic
  Diabetes       9          2
  Healthy      223         10
, , B = <=22, A = 60+
          E
C          Arsenic No Arsenic
  Diabetes       0          2
  Healthy       72         18
, , B = >22, A = 60+
          E
C          Arsenic No Arsenic
  Diabetes       2          3
  Healthy      102          7
> sum(Rahman1998)
[1] 1017
```

PROBLEM SET #2 STATISTICS 501 SPRING 2019: DATA PAGE 2

Due at noon on Wednesday 8 May 2019, 11:00am, my office 473 JMHH.

This is an exam. Do not discuss it with anyone.

There are four variables.

D = diabetes or healthy.

E = exposure status, either exposed to arsenic in drinking water or not exposed

B = BMI or body-mass index.

A = Age.

So we have a 4-way table, D x E x B x A = 2 x 2 x 2 x 3.

Important:

- **Refer to the four variables by letter**, D, E, B, A, as above. For instance, [DE] refers to the marginal table for diabetes x exposure.
- **Refer to models using the standard notation**. For instance [D][E][BA] has a constant term, main effects of all four variables, plus the BA interaction.
- **Set eps=0.001** in your calls to loglin, so that there will be negligible computational error.

Please report estimated **odds ratios** rounded to **two significant digits after the decimal**, 0.25 not 0.2540981234, and 2.06 not 2.05681. Give **fitted probabilities** rounded to 3 digits, 0.001, say, or 0.245.

- Test goodness-of-fit and compare models using G^2, that is, the **likelihood ratio chi-square**, not Pearson's chi-square.
- Set **eps**=0.001.

Follow instructions. **Write your name and id#, last name first,** on **both** sides of the answer page. If a question has several parts, **answer every part**. Turn in **only the answer page**. **Brief answers suffice**. If a question asks you to circle an answer, then you are correct if you **circle the correct answer**. If you cross out an answer, no matter which answer you cross out, the answer is wrong. **You may turn in the exam early**, by leaving it in my mail box in the statistics department in an sealed envelope addressed to me. **Make and keep a photocopy of your answer page.** After the exam, you can compare your photocopy to the posted answer key in the updated bulkpack. This is an exam. **Do not discuss this exam with anyone.** If you discuss the exam, you have cheated on an exam. The single dumbest thing a PhD student at Penn can do is cheat on an exam.

HAVE A GREAT SUMMER!

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone. Due noon May 8.

1.1 Give the marginal table for the single variable D.	Diabetes | Healthy |
1.2 Does any one of the four 3-way marginal tables have a zero count?	CIRCLE ONE YES NO
1.3 The one zero count in Rahman1998 is a fixed zero (aka structural zero).	CIRCLE ONE TRUE FALSE
1.4 Compute the 95% confidence interval for the odds ratio in the 2-way DxE marginal table.	[,]
1.5 In **standard model notation**, state which model is the model of conditional independence of D=diabetes and E=arsenic exposure given the other two variables.	(See data page re standard notation)
1.6 Test the goodness of the model in 1.5. Give the value of G^2, its degrees of freedom (df), the P-value, and state whether this model could plausibly have generated the data.	G^2=_____ df=_____ P-value=_____ **CIRCLE ONE** PLAUSIBLE NOT PLAUSIBLE
1.7 Test the goodness of the model [DBA][EBA][DEA]. Give the value of G^2, its degrees of freedom (df), the P-value, and state whether this model could plausibly have generated the data.	G^2=_____ df=_____ P-value=_____ **CIRCLE ONE** PLAUSIBLE NOT PLAUSIBLE
1.8 The model in 1.7 includes the u_{DEA} three-factor term. In the model in 1.7, test the null hypothesis H_0 that this term is not needed, H_0:0=u_{DEA}. Is H_0 plausible?	G^2=_____ df=_____ P-value=_____ **CIRCLE ONE** H_0 is PLAUSIBLE NOT PLAUSIBLE
1.9 Were [DBA][EBA][DEA] the true model, it would imply that D=diabetes is independent of B=BMI.	CIRCLE ONE TRUE FALSE
1.10 Were [DBA][EBA][DEA] the true model, it would imply that the odds ratio linking D=diabetes and E=arsenic exposure varies with B=BMI but not with A=age.	CIRCLE ONE TRUE FALSE

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2019: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone. Due noon May 8.

2. Fit model [DBA][EBA][DEA] with eps=0.001 and use it for part 2.

Fill in or **circle** the answer

2.1 From the fitted counts for [DBA][EBA][DEA] compute 6 odds ratios linking D=diabetes and E=arsenic exposure for each of the 6 combinations of age and BMI. Put these six fitted odds ratios in the table.

	BMI<=22	BMI>22
Age 30-44		
Age 45-59		
Age 60+		

2.2 From the fitted counts for [DBA][EBA][DEA] compute 12 estimated probabilities of D=Diabetes rather than D=Healthy. Enter the probability of D=Diabetes in the table, where the probability of being Healthy is one minus the probability you entered. Report fitted probabilities rounded to 3 digits, 0.001 or 0.254, say.

Age	BMI	Arsenic	No arsenic
30-44	<=22		
30-44	>22		
45-59	<=22		
45-59	>22		
60+	<=22		
60+	>22		

2.3 The model [DBA][EBA][DEA] preserves the 3-way marginal table that collapses over B=BMI

CIRCLE ONE

TRUE FALSE

2.4 If you use the fitted counts from [DBA][EBA][DEA] to estimate the odds ratio linking D and E for Age=30-44 and BMI<=22, you obtain the same fitted odds ratio as you would if you collapsed the same fitted table over BMI to DxExA and calculated the odds ratio odds ratio linking D and E for Age=30-44

CIRCLE ONE

TRUE FALSE

2.5 The fit of the model [DBA][EBA][DEA] finds a stronger association between D=diabetes and E=arsenic exposure at older ages.

CIRCLE ONE

TRUE FALSE

2.6 Quasi-independence implies independence: if two variables in a 2-way table with structural zeros exhibit quasi-independent, then those two variables are independent.

CIRCLE ONE

TRUE FALSE

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone. Due noon May 8.

1.1 Give the marginal table for the single variable D.	Diabetes: 46 | Healthy: 971
1.2 Does any one of the four 3-way marginal tables have a zero count?	CIRCLE ONE YES (NO)
1.3 The one zero count in Rahman1998 is a fixed zero (aka structural zero).	CIRCLE ONE TRUE (FALSE)
1.4 Compute the 95% confidence interval for the odds ratio in the 2-way DxE marginal table.	[2.53 , 9.38]
1.5 In **standard model notation**, state which model is the model of conditional independence of D=diabetes and E=arsenic exposure given the other two variables.	(See data page re standard notation) [DBA] [EBA]
1.6 Test the goodness of the model in 1.5. Give the value of G^2, its degrees of freedom (df), the P-value, and state whether this model could plausibly have generated the data.	G^2=38.449 df=6 P-value=9.18×10^{-7} **CIRCLE ONE** PLAUSIBLE (NOT PLAUSIBLE)
1.7 Test the goodness of the model [DBA][EBA][DEA]. Give the value of G^2, its degrees of freedom (df), the P-value, and state whether this model could plausibly have generated the data.	G^2=2.010 df=3 P-value=0.57 **CIRCLE ONE** (PLAUSIBLE) NOT PLAUSIBLE
1.8 The model in 1.7 includes the u_{DEA} three-factor term. In the model in 1.7, test the null hypothesis H_0 that this term is not needed, H_0:0=u_{DEA}. Is H_0 plausible?	G^2=7.49 df=2 P-value=0.0236 **CIRCLE ONE** H_0 is PLAUSIBLE (NOT PLAUSIBLE)
1.9 Were [DBA][EBA][DEA] the true model, it would imply that D=diabetes is independent of B=BMI.	CIRCLE ONE TRUE (FALSE)
1.10 Were [DBA][EBA][DEA] the true model, it would imply that the odds ratio linking D=diabetes and E=arsenic exposure varies with B=BMI but not with A=age.	CIRCLE ONE TRUE (FALSE)

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2019: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone. Due noon May 8.

2. Fit model [DBA][EBA][DEA] with eps=0.001 and use it for part 2.

Fill in or **circle** the answer

2.1 From the fitted counts for [DBA][EBA][DEA] compute 6 odds ratios linking D=diabetes and E=arsenic exposure for each of the 6 combinations of age and BMI. Put these six fitted odds ratios in the table.

	BMI<=22	BMI>22
Age 30-44	1.65	1.65
Age 30-44	10.05	10.05
Age 60+	28.02	28.02

2.2 From the fitted counts for [DBA][EBA][DEA] compute 12 estimated probabilities of D=Diabetes rather than D=Healthy. Enter the probability of D=Diabetes in the table, where the probability of being Healthy is one minus the probability you entered. Report fitted probabilities rounded to 3 digits, 0.001 or 0.254, say.

Age	BMI	Arsenic	No arsenic
30-44	<=22	.031	0.019
30-44	>22	.070	.044
45-59	<=22	.224	.028
45-59	>22	.261	.034
60+	<=22	.088	0.003
60+	>22	.325	0.017

2.3 The model [DBA][EBA][DEA] preserves the 3-way marginal table that collapses over B=BMI

CIRCLE ONE

(TRUE) FALSE

2.4 If you use the fitted counts from [DBA][EBA][DEA] to estimate the odds ratio linking D and E for Age=30-44 and BMI<=22, you obtain the same fitted odds ratio as you would if you collapsed the same fitted table over BMI to DxExA and calculated the odds ratio odds ratio linking D and E for Age=30-44

CIRCLE ONE

TRUE (FALSE)

2.5 The fit of the model [DBA][EBA][DEA] finds a stronger association between D=diabetes and E=arsenic exposure at older ages.

CIRCLE ONE

(TRUE) FALSE

2.6 Quasi-independence implies independence: if two variables in a 2-way table with structural zeros exhibit quasi-independent, then those two variables are independent.

CIRCLE ONE

TRUE (FALSE)

Spring 2019 Final
Doing the Problem Set in R

```
R<-Rahman1998

or<-function(tb){
  tb[1,1]*tb[2,2]/(tb[1,2]*tb[2,1])
}

#1.1
margin.table(R,1)
#1.2
margin.table(R,c(1,2,3))
margin.table(R,c(1,2,4))
margin.table(R,c(1,3,4))
margin.table(R,c(2,3,4))
#1.4
fisher.test(margin.table(R,c(1,2)))
#1.6
loglin(R,list(c(1,3,4),c(2,3,4)),eps=0.001)
1-pchisq(38.449,6)
#1.7
loglin(R,list(c(1,3,4),c(2,3,4),c(1,2,4)),eps=0.001)
1-pchisq(2.010018,3)
#1.8 Compare two models
loglin(R,list(c(1,3,4),c(2,3,4),c(1,2)),eps=0.001)
c(9.502532-2.010018,5-3)
1-pchisq(9.502532-2.010018,5-3)

#2.1
or(ft[,,1,1])
or(ft[,,2,1])
or(ft[,,1,2])
or(ft[,,2,2])
or(ft[,,1,3])
or(ft[,,2,3])
#2.2
round(prop.table(ft,c(2,3,4))[1,,,],3)
#2.4
or(ft[,,1,1])
or(margin.table(ft,c(1,2,4))[,,1])
```

PROBLEM SET #1 STATISTICS 501 SPRING 2018: DATA PAGE 1

Due at noon on Thursday 29 March 2018, noon, in class.

This is an exam. Do not discuss it with anyone.

The data are from a paper by Sarto et al. (1984) concerning the possibility that occupational exposures to ethylene oxide cause genetic damage. The paper is available from the library web-page, but there is no reason to look at the paper unless you want to. The paper begins: "Ethylene oxide (**EO**) is widely used for sterilization in hospitals: according to NIOSH (1981), about 75 000 sanitary workers were potentially exposed to EO in 1977 in the U.S.A." It continues: "We examined 41 sanitary workers employed in the sterilizing unit of 8 hospitals in the Venice Region. In 6 hospitals, old (lst generation) gas sterilizers were employed, whereas 2 hospitals used more modern (2nd generation) sterilizers. Environmental analyses demonstrated that, in the hospitals where 1st generation sterilizers" were used the ethylene oxide levels were about ten times higher than those with second generation sterilizers. "The control group consisted of 41 healthy volunteers, sanitary workers, not exposed professionally to EO … [where] controls were chosen by pairing each exposed subject with a suitable control of the same sex, age (within 5 years) and smoking habits (within 5 cigarettes per day). Subjects smoking 5 or more cigarettes per day were considered to be smokers." The article contains additional detail.

In the course workspace, the data are sarto501. You will need to download the workspace again. The data are also available for a limited time as a csv-file in the link to data.csv on my home page.

```
> dim(sarto501)
[1] 82  9
> head(sarto501)
  Subject Age Cigarettes Exposure  SCE worker pair   type smoke5
1      C1  40        3.5        0 10.7      0    1 higher      0
2      E1  42        2.5        7 10.9      1    1 higher      0
3      C2  28       20.0        0 13.3      0    2 higher      1
4      E2  28       20.0        5 13.9      1    2 higher      1
```

In "Subject", C indicates a control, E an exposed worker. The same information is in "worker" and "pair". The outcome is SCE, for sister chromatid exchange, an assay used to measure genetic damage, with higher values suggesting greater damage. Age is age in years. Cigarettes are cigarettes per day, and smoke5 is 1 for someone who smoked 5 or more cigarettes per day. "Exposure" is years of exposure to EO, and is zero for controls. "type" refers to the type of sterilizer, 1^{st} or 2^{nd} generation, with "higher" signifying the higher exposures of 1^{st} generation sterilizers.

You should plot the data in various ways to become familiar with it. Do not turn in the plots. For instance, **do the following plots** of the matched pair differences in SCE:

```
> dif<-SCE[worker==1]-SCE[worker==0]
> boxplot(dif)
> abline(h=0)
> boxplot(dif~type[worker==1])
```

PROBLEM SET #1 STATISTICS 501 SPRING 2018: DATA PAGE 2

Due at noon on Thursday 29 March 2018, noon, in class.

This is an exam. Do not discuss it with anyone.

You will need to **construct** and understand an ordered factor, **grp**. It is an ordered factor that anticipates low SCE for workers with short exposure, or with type=lower, or both. Note that the possible category with long exposure at type=lower is empty.

```
grp<-(Exposure[worker==1]>7)+(type[worker==1]=="higher")
grp<-factor(grp,levels=0:2,labels=c("lower,<=7 years",
       "higher, <=7 years","higher, >7 years"),ordered=TRUE)
table(grp)
table(Exposure[worker==1]>7,grp)
table(type[worker==1],grp)
boxplot(dif~grp)
boxplot(SCE[worker==1]~grp)
boxplot(SCE[worker==0]~grp)
```

Notice that SCE[worker==1] picks out the SCE values for the 41 workers, while SCE[worker==0] picks out the controls. Be careful: some questions ask you to analyze pair differences, other questions ask about SCE for workers or for controls.

References

Sarto, F., Cominato, I., Pinton, A. M., Brovedani, P. G., Faccioli, C. M., Bianchi, V., & Levis, A. G. (1984). Cytogenetic damage in workers exposed to ethylene oxide. Mutation Research/Genetic Toxicology, 138(2-3), 185-195.

Important: One question asks you to use the **Jonckheere-Terpstra** statistic in section 6.2 of Hollander, Wolfe and Chicken (HWC). You can use the **pJCK** function from NSM3 with **method="Asymptotic"** for this question. The function is both in the course workspace and in the NSM3 package, so you do not need the NSM3 package. Package documentation without the package is at: https://cran.r-project.org/web/packages/NSM3/NSM3.pdf

Extra Credit: There is an optional extra credit problem that covers material in the textbook that we did not cover in class and that uses the NSM3 package. You can get a 100% grade on the exam while not answering this question. If you cannot access the NSM3 package, skip this question.

Follow instructions. **Write your name and id#**, last name first, on both sides of the answer page. If a question has several parts, **answer every part**. Turn in **only the answer page**. **Do not turn in additional pages**. Do not turn in graphs. **Brief answers suffice**. If a question asks you to circle an answer, then you are correct if you **circle the correct answer**. If you cross out an answer, no matter which answer you cross out, the answer is wrong. Do not circle TRUE adding a note explaining why it is also FALSE. If a true/false question says A&B&C and if C is false, then A&B&C is false, even if A&B is true. This is an exam. **Do not discuss the exam with anyone**. If you discuss the exam, you have **cheated on an exam**. The single dumbest thing a PhD student at Penn can do is cheat on an exam.

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #1 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone. Due noon 3/29

	Fill in or **circle** the answer
1.1 Use a Wilcoxon test to test the hypothesis H_0 that the work-minus-control pair differences, Z_i, in SCE are symmetrically distributed about zero. Give the **value** of the Wilcoxon statistic, as reported by R, and the **two-sided P-value**. Is H_0 **plausible**?	Value: _____ P-value:_____ Circle one Plausible Not Plausible
1.2 When you estimate the center of symmetry of a continuous random variable, Z, you are assuming that there exists some value, θ, such $Pr(Z>\theta+a) = Pr(Z<\theta-a)$ for every number a.	Circle one TRUE FALSE
1.3 Give the Hodges-Lehmann point **estimate** and 95% two-sided confidence interval (**CI**) for the center of symmetry, θ, of worker-minus-control pair differences in SCE for the test in 1.1.	Estimate:_____ 95% CI: [_____, _____]
1.4 Continuing questions 1.1 and 1.3, use a Wilcoxon test to test H_0: $\theta=1$. Give the **value** of the Wilcoxon statistic, as reported by R, and the **two-sided P-value**. Is H_0 **plausible**?	Value: _____ P-value:_____ Circle one Plausible Not Plausible
1.5 As in your text, define eta = $\eta = Pr(Z_i+Z_j>0)$ as the probability of a positive Walsh average. What is the estimate of η for SCE of the probability of a positive Walsh average from the Wilcoxon test? With 41 pair differences, Z_i, if η = 0.8, then the power of Wilcoxon's test in 1.1 is <80%.	Estimate: _____ Power is <80% (Circle one) TRUE FALSE
Optional extra credit problem. Use the Randles, Fligner, Policello, Wolfe statistic to test the null hypothesis H_0 that the 41 pair differences are symmetric about some θ.	Chapter 3 in HWC. P-value:_____ H_0 is: Plausible Not Plausible

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #1 STATISTICS 501 SPRING 2018: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone. Due noon 3/29

<table>
<tr><td>Create grp discussed on the data page and use it in part 2.</td><td>Fill in or circle the answer</td></tr>
<tr><td>2.1 Use the Jonckheere-Terpstra statistic for ordered alternatives to test the null hypothesis H_0 of no difference in distributions of SCE among workers against the predicted order in grp. Repeat the test for controls. Repeat the test for worker-minus-control pair differences.</td><td><table><tr><td>Comparison of SCE</td><td>P-value</td><td>H_0 is plausible</td></tr><tr><td>Workers</td><td></td><td>TRUE FALSE</td></tr><tr><td>Controls</td><td></td><td>TRUE FALSE</td></tr><tr><td>Difference</td><td></td><td>TRUE FALSE</td></tr></table>See “important” on data page.</td></tr>
<tr><td>2.2 Use the Kruskal-Wallis test to test the same null hypothesis about pair differences as in question 2.1.</td><td>P-value:_____
H_0 is (circle one):
Plausible Not plausible</td></tr>
<tr><td>2.3 The issue with the Jonckheere test in 2.1, when compared to the Kruskal-Wallis test in 2.2 is that a 0.05-level Jonckheere test is more likely to reject the same null hypothesis when it is actually true.</td><td>Circle one:

TRUE FALSE</td></tr>
<tr><td>2.4 Use Holm’s method with the Wilcoxon test to compare the three groups defined by grp in terms of SCE values for workers. Which pairs of groups differ in two-sided tests that control the family-wise error rate at 0.05? Circle YES or NO. Give the P-Adj = p-value adjusted by Holm’s method and P-Una = unadjusted P-value.</td><td><table><tr><td>grp</td><td>grp</td><td>Differ</td><td>P-Adj</td><td>P-Una</td></tr><tr><td>L<=7</td><td>H<=7</td><td>YES NO</td><td></td><td></td></tr><tr><td>L<=7</td><td>H>7</td><td>YES NO</td><td></td><td></td></tr><tr><td>H<=7</td><td>H>=7</td><td>YES NO</td><td></td><td></td></tr></table>H=higher, L=lower
<=7 is <= 7 years exposure
>7 is >7 years exposure</td></tr>
<tr><td>2.5 The problem with unadjusted P-values in 2.4 is that they control the family-wise error rate in the weak sense, but not in the strong sense.</td><td>Circle one:

TRUE FALSE</td></tr>
<tr><td>2.6 For the 41 workers only, what is the Kendall correlation between SCE and duration of Exposure? Use this correlation to test the null hypothesis H_0 that these variables are independent for workers.</td><td>Kendall’s correlation:_____

Two-sided P-value:_____
H_0 is:
Plausible Not Plausible</td></tr>
</table>

ANSWERS

PROBLEM SET #1 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone.

	Fill in or **circle** the answer
1.1 Use a Wilcoxon test to test the hypothesis H_0 that the work-minus-control pair differences, Z_i, in SCE are symmetrically distributed about zero. Give the **value** of the Wilcoxon statistic, as reported by R, and the **two-sided P-value**. Is H_0 **plausible**?	Value: 757.5 P-value: 2.321×10^{-5} Circle one Plausible **Not Plausible**
1.2 When you estimate the center of symmetry of a continuous random variable, Z, you are assuming that there exists some value, θ, such $Pr(Z>\theta+a) = Pr(Z<\theta-a)$ for every number a.	Circle one **TRUE** FALSE
1.3 Give the Hodges-Lehmann point **estimate** and 95% two-sided confidence interval (**CI**) for the center of symmetry, θ, of worker-minus-control pair differences in SCE for the test in 1.1.	Estimate: 1.80 95% CI: [1.10, 2.50]
1.4 Continuing questions 1.1 and 1.3, use a Wilcoxon test to test H_0: $\theta=1$. Give the **value** of the Wilcoxon statistic, as reported by R, and the **two-sided P-value**. Is H_0 **plausible**?	You know from the CI that the P-value is <=0.05. Value: 578 P-value:0.024 Circle one Plausible **Not Plausible**
1.5 As in your text, define eta = $\eta = Pr(Z_i+Z_j>0)$ as the probability of a positive Walsh average. What is the estimate of η for SCE of the probability of a positive Walsh average from the Wilcoxon test? With 41 pair differences, Z_i, if η = 0.8, then the power of Wilcoxon's test in 1.1 is <80%.	Estimate: 0.8798 Power is <80% (Circle one) TRUE **FALSE**
Optional extra credit problem. Use the Randles, Fligner, Policello, Wolfe statistic to test the null hypothesis H_0 that the 41 pair differences are symmetric about some θ.	Chapter 3 in HWC. P-value: 0.99 H_0 is: **Plausible** Not Plausible

ANSWERS

PROBLEM SET #1 STATISTICS 501 SPRING 2018: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone.

<table>
<tr><td>Create grp discussed on the data page and use it in 2.</td><td>Fill in or circle the answer</td></tr>
<tr><td>2.1 Use the Jonckheere-Terpstra statistic for ordered alternatives to test the null hypothesis H_0 of no difference in distributions of SCE among workers against the predicted order in grp. Repeat the test for controls. Repeat the test for worker-minus-control pair differences.</td><td>
<table>
<tr><td>Comparison of SCE</td><td>P-value</td><td>H_0 is plausible</td></tr>
<tr><td>Workers</td><td>0.000103</td><td>TRUE FALSE</td></tr>
<tr><td>Controls</td><td>0.184</td><td>TRUE FALSE</td></tr>
<tr><td>Difference</td><td>0.000858</td><td>TRUE FALSE</td></tr>
</table>
See “important” on data page.
</td></tr>
<tr><td>2.2 Use the Kruskal-Wallis test to test the same null hypothesis about pair differences as in 2.1.</td><td>P-value: 0.011
H_0 is (circle one):
Plausible Not plausible</td></tr>
<tr><td>2.3 The issue with the Jonckheere test in 2.1, when compared to the Kruskal-Wallis test in 2.2 is that a 0.05-level Jonckheere test is more likely to reject the same null hypothesis when it is actually true.</td><td>Circle one:
TRUE FALSE
The two tests both ~~falsely~~ reject 1 true hypothesis in 20 uses. They differ in power against ordered alternatives.</td></tr>
<tr><td>2.4 Use Holm’s method with the Wilcoxon test to compare the three groups defined by grp in terms of SCE values for workers. Which pairs of groups differ in two-sided tests that control the family-wise error rate at 0.05? Circle YES or NO. Give the P-Adj = p-value adjusted by Holm’s method and P-Una = unadjusted P-value.</td><td>
<table>
<tr><td>grp</td><td>grp</td><td>Differ</td><td>P-Adj</td><td>P-Una</td></tr>
<tr><td>L<=7</td><td>H<=7</td><td>YES NO</td><td>.0061</td><td>.002</td></tr>
<tr><td>L<=7</td><td>H>7</td><td>YES NO</td><td>.0288</td><td>.014</td></tr>
<tr><td>H<=7</td><td>H>=7</td><td>YES NO</td><td>.2533</td><td>.253</td></tr>
</table>
Notice that the sample size is much smaller for the third comparison.
</td></tr>
<tr><td>2.5 The problem with unadjusted P-values in 2.4 is that they control the family-wise error rate in the weak sense, but not in the strong sense.</td><td>Circle one:
TRUE FALSE
Unadjusted P-values do not control the familywise error in weak or strong senses.</td></tr>
<tr><td>2.6 For the 41 workers only, what is the Kendall correlation between SCE and Exposure? Use this to test the null hypothesis H_0 that these variables are independent for workers.</td><td>Kendall’s correlation: 0.3147
Two-sided P-value:0.0057
H_0 is:
Plausible Not Plausible</td></tr>
</table>

SPRING 2018
DOING THE PROBLEM SET IN R

```
attach(sarto501)
dif<-SCE[worker==1]-SCE[worker==0]
boxplot(dif)
abline(h=0)

#1.1 and 1.3
wilcox.test(dif,conf.int=TRUE)
#1.4
wilcox.test(dif-1)
#1.5
wilcox.test(dif)
757.5/(41*42/2)
#1.6
#The function srspower is in the course workspace
srspower<-function (eta, alpha = 0.025, beta = 0.05)
{
  zalpha <- qnorm(1 - alpha)
  zbeta <- qnorm(1 - beta)
  n <- ((zalpha + zbeta)^2)/(3 * (eta - 0.5)^2)
  round(n, 1)
}
srspower(.8,beta=.2)

#extra credit
library(NSM3)
RFPW(dif)

grp<-(Exposure[worker==1]>7)+(type[worker==1]=="higher")
grp<-factor(grp,levels=0:2,labels=c("lower,<=7 years",
                                    "higher, <=7 years","higher,
>7 years"),ordered=TRUE)
table(Exposure[worker==1]>7,grp)
table(type[worker==1],grp)
#2.1
pJCK(SCE[worker==1],g=grp,method="Asymptotic")
pJCK(SCE[worker==0],g=grp,method="Asymptotic")
pJCK(dif,g=grp,method="Asymptotic")
#2.2
kruskal.test(dif,grp)
#2.4
pairwise.wilcox.test(SCE[worker==1],grp)
pairwise.wilcox.test(SCE[worker==1],grp,p.adjust.method="none")
#2.6
cor.test(SCE[worker==1],Exposure[worker==1],method="kendall")

detach(sarto501)
```

PROBLEM SET #2 STATISTICS 501 SPRING 2018: DATA PAGE 1

Due at noon on Friday 4 May 2018, my office 473 JMHH.

This is an exam. Do not discuss it with anyone.

The data are from a paper by Rafael Lalive, Jan van Ours, Josef Zweimüller (2006) How Changes in Financial Incentives Affect the Duration of Unemployment, *The Review of Economic Studies*, 73, 1009-1038. There is no need to look at the paper unless you want to. They asked about the relationship between the length of unemployment benefits and the duration of unemployment?

In July 1989, the government of Austria changed its unemployment benefits. The changes were extensive, but we will look at the subgroup of people where the biggest change occurred (ePBD-RR group in Table 3 of Lalive et al. (2006)). In this group, people received an increase in the amount of money they received plus an increase in the duration of unemployment benefits. Before July 1989, in this group, people received <35 weeks of benefits, with a median of 30 weeks, while after August 1989 they received at least 39 weeks of benefits with a median of 39 weeks. For Lalive et al, a key question is whether people tended to stay out of work longer after the duration of benefits was increased.

The data describe 1987-1991, roughly two years on either side of the change in benefits.

There are four binary variables.

D = duration of unemployment in weeks, either >=35 weeks or <35 weeks.

A = after. Did unemployment start after the increase in benefits in July 1989?

L = layoff. Either a temporary layoff or a permanent end of the job.

S = seasonal job. Did the person lose a job in a seasonal industry (construction or tourism) or in some other industry.

Everyone in this group is between age 40 and 55.

So we have a 4-way table, D x A x L x S = 2 x 2 x 2 x 2.

Important:

- **Refer to the four variables by letter**, D, A, L and S. For instance, [LS] refers to the marginal table for layoff x seasonal job.
- **Refer to models using the standard notation**. For instance [D][A][LS] has a constant term, main effects of all four variables, plus the LS interaction.
- **Set eps=0.0001** in your calls to loglin, so that there will be negligible computational error.
- Please report estimated odds ratios and probabilities rounded to **two significant digits after the decimal**, 0.25 not 0.2540981234, and 0.025 not 0.02540981234.
- **For question 1**, you will need to construct a 2x2x2 table for A, L, S, ignoring D. Do this with **mt<-margin.table(lalive.tab,c(2,3,4))**

PROBLEM SET #2 STATISTICS 501 SPRING 2018: DATA PAGE 2

Due at noon on Friday 4 May 2018, my office 473 JMHH.

This is an exam. Do not discuss it with anyone.

The data are in an object, lalive.tab, which is reproduced on the below. So 58 people were out of work for more at least 35 weeks after the change in benefits among people who had a temporary layoff from a seasonal job.

lalive.tab

```
, , L = Temporary, S = Seasonal
            A
D            After Before
  >=35 weeks    58     17
  <35 weeks   1208    756
, , L = Permanent, S = Seasonal
            A
D            After Before
  >=35 weeks   224    160
  <35 weeks   1138   2593
, , L = Temporary, S = Other
            A
D            After Before
  >=35 weeks   172     68
  <35 weeks   1833   1286
, , L = Permanent, S = Other
            A
D            After Before
  >=35 weeks  1421    913
  <35 weeks   3128   6199
```

A preliminary question is the topic of Question 1. Before thinking about the duration of unemployment: Did temporary layoffs and losses of seasonal jobs change from before July 1989 to after. It would be nice for the investigators if they did not change, because then they would have less to worry about when comparing unemployment duration before and after.

Follow instructions. **Write your name and id#**, **last name first**, on **both** sides of the answer page. If a question has several parts, **answer every part**. Turn in **only the answer page**. **Brief answers suffice**. If a question asks you to circle an answer, then you are correct if you **circle the correct answer**. If you cross out an answer, no matter which answer you cross out, the answer is wrong. **You may turn in the exam early**, either by giving it to Noelle at the front desk in the Statistics Dept, 4th floor JMHH, or by leaving it in my mail box in the statistics department in an envelope addressed to me. **Make and keep a photocopy of your answer page**. After the exam, you can compare your photocopy to the posted answer key. This is an exam. **Do not discuss this exam with anyone**. If you discuss the exam, you have cheated on an exam. The single dumbest thing a PhD student at Penn can do is cheat on an exam.

HAVE A GREAT SUMMER!

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone. Due noon May 4.

1. Use the [ALS] marginal table **mt** to answer the questions in part 1. **See the data page**.	**Use the 3-way table for part 1** Fill in or **circle** the answer
1.1 In the 3-way marginal table **mt**, the model [A][LS] says that the four level variable defined by L and S is independent of A.	Circle one TRUE FALSE
1.2 Use the likelihood ratio chi square X^2 to test goodness of fit of the model [A][LS] in the **3-way marginal table mt**. Give the value of **X^2**, its degrees of freedom (**df**), its **P-value**, and state whether [A][LS] fits adequately.	X^2 = _____ df = _____ P-value = _____ Circle one: ADEQUATE FIT NOT ADEQUATE
1.3 Use the same method as in 1.2 to test the fit of the model [AL][AS][LS] in **mt.**	Circle one: ADEQUATE FIT NOT ADEQUATE
1.4 In **mt**, considering just seasonal workers (S=seasonal), what is the odds ratio linking After with Temporary Layoff? Compute this from the data, mt, not a model. What is the parallel odds ratio for nonseasonal workers (S=other)	Give two AxL odds ratios S=seasonal _____ S=other _____

2. Question 2 refers to the 4-way table **lalive.tab**, not to mt.	**Use the 4-way table for part 2** Fill in or **circle** the answer
2.1. The model [DLS][ALS] says that D and A are conditionally independent given the 4-level variable LS.	Circle one TRUE FALSE
2.2 If the model [DLS][ALS] were true, then duration of unemployment D and time period A might be dependent, but D and A would be independent among seasonal workers who were temporarily laid off. **Circle** the correct answers.	D and A might be dependent TRUE FALSE D and A independent for (L=temporary,S=seasonal) TRUE FALSE
2.3 Use likelihood ratio chi square X^2 to test the fit of the model [DLS][ALS] in lalive.tab. Give X^2, df, P-value, and indicate whether this model fits adequately.	X^2=_____df=____P-value=_____ Circle one: ADEQUATE FIT NOT ADEQUATE

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone. Due noon May 4.

<table>
<tr><td>3. Question 2 refers to the 4-way table lalive.tab, not mt.</td><td>Use the 4-way table for part 3
Fill in or circle the answer</td></tr>
<tr><td>3.1 The model [DA][DLS][ALS] has the same odds ratio linking D and A at all four levels of the merged variable LS.</td><td>Circle one

TRUE FALSE</td></tr>
<tr><td>3.2 In model [DAS][DLS][ALS], the four odds ratios linking D and A are the same for L=temporary and L=permanent, but vary with S.</td><td>Circle one

TRUE FALSE</td></tr>
<tr><td>3.3 The model [DAS][DLS][ALS] is nested within the model [DAL][DLS][ALS].</td><td>Circle one
TRUE FALSE</td></tr>
<tr><td>3.4 A likelihood ratio test comparing [DA][DLS][ALS] to model [DAL][DLS][ALS] tests the hypothesis that H_0:$u_{DAL(ijk)}$=0 in the model [DAL][DLS][ALS].</td><td>Circle one

TRUE FALSE</td></tr>
<tr><td>3.5 Do a likelihood ratio test comparing [DA][DLS][ALS] to model [DAL][DLS][ALS]. Give the likelihood ratio chi-square and its degrees of freedom (df), the P-value, and state whether the simpler of the two models is plausible.</td><td>Chi square = _____ df = ____

P-value = _____
Circle one:

PLAUSIBLE NOT PLAUSIBLE</td></tr>
<tr><td>3.6 Use the fitted counts under the model [DAL][DLS][ALS] to estimate the odds ratio linking D and A at the four levels of LS. Give 4 odds ratios.</td><td><table><tr><td></td><td>S=seasonal</td><td>S=other</td></tr><tr><td>L= temporary</td><td></td><td></td></tr><tr><td>L= permanent</td><td></td><td></td></tr></table></td></tr>
<tr><td>3.7 Use the fitted counts under the model [DAL][DLS][ALS] to estimate the probability of an unemployment duration >=35 weeks at the eight levels of ALS. Give 8 probabilities.</td><td><table><tr><td></td><td>S=seasonal</td><td>S=other</td></tr><tr><td>L= Tempor-ary</td><td>After= _____
Before= _____</td><td>After= _____
Before= _____</td></tr><tr><td>L= Perman-ent</td><td>After= _____
Before= _____</td><td>After= _____
Before= _____</td></tr></table></td></tr>
<tr><td>3.8 The analysis suggests that unemployment durations of >=35 weeks were relatively more common in the after period, the strength of this association being weaker for temporary layoffs than permanent jobs.</td><td>Circle one

TRUE FALSE</td></tr>
</table>

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone.

1. Use the [ALS] marginal table **mt** to answer the questions in part 1. **See the data page**.	**Use the 3-way table for part 1** Fill in or **circle** the answer
1.1 In the 3-way marginal table **mt**, the model [A][LS] says that the four level variable defined by L and S is independent of A.	Circle one (TRUE) FALSE
1.2 Use the likelihood ratio chi square X^2 to test goodness of fit of the model [A][LS] in the **3-way marginal table mt**. Give the value of **X^2**, its degrees of freedom (**df**), its **P-value**, and state whether [A][LS] fits adequately.	X^2 = 920.89 df = 3 P-value = <0.00001 Circle one: ADEQUATE FIT (NOT ADEQUATE)
1.3 Use the same method as in 1.2 to test the fit of the model [AL][AS][LS] in **mt.**	Circle one: ADEQUATE FIT (NOT ADEQUATE)
1.4 In **mt**, considering just seasonal workers (S=seasonal), what is the odds ratio linking After with Temporary Layoff? Compute this from the data, mt, not a model. What is the parallel odds ratio for nonseasonal workers (S=other)	Give two AxL odds ratios S=seasonal 3.31 S=other 2.32 Employment benefits were not the only change over time. The types of workers losing jobs changed also, perhaps for unrelated reasons.

2. Question 2 refers to the 4-way table **lalive.tab**, not to mt.	**Use the 4-way table for part 2** Fill in or **circle** the answer
2.1. The model [DLS][ALS] says that D and A are conditionally independent given the 4-level variable LS.	Circle one (TRUE) FALSE
2.2 If the model [DLS][ALS] were true, then duration of unemployment D and time period A might be dependent, but D and A would be independent among seasonal workers who were temporarily laid off. **Circle** correct.	D and A might be dependent (TRUE) FALSE D and A independent for (L=temporary,S=seasonal) worker (TRUE) FALSE
2.3 Use likelihood ratio chi square X^2 to test the fit of the model [DLS][ALS] in lalive.tab. Give X^2, df, P-value, and indicate whether this model fits adequately.	X^2=711.96 df=4 P-value=<0.00001 Circle one: ADEQUATE FIT (NOT ADEQUATE)

Name (**Last**, First): _____,_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2018: ANSWER PAGE 2

3. Question 2 refers to the 4-way table **lalive.tab**, not mt.	**Use the 4-way table for part 3** Fill in or **circle** the answer
3.1 The model [DA][DLS][ALS] has the same odds ratio linking D and A at all four levels of the merged variable LS.	Circle one (TRUE) FALSE
3.2 In model [DAS][DLS][ALS], the four odds ratios linking D and A are the same for L=temporary and L=permanent, but vary with S.	Circle one (TRUE) FALSE
3.3 The model [DAS][DLS][ALS] is nested within the model [DAL][DLS][ALS].	Circle one TRUE (FALSE)
3.4 A likelihood ratio test comparing [DA][DLS][ALS] to model [DAL][DLS][ALS] tests the hypothesis that $H_0: u_{DAL(ijk)}=0$ in the model [DAL][DLS][ALS].	Circle one (TRUE) FALSE
3.5 Do a likelihood ratio test comparing [DA][DLS][ALS] to model [DAL][DLS][ALS]. Give the likelihood ratio chi-square and its degrees of freedom (**df**), the P-value, and state whether the simpler of the two models is plausible.	Chi square = 13.23 **df** = 1 P-value = 0.000275 Circle one: PLAUSIBLE (NOT PLAUSIBLE)
3.6 Use the fitted counts under the model [DAL][DLS][ALS] to estimate the odds ratio linking D and A at the four levels of LS. Give 4 odds ratios.	<table><tr><td></td><td>S=seasonal</td><td>S=other</td></tr><tr><td>L= temporary</td><td>1.85</td><td>1.85</td></tr><tr><td>L= permanent</td><td>3.10</td><td>3.10</td></tr></table>
3.7 Use the fitted counts under the model [DAL][DLS][ALS] to estimate the probability of an unemployment duration >=35 weeks at the eight levels of ALS. Give 8 probabilities.	<table><tr><td></td><td>S=seasonal</td><td>S=other</td></tr><tr><td>L= Tempor-ary</td><td>After= 0.044 Before= 0.024</td><td>After= 0.087 Before= 0.049</td></tr><tr><td>L= Perman-ent</td><td>After= 0.163 Before= 0.059</td><td>After= 0.313 Before= 0.128</td></tr></table>
3.8 The analysis suggests that unemployment durations of >=35 weeks were relatively more common in the after period, the strength of this association being weaker for temporary layoffs than permanent jobs.	Circle one (TRUE) FALSE

```
# Doing the 2018 Statistics 501 Final in R


mt<-margin.table(lalive.tab,c(2,3,4))

# Question 1.2
loglin(mt,list(1,c(2,3)),eps=0.0001)
1-pchisq(920.8895,3)

# Question 1.3
loglin(mt,list(c(1,2),c(1,3),c(2,3)),eps=0.001)
1-pchisq(26.90355,1)

# Question 1.4
or(mt[,,1])
or(mt[,,2])

# Question 2.3
loglin(lalive.tab,list(c(1,3,4),c(2,3,4)),eps=0.0001)
1-pchisq(711.9607,4)

# Question 3.5
reduced<-
loglin(lalive.tab,list(c(1,3,4),c(1,2),c(2,3,4)),eps=0.0001,fit=T
)
full<-
loglin(lalive.tab,list(c(1,3,4),c(1,2,3),c(2,3,4)),eps=0.0001,fit
=T)
reduced$lrt-full$lrt
reduced$df-full$df
1-pchisq(reduced$lrt-full$lrt,1)

# Question 3.6
mhat<-full$fit
or(mhat[,,1,1])
or(mhat[,,1,2])
or(mhat[,,2,1])
or(mhat[,,2,2])

# Question 3.7
prop.table(mhat,margin=c(2,3,4))
#or
prop.table(mhat,margin=c(2,3,4))[1,,,]
```

PROBLEM SET #1 STATISTICS 501 SPRING 2017: DATA PAGE 1

Due at noon in class on Thursday April 13 (2 weeks).

This is an exam. Do not discuss it with anyone.

There is a persistent theory, possibly correct, that long-term use of nonsteroidal anti-inflammatory drugs (NSAIDs) like ibuprofen reduce the risk of Alzheimer disease. See, for instance, McGeer et al. (1996) and in 't Veld (2002).

A problem with asking people about long term use of NSAIDs is that a person with Alzheimer disease may recall the past differently than a person without Alzheimer disease.

Some studies, including several reviewed by McGeer et al. (1996), compared people with arthritis to controls without arthritis, reasoning that the former were likely to be long term users of NSAIDs and the latter were not. Obviously, there would be exceptions in both groups, but such a comparison relies less on recall of the past.

The data are in an object **wordrecall**. You will have to download the course workspace again. It is also in the csv file data.csv on my web page for a short time.

```
> head(wordrecall)
  X Arthritis Control Education
1 1        12       4         1
2 2         7      14         1
3 3        11       4         1
> dim(wordrecall)
[1] 253   4
```

The data you will analyze are from a longitudinal survey of the elderly. In your version of the data, there are 253 matched pairs of two people 75 years old or older, matched for age, sex and education. One person in a pair has osteoarthritis and the other does not. For each person, there is a score on a word recall test. People are read a list of words and asked to remember them. They are asked twice to recall as many words as they can, once right after hearing the list, once after a delay. The score you have is the sum of these two scores, the number of words remembered. The first person with Arthritis remembered 12 words, while the matched control remembered 4 words. A higher score is simply more words remembered. The delayed word recall test is considered a good but inexpensive measure of dementia. It has a limitation that you will consider below.

The third variable is the education level of the control, 1 for "less than high school," 2 for "high school", 3 for "at least some college". Category 3 includes a two-year associate's degree, a BA, or more. Usually, the education of both people in a pair is the same, but you have the education of the control. A common issue in studying dementia using cognitive tests is that better educated people often get better scores on such tests. This happens when they are young and not demented and also when they are old. Again, the pairs are matched for education. Better educated people have taken lots of tests (a thought that

may be on your mind at the moment), and they tend to do better when they take another one. Anyway, you will take a look to see if education predicts the memory test score of the control.

You should think about what you expect to see if long-term NSAID use reduces the risk of Alzheimer disease. You should think about what you expect to see if cognitive test performance is related to education.

You should plot the data in various ways to get acquainted with it. Do not turn in the plots. Think about the plots. One of many interesting plots is:

```
> qqplot(Control,Arthritis)
> abline(0,1)
> abline(1,1,lty=2)
```

References

B. A. in ‘t Veld, L. J. Launer, M. M. B. Breteler, A. Hofman, B. H. Ch. Stricker (2002). Pharmacologic Agents Associated with a Preventive Effect on Alzheimer’s Disease: A Review of the Epidemiologic Evidence. *Epidemiologic Reviews*, 24 (2): 248-268.

McGeer, P. L., Schulzer, M., & McGeer, E. G. (1996). Arthritis and anti-inflammatory agents as possible protective factors for Alzheimer's disease A review of 17 epidemiologic studies. *Neurology*, 47(2), 425-432.

Important: **Question 1.4** is slightly subtle and is related to **question 1.3** about zero differences. Question 1.4 requires you to be careful about zero differences in the sign test. Hopefully, it will help you understand zero differences. You may want to consult the textbook. You can use the signCI function in the course workspace to build the confidence interval for the median in **question 1.5**. A closed interval includes its endpoints, so [5,9] includes 5 and 9 and everything in-between. A half-open interval includes one endpoint and excludes the other, so (5,9] includes 9 but excludes 5, yet it includes everything between 5 and 9. Please use the **npsm package** to do the ordered alternatives test in **question 2.2**. Remember, you must install a package once and load it each time to use it.

Follow instructions. **Write your name and id#**, last name first, on both sides of the answer page. If a question has several parts, **answer every part**. Turn in **only the answer page**. **Do not turn in additional pages**. Do not turn in graphs. **Brief answers suffice**. If a question asks you to circle an answer, then you are correct if you **circle the correct answer**. If you cross out an answer, no matter which answer you cross out, the answer is wrong. Do not circle TRUE adding a note explaining why it is also FALSE. If a true/false question says A&B&C and if C is false, then A&B&C is false, even if A&B is true. This is an exam. **Do not discuss the exam with anyone**. If you discuss the exam, you have cheated on an exam. The single dumbest thing a PhD student at Penn can do is cheat on an exam.

Name (**Last**, First): _____ ID# _____

PROBLEM SET #1 STATISTICS 501 SPRING 2017: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone. Due noon 4/13.

Answer every part of a question	Fill in/**CIRCLE** the answer.
1.1 Use the appropriate Wilcoxon test to test the null hypothesis that there is no difference in word recall for paired people with and without arthritis. Give the **full name** of the test, the numerical **value** of the test statistic, the two-sided P-value and state whether the null hypothesis is plausible.	Name: Value: P-value: The null hypothesis is: Circle one PLAUSIBLE NOT PLAUSIBLE
1.2 Assuming that the pair differences, Arthritis-Control, are symmetric about a number θ, give a **point estimate** and two-sided 95% **confidence interval** (CI) for θ based on the appropriate Wilcoxon test. In what **units** – inches, pounds, dollars, whatever – is the parameter θ measured.	Point estimate: 95% CI: [,] Units:
1.3 There are zero differences among the Arthritis-Control differences whenever both people in a pair remembered the same number of words. How many **zero differences** are there? How many **nonzero differences**? Would R's Wilcoxon output **change** if you removed the zero differences?	Zeros: Nonzeros: Output: Circle one CHANGE DOES NOT CHANGE
1.4 Use the sign test to test 3 hypotheses about the population median, say κ, of the Arthritis-Control differences: $H_0: \kappa=0$, $H_1: \kappa=0.0001$, $H_2: \kappa=-0.0001$. Give the **two-sided P-value** in for each hypothesis. Is "no difference" or $H_0: \kappa=0$ plausible? **See the data page!**	$H_0: \kappa=0$: $H_0: \kappa=0.0001$: $H_0: \kappa=-0.0001$: "No difference" is: Circle one PLAUSIBLE NOT PLAUSIBLE
1.5 Give the two-sided 95% **confidence interval** for κ from question 1.4. In light of 1.4, is the left endpoint of the interval **open or closed**?	**95% CI**: Circle one OPEN CLOSED

Name (**Last**, First): _____ ID# _____

PROBLEM SET #1 STATISTICS 501 SPRING 2017: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone. Due noon 4/13.

Use Control and Education for 2	Fill in/**CIRCLE** the answer.
2.1 Use the Kruskal-Wallis test to compare the words recalled by Controls in the three Education groups for Controls. Give the **value** of statistic, its degrees of freedom (**DF**) and the **P-value**. It is **plausible** that the distribution of words recalled is the same for the three education groups?	Value: DF: P-value: Circle one PLAUSIBLE NOT PLAUSIBLE
2.2 Use the nonparametric test for ordered alternatives in npsm to test the null hypothesis of no difference against the alternative that more education is associated with more words remembered. Give the **value** of statistic, its null expectation, its null variance, and the **P-value**. It is **plausible** that the distribution of words recalled is the same for the three education groups?	Value: Expectation: Variance: P-value: Circle one PLAUSIBLE NOT PLAUSIBLE
2.3 The test in 2.1 is analogous to a one-sided test, but the test in 2.2 is analogous to a two-sided test.	Circle one TRUE FALSE
2.4 The test in 2.2 compared higher to lower education groups, predicting more words recalled for higher education groups, and it was correct in 92.1% of such predictions.	Circle one TRUE FALSE
2.5 Use the Wilcoxon/Holm method to compare the words remembered by the control in the three education groups. If you control the family-wise error rate at 0.05, which pairs of education groups differ significantly?	List all pairs of groups that differ significantly, e.g. (1,2) if groups 1 and 2 differ significantly. If no pairs differ significantly, write none.
2.6 Repeat question 2.5 but control the family-wise error rate at 0.01.	

PROBLEM SET #1 STATISTICS 501 SPRING 2017: ANSWER PAGE 1

This is an exam. Do not discuss it with anyone.

Answer every part of a question	Fill in/**CIRCLE** the answer.
1.1 Use the appropriate Wilcoxon test to test the null hypothesis that there is no difference in word recall for paired people with and without arthritis. Give the **full name** of the test, the numerical **value** of the test statistic, the two-sided P-value and state whether the null hypothesis is plausible.	Name: Wilcoxon's signed rank test Value: 16702 P-value: 0.004314 The null hypothesis is: Circle one PLAUSIBLE NOT PLAUSIBLE
1.2 Assuming that the pair differences, Arthritis-Control, are symmetric about a number θ, give a **point estimate** and two-sided 95% **confidence interval** (CI) for θ based on the appropriate Wilcoxon test. In what **units** – inches, pounds, dollars, whatever – is the parameter θ measured.	Point estimate: 1.0 95% CI: [0.5, 2.0] Units: words
1.3 There are zero differences among the Arthritis-Control differences whenever both people in a pair remembered the same number of words. How many **zero differences** are there? How many **nonzero differences**? Would R's Wilcoxon output **change** if you removed the zero differences?	Zeros: 19 Nonzeros: 234 Output: Circle one CHANGE DOES NOT CHANGE
1.4 Use the sign test to test 3 hypotheses about the population median, say κ, of the Arthritis-Control differences: $H_0: \kappa=0$, $H_1: \kappa=0.0001$, $H_2: \kappa=-0.0001$. Give the **two-sided P-value** in for each hypothesis. Is "no difference" or $H_0: \kappa=0$ plausible? **See the data page!**	$H_0: \kappa=0$: 0.01539 $H_0: \kappa=0.0001$: 0.2577 $H_0: \kappa=-0.0001$: 0.0004091 "No difference" is: Circle one PLAUSIBLE NOT PLAUSIBLE
1.5 Give the two-sided 95% **confidence interval** for κ from question 1.4. In light of 1.4, is the left endpoint of the interval **open or closed**?	**95% CI**: [0.0, 2.0] Circle one OPEN CLOSED

PROBLEM SET #1 STATISTICS 501 SPRING 2017: ANSWER PAGE 2

This is an exam. Do not discuss it with anyone.

Use Control and Education for 2	Fill in/**CIRCLE** the answer.
2.1 Use the Kruskal-Wallis test to compare the words recalled by Controls in the three Education groups for Controls. Give the **value** of statistic, its degrees of freedom (**DF**) and the **P-value**. It is **plausible** that the distribution of words recalled is the same for the three education groups?	Value: 22.419 DF: 2 P-value: 1.355×10^{-5} Circle one PLAUSIBLE (NOT PLAUSIBLE)
2.2 Use the nonparametric test for ordered alternatives in nsmp to test the null hypothesis of no difference against the alternative that more education is associated with more words remembered. Give the **value** of statistic, its null expectation, its null variance, and the **P-value**. It is **plausible** that the distribution of words recalled is the same for the three education groups?	Value: 1.054350×10^{4} Expectation: 7.906000×10^{3} Variance: 3.089690×10^{5} P-value: 1.042599×10^{-6} Circle one PLAUSIBLE (NOT PLAUSIBLE)
2.3 The test in 2.1 is analogous to a one-sided test, but the test in 3.2 is analogous to a two-sided test.	Circle one TRUE (FALSE)
2.4 The test in 2.2 compared higher to lower education groups, predicting more words recalled for higher education groups, and it was correct in 92.1% of such predictions.	Circle one TRUE (FALSE)
2.5 Use the Wilcoxon/Holm method to compare the words remembered by the control in the three education groups. If you control the family-wise error rate at 0.05, which pairs of education groups differ significantly?	List all pairs of groups that differ significantly, e.g. (1,2) if groups 1 and 2 differ significantly. If no pairs differ significantly, write none. (1,2) (1,3)
2.6 Repeat question 2.5 but control the family-wise error rate at 0.01.	(1,3)

Doing the Problem Set in R
Spring 2017

```
attach(wordrecall)
dif<-Arthritis-Control
wilcox.test(dif,conf.int=TRUE) #Questions 1.1 and 1.2
length(dif)
u<-(dif!=0)
sum(u) #Question 1.3
wilcox.test(dif[u],conf.int=TRUE) #Question 1.3
binom.test(sum((dif[u])>0),length(dif[u])) #Question 1.4
binom.test(sum((dif-.00001)>0),length(dif)) #Question 1.4
binom.test(sum((dif-(-.00001))>0),length(dif)) #Question 1.4
signCI(dif) #Question 1.5
kruskal.test(Control,Education) #Question 2.1
library(npsm)
jonckheere(Control,Education) #Question 2.2
(1.054350e+04)/(2*7.906000e+03) #Question 2.4
pairwise.wilcox.test(Control,Education) #Questions 2.5 and 2.6
```

PROBLEM SET #2 STATISTICS 501 SPRING 2017: DATA PAGE 1

Due at noon on Tuesday 9 May 2017.

This is an exam. Do not discuss it with anyone.

The data are from NHANES 2013-2014. You can obtain the original data at https://www.cdc.gov/nchs/nhanes/ , but there is no reason to do this unless you want to. The data are a 2x2x2x2 table recording the answers to the following questions for people who are at least 21 years old. The table is in an object, **dsbmi**, in the course workspace. You will need to download the workspace again.

1=drugs Have you ever used cocaine, crack cocaine, heroin, or methamphetamine? (DUQ240) (Yes or No) (Described as "**hard drugs**" in the quesions.)

2=smoke100 Have you smoked at least 100 cigarettes in your entire life? (SMQ020) (>=100 or <100)

3=bmi Body Mass Index (kg/m**2) (BMXBMI) (>=35 or <35)
https://www.nhlbi.nih.gov/health/educational/lose_wt/BMI/bmicalc.htm

4=gender Gender (RIAGENDR) (Male, Female)

In the questions, **variables are often mentioned by number**, eg, 4 for gender. Term u_{12} links 1=drugs and 2=smoke100.

```
> dsbmi
, , bmi = >=35, gender = Male
     smoke100
drugs >=100 <100
  Yes    30   13
  No     86  134
, , bmi = <35, gender = Male
     smoke100
drugs >=100 <100
  Yes   310   74
  No    584  748
, , bmi = >=35, gender = Female
     smoke100
drugs >=100 <100
  Yes    49   12
  No    162  268
, , bmi = <35, gender = Female
     smoke100
drugs >=100 <100
  Yes   148   61
  No    411  992
```

PROBLEM SET #2 STATISTICS 501 SPRING 2017: DATA PAGE 2

Important: When fitting log-linear models in this problem set: (i) all questions refer to **hierarchical models**, without explicit mention of this fact, (ii) always fit hierarchical models, (iii) do all tests with the **likelihood ratio chi squares**, not Pearson's chi squares, (iv) **set eps=0.001** when using loglin. If you do (iv) then your numbers will be (a) very close to convergence and (b) exactly the same as the numbers on the answer key. At various stages in the problem set, reference is made to "all two-factor terms" or to "all pairs of two variables" or similar things. How many pairs of 2 variables are there for dsbmi which includes 4 variables? There are 6: (1,2), (1,3), (1,4), (2,3), (2,4), (3,4). **Don't lose many points in a silly way by leaving out one of the six!**

Some questions ask you to discuss the estimate of an **odds ratio based on the fitted counts from some model**. For example, the odds ratio linking having tried hard drugs and having smoked 100 cigarettes for women with a bmi<35 is

$$(m_{1122} \times m_{2222})/(m_{1222} \times m_{2122})$$

and you estimate this under a model by substituting the fitted counts for the true expected counts.

Follow instructions. **Write your name and id#**, last name first, on both sides of the answer page. If a question has several parts, **answer every part**. Turn in **only the answer page**. **Do not turn in additional pages**. Do not turn in graphs. **Brief answers suffice**. If a question asks you to circle an answer, then you are correct if you **circle the correct answer**. If you cross out an answer, no matter which answer you cross out, the answer is wrong. Do not circle TRUE adding a note explaining why it is also FALSE. If a true/false question says A&B&C and if C is false, then A&B&C is false, even if A&B is true. **This is an exam**. **Do not discuss the exam with anyone**. If you discuss the exam, you have cheated on an exam. The single dumbest thing a PhD student at Penn can do is cheat on an exam. The exam is due **on the exam date at noon, at my office, 473 JMHH**. You may turn in the exam early by placing it in an envelope addressed to me and leaving it in my mail box in statistics, 4th floor, JMHH. If you prefer, give it to Noel at the front desk in statistics. Do not slip the exam under the door of the Statistics Department when the Department is closed – the exam will get lost or thrown out by a cleaner. **Make and keep a photocopy of your answer page**. The answer key will be posted in the revised bulk pack on-line. **Have a great summer!**

Name (**Last**, First):_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2017: ANSWER PAGE 1

This is an exam. Do not discuss it. Due noon 9 May 2017.

Question	Fill in/CIRCLE the answer
1.1 In this data set, more men than women have smoked >=100 cigarettes.	CIRCLE ONE TRUE FALSE
1.2 Ignoring drugs and bmi, using the marginal table, give the point **estimate** and 95% confidence interval (**CI**) for the odds ratio linking gender and having smoked >=100 cigarettes.	Estimate: 95% CI:
1.3 Ignoring bmi and gender, using the marginal table, having smoked >=100 cigarettes is negatively associated with having tried hard drugs.	CIRCLE ONE TRUE FALSE
1.4 Fit the hierarchical log-linear model that includes **all** 2-factor terms but **no** 3-factor terms. Does this model fit well? Give the likelihood ratio **chi-square** test of fit, its **degrees of freedom** (DF) its **P-value**, and state whether the model fits **acceptably**.	Chi-square: DF: P-value: CIRCLE ONE ACCEPTABLE FIT OTHER
1.5 The results in 1.4 by themselves strongly indicate that all two-factor terms must be in a hierarchical log-linear model if it is to fit the dsbmi data.	CIRCLE ONE TRUE FALSE
1.6 The results in 1.4 strongly indicate that at least one three-factor term must be in a hierarchical log-linear model if it is to fit the dsbmi data.	CIRCLE ONE TRUE FALSE
1.7 A hierarchical log-linear model that omits $u_{12(ij)}$ says 1 and 2 are conditionally independent given the other variables.	CIRCLE ONE TRUE FALSE

Name (**Last**, First):_____ ID# _____

PROBLEM SET #2 STATISTICS 501 SPRING 2017: ANSWER PAGE 1

This is an exam. Do not discuss it. Due noon 9 May 2017.

<table>
<tr><th>Question</th><th>Fill in/CIRCLE the answer</th></tr>
<tr><td>2.1 Add to the model in 1.4 one more u-term namely u_{234}. For this new model, answer the questions from 1.4. The model has 6 two-factor u-terms and one 3-factor term.</td><td>Chi-square: DF:

P-value:
CIRCLE ONE
ACCEPTABLE FIT OTHER</td></tr>
<tr><td>2.2 Remove from the model in 2.1 the u-term u_{13}. So you have all two-factor terms except u_{13}, but you have one 3-factor term u_{234}. For this new model, answer the questions from 1.4.</td><td>Chi-square: DF:

P-value:
CIRCLE ONE
ACCEPTABLE FIT OTHER</td></tr>
<tr><td>2.3 Do a likelihood ratio test comparing the model in 2.1 to the model in 2.2; that is, test the null hypothesis H_0: $u_{13}=0$ in the model in 2.1. Is H_0 rejected at the conventional 0.05 level?</td><td>Chi-square: DF:

P-value:
CIRCLE ONE

REJECTED NOT REJECTED</td></tr>
<tr><td>2.4 Use the fitted counts from the model in 2.1 to estimate the odds ratio linking having tried hard drugs and having smoked 100 cigarettes for males and females with bmi above or below 35. Put the 4 odds ratios in the table.</td><td><table><tr><th></th><th>Male</th><th>Female</th></tr><tr><td>bmi>=35</td><td></td><td></td></tr><tr><td>bmi<35</td><td></td><td></td></tr></table></td></tr>
<tr><td>2.5 Use fitted counts from the model in 2.1 to estimate the odds ratio linking having smoked 100 cigarettes with bmi>=35 for males and females who have or have not tried hard drugs.</td><td><table><tr><th></th><th>Male</th><th>Female</th></tr><tr><td>drugs: yes</td><td></td><td></td></tr><tr><td>drugs: no</td><td></td><td></td></tr></table></td></tr>
<tr><td>2.6 The model in 1.4 says the odds ratio linking any two variables is the same at all levels of the other two variables.</td><td>CIRCLE ONE

TRUE FALSE</td></tr>
</table>

ANSWERS: PROBLEM SET #2 STATISTICS 501 SPRING 2017

This is an exam. Do not discuss it. 7 points each.

Question	Fill in/CIRCLE the answer
1.1 In this data set, more men than women have smoked >=100 cigarettes.	CIRCLE ONE (TRUE) FALSE
1.2 Ignoring drugs and bmi, using the marginal table, give the point **estimate** and 95% confidence interval (**CI**) for the odds ratio linking gender and having smoked >=100 cigarettes.	Estimate: 1.80 95% CI: [1.59, 2.05]
1.3 Ignoring bmi and gender, using the marginal table, having smoked >=100 cigarettes is negatively associated with having tried hard drugs.	CIRCLE ONE TRUE (FALSE)
1.4 Fit the hierarchical log-linear model that includes **all** 2-factor terms but **no** 3-factor terms. Does this model fit well? Give the likelihood ratio **chi-square** test of fit, its **degrees of freedom** (DF) its **P-value**, and state whether the model fits **acceptably**.	Chi-square: 17.04941 DF: 5 P-value: 0.00441 CIRCLE ONE ACCEPTABLE FIT (OTHER)
1.5 The results in 1.4 by themselves strongly indicate that all two-factor terms must be in a hierarchical log-linear model if it is to fit the dsbmi data.	CIRCLE ONE TRUE (FALSE)
1.6 The results in 1.4 strongly indicate that at least one three-factor term must be in a hierarchical log-linear model if it is to fit the dsbmi data.	CIRCLE ONE (TRUE) FALSE
1.7 A hierarchical log-linear model that omits $u_{12(ij)}$ says 1 and 2 are conditionally independent given the other variables.	CIRCLE ONE (TRUE) FALSE

ANSWERS: PROBLEM SET #2 STATISTICS 501 SPRING 2017
7 points each, except as noted.

<table>
<tr><th>Question</th><th>Fill in/CIRCLE the answer</th></tr>
<tr><td>2.1 Add to the model in 1.4 one more u-term namely u_{234}. For this new model, answer the questions from 1.4. The model has 6 two-factor u-terms and one 3-factor term.</td><td>10 points
Chi-square: 2.030219 DF: 4

P-value: 0.730
CIRCLE ONE
ACCEPTABLE FIT OTHER</td></tr>
<tr><td>2.2 Remove from the model in 2.1 the u-term u_{13}. So you have all two-factor terms except u_{13}, but you have one 3-factor term u_{234}. For this new model, answer the questions from 1.4.</td><td>10 points
Chi-square: 6.138655 DF: 5

P-value: 0.293
CIRCLE ONE
ACCEPTABLE FIT OTHER</td></tr>
<tr><td>2.3 Do a likelihood ratio test comparing the model in 2.1 to the model in 2.2; that is, test the null hypothesis H_0: $u_{13}=0$ in the model in 2.1. Is H_0 rejected at the conventional 0.05 level?</td><td>10 points
Chi-square: 4.108436 DF: 1

P-value: 0.0426698
CIRCLE ONE

REJECTED NOT REJECTED</td></tr>
<tr><td>2.4 Use the fitted counts from the model in 2.1 to estimate the odds ratio linking having tried hard drugs and having smoked 100 cigarettes for males and females with bmi above or below 35. Put the 4 odds ratios in the table.</td><td><table><tr><th></th><th>Male</th><th>Female</th></tr><tr><td>bmi>=35</td><td>5.51</td><td>5.51</td></tr><tr><td>bmi<35</td><td>5.51</td><td>5.51</td></tr></table></td></tr>
<tr><td>2.5 Use fitted counts from the model in 2.1 to estimate the odds ratio linking having smoked 100 cigarettes with bmi>=35 for males and females who have or have not tried hard drugs.</td><td><table><tr><th></th><th>Male</th><th>Female</th></tr><tr><td>drugs: yes</td><td>0.769</td><td>1.485</td></tr><tr><td>drugs: no</td><td>0.769</td><td>1.485</td></tr></table></td></tr>
<tr><td>2.6 The model in 1.4 says the odds ratio linking any two variables is the same at all levels of the other two variables.</td><td>CIRCLE ONE

TRUE FALSE</td></tr>
</table>

DOING THE PROBLEM SET IN R

```
margin.table(dsbmi,c(2,4)) #Question 1.1
fisher.test(margin.table(dsbmi,c(2,4))) #Question 1.2
fisher.test(margin.table(dsbmi,c(1,2))) #Question 1.3
loglin(dsbmi,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)),eps=
0.001) #Question 1.4
1-pchisq(17.04941,5) #Question 1.4
loglin(dsbmi,list(c(1,2),c(1,3),c(1,4),c(2,3,4)),eps=0.001)
#Question 2.1
1-pchisq(2.030219,4) #Question 2.1
loglin(dsbmi,list(c(1,2),c(1,4),c(2,3,4)),eps=0.001) #Question
2.2
1-pchisq(6.138655,5) #Question 2.2
1-pchisq(6.138655-2.030219,5-4) #Question 2.3
or<-function(tb){tb[1,1]*tb[2,2]/(tb[1,2]*tb[2,1])} #Speed up
calculating an odds ratio
ft<-
loglin(dsbmi,list(c(1,2),c(1,3),c(1,4),c(2,3,4)),eps=0.001,fit=TR
UE)$fit #Question 2.4
or(ft[,,1,1]) #Question 2.4
or(ft[,,1,2]) #Question 2.4
or(ft[,,1,1]) #Question 2.4
or(ft[,,2,2]) #Question 2.4
or(ft[1,,,1]) #Question 2.5
or(ft[1,,,2]) #Question 2.5
or(ft[2,,,1]) #Question 2.5
or(ft[2,,,2]) #Question 2.5
```

Statistics 501, Spring 2015, Midterm: Data Page #1

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. Cheating on an exam is the dumbest thing a PhD student at Penn can do.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question.

The data are from a paper by Chen Zhijian et al. (2006), Evaluating the genotoxic effects of workers exposed to lead using micronucleus assay, comet assay and TCR gene mutation test, *Toxicology*, 223(3), 219-226. There is no need to consult the paper unless you want to. The data are in an object, **storagebattery**, in the course workspace. You will need to download the workspace again. If it is not there, then you need to clear your browser's memory and download again. The first few lines are below. Alternatively, there is a csv file of the data on my webpage at the link **data.csv**.

```
> head(storagebattery)
  pair wsex csex wage cage wyears wlead clead wmnr cmnr wmtm cmtm
wmftcr cmftcr leadgrp leadgrpi
1    1    M    M   20   20    2.0   560    38    8    1 1.24 0.16
1.89   1.22    high        3
2    2    M    M   22   22    3.0   250    28   14    2 0.82 0.14
1.21   2.19  medium        2
3    3    M    M   23   22    2.0   620    18   38    3 0.73 0.26
1.07   2.12    high        3
4    4    F    F   28   25    3.0   350    20   14    0 0.70 0.61
1.39   1.00  medium        2
5    5    M    M   28   28    2.5   340    47    8    2 0.76 0.39
1.31   0.75  medium        2
6    6    M    M   28   32    3.0   160     2    3    1 0.97 0.21
1.07   1.20     low        1
```

The data describe 50 people in 25 matched pairs. The worker (w) was exposed to lead while involved in the production of storage batteries. The paper concerns the possibility of genotoxic effects of lead exposure. The controls (c) were not known to be exposed to lead. The pairs were matched for gender (wsex or ccex) and age (wage or cage). Workers were exposed for wyears. Blood lead levels are wlead and clead recorded in μg/l. There are three measures of genetic damage based on lymphocytes in a blood sample. The micronucleus rate (wmnr and cmnr) is the number of micronuclei per 1000 binucleated lymphocytes, that is, a measure of the extent to which cell divisions went wrong, producing not two intact nuclei but rather additional micronuclei containing genetic material. The mean tail moment (wmtm and cmtm) of the comet assay is a fairly direct measure of damage to DNA with larger values signifying greater damage. Also, wmftcr and cmftcr are results of the T-cell receptor gene mutation test. The variable leadgrp cuts wlead at its thirds into low, medium, high, and leadgrpi is as.integer(leadgrp).

In answering questions, please remember: (i) the workers and controls are paired to have the same gender and similar age, (ii) if an ordered alternative is considered, it is natural to look for greater genetic damage in workers with more lead in their blood. You should plot the data in various ways. Do not submit the plots. Question 1 asks you to compare workers (wmtm) and controls (cmtm) in terms of the mean tail moment of the comet assay. Question 2 asks you to set aside the controls and to look at the mean tail moment of the comet assay for workers (wmtm) in relation to the lead groups for workers (either leadgrp or leadgrpi). Question 3 asks you to set aside the controls and to look at the micronucleus rate for workers (wmnr) in relation to the lead levels for workers (wlead). So Question 2 refers to lead groups for workers, but question 3 refers to the numeric lead levels for workers. Question 3 asks you to test the null hypothesis of zero correlation against a one-sided alternative of a correlation greater than zero. Most journals would require a two-sided test. Of course, the authors are looking for genetic damage from higher lead levels.

Statistics 501, Midterm, Answer Page #1. This is an exam. Do not discuss it with anyone.

Questions in part 1 refer to the mean tail moments (mtm) of the comet assay.	FILL IN OR **CIRCLE** THE CORRECT ANSWER
1.1 In a Normal-quantile plot, do the worker-minus-control pair differences in mtm look Normal? This Normal quantile plot shows a positive outlier (true or false). If the quantile plot shows any outliers, give the pair number of the one most extreme outlier. If none, write "none".	Look Normal? YES NO Positive outlier? TRUE FALSE Identify one outlier: _____
1.2 Test the null hypothesis that the worker-minus-control pair differences in mtm are Normal. Give the P-value. Is the null hypothesis plausible?	P-value: _____ PLAUSIBLE NOT PLAUSIBLE
1.3 Do an appropriate two-sided Student's t-test to compare mean tail moments (mtm) of the comet assay for workers and matched controls. Give the two-sided P-value, the two-sided 95% confidence interval, and the associated point estimate of the typical difference.	P-value: _____ 95% CI: [,] Estimate:_____
1.4 Do an appropriate two-sided Wilcoxon test to compare mean tail moments (mtm) of the comet assay for workers and matched controls. Give the two-sided P-value, the two-sided 95% confidence interval, and the associated point estimate of the typical difference.	P-value: _____ 95% CI: [,] Estimate:_____
1.5 Divide the length of the 95% confidence interval from the t-test (numerator) by the length of the 95% confidence interval from the Wilcoxon test (denominator).	Ratio of lengths: _____
1.6 The exact t-test confidence interval in problem 1.3 and the Wilcoxon confidence interval in 1.4 both assume the differences in problem 1.2 are symmetrically distributed about their population median, but the t-test assumes more than this.	TRUE FALSE
1.7 Use the Randles-Fligner-Policello-Wolfe test to test that the null hypothesis that the worker-minus-control differences in question 1.2 are symmetrically distributed about the population median. Give the P-value and state whether symmetry is plausible.	P-value: _____ PLAUSIBLE NOT PLAUSIBLE
1.8 If you used the t-test under Normality assumptions to test the null hypothesis H_0 that the differences in problem 1.2 are symmetric about $\mu_0=0.4$ then you would accept H_0 at the two-sided 0.05 level, but if you tested H_0 using the appropriate Wilcoxon test, then you would reject H_0 at the two-sided 0.05 level.	TRUE FALSE

Print LAST name: _____, First:_____ ID#_____

Statistics 501, Spring 2014, Midterm, Answer Page #2.

This is an exam. Do not discuss it with anyone. Read the data page. Due noon March 31, 2015.

Question 2 refers to wmtm and leadgrp or leadgrpi; i.e., set aside the controls; see the data page.	FILL IN OR **CIRCLE** THE CORRECT ANSWER
2.1 Test the null hypothesis that wmtm has the same distribution in the three lead groups using the Kruskal Wallis test. Give the P-value and state whether the null hypothesis is plausible.	P-value: _____ PLAUSIBLE NOT PLAUSIBLE
2.2 Test the null hypothesis that wmtm has the same distribution in the three lead groups against the ordered alternative that the ordering that a higher lead group predicts a higher wmtm. Give the exact and asymptotic P-values. (R computes the exact P-value in this case.)	Exact P-value: _____ Asymptotic P-value: _____
2.3 Use pairwise two-sided Wilcoxon tests to compare wmtm in all three pairs of two groups defined by leadgrp. Which two groups have the smallest unadjusted P-value? What is this smallest unadjusted P-value? What is the corresponding P-value adjusted by the Bonferroni method? What is the corresponding P-value adjusted by the Holm method? What is the corresponding P-value adjusted by the Shaffer method?	Two groups: _____ _____ Unadjusted: _____ Bonferroni: _____ Holm: _____ Shaffer: _____
2.4 If you strongly control the familywise error rate at 0.05 in a multiple testing problem (like 2.3), then in the experiment as a whole, the probability that at least one true alternative hypothesis is not rejected is at most 5%.	TRUE FALSE

3. Question 3 refers to **wmnr** and **wlead** for workers only; see the data page. Not wmtm!	FILL IN OR **CIRCLE** THE CORRECT ANSWER
3.1 Plot y=wmnr against x=wlead. Think about it.	Free points. (Happiness from plotting and thinking)
3.2 Test the null hypothesis of zero correlation against the one-sided alternative of positive correlations using Pearson's (the usual) correlation. Give the correlation and one-sided P-value.	One-sided Correlation: _____ P-value:_____
3.3 Test the null hypothesis of zero correlation against the one-sided alternative of positive correlations using Kendalls's correlation. Give the correlation and one-sided P-value.	One-sided Correlation: _____ P-value:_____
3.4 Fit the model wmnr = $\beta_0 + \beta_1$ wlead + e with symmetric independent errors using M-estimation with the default settings for rlm in the MASS. Give the estimate of the slope, β_1, its estimated standard error and the t-value (aka z value) formed as the ratio of the estimate to its standard error.	Estimate: _____ Estimated standard error: _____ t = z value: _____

Answers: Statistics 501, Spring 2014, Midterm, Answer Page #1.
This is an exam. Do not discuss it with anyone. Read the data page.

Questions in part 1 refer to the mean tail moments (mtm) of the comet assay.	FILL IN OR **CIRCLE** THE CORRECT ANSWER
1.1 In a Normal-quantile plot, do the worker-minus-control pair differences in mtm look Normal? This Normal quantile plot shows a positive outlier (true or false). If the quantile plot shows any outliers, give the pair number of the one most extreme outlier. If none, write "none".	Look Normal? YES (NO) Positive outlier? TRUE (FALSE) Identify one outlier: #11
1.2 Test the null hypothesis that the worker-minus-control pair differences in mtm are Normal. Give the P-value. Is the null hypothesis plausible?	P-value: 4.024×10^{-5} PLAUSIBLE (NOT PLAUSIBLE)
1.3 Do an appropriate two-sided Student's t-test to compare mean tail moments (mtm) of the comet assay for workers and matched controls. Give the two-sided P-value, the two-sided 95% confidence interval, and the associated point estimate of the typical difference.	P-value: 1.007×10^{-5} 95% CI: [0.348, 0.758] Estimate: 0.553
1.4 Do an appropriate two-sided Wilcoxon test to compare mean tail moments (mtm) of the comet assay for workers and matched controls. Give the two-sided P-value, the two-sided 95% confidence interval, and the associated point estimate of the typical difference.	P-value: 0.000227 95% CI: [0.465, 0.740] Estimate: 0.595
1.5 Divide the length of the 95% confidence interval from the t-test (numerator) by the length of the 95% confidence interval from the Wilcoxon test (denominator).	Ratio of lengths: 1.49 t-interval is 50% longer!
1.6 The exact t-test confidence interval in problem 1.3 and the Wilcoxon confidence interval in 1.4 both assume the differences in problem 1.2 are symmetrically distributed about their population median, but the t-test assumes more than this.	(TRUE) FALSE
1.7 Use the Randles-Fligner-Policello-Wolfe test to test that the null hypothesis that the worker-minus-control differences in question 1.2 are symmetrically distributed about the population median. Give the P-value and state whether symmetry is plausible.	P-value: 0.785 (PLAUSIBLE) NOT PLAUSIBLE
1.8 If you used the t-test under Normality assumptions to test the null hypothesis H_0 that the differences in problem 1.2 are symmetric about μ_0=0.4 then you would accept H_0 at the two-sided 0.05 level, but if you tested H_0 using the appropriate Wilcoxon test, then you would reject H_0 at the two-sided 0.05 level.	(TRUE) FALSE You can just look at the 95% confidence intervals, or you can do the tests with μ_0 = .4

Answers

Statistics 501, Spring 2014, Midterm, Answer Page #2.

This is an exam. Do not discuss it with anyone. Read the data page. Due noon March 31, 2015.

Question 2 refers to wmtm and leadgrp or leadgrpi; i.e., set aside the controls; see the data page.	FILL IN OR **CIRCLE** THE CORRECT ANSWER
2.1 Test the null hypothesis that wmtm has the same distribution in the three lead groups using the Kruskal Wallis test. Give the P-value and state whether the null hypothesis is plausible.	P-value: 0.2527 (PLAUSIBLE) NOT PLAUSIBLE
2.2 Test the null hypothesis that wmtm has the same distribution in the three lead groups against the ordered alternative that the ordering that a higher lead group predicts a higher wmtm. Give the exact and asymptotic P-values. (R computes the exact P-value in this case.)	Exact P-value: 0.053 Asymptotic P-value: 0.05 Remember: you cannot shop for p-values, doing all three tests in 2.1 & 2.2. Most appropriate here is the exact ordered test with p-value 0.053.
2.3 Use pairwise two-sided Wilcoxon tests to compare wmtm in all three pairs of two groups defined by leadgrp. Which two groups have the smallest unadjusted P-value? What is this smallest unadjusted P-value? What is the corresponding P-value adjusted by the Bonferroni method? What is the corresponding P-value adjusted by the Holm method? What is the corresponding P-value adjusted by the Shaffer method?	Two groups: low high The smallest adjusted p-values are all 3 times the unadjusted p-value, or approximately 0.34~3x.11 Unadjusted: 0.11 Bonferroni: 0.34 Holm: 0.34 Shaffer: 0.34 Holm and Shaffer can win over Bonferroni only if the smallest p-value meets the Bonferroni standard of 0.05/(number of tests), but that did not happen here.
2.4 If you strongly control the familywise error rate at 0.05 in a multiple testing problem (like 2.3), then in the experiment as a whole, the probability that at least one true alternative hypothesis is not rejected is at most 5%.	TRUE (FALSE) The promise is about falsely rejecting true null hypotheses. The promise does not refer to the alternative hypothesis.

3. Question 3 refers to **wmnr** and **wlead** for workers only; see the data page. Not wmtm!	FILL IN OR **CIRCLE** THE CORRECT ANSWER
3.1 Plot y=wmnr against x=wlead. Think about it.	Free points. (Happiness from plotting and thinking)
3.2 Test the null hypothesis of zero correlation against the one-sided alternative of positive correlations using Pearson's (the usual) correlation. Give the correlation and one-sided P-value.	One-sided Correlation: 0.358 P-value: 0.039 But it is all one outlier.
3.3 Test the null hypothesis of zero correlation against the one-sided alternative of positive correlations using Kendalls's correlation. Give the correlation and one-sided P-value.	One-sided Correlation: 0.041 P-value: 0.389
3.4 Fit the model wmnr = $\beta_0 + \beta_1$ wlead + e with symmetric independent errors using M-estimation with the default settings for rlm in the MASS. Give the estimate of the slope, β_1, its estimated standard error and the t-value (aka z value) formed as the ratio of the estimate to its standard error.	Estimate: 0.0072 Estimated standard error: 0.0090 t = z value: 0.8033

Doing the Problem Set in R

Midterm Spring 2015 Statistics 501

```
Problem 1:
1.1
> dmtm<-wmtm-cmtm
> qqnorm(dmtm)
FALSE because there is a negative, not a positive, outlier.
> which.min(dmtm)
[1] 11
> storagebattery[11,]
   pair wsex csex wage cage wyears wlead clead wmnr cmnr wmtm
cmtm wmftcr cmftcr leadgrp leadgrpi
11   11    F    F   39   35      3   260     2    4    0 1.05
2.47   1.37    0.9  medium        2
In this one pair, the control had a high mtm.
1.2
> shapiro.test(dmtm)
Shapiro-Wilk normality test.  data:  dmtm
W = 0.7524, p-value = 4.024e-05
1.3
> t.test(dmtm)
        One Sample t-test   data:  dmtm
t = 5.5629, df = 24, p-value = 1.007e-05
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.3477058 0.7578942
sample estimates: mean of x
   0.5528
1.4
> wilcox.test(dmtm,conf.int=T)
Wilcoxon signed rank test with continuity correction data:  dmtm
V = 300, p-value = 0.0002273
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 0.4650308 0.7400173
sample estimates: (pseudo)median
     0.5950558
1.5
> (0.7578942-0.3477058)/(0.7400173-0.4650308)
[1] 1.491667
The t-interval is 50% longer!
1.6  The t-test is an exact test if the data are Normal, hence
symmetric about their population median.
1.7
> library(NSM3)
> RFPW(dmtm)
$obs.stat
[1] -0.2734514
```

```
$p.val
[1] 0.7845063
1.8 Look at the 95% confidence intervals.
Question 2.
2.1
> kruskal.test(wmtm,leadgrp)
Kruskal-Wallis rank sum test.  data:  wmtm and leadgrp
Kruskal-Wallis chi-squared = 2.7508, df = 2, p-value = 0.2527
2.2
> pJCK(wmtm,leadgrpi) #exact because of small samples, no ties
Group sizes:  9 8 8 Jonckheere-Terpstra J  Statistic:  137
Exact  upper-tail probability:  0.053
> pJCK(wmtm,leadgrpi,method="Asymptotic")
Group sizes:  9 8 8 Jonckheere-Terpstra J*  Statistic:  1.6445
Asymptotic  upper-tail probability:  0.05
2.3
> pairwise.wilcox.test(wmtm,leadgrp,p.adjust.method="none")
       low  medium
medium 0.54 -
high   0.11 0.38
>
pairwise.wilcox.test(wmtm,leadgrp,p.adjust.method="bonf").34~.11x
3
>
pairwise.wilcox.test(wmtm,leadgrp,p.adjust.method="holm").34~.11x
3
Question 3.
3.2
> cor.test(wmnr,wlead,alternative="greater")
Pearson's product-moment correlation  data:  wmnr and wlead
t = 1.8399, df = 23, p-value = 0.03936
alternative hypothesis: true correlation is greater than 0
95 percent confidence interval:  0.0241278 1.0000000
sample estimates:  cor   0.3581974
3.3
> cor.test(wmnr,wlead,alternative="greater",method="k")
Kendall's rank correlation tau  data:  wmnr and wlead
z = 0.2819, p-value = 0.389
alternative hypothesis: true tau is greater than 0
sample estimates:  tau 0.04131109
3.4
> library(MASS)
> summary(rlm(wmnr~wlead))
Call: rlm(formula = wmnr ~ wlead)
Coeff:      Value  Std. Error t value
(Intercept) 5.8644 3.0764     1.9063
wlead       0.0072 0.0090     0.8033
```

Statistics 501 Spring 2015 Final Exam: Data Page 1

This is an exam. Do not discuss it with anyone. Due May 7, 2015, noon.

The data are from a paper, Benson, P. (1981) "Political alienation and public satisfaction with police services," *Pacific Sociological Review*, 24, 45-64. The paper is available in jstor, but there is no need to look at it unless you want to – they used different methods, and I have reduced the number of variables to make the problem set simpler. The data were from a telephone survey of the St. Louis SMSA during summer 1977. The table used here is a 2x2x2x2 table with dimensions PIntegrity, Evaluation, Alienation, and Race. PIntegrity concerned the respondent's opinion of the integrity of the police, either "not low" or "low", and it was based on the response to two statements, "Policemen in your neighborhood are basically honest" and "The police in your neighborhood treat all citizens equally according to the law." Evaluation concerned the respondent's evaluation of police performance, and it was either "Positive", or "Negative". Alienation was an indicator of the respondent's political alienation, either "Alienated" or "NotA" for "not alienated", and it was based on the response to two statements, "The local government is concerned about your neighborhood" and "A person can't get any satisfaction out of talking to the public officials in your community." Race was either "White" or "Other", where "Other" included black, Latino, native American, and others. Remember that I, E and A refer to opinions expressed by respondents to a survey.

The data are in an object, `policeStL`, in the course workspace. You will need to download the work space again. You may need to clear your web browser's memory to download the workspace. The table appears on the second data page, consists of 16 numbers, and may be easily entered into any program by hand. The first cell of the table indicates that 1345 respondents had a positive view of police performance, thought police integrity was not low, were not politically alienated, and were white.

Important: In referring to models, use the short form I for PIntegrity, E for evaluation, A for alienation, and R for race, so the standard hierarchical notation for the saturated model is [IEAR]. If you mess up this **notation** you may lose many points for no good reason, so don't mess up the notation. Make sure you know how to use the standard hierarchical notation – e.g., the model [IE] [AR] and how it differs from model [I] [EAR]. **Important**: All chi-square tests should use the **likelihood ratio chi-square, not the Pearson chi-square**. If you mess up and use the wrong chi-square, you may lose many points for no good reason, so don't mess up. Remember that a goodness-of-fit test is one that tests a model H_0 against the alternative that H_0 is false, whereas some other tests have more specific alternative hypotheses.

```
> dimnames(policeStL)
$PIntegrity     (Short form I)
[1] "NotLow" "Low"
$Evaluation     (Short form E)
[1] "Positive" "Negative"
$Alienation     (Short form A)
[1] "NotA"       "Alienated"
$Race           (Short form R)
[1] "White" "Other"
```

Statistics 501 Spring 2015 Final Exam: Data Page 2
This is an exam. Do not discuss it with anyone. Due May 7, 2015, noon.

```
> policeStL
, , Alienation = NotA, Race = White
          Evaluation
PIntegrity Positive Negative
    NotLow     1345       18
    Low         135       23

, , Alienation = Alienated, Race = White
          Evaluation
PIntegrity Positive Negative
    NotLow       69       11
    Low          36       22

, , Alienation = NotA, Race = Other
          Evaluation
PIntegrity Positive Negative
    NotLow      599       31
    Low         203       64

, , Alienation = Alienated, Race = Other
          Evaluation
PIntegrity Positive Negative
    NotLow       64       16
    Low          68       44
```

Make and keep a photocopy of your answer page. **The exam is due in my office, 473 Huntsman, on Thursday May 7, 2015, noon.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman or by giving it to Noelle at the front desk in statistics, but if you turn in the exam early, place it in an envelope addressed to me. When all of the exams are graded, I will add an **answer key** to the on-line bulk-pack for the course. You can compare the answer key to your photocopy of your exam. Your course grade will be available from the Registrar. I no longer distribute answer keys and graded exams by US Mail. **Turn in only the answer page**. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question

This is an exam. Do not discuss it with anyone.

Have a great summer!

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2015 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone. Due: Due May 7, 2015, noon.

Before you do anything else, read the important notes on Data Page 1.	**Fill in or Circle the Correct Answer**
1.1 Test the one null hypothesis H_0 that I, E, A and R are all independent against the alternative hypothesis that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: _____ Value: _____ DF: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
1.2 Test the null hypothesis H_0 that the evaluation E of the police is independent of the other variables, permitting any kind of dependence among the other three variables. Test against the alternative that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: _____ Value: _____ DF: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
1.3 Test the null hypothesis H_0 that police integrity I is conditionally independent of the evaluation E of the police given both the level of political alienation A and the race of the respondent R. Test against the alternative that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: _____ Value: _____ DF: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
1.4 Test the null hypothesis H_0 that police integrity I and evaluation E of the police are related in the same way (i.e., same odds ratio) for all categories of Alienation A and Race R, where I, A and R can have any possible relationship and E, A and R can have any possible relationship. Test against the alternative that H_0 is false. Give the notation for the log-linear model corresponding with H_0. Give the value of the statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: _____ Value: _____ DF: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2015 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone. Due: Due May 7, 2015, noon.

<table>
<tr><th>Before you do anything else, read the important notes on Data Page 1.</th><th>Fill in or Circle the Correct Answer</th></tr>
<tr><td>2.1 The model [IEA] [IAR] [EAR] permits the relationship between perceieved police integrity I and evaluation E to be related in a different way depending upon political alienation A.</td><td>TRUE FALSE</td></tr>
<tr><td>2.2 Test the goodness-of-fit of the model in 2.1. Give the value of the test statistic, the degrees of freedom, the P-value, and state whether the model is plausible based on the test.</td><td>Value: _____ DF: _____ P-value:_____

CIRCLE ONE
PLAUSIBLE NOT PLAUSIBLE</td></tr>
<tr><td>2.3 Test the null hypothesis H_0 that the model in question 1.4 is the correct model against the alternative that the model in 2.1 is the correct model. Give the value of the test statistic, the degrees of freedom, the P-value, and state whether H_0 is plausible.</td><td>Value: _____ DF: _____ P-value:_____

CIRCLE ONE
PLAUSIBLE NOT PLAUSIBLE</td></tr>
<tr><td>2.4 Fit the model [IEA] [IAR] [EAR] in question 2.1 with eps=0.0001 keeping the fitted counts. From the fitted counts, compute 4 odds ratios linking I and E, one at each level of A and R. Put I=notlow and E=positive in the numerator of the odds ratio.</td><td>Put odds ratios in the table.<table><tr><th></th><th>A=notA</th><th>A=alienated</th></tr><tr><td>R=white</td><td></td><td></td></tr><tr><td>R=other</td><td></td><td></td></tr></table></td></tr>
<tr><td>2.5 Fit the model [IEA] [IAR] [EAR] in question 2.1 with eps=0.0001 keeping the fitted counts. From the fitted counts, compute the 8 fitted probabilities of a negative evaluation of police performance.</td><td>Put estimated probabilities in the table.<table><tr><th></th><th>I=not low</th><th>I=low</th></tr><tr><td>R=white
A=notA</td><td></td><td></td></tr><tr><td>R=white
A=alienated</td><td></td><td></td></tr><tr><td>R=other
A=notA</td><td></td><td></td></tr><tr><td>R=other
A=alienated</td><td></td><td></td></tr></table></td></tr>
<tr><td>2.6 The model [IEA] [IAR] [EAR] preserves the [IER] marginal table and is the smoothest (i.e., maximum entropy) table that dose this.</td><td>TRUE FALSE</td></tr>
</table>

Answers: Stat 501 S-2015 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone.

Before you do anything else, read the important notes on Data Page 1.	**Fill in or Circle the Correct Answer**
1.1 Test the one null hypothesis H_0 that I, E, A and R are all independent against the alternative hypothesis that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: [I] [E] [A] [R] Value: 709.98 DF: 11 P-value: <0.0001 CIRCLE ONE PLAUSIBLE **NOT PLAUSIBLE**
1.2 Test the null hypothesis H_0 that the evaluation E of the police is independent of the other variables, permitting any kind of dependence among the other three variables. Test against the alternative that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: [E] [IAR] Value: 341.32 DF: 7 P-value: <0.0001 CIRCLE ONE PLAUSIBLE **NOT PLAUSIBLE**
1.3 Test the null hypothesis H_0 that police integrity I is conditionally independent of the evaluation E of the police given both the level of political alienation A and the race of the respondent R. Test against the alternative that H_0 is false. Give the standard notation for the log-linear model corresponding with H_0. Give the value of the test statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: [IAR] [EAR] Value: 138.53 DF: 4 P-value: <0.0001 CIRCLE ONE PLAUSIBLE **NOT PLAUSIBLE**
1.4 Test the null hypothesis H_0 that police integrity I and evaluation E of the police are related in the same way (i.e., same odds ratio) for all categories of Alienation A and Race R, where I, A and R can have any possible relationship and E, A and R can have any possible relationship. Test against the alternative that H_0 is false. Give the notation for the log-linear model corresponding with H_0. Give the value of the statistic, the degrees of freedom, the P-value. Is H_0 plausible?	Model in standard notation: [IE] [IAR] [EAR] Value: 12.00 DF: 3 P-value: 0.00738 CIRCLE ONE PLAUSIBLE **NOT PLAUSIBLE**

Answers: Stat 501 S-2015 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone. Due:

<table>
<tr><th>Before you do anything else, read the important notes on Data Page 1.</th><th>Fill in or Circle the Correct Answer</th></tr>
<tr><td>2.1 The model [IEA] [IAR] [EAR] permits the relationship between perceived police integrity I and evaluation E to be related in a different way depending upon political alienation A.</td><td>TRUE FALSE</td></tr>
<tr><td>2.2 Test the goodness-of-fit of the model in 2.1. Give the value of the test statistic, the degrees of freedom, the P-value, and state whether the model is plausible based on the test.</td><td>Value: 3.88 DF: 2 P-value: 0.144

CIRCLE ONE
PLAUSIBLE NOT PLAUSIBLE</td></tr>
<tr><td>2.3 Test the null hypothesis H_0 that the model in question 1.4 is the correct model against the alternative that the model in 2.1 is the correct model. Give the value of the test statistic, the degrees of freedom, the P-value, and state whether H_0 is plausible.</td><td>Value: 12.00068-3.880125=8.120555
DF: 3-2=1 P-value: 0.0044

CIRCLE ONE
PLAUSIBLE NOT PLAUSIBLE</td></tr>
<tr><td>2.4 Fit the model [IEA] [IAR] [EAR] in question 2.1 with eps=0.0001 keeping the fitted counts. From the fitted counts, compute 4 odds ratios linking I and E, one at each level of A and R. Put I=notlow and E=positive in the numerator of the odds ratio.</td><td>Put odds ratios in the table.
<table><tr><th></th><th>A=notA</th><th>A=alienated</th></tr><tr><td>R=white</td><td>7.87</td><td>3.03</td></tr><tr><td>R=other</td><td>7.87</td><td>3.03</td></tr></table></td></tr>
<tr><td>2.5 Fit the model [IEA] [IAR] [EAR] in question 2.1 with eps=0.0001 keeping the fitted counts. From the fitted counts, compute the 8 fitted probabilities of a negative evaluation of police performance. Round to 2 digits after the decimal, as in 0.99.</td><td>Put estimated probabilities in the table.
<table><tr><th></th><th>I=not low</th><th>I=low</th></tr><tr><td>R=white A=notA</td><td>0.02</td><td>0.12</td></tr><tr><td>R=white A=alienated</td><td>0.15</td><td>0.36</td></tr><tr><td>R=other A=notA</td><td>0.04</td><td>0.26</td></tr><tr><td>R=other A=alienated</td><td>0.18</td><td>0.40</td></tr></table></td></tr>
<tr><td>2.6 The model [IEA] [IAR] [EAR] preserves the [IER] marginal table and is the smoothest (i.e., maximum entropy) table that dose this.</td><td>TRUE FALSE</td></tr>
</table>

Statistics 510 Final 2015 Answer Page

1.1

```
> loglin(policeStL,list(1,2,3,4))
2 iterations: deviation 4.547474e-13
$lrt
[1] 709.9806
$df
[1] 11
> 1-pchisq(709.9806,11)
[1] 0
```

1.2

```
> loglin(policeStL,list(2,c(1,3,4)))
2 iterations: deviation 7.105427e-15
$lrt
[1] 341.3207
$df
[1] 7
> 1-pchisq(341.3207,7)
[1] 0
```

1.3

```
> loglin(policeStL,list(c(1,3,4),c(2,3,4)))
2 iterations: deviation 0
$lrt
[1] 138.5315
$df
[1] 4
> 1-pchisq(138.5315,4)
[1] 0
```

1.4

```
> loglin(policeStL,list(c(1,2),c(1,3,4),c(2,3,4)))
5 iterations: deviation 0.09289019
$lrt
[1] 12.00068
$df
[1] 3
> 1-pchisq(12.00068,3)
[1] 0.007380831
```

```
2.2
> loglin(policeStL,list(c(1,2,3),c(1,3,4),c(2,3,4)))
5 iterations: deviation 0.01297741
$lrt
[1] 3.880125
$df
[1] 2
> 1-pchisq(3.880125,2)
[1] 0.143695

2.3 Compare the full and reduced models in terms of the
likelihood ratio chi-square.
> 12.00068-3.880125
[1] 8.120555
> 3-2
[1] 1
> 1-pchisq(8.120555,1)
[1] 0.004376616

2.4
> ft<-loglin(policeStL,list(c(1,2,3),c(1,3,4),c(2,3,4)),
    eps=0.0001,fit=T)$fit
7 iterations: deviation 6.614585e-05
> ft
, , Alienation = NotA, Race = White
          Evaluation
PIntegrity  Positive Negative
    NotLow 1340.4677 22.53229
    Low     139.5323 18.46771
, , Alienation = Alienated, Race = White
          Evaluation
PIntegrity Positive Negative
    NotLow 67.65754 12.34246
    Low    37.34246 20.65754
, , Alienation = NotA, Race = Other
          Evaluation
PIntegrity Positive Negative
    NotLow 603.5323 26.46771
    Low    198.4677 68.53229
, , Alienation = Alienated, Race = Other
          Evaluation
PIntegrity Positive Negative
    NotLow 65.34246 14.65754
    Low    66.65754 45.34246
> 1340.4677*18.46771/(139.5323*22.53229)
[1] 7.873889
```

```
> 67.65754*20.65754/(37.34246*12.34246)
[1] 3.032426
> 603.5323*68.53229/(198.4677*26.46771)
[1] 7.873894
> 65.34246*45.34246/(66.65754*14.65754)
[1] 3.032426

2.5
> prop.table(ft,c(1,3,4))
, , Alienation = NotA, Race = White
          Evaluation
PIntegrity  Positive   Negative
    NotLow 0.9834686 0.01653139
    Low    0.8831157 0.11688425
, , Alienation = Alienated, Race = White
          Evaluation
PIntegrity  Positive  Negative
    NotLow 0.8457193 0.1542807
    Low    0.6438355 0.3561645
, , Alienation = NotA, Race = Other
          Evaluation
PIntegrity  Positive   Negative
    NotLow 0.9579878 0.04201224
    Low    0.7433248 0.25667524
, , Alienation = Alienated, Race = Other
          Evaluation
PIntegrity  Positive  Negative
    NotLow 0.8167807 0.1832193
    Low    0.5951566 0.4048434
```

Statistics 501, Spring 2014, Midterm: Data Page #1

Due in class, 1 April 2014 at noon.

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. The University often expels students caught cheating on exams. Cheating on an exam is the single dumbest thing a PhD student at Penn can do.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question. **Due in class Tuesday 1 April, 2014.**

The data for this problem are at in the latest Rst501.RData for R users as the object nhanesInsurance and in the nhanesInsurance.csv file at http://stat.wharton.upenn.edu/statweb/course/Spring-2008/stat501 The list is case sensitive, so nhanesInsurance.csv is with lower case items.

The data are from NHANES 2011-2012. They described 801 people who report they have no health insurance and 801 paired people who report they do have health insurance. Everyone is at least 25 years old and under 65. The pairing if for age and gender.
SEQN = NHANES identification number
age = age in years (RIDAGEYR)
female = 1 for female, 0 for male (RIAGENDR)
educ = education categories (DMDEDUC2)
povertyratio = ratio of income to the poverty level, capped at 5 times (INDFMPIR)
bmi = body mass index (BMXBMI)
sad1, sad2 = Sagittal abdominal diameter measured twice in cm (BMXSAD1, BMXSAD2)
noplace = 1 if respondent said he/she had no routine place to go for healthcare (HUQ030==2)
nocare = 1 if respondent said he/she received no healthcare in the last 12 month (HUQ050 == 0)
noinsurance = 1 if respondent said he/she had no health insurance (including no Medicaid) (HIQ011 == 2)
systolic blood pressure measured 3 times, systolic1, systolic2, systolic3, (BPXSY1, BPXSY2, BPXSY3)
diastolic blood pressure measured 3 times, diastolic1, diastolic2, diastolic3, (BPXDI1, BPXDI2, BPXDI3)
bpmedication = respondent says he/she is on blood pressure medication (BPQ050A)
pair = 1, 2, … , 801, for 801 pairs of two people, one with health insurance, the other without.

The Sagittal abdominal diameter (cm) attempts to measure waist size as it related to abdominal fat. http://en.wikipedia.org/wiki/Sagittal_Abdominal_Diameter BMI is an index of obestity https://www.nhlbi.nih.gov/guidelines/obesity/BMI/bmicalc.htm For information about blood pressure, see http://www.heart.org/HEARTORG/Conditions/HighBloodPressure/AboutHighBloodPressure/Understanding-Blood-Pressure-Readings_UCM_301764_Article.jsp

The NHLBI writes “Metabolic syndrome is the name for a group of risk factors that raises your risk for heart disease and other health problems, such as diabetes and stroke.” Among the risk factors are a large waistline, high blood pressure (or being treated for high blood pressure). The write “Successfully controlling metabolic syndrome requires long-term effort and teamwork with your health care providers.” http://www.nhlbi.nih.gov/health/health-topics/topics/ms/

In that spirit, you will be looking at whether having health insurance is related to better markers for metabolic syndrome, controlling for age and sex. There are many possibilities here because having health insurance is related to SES, education, income and many other things.

The data you have consists of 801 matched pairs, indicated by the pair variable, so the first two people are paired. The first person in the pair has no health insurance, while the second person does have health insurance. The pairs were matched for age and gender. It is important that you take appropriate account of the pairing in selecting and using statistical methods.

You should look at the data to understand its structure before starting the exam. For example:

```
> nhanesInsurance[1:4,c(1,2,3,6,19)]
      SEQN age female  bmi pairID
1    62208  38      0 22.2      1
2560 70910  38      0 32.1      1
107  63401  49      1 21.0      2
2735 71657  49      1 29.4      2
```

So pair 1 consists of two men aged 38, while pair 2 consists of two women aged 49.

```
> attach(nhanesInsurance)
```

Consecutive people are paired:

```
> table(pairID[noinsurance==1]==pairID[noinsurance==0])
TRUE
 801
```

Age is balanced by pairing:

```
> boxplot(age[noinsurance==1],age[noinsurance==0])
```

Age differs within a pair by at most one year:

```
> boxplot(age[noinsurance==1]-age[noinsurance==0])
> table(female[noinsurance==1],female[noinsurance==0])
      0   1
  0 445   0
  1   0 356
> plot(density(bmi))
> abline(v=25)
> abline(v=30)
> abline(v=35)
```

Pair difference in bmi, noinsurance-minus-insurance:

```
> bmidif<-bmi[noinsurance==1]-bmi[noinsurance==0]
```

If you are not sure what this does, look at bmi, at noinsurance==1, at bmi[noinsurance==1], etc so that you do kwno what this does.

```
> summary(bmidif)
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-43.9000  -5.2000   0.2000   0.3839   6.0000  36.1000
```

Models and terminology

Model 1: Z_i are independent, identically distributed (iid), with a continuous distribution symmetric about θ, or $Z_i = \theta + e_i$ where e_i are iid with continuous distribution symmetric about 0.

Model 2: Z_i are independent distributed, with continuous distributions with median θ, or $Z_i = \theta + e_i$ where e_i are independent with continuous distributions with median 0. The observations need not have identical distributions.

Model 3: X_i are independent, identically distributed with a continuous distribution. Y_i are independent, identically distributed with a continuous distribution, possibly different from the distribution of the X's. The X's and Y's are independent.

Model 4: $X_i = e_i$ $i=1,\ldots,m$, and $Y_j = \theta + e_{m+j}$ $j=1,\ldots,n$, where the e_k are m+n independent, identically distributed observations with a continuous distribution.

Model 5: (X_i, Y_i) are independent bivariate observations.

Pair differences always mean noinsurance-minus-insurance and there are 801 pair differences.

Print **LAST name**: _____, first:_____ ID#_____

Statistics 501, Spring 2014, Midterm, Answer Page #1 Due in class, 1 April2014, noon.

This is an exam. Do not discuss it with anyone. Read the data page.

Models are defined on the data page. Also, see the definition of a pair difference on the data page.	Fill in or CIRCLE the correct answer
1.1 Under model 1, test the null hypothesis H_0 that the pair differences in (first) systolic blood pressure (**systolic1**) are symmetric about zero using the appropriate Wilcoxon test. Give the value of name of the test, the value the test statistic (as reported by R) and the two-sided P-value. Is H_0 plausible?	Name of test:_____ Value: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
1.2 Under model 1, give the 95% confidence interval and the Hodges-Lehmann point estimate for the typical pair difference in (first) systolic blood pressure (systolic1), that is, the center of symmetry.	95% interval: [,] Point estimate: _____
1.3 Repeat questions 1.1 and 1.2 using (first) Sagittal abdominal diameter (**sad1**) in place of blood pressure.	Value: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE 95% interval: [,] Point estimate: _____
1.4 Under model 2, test the null hypothesis that the population median pair difference in **bmi** is zero. Give the name of the test, and the two-sided P-value, correcting appropriately for ties. How many of the 801 pairs contribute to the test?	Name of test:_____ P-value:_____ How many pairs contribute? _____
1.5 Under model 2, give the 95% confidence interval for the median pair difference in **bmi** and the associated point estimate. (These are not adjusted for ties.)	95% interval: [,] Point estimate: _____
1.6 You cannot appropriately use the method in question 1.1 with the 801 pair differences in bmi, because it is clear that the 1602 bmi values are skewed right.	CIRCLE ONE TRUE FALSE

Question 2 asks about the relationship between the 801 Sagittal abdominal diameter (**sad1**) and the 801 (first) systolic blood pressures (**systolic1**) for the 801 people without health insurance. **Do not use** their paired controls with health insurance.	Fill in or CIRCLE the correct answer
2.1 Use Kendall's rank correlation to test the null hypothesis that sad1 and systolic1 are independent for the 801 people without health insurance. Give the value of the correlation coeffient and the two-sided P-value. Is the null hypothesis plausible?	Value: _____ P-value:_____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
2.2 Give the 95% (asymptotic) confidence interval for Kendall's rank correlation for the data in 2.1.	95% interval: [,]
Use the results in 2.1 and 2.2 to give the estimate of the probability of concordance and the 95% confidence interval for that probability.	Estimate: _____ 95% interval: [,]

Print **LAST name**, then first: _____, _____ ID#_____

Statistics 501, Spring 2014, Midterm, Answer Page #2 Due in class, 1 April 2014, noon.

This is an exam. Do not discuss it with anyone. Read the data page

For this question, you should boxplot the pair difference in sad1 for pairs containing men versus pairs containing women. Do not turn in the plot.	Fill in or CIRCLE the correct answer
3.1 Of the 801 pairs, how many contain two women? How many contain two men?	2 women:_____ + 2 men _____ = 801
3.2 Test the null hypothesis that the pair difference in **sad1** have the same distribution for female pairs and for male pairs using the appropriate Wilcoxon test. Give the name of the test and the two-sided P-value. Is the null hypothesis plausible?	Name:_____ P-value: _____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
3.3 Assuming model 4, build a 95% confidence interval and point estimate for the shift, Δ, female-minus-male difference in noinsurance-minus-insurance pair difference in **sad1**. What are the units of measurement (miles, weeks, dollars, etc.)?	Estimate: _____ 95% interval: [,] Units of measurement: _____
3.4 Estimate the probability that the pair difference in sad1, noinsurance-minus-insurance, will be larger a female pair than for a male pair.	Estimate: _____
3.5 The test in 3.2 and the estimate in 3.4 are not valid if model 4, the shift model, is false.	CIRCLE ONE TRUE FALSE
3.6 Test the same hypothesis as in 3.2 but use LePage's test. Give the two-sided asymptotic P-value.	P-value: _____
3.7 Use the Kolomogorov-Smirnov test to test the same hypothesis as in 3.2. What is the two-sided P-value?	P-value: _____

Question 4 looks just at the bmi for the 801 people without insurance by whether they no place to go for health care (noplace=1) and whether they received no health care in the previous year (nocare=1), making 4 groups.

```
> bmiNoI<-bmi[noinsurance==1]
> grp<-(factor(noplace):factor(nocare))[noinsurance==1]
> table(grp)
```

Question 4 refers only to the 801 people with no health insurance. See above.	Fill in or CIRCLE the correct answer
Use the Kruskal Wallis test the null hypothesis that the distribution of bmi is the same over the four groups defined by grp. Give the P-value. Is the null hypothesis plausible?	P-value: _____ CIRCLE ONE PLAUSIBLE NOT PLAUSIBLE
Compare all four groups using Wilcoxon two sample tests adjusting using Holm's procedure. List all **pairs** of groups that differ significantly at the 0.05 level after adjustment. If none, write "none". Example: listing (0,1):(0,0) means (noplace,nocare) = (0,1) differs from (noplace,nocare) = (0,0).	
The chance that Holm's procedure will reject at least one false null hypothesis at the 5% level is at most 5%.	CIRCLE ONE TRUE FALSE

Statistics 501 Spring 2104 Midterm Answer page

Models are defined on the data page. Also, see the definition of a pair difference on the data page.	Fill in or CIRCLE the correct answer
1.1 Under model 1, test the null hypothesis H_0 that the pair differences in (first) systolic blood pressure (**systolic1**) are symmetric about zero using the appropriate Wilcoxon test. Give the value of name of the test, the value the test statistic (as reported by R) and the two-sided P-value. Is H_0 plausible?	Name of test Wilcoxon signed rank test Value:152295.5 P-value: 0.31 CIRCLE ONE (PLAUSIBLE) NOT PLAUSIBLE
1.2 Under model 1, give the 95% confidence interval and the Hodges-Lehmann point estimate for the typical pair difference in (first) systolic blood pressure (systolic1), that is, the center of symmetry.	95% interval: [-1.00, 2.00] Point estimate: 1.00
1.3 Repeat questions 1.1 and 1.2 using (first) Sagittal abdominal diameter (**sad1**) in place of blood pressure.	Value162915.2 P-value: 0.36 CIRCLE ONE (PLAUSIBLE) NOT PLAUSIBLE 95% interval: [-0.25, 0.60] Point estimate: 0.20
1.4 Under model 2, test the null hypothesis that the population median pair difference in **bmi** is zero. Give the name of the test, and the two-sided P-value, correcting appropriately for ties. How many of the 801 pairs contribute to the test?	Name of test: sign test P-value: 0.697 How many pairs contribute? 392+404 = 796
1.5 Under model 2, give the 95% confidence interval for the median pair difference in **bmi** and the associated point estimate. (These are not adjusted for ties.)	95% interval: [-0.5, 1.1] Point estimate: 0.20
1.6 You cannot appropriately use the method in question 1.1 with the 801 pair differences in bmi, because it is clear that the 1602 bmi values are skewed right.	CIRCLE ONE TRUE (FALSE)

Question 2 asks about the relationship between the 801 Sagittal abdominal diameter (**sad1**) and the 801 (first) systolic blood pressures (**systolic1**) for the 801 people without health insurance. Do not use their paired controls with health insurance.	Fill in or CIRCLE the correct answer
2.1 Use Kendall's rank correlation to test the null hypothesis that sad1 and systolic1 are independent for the 801 people without health insurance. Give the value of the correlation coeffient and the two-sided P-value. Is the null hypothesis plausible?	Value: 0.206 P-value: 2.2×10^{-16} CIRCLE ONE PLAUSIBLE (NOT PLAUSIBLE)
2.2 Give the 95% (asymptotic) confidence interval for Kendall's rank correlation for the data in 2.1.	95% interval: [0.159, 0.253]
Use the results in 2.1 and 2.2 to give the estimate of the probability of concordance and the 95% confidence interval for that probability.	Estimate: 0.603 95% interval: [0.5795, 0.6265]

Statistics 501 Spring 2104 Midterm Answer page

For this question, you should boxplot the pair difference in sad1 for pairs containing men versus pairs containing women. Do not turn in the plot.	Fill in or CIRCLE the correct answer
3.1 Of the 801 pairs, how many contain two women? How many contain two men?	2 women: 356 + 445 = 801
3.2 Test the null hypothesis that the pair difference in **sad1** have the same distribution for female pairs and for male pairs using the appropriate Wilcoxon test. Give the name of the test and the two-sided P-value. Is the null hypothesis plausible?	Name: Wilcoxn's rank sum P-value: 0.009372 CIRCLE ONE PLAUSIBLE (NOT PLAUSIBLE)
3.3 Assuming model 4, build a 95% confidence interval and point estimate for the shift, Δ, female-minus-male difference in noinsurance-minus-insurance pair difference in **sad1**. What are the units of measurement (miles, weeks, dollars, etc.)?	Estimate: 1.10 95% interval:[0.30, 1.90] Units of measurement: cm
3.4 Estimate the probability that the pair difference in sad1, noinsurance-minus-insurance, will be larger a female pair than for a male pair.	Estimate: 0.553
3.5 The test in 3.2 and the estimate in 3.4 are not valid if model 4, the shift model, is false.	CIRCLE ONE TRUE (FALSE)
3.6 Test the same hypothesis as in 3.2 but use LePage's test. Give the two-sided asymptotic P-value.	P-value: 0.0226
3.7 Use the Kolomogorov-Smirnov test to test the same hypothesis as in 3.2. What is the two-sided P-value?	P-value: 0.006937

Question 4 looks just at the bmi for the 801 people without insurance by whether they no place to go for health care (noplace=1) and whether they received no health care in the previous year (nocare=1), making 4 groups.

```
> bmiNoI<-bmi[noinsurance==1]
> grp<-(factor(noplace):factor(nocare))[noinsurance==1]
> table(grp)
```

Question 4 refers only to the 801 people with no health insurance. See above.	Fill in or CIRCLE the correct answer
Use the Kruskal Wallis test the null hypothesis that the distribution of bmi is the same over the four groups defined by grp. Give the P-value. Is the null hypothesis plausible?	P-value: 0.01107 CIRCLE ONE PLAUSIBLE (NOT PLAUSIBLE)
Compare all four groups using Wilcoxon two sample tests adjusting using Holm's procedure. List all **pairs** of groups that differ significantly at the 0.05 level after adjustment. If none, write "none". Example: listing (0,1):(0,0) means (noplace,nocare) = (0,1) differs from (noplace,nocare) = (0,0).	(0,0):(1,1) or equivalently (someplace,somecare) differs from (noplace,nocare)
The chance that Holm's procedure will reject at least one false null hypothesis at the 5% level is at most 5%.	CIRCLE ONE TRUE (FALSE)

Stat 501 Spring 2104 Midterm: Doing the problem set in R

1.1-1.2

```
> difsystolic1<-systolic1[noinsurance==1]-
      systolic1[noinsurance==0]
> boxplot(difsystolic1)
> wilcox.test(difsystolic1,conf.int=T)
        Wilcoxon signed rank test with continuity
correction
data:  difsystolic1
V = 152295.5, p-value = 0.3109
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -0.9999988  2.0000214
sample estimates:
(pseudo)median
     0.9999535
```

1.3

```
> difsad<-sad1[noinsurance==1]-sad1[noinsurance==0]
> wilcox.test(difsad,conf.int=T)
        Wilcoxon signed rank test with continuity
correction
data:  difsad
V = 162912.5, p-value = 0.3598
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -0.2499814  0.6000532
sample estimates:
(pseudo)median
     0.1999492
```

1.4

```
> difbmi<-bmi[noinsurance==1]-bmi[noinsurance==0]
> table(sign(difbmi))
 -1   0   1
392   5 404              Five 0's (ties) are removed.
> prop.test(392,392+404,p=1/2)
        1-sample proportions test with continuity
correction
data:  392 out of 392 + 404, null probability 1/2
X-squared = 0.152, df = 1, p-value = 0.6966
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.4572270 0.5277714
sample estimates:
        p 0.4924623
```

```
1.5
> signCI(difbmi)
$CI
[1] -0.5  1.1
$coverage
[1] 0.9522137
> median(difbmi)
[1] 0.2
2.1
>
cor.test(systolic1[noinsurance==1],sad1[noinsurance==1],met
hod="k")   Kendall's rank correlation tau
data:  systolic1[noinsurance == 1] and sad1[noinsurance ==
1]
z = 8.5379, p-value < 2.2e-16
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau 0.2060076
2.2
> library(NSM3)
>
kendall.ci(systolic1[noinsurance==1],sad1[noinsurance==1])
1 - alpha = 0.95 two-sided CI for tau:
0.159, 0.253
2.3 Just transform the correlation.
> (c(0.206,0.159, 0.253)+1)/2
[1] 0.6030 0.5795 0.6265
3.1 – 3.4
> fem<-1==female[noinsurance==1]
> table(fem)
fem
  0   1
445 356
> wilcox.test(difsad[fem==1],difsad[fem==0],conf.int=T)
        Wilcoxon rank sum test with continuity correction
data:  difsad[fem == 1] and difsad[fem == 0]
W = 87664.5, p-value = 0.009372
alternative hypothesis: true location shift is not equal to
0
95 percent confidence interval:  0.2999803 1.9000161
sample estimates difference in location 1.10002
> 87664.5/(445*356)
[1] 0.5533676

3.6
>
pLepage(difsad[fem==1],difsad[fem==0],method="Asymptotic")
```

```
Ties are present, so p-values are based on conditional null
distribution.
Number of X values:  356 Number of Y values:  445
Lepage D  Statistic:  7.5763
Asymptotic  upper-tail probability:  0.0226
3.7
> ks.test(difsad[fem==1],difsad[fem==0])
        Two-sample Kolmogorov-Smirnov test
data:  difsad[fem == 1] and difsad[fem == 0]
D = 0.1197, p-value = 0.006937
alternative hypothesis: two-sided

4
> bmiNoI<-bmi[noinsurance==1]
> grp<-(factor(noplace):factor(nocare))[noinsurance==1]
> kruskal.test(bmiNoI~grp)
        Kruskal-Wallis rank sum test
data:  bmiNoI by grp
Kruskal-Wallis chi-squared = 11.125, df = 3, p-value =
0.01107
> pairwise.wilcox.test(bmiNoI,grp)
        Pairwise comparisons using Wilcoxon rank sum test
data:  bmiNoI and grp
    0:0   0:1   1:0
0:1 0.363 -     -
1:0 0.114 1.000 -
1:1 0.019 1.000 1.000
P value adjustment method: holm
```

Statistics 501 Spring 2014 Final Exam: Data Page 1
This is an exam. Do not discuss it with anyone.
Due: Monday, May 12, at 12:00am

The data are from NHANES 2011-2012. It is a 2^4 table. It was built from four questions, WHQ030M, WHQ500, RIAGENDR, BMXBMI, with some categories changed to make them binary. The variable "thinkfat" asks about a person's weight, and people either think they are "fat or overweight" or "about the right weight"; there were other categories, but they are not represented here. The variable "trying to" asks whether a person is trying to lose weight or is not trying to make a change in weight; again there were other categories. The variable "bmi25" is based on measurements of body mass index, and is <25 or >=25, where >=25 is the conventional cut for overweight. The last variables is gender, male or female. The table is in nhanesWeight in the R workspace for the course. You will need to download the workspace again, and may need to clear your web browser's memory. If you are using some other software, you can enter the following 16 numbers by hand.

```
> nhanesWeight
, , bmi25 = <25, gender = male
                tryingto
thinkfat         lose.weight no.change
  fat/overweight          38         4
  about.right             85       295
, , bmi25 = >=25, gender = male
                tryingto
thinkfat         lose.weight no.change
  fat/overweight          65         6
  about.right             43        16
, , bmi25 = <25, gender = female
                tryingto
thinkfat         lose.weight no.change
  fat/overweight          32         3
  about.right            114       318
, , bmi25 = >=25, gender = female
                tryingto
thinkfat         lose.weight no.change
  fat/overweight          82         5
  about.right             41        11
```

Very important: There are 4 variables in this table. Variable 1 is thinkfat and is abbreviated in this exam as variable F. Variable 2 is tryingto and is abbreviated as T. Variable 3 is bmi25 and is abbreviated as B. Variable 4 is gender ad is abbreviated as G. If you mess up and use T to refer to thinkfat (wrong) instead of tryingto (right), then you will get many questions wrong for a tiny error. **Don't mess up** that way: check that you are using the correct abbreviations.

Very important: As always, model [FT][BG] is the abbreviation for the log linear model
$\log(m_{ijkn}) = u + u_{F(i)} + u_{T(j)} + u_{B(k)} + u_{G(n)} + u_{FT(ij)} + u_{BG(kn)}$
Make sure you understand this notation in terms of variables before attempting the exam. The notation is used in Fienberg's book (and everywhere else). When a question asks for a model, give the model in this abbreviated notation; eg [FT][BG]. If a question speaks of a model it will use this notation. Keep in mind that [F][T][B][G] and [FTBG] are very different models, and FTBG does not denote a model: brackets matter. Don't invent a new notation.

Very important: Always use the likelihood ratio chi-square, not Pearson's chi-square.

```
> dimnames(nhanesWeight)
$thinkfat (F)
[1] "fat/overweight" "about.right"
$tryingto (T)
[1] "lose.weight" "no.change"
$bmi25 (B)
[1] "<25"  ">=25"
$gender (G)
[1] "male"   "female"
```

Claim 3.2 is related to question 3.2.
Claim 3.2: Thinking you are fat/overweight is positively related to trying to lose weight, but the relationship is much stronger for people with BMI<25 than for people with BMI>=25, and this is true for both men and women.

Make and keep a photocopy of your answer page. **The exam is due in my office, 473 Huntsman, on Monday 12 May 2014 at noon.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman or by giving it to Noelle at the front desk in statistics, but if you turn in the exam early, place it in an envelope addressed to me. When all of the exams are graded, I will add an **answer key** to the on-line bulk-pack for the course. You can compare the answer key to your photocopy of your exam. Your course grade will be available from the Registrar. I no longer distribute answer keys and graded exams by US Mail. **Turn in only the answer page**. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question

This is an exam. Do not discuss it with anyone.

Have a great summer!

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2014 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone. Due: Monday, May 12, at 12:00am

Use the abbreviations listed as very important on the data page, eg, F, T and [FT]	Fill in or circle the correct answer.
1.1 Use the [] notation to give the log-linear model that corresponds with the four variables, F, T, B and G being independent.	Model:
1.2 Using the likelihood ratio test of goodness of fit, test the null hypothesis that the model in 1.1 is correct. Give the value of the statistic, the DF and P-value. Is the model plausible?	Value (one number): Degrees of freedom: P-value: Circle one: PLAUSIBLE NOT PLAUSIBLE
1.3 Under model [FB][TG], gender (G) is independent of body mass index <25 (B).	Circle one: TRUE FALSE
1.4 Under model [FB][TG][TB], the odds ratio linking F and B is the same for males and females.	Circle one: TRUE FALSE
1.5 In model [FTB][TBG][FG], feeling fat/overweight (F) is conditionally independent of gender (G) given T and B.	Circle one: TRUE FALSE
1.6 Model [FTB][TBG][FG] can be collapsed over T without changing the odds ratio linking F and G.	Circle one: TRUE FALSE
1.7 In model [FTB][TBG], feeling fat/overweight (F) is independent of gender (G).	Circle one: TRUE FALSE
1.8 In model [FTB][TBG], at each of the 4 levels of T-and-B, the odds ratio linking feeling gender (G) and feeling fat/overweight (F) equals 1.	Circle one: TRUE FALSE
1.9 In model [FTB][G], G and B are **not** independent but **are** conditionally independent given F-and-T.	Circle one: TRUE FALSE

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2014 Final Exam: Answer Page 2 This is an exam. Do not discuss it with anyone. Due: Monday, May 12, at 12:00am

	Fill in/circle the answer.
2.1 Test the goodness of fit of model [FTB][G]. Give the value of the likelihood ratio chi-square, the degrees of freedom, the P-value. Based on this test alone, is the null hypothesis that this model is correct plausible?	Value (one number): Degrees of freedom: P-value: Circle one: PLAUSIBLE NOT PLAUSIBLE
2.2 Test the null hypothesis that [FTB][G] is the correct model against the alternative hypothesis that [FTB][TG] is the correct model. Give the value of the likelihood ratio chi-square test statistic, its degrees of freedom, and P-value and state whether the null hypothesis is plausible.	Value (one number): Degrees of freedom: P-value: Circle one: PLAUSIBLE NOT PLAUSIBLE
2.3 Test the null hypothesis that [FT][FB][TB][G] is the correct model against the alternative hypothesis that [FTB][G] is the correct model. Answer the same questions for this comparison as in 2.2.	Value (one number): Degrees of freedom: P-value: Circle one: PLAUSIBLE NOT PLAUSIBLE
2.4 Model [FTB][G] can be collapsed over gender G without changing the odds ratios linking the other three variables, F, T and B.	Circle one: TRUE FALSE

Use fitted counts from [FTB][G] for question 3.	Fill in or circle the correct answer.
3.1 Give the four estimated odds ratios linking F and T at each level of B-and-G. You are to enter 4 numbers, and all 4 are >=1.	<table><tr><td></td><td>G=Male</td><td>G=Female</td></tr><tr><td>B is <25</td><td></td><td></td></tr><tr><td>B is >=25</td><td></td><td></td></tr></table>
3.2 Claim 3.2 on the data page is a reasonable summary of the odds ratios in 3.1.	Circle one: TRUE FALSE

Statistics 501 Spring 2014 Final Exam: Answers

Use the abbreviations listed as very important on the data page, eg, F, T and [FT]	Fill in or circle the correct answer.
1.1 Use the [] notation to give the log-linear model that corresponds with the four variables, F, T, B and G being independent.	Model: [F][T][B][G]
1.2 Using the likelihood ratio test of goodness of fit, test the null hypothesis that the model in 1.1 is correct. Give the value of the statistic, the DF and P-value. Is the model plausible?	Value (one number): 715.5127 Degrees of freedom: 11 P-value: <0.0001 Circle one: PLAUSIBLE NOT PLAUSIBLE
1.3 Under model [FB][TG], gender (G) is independent of body mass index <25 (B).	Circle one: TRUE FALSE
1.4 Under model [FB][TG][TB], the odds ratio linking F and B is the same for males and females.	Circle one: TRUE FALSE
1.5 In model [FTB][TBG][FG], feeling fat/overweight (F) is conditionally independent of gender (G) given T and B.	Circle one: TRUE FALSE
1.6 Model [FTB][TBG][FG] can be collapsed over T without changing the odds ratio linking F and G.	Circle one: TRUE FALSE
1.7 In model [FTB][TBG], feeling fat/overweight (F) is independent of gender (G).	Circle one: TRUE FALSE
1.8 In model [FTB][TBG], at each of the 4 levels of T-and-B, the odds ratio linking feeling gender (G) and feeling fat/overweight (F) equals 1.	Circle one: TRUE FALSE
1.9 In model [FTB][G], G and B are **not** independent but **are** conditionally independent given F-and-T.	Circle one: TRUE FALSE

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2014 Final Exam: Answer Page 2 This is an exam. Do not discuss it with anyone. Due: Monday, May 12, at 12:00am

	Fill in/circle the answer.
2.1 Test the goodness of fit of model [FTB][G]. Give the value of the likelihood ratio chi-square, the degrees of freedom, the P-value. Based on this test alone, is the null hypothesis that this model is correct plausible?	Value (one number): 6.283948 Degrees of freedom: 7 P-value: 0.507013 Circle one: PLAUSIBLE NOT PLAUSIBLE
2.2 Test the null hypothesis that [FTB][G] is the correct model against the alternative hypothesis that [FTB][TG] is the correct model. Give the value of the likelihood ratio chi-square test statistic, its degrees of freedom, and P-value and state whether the null hypothesis is plausible.	Value (one number): 0.760835 Degrees of freedom: 1 P-value: 0.3830673 Circle one: PLAUSIBLE NOT PLAUSIBLE
2.3 Test the null hypothesis that [FT][FB][TB][G] is the correct model against the alternative hypothesis that [FTB][G] is the correct model. Answer the same questions for this comparison as in 2.2.	Value (one number): 12.7778 Degrees of freedom: 1 P-value: 0.0003507572 Circle one: PLAUSIBLE NOT PLAUSIBLE
2.4 Model [FTB][G] can be collapsed over gender G without changing the odds ratios linking the other three variables, F, T and B.	Circle one: TRUE FALSE

Use fitted counts from [FTB][G] for question 3.	Fill in or circle the correct answer.
3.1 Give the four estimated odds ratios linking F and T at each level of B-and-G. You are to enter 4 numbers, and all 4 are >=1.	<table><tr><th></th><th>G=Male</th><th>G=Female</th></tr><tr><td>B is <25</td><td>30.8</td><td>30.8</td></tr><tr><td>B is >=25</td><td>4.3</td><td>4.3</td></tr></table>
3.2 Claim 3.2 on the data page is a reasonable summary of the odds ratios in 3.1.	Circle one: TRUE FALSE

Doing the Problem Set in R

1.

```
> loglin(nhanesWeight,list(1,2,3,4))
2 iterations: deviation 1.136868e-13
$lrt
[1] 715.5127
$pearson
[1] 978.587
$df
[1] 11
> 1-pchisq(715.5127,11)
[1] 0
```

2.1

```
> loglin(nhanesWeight,list(c(1,2,3),4))
2 iterations: deviation 2.273737e-13
$lrt
[1] 6.283948
$df
[1] 7
> 1-pchisq(6.283948,7)
[1] 0.507013
```

2.2

```
> loglin(nhanesWeight,list(c(1,2,3),c(2,4)))
2 iterations: deviation 5.684342e-14
$lrt
[1] 5.523113
$df
[1] 6
> 6.283948-5.523113
[1] 0.760835
> 7-6
[1] 1
> 1-pchisq(0.760835,1)
[1] 0.3830673
```

2.3

```
> loglin(nhanesWeight,list(c(1,2),c(1,3),c(2,3),4))
6 iterations: deviation 0.03227441
$lrt
[1] 19.06175
$df
[1] 8
> 19.06175-6.283948
[1] 12.7778
> 1-pchisq(12.7778,1)
[1] 0.0003507572
```

3.

```
> ft<-loglin(nhanesWeight,list(c(1,2,3),4),fit=T)$fit
2 iterations: deviation 2.273737e-13
> ft
, , bmi25 = <25, gender = male
                tryingto
thinkfat         lose.weight  no.change
  fat/overweight   33.367876   3.336788
  about.right      94.860104 292.207254
, , bmi25 = >=25, gender = male
                tryingto
thinkfat         lose.weight  no.change
  fat/overweight   70.072539   5.243523
  about.right      40.041451  12.870466
, , bmi25 = <25, gender = female
                tryingto
thinkfat         lose.weight  no.change
  fat/overweight   36.632124   3.663212
  about.right     104.139896 320.792746
, , bmi25 = >=25, gender = female
                tryingto
thinkfat         lose.weight  no.change
  fat/overweight   76.927461   5.756477
  about.right      43.958549  14.129534
> 33.367876*292.207254/(94.860104*3.336788)
[1] 30.80402
> 70.072539*12.870466/(40.041451*5.243523)
[1] 4.295455
> 36.632124*320.792746/(104.139896*3.663212)
[1] 30.80402
> 76.927461*14.129534/(43.958549*5.756477)
[1] 4.295454
```

Statistics 501, Spring 2013, Midterm: Data Page #1

Due in class, noon, Tuesday March 26, 2013

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. The University often expels students caught cheating on exams. Cheating on an exam is the single dumbest thing a PhD student at Penn can do.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question. **Due in class Tuesday March 26, 2013.**

The data for this problem are at in the latest Rst501.RData for R users as the object garki and in the garki.csv file at http://stat.wharton.upenn.edu/statweb/course/Spring-2008/stat501 The list is case sensitive, so garki.csv is with lower case items.

The data are from a study by Molineaux and Gramiccia (1980) The GARKI project: Research on the epidemiology and control of malaria in the Sudan Savanna of West Africa, Geneva: World Health Organization. The study looked at several treatments and a control. We will look at one treatment and the control. The treatment involved spraying an insecticide, propoxur, and administering a drug, sulfalene-pyrimethamine at high frequency. The controls did not receive these interventions. In the example here, there are 1560 treated individuals matched in pairs to 1560 controls, the matching being for age and gender. The outcome is the frequency of Plasmodium falciparum in blood samples, that is the frequency of a protozoan parasite that causes malaria. A slide containing blood is divided into 200 fields and the outcome is the number of fields with the parasite, 0-200. Low numbers are better. Each person has two measures responses, one before the treatment period started, the other after the treatment period. Each response is the average of 2 to 4 blood samples. Each row of data contains a treated person (treated) and a match control person (control), their response before and after, their ages, their genders, and id numbers. The first 3 lines of data are below. In the first line, there are two men aged 35 years, the treated man declining from .50 before treatment to 0 after treatment, the control staying the same from .5 before to .5 after. In the control group, nothing happened between before and after, just the passage of time. You are to assume that the 1560 distinct pairs are independent, although of course the pairing may make the two people within a pair dependent.

```
> dim(garki)
[1] 1560   11
> garki[1:3,]
  matched.id treated.before treated.after control.before
1          1           0.50             0           0.50
2          2           1.75             0           6.25
3          3           1.50             0          20.00
  control.after treated.age control.age treated.male control.male
1           0.5          35          35            1            1
2           0.0          30          30            0            0
3           5.5          10          10            1            1
  control treated
1   12059    6242
2    6209    6243
3    6109    6244
```

In your analyses of the garki data, please (i) assume that different rows of the garki data frame are independent, (ii) act as if the parasite levels were untied (that is, ignore ties, letting R do its thing with ties). The matching is very close but not perfect. In two of 1560 pairs, a male is paired with a female. Use treated.male=1 for a male pair, and treated.male=0 for a female pair, ignoring the two mismatches.

STATISTICS 501, SPRING 2012, MIDTERM DATA PAGE #2

Due in class, noon, Tuesday March 26, 2013

Define a change as after-minus-before, for instance,

```
tamb <- treated.after-treated.before

camb <- control.after-control.before
```

Define the difference-in-differences to be `dind <- tamb- camb` or

```
dind <- (treated.after-treated.before)-(control.after-control.before)
```

Define three factors

```
> young<-factor(treated.age<=10,levels=c(F,T),labels=c("NotYoung","Young"))
      > table(young)
      young
      NotYoung    Young
          1113      447
> male<-factor(treated.male,levels=c(0,1),labels=c("Female","Male"))
> table(male)
      male
      Female   Male
         766    794
> group<-young:male
> table(group)
      group
      NotYoung:Female   NotYoung:Male    Young:Female      Young:Male
                  570             543             196             251
```

Question 3 asks you to look at this boxplot.

```
> boxplot(dind~young)
```

Question 4 refers to a variable, avage, which is the average age in a treated-versus-control pair.

```
> avage<-(treated.age+control.age)/2
```

Question 4 refers to a variable, `young10`, which is a binary version of the factor `young`.

```
> young10<-1*(treated.age<=10)
```

Print Name **LAST name**, then first: _____ ID#_____

Statistics 501, Spring 2013, Midterm, Answer Page #1 Due in class, noon, Tuesday March 26

This is an exam. Do not discuss it with anyone.

Use the appropriate Wilcoxon test to answer the questions in part 1.	Fill in or CIRCLE the correct answer
1.1 Apply the appropriate Wilcoxon test to the change in outcome among controls, camb. Give the two sided P-value, point estimate and 95% confidence interval. Is no change plausible?	P-value: _____ Estimate: _____ CI:[,] Circle one: Plausible Not plausible
1.2 Apply the appropriate Wilcoxon test to the change in outcome among treated subjects, tamb. Give the two sided P-value, point estimate and 95% confidence interval. Is no change plausible?	P-value: _____ Estimate: _____ CI:[,] Circle one: Plausible Not plausible
1.3 Apply the appropriate Wilcoxon test to whether the typical difference-in-differences is zero, dind. Give the two sided P-value, point estimate and 95% confidence interval. Is zero plausible?	P-value: _____ Estimate: _____ CI:[,] Circle one: Plausible Not plausible
1.4 In question 1.3, the appropriate Wilcoxon test is Wilcoxon's rank sum test (from chapter 4 in H&W) because treated and control groups are unrelated.	Circle one: TRUE FALSE
1.5 In question 1.2, the boxplot of changes for the 1560 treated subjects does not look symmetric about its center. So, the P-value in 1.2 has no meaning as a test of the null hypothesis of symmetry of changes about zero..	Circle one: Doesn't look symmetric TRUE FALSE P-value meaningless TRUE FALSE
1.6 In question 1.1, there are 1,217,580 Walsh averages for the 1560 changes in the control group, and more than 80% of these are negative.	Circle one: TRUE FALSE
1.7 Based on your answer to 1.3, the treatment was associated with a greater increase parasites in the blood of treated subjects than in controls.	Circle one: TRUE FALSE

2. Define the `group` variable as on the data page. It refers to age and gender of the treated person in a pair. Use it to study how `dind` varies among the four groups. Use appropriate nonparametric tests for all comparisons.	Fill in or CIRCLE the correct answer
2.1 Is it plausible that `dind` has the same distribution in the four groups defined by `group`? What is the name of the appropriate nonparametric test? What is the value of the test statistic? What is the P-value? Is the null hypothesis of no difference plausible?	Name of test: Value: _____ P-value:_____ Circle one: Plausible Not plausible
2.2 Compare all six pairs of two of the four groups from 2.1. Use Holm's method with an appropriate nonparametric test. List all pairs of groups as (A,B) that do not differ significantly at the 0.05 level, for instance (young.male,notyoungmale). List up to 6 pairs. If none, write none.	
2.3 In all data sets, Holm's procedure rejects each hypothesis rejected by the Bonferroni method and	Circle one: TRUE FALSE

may reject additional hypotheses.	

Print Name **LAST name**, then first: _____ ID#_____

Statistics 501, Spring 2013, Midterm, Answer Page #2 Due in class, noon, Tuesday March 26

This is an exam. Do not discuss it with anyone.

3. Compare `dind` by `young` on the data page, starting with the boxplot `boxplot(dind~young)`	Fill in or CIRCLE the correct answer
3.1 The boxplot above suggests the quantity `dind` is lower in pairs with a treated subject 10 years or younger, but `dind` is also more dispersed in the young group.	Circle one: TRUE FALSE
3.2 Given what you saw in the boxplot, you cannot appropriately use Wilcoxon's rank sum test to test the null hypothesis that `dind` has the same distribution in `young` and `notyoung` groups.	Circle one: TRUE FALSE
3.3 If you compare `Young` and `NotYoung` groups in terms of `dind` in all 1113x447=497511 possible ways, in more than 70% of such comparisons, the `dind` value is a larger number for the person in the `NotYoung` group.	Circle one: TRUE FALSE
3.4 If you assumed `dind` was symmetric about its medians in `Young` and `NotYoung` groups but the group dispersions were different, then you could not appropriately test that the two groups had equal medians (with possibly unequal dispersions) using Wilcoxon's rank sum test in section 4.1 of Hollander and Wolfe (2nd ed) but you could use the method of Fligner and Policello in section 4.4.	Circle one: TRUE FALSE

4. Use the variables `avage` and `young10` defined on the data page. You also need to install, then load the `Rfit` package.	Fill in or CIRCLE the correct answer
4.1 What is the Kendall correlation between avage and dind? What is the P-value testing independence? What is the estimate of the probability of concordance?	Cor:_____ P-value:_____ Prob Concordance: _____
4.2 Use rfit to fit a rank regression of dind on three predictors, `avage, young10, treated.male`. What is the estimated coefficient of avage in this regression? What is the P-value for testing the null hypothesis that the coefficient is zero.	Estimate:_____ P-value:_____
4.3 In the model you fitted using rfit in 4.2, test the one hypothesis that both the coefficient of `avage` and the coefficient of `young 10` are simultaneously zero. Do this using the methods for a rank regression fitted by rfit. What is the value of the test statistic? What is the P-value?	Value:_____ P-value:_____
4.4 Appropriately used, the rfit function assumes that the errors around the linear model are Normal, independent, with equal dispersion.	Circle one: TRUE FALSE

Answers

Statistics 501, Spring 2013, Midterm, Answer Page #1

(H&W refers to the text, Hollander and Wolfe 1999 2nd Ed)

Use the appropriate Wilcoxon test to answer the questions in part 1.	Fill in or CIRCLE the correct answer 6 points each
1.1 Apply the appropriate Wilcoxon test to the change in outcome among controls, camb. Give the two sided P-value, point estimate and 95% confidence interval. Is no change plausible?	P-value: 2.2×10^{-16} Estimate: -4.79 CI: [-5.87, -3.87] Circle one: Plausible (Not plausible)
1.2 Apply the appropriate Wilcoxon test to the change in outcome among treated subjects, tamb. Give the two sided P-value, point estimate and 95% confidence interval. Is no change plausible?	P-value: 2.2×10^{-16} Estimate: -17.5 CI:[-20.08, -15.12] Circle one: Plausible (Not plausible)
1.3 Apply the appropriate Wilcoxon test to whether the typical difference-in-differences is zero, dind. Give the two sided P-value, point estimate and 95% confidence interval. Is zero plausible?	P-value: 2.2×10^{-16} Estimate: -5.52 CI:[-7.04, -4.25] Circle one: Plausible (Not plausible)
1.4 In question 1.3, the appropriate Wilcoxon test is Wilcoxon's rank sum test (from chapter 4 in H&W) because treated and control groups are unrelated.	Circle one: TRUE (FALSE) Signed rank, because of matched pairs
1.5 In question 1.2, the boxplot of changes for the 1560 treated subjects does not look symmetric about its center. So, the P-value in 1.2 has no meaning as a test of the null hypothesis of symmetry of changes about zero.	Circle one: Doesn't look symmetric (TRUE) FALSE P-value meaningless TRUE (FALSE) H&W page 49, comment #14.
1.6 In question 1.1, there are 1,217,580 Walsh averages for the 1560 changes in the control group, and more than 80% of these are negative.	I did not grade this question. There were lots of ties. A student pointed out that R's (correct) handling of ties was surprising. I did not intend this to be a complex question, so I did not grade it.
1.7 Based on your answer to 1.3, the treatment was associated with a greater increase parasites in the blood of treated subjects than in controls.	Circle one: TRUE (FALSE)

2. Define the `group` variable as on the data page. It refers to age and gender of the treated person in a pair. Use it to study how `dind` varies among the four groups. Use appropriate nonparametric tests for all comparisons.	Fill in or CIRCLE the correct answer 6 points each
2.1 Is it plausible that `dind` has the same distribution in the four groups defined by `group`? What is the name of the appropriate nonparametric test? What is the value of the test statistic? What is the P-value? Is the null hypothesis of no difference plausible?	Name of test: Kruskal Wallis test. Value: 200.65 P-value: 2.2×10^{-16} Circle one: Plausible (Not plausible)
2.2 Compare all six pairs of two of the four groups from 2.1. Use Holm's method with an appropriate nonparametric test. List all pairs of groups as (A,B) that do **not** differ significantly at the 0.05 level, for instance (young.male,notyoungmale). List up to 6 pairs. If none, write none.	(NotYoung:Male, NotYoung:Female) (Young:Male, Young:Female)
2.3 In all data sets, Holm's procedure rejects each hypothesis rejected by the Bonferroni method and may reject additional hypotheses.	Circle one: (TRUE) FALSE

Answers, continued

Statistics 501, Spring 2013, Midterm, Answer Page #2 Due in class, noon, Tuesday March 26

This is an exam. Do not discuss it with anyone.

3. Compare `dind` by `young` on the data page, starting with the boxplot `boxplot(dind~young)`	Fill in or CIRCLE the correct answer 6 points each
3.1 The boxplot above suggests the quantity `dind` is lower in pairs with a treated subject 10 years or younger, but `dind` is also more dispersed in the young group.	Circle one: (TRUE) FALSE
3.2 Given what you saw in the boxplot, you cannot appropriately use Wilcoxon's rank sum test to test the null hypothesis that `dind` has **the same distribution** in `young` and `notyoung` groups.	Circle one: TRUE (FALSE) H&W page 123, comment #14.
3.3 If you compare `Young` and `NotYoung` groups in terms of `dind` in all 1113x447=497511 possible ways, in more than 70% of such comparisons, the `dind` value is a larger number for the person in the `NotYoung` group.	Circle one: (TRUE) FALSE H&W page 117, comment #7
3.4 If you assumed `dind` was symmetric about its medians in `Young` and `NotYoung` groups but the group dispersions were different, then you could not appropriately test that the **two groups had equal medians (with possibly unequal dispersions)** using Wilcoxon's rank sum test in section 4.1 of Hollander and Wolfe (2nd ed) but you could use the method of Fligner and Policello in section 4.4.	Circle one: (TRUE) FALSE H&W page 135, section 4.4, paragraph 1 and H&W page 120, comment #11. Wilcoxon's test can test that the null hypothesis that two distributions are **the same** but not that they have **the same medians with different dispersions**.

4. Use the variables `avage` and `young10` defined on the data page. You also need to install, then load the `Rfit` package.	Fill in or CIRCLE the correct answer 6 points each, except 4.4 for 4 points
4.1 What is the Kendall correlation between avage and dind? What is the P-value testing independence? What is the estimate of the probability of concordance?	Cor: 0.237 P-value: 2.2×10^{-16} Prob Concordance: 0.618
4.2 Use rfit to fit a rank regression of dind on three predictors, `avage, young10, treated.male`. What is the estimated coefficient of avage in this regression? What is the P-value for testing the null hypothesis that the coefficient is zero.	Estimate: 0.079 P-value: 0.000870
4.3 In the model you fitted using rfit in 4.2, test the one hypothesis that both the coefficient of `avage` and the coefficient of `young 10` are simultaneously zero. Do this using the methods for a rank regression fitted by rfit. What is the value of the test statistic? What is the P-value?	Value: 373.77 P-value: 0.00 Use the drop.test function in the Rfit package: it is analogous to the F-test of a general linear hypothesis
4.4 Appropriately used, the rfit function assumes that the errors around the linear model are **Normal**, independent, with equal dispersion.	TRUE (FALSE) Errors are not assumed Normal. H&W page 439 section 9.6, assumption C2.

Doing the Problem Set in R
Stat 501, Spring 2013, Midterm

```
> attach(garki)
> tamb<-treated.after-treated.before
> camb<-control.after-control.before
> dind<-tamb-camb

Question 1.1
> wilcox.test(camb,conf.int=T)
        Wilcoxon signed rank test with continuity correction
data:  camb
V = 216499, p-value < 2.2e-16
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -5.874995 -3.874996
sample estimates:
(pseudo)median
     -4.791616
Question 1.2
> wilcox.test(tamb,conf.int=T)
        Wilcoxon signed rank test with continuity correction
data:  tamb
V = 3269.5, p-value < 2.2e-16
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -20.08338 -15.12499
sample estimates:
(pseudo)median
     -17.49996
Question 1.3
> wilcox.test(dind,conf.int=T)
        Wilcoxon signed rank test with continuity correction
data:  dind
V = 336360.5, p-value < 2.2e-16
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -7.041657 -4.250007
sample estimates:
(pseudo)median
     -5.517102
Question 1.6
> 1560*1561/2
[1] 1217580
> 216499/1217580
[1] 0.1778109
> 1-0.1778109
[1] 0.8221891
> 0.8221891>.8
[1] TRUE

Question 2.1
> kruskal.test(dind~group)
        Kruskal-Wallis rank sum test
data:  dind by group
Kruskal-Wallis chi-squared = 200.6542, df = 3, p-value < 2.2e-16
Question 2.2
> pairwise.wilcox.test(dind,group)
        Pairwise comparisons using Wilcoxon rank sum test
data:  dind and group
```

```
             NotYoung:Female NotYoung:Male Young:Female
NotYoung:Male 0.990           -             -
Young:Female  2.9e-12         2.9e-12       -
Young:Male    < 2e-16         < 2e-16       0.083
P value adjustment method: holm
Question 4.1
> cor.test(avage,dind,method="k")
        Kendall's rank correlation tau
data:  avage and dind
z = 13.7758, p-value < 2.2e-16
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.2366609
> (0.2366609+1)/2
[1] 0.6183304
Question 4.2
> md<-rfit(dind~treated.age+young10+treated.male)
> summary(md)
Coefficients:
               Estimate Std. Error  t.value   p.value
             -3.276001   0.868523  -3.7719 0.0001681 ***
treated.age   0.079314   0.023775   3.3360 0.0008700 ***
young10     -30.924315   0.921458 -33.5602 < 2.2e-16 ***
treated.male  -0.982663   0.547096  -1.7961 0.0726660 .
---
Multiple R-squared (Robust): 0.3260413
Reduction in Dispersion Test: 250.9156 p-value: 0
Question 4.3
Compare the full model to the reduced model.
> mdr<-rfit(dind~treated.male)
rfit.default(formula = dind ~ treated.male)
             treated.male
   -1.000000    -1.249973
> drop.test(md,mdr)
Drop in Dispersion Test
F-Statistic     p-value
     373.77        0.00
```

Statistics 501 Spring 2013 Final Exam: Data Page 1
This is an exam. Do not discuss it with anyone.
Due: Monday, April 29, at 11:00am

The data are from NHANES 2009-2010. It is a 2^5 table. The data are in the nhanesD object in the workspace, and the table is below. As suggested by NHANES, a person is judged depressed if their score on the 9 item depression screener (DPQ) is 10 or more. The other variables are alcohol last year, age, married, and gender.

```
> dimnames(nhanesD)
$depressed
[1] "Depressed"     "Not Depressed"
$alcohol
[1] "<12 drinks last year"  ">=12 drinks last year"
$age
[1] "<50"  ">=50"
$married
[1] "married" "other"
$gender
[1] "male"   "female"
```

IMPORTANT: **Please refer to the variables with the letters** d=depressed, b=alcohol (booze), a=age, m=married and g=gender. Use the margin-preservation notation with these letters to refer to log-linear models. For example, you would refer to model of independence as [d][b][a][m][g]. **Use the likelihood ratio chi-square**.

```
        d-1         b-2         a-3         m-4         g-5
"depressed"   "alcohol"       "age"   "married"    "gender"
```

Questions 2.3-2.6 asks you to calculate two odds ratios or probabilities from fitted counts. This refers to the fitted counts in the full nhanesD table as that table is currently structured, with the 11 and 22 cells in the numerator. The program, loglin, fits iteratively, and the question asks you to set eps=0.000001 in the loglin call and report odds ratios to 2 significant digits. If the odds are twice as great, we speak in English as twice as likely. **Make and keep a photocopy of your answer page**. **The exam is due in my office, 473 Huntsman, on Monday April 29 at 11:00am.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman or by giving it to Adam at the front desk in statistics, but if you turn in the exam early, place it in an envelope addressed to me. When all of the exams are graded, I will add an **answer key** to the on-line bulk-pack for the course. You can compare the answer key to your photocopy of your exam. Your course grade will be available from the Registrar. I no longer distribute answer keys and graded exams by US Mail. **Turn in only the answer page**. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question

Have a great summer!

This is an exam. Do not discuss it with anyone.

```
> nhanesD
, , age = <50, married = married, gender = male
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                         5                    27
  Not Depressed                    70                   499
, , age = >=50, married = married, gender = male
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                         6                    36
  Not Depressed                   154                   695
, , age = <50, married = other, gender = male
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                        10                    53
  Not Depressed                    71                   559
, , age = >=50, married = other, gender = male
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                         6                    35
  Not Depressed                    61                   316
, , age = <50, married = married, gender = female
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                        19                    43
  Not Depressed                   201                   374
, , age = >=50, married = married, gender = female
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                        25                    24
  Not Depressed                   235                   328
, , age = <50, married = other, gender = female
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                        33                    81
  Not Depressed                   182                   458
, , age = >=50, married = other, gender = female
                alcohol
depressed        <12 drinks last year >=12 drinks last year
  Depressed                        42                    58
  Not Depressed                   270                   293
```

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2013 Final Exam: Answer Page 1 This is an exam. Do not discuss it with anyone. Due Monday, April 29, 2013, at 11:00am.

Use letters d, b, a, m and g to refer to variables and the [] notation to refer to log-linear models. In question 1.1, this is done for you. See the data page.	Fill in or CIRCLE the correct answer
1.1 Which log-linear model says the five variables are independent? Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Is independence of all 5 variables plausible?	Model: `[d][b][a][m][g]` Value: ____ df:____ P:_____ Circle One: Plausible Not Plausible
1.2 Which log-linear model says that alcohol last year (b) and marital status (m) are conditionally independent given the other three variables? Write in the model, as in 1.1. Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible?	Model: _____ Value: ____ df:____ P:_____ Circle One: Plausible Not Plausible
1.3 Which log-linear model says being depressed (d) and alcohol (b) are related, but related in a simple way, specifically with the same odds ratio at all values of the other variables, and subject to that condition, the other variables may have any relationship at all? Write in the model. Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible?	Model: Value: ____ df:____ P:_____ Circle One: Plausible Not Plausible
1.4 Consider [dm][dg][ba][bg][amg] as the model. Give the value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible?	Value: _____ df:_____ P:_____ Circle One: Plausible Not Plausible
1.5 The model [dm][dg][ba][bg][amg] in question 1.4 says being depressed (d) is independent of age (a).	Circle One: TRUE FALSE
1.6 The model [dm][dg][ba][bg][amg] in question 1.4 says the odds ratio (in the full nhanesD table) linking being depressed (d) with being married (m) is different for men and women (g).	Circle One: TRUE FALSE

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2013 Final Exam: Answer Page 2 This is an exam. Do not discuss it with anyone. Due Monday, April 29, 2013, at 11:00am.

See the data page.	Fill in or CIRCLE the correct answer
2.1 Test the null hypothesis that the model [dm][dg][ba][bg][amg] in 1.4 is adequate against the alternative hypothesis that the [dmg] u-term needs to be added to the model. Give the value of chi-square for this test, its degrees of freedom, and indicate whether the null hypothesis is plausible.	Value: _____ df:_____ P:_____ Circle One: Plausible Not Plausible
2.2 Are there any u-terms in the model [dm][dg][ba][bg][amg] that may be removed without a statistically significant degradation in fit at the 0.05 level. If yes, list any and all u-terms that may be removed (one at a time) without degradation of fit. If none, write "none".	
2.3 In the model [dm][dg][ba][bg][amg], give the fitted odds ratio linking being depressed with being married for men, under 50, who had fewer than 12 alcoholic drinks last year. Repeat for women, under 50, who had fewer than 12 alcoholic drinks last year. See the data page.	Set eps=0.000001 in the loglin call. Report odds ratios to 2 significant digits. Men, <50, <12 drinks: _____ Women, <50, <12 drinks: _____
2.4 Consider just individuals who are under 50 and had fewer than 12 alcoholic drinks last year. For these individuals, based on your answer to question 2.3, the point estimates of odds ratios suggest that married men are about half as likely as unmarried men to be depressed, but women in this group are twice as likely to be depressed.	Circle One: TRUE FALSE
2.5 In the model [dm][dg][ba][bg][amg], under age 50, with fewer than 12 alcoholic drinks last year, married men are estimated to be about 5 times more likely than married women to be depressed. (Use fitted odds ratios).	Circle One: TRUE FALSE
2.6 In model [dm][dg][ba][bg][amg], married men under age 50 with fewer than 12 drinks last year are estimated to have a probability of depression of about 0.05.	Circle One: TRUE FALSE

Stat 501 S-2013 Final Exam: Answer Page 1 Answers.

Use letters d, b, a, m and g to refer to variables and the [] notation to refer to log-linear models. In question 1.1, this is done for you. See the data page.	Fill in or CIRCLE the correct answer 8 points each except as noted
1.1 Which log-linear model says the five variables are independent? Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Is independence of all 5 variables plausible?	Model: `[d][b][a][m][g]` Value: 729.894 df: 26 P: ~0 Circle One: Plausible **Not Plausible**
1.2 Which log-linear model says that alcohol last year (b) and marital status (m) are conditionally independent given the other three variables? Write in the model, as in 1.1. Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible? (10 points)	Model: [dbag][damg] Value: 12.505 df: 8 P: 0.13 Circle One: **Plausible** Not Plausible
1.3 Which log-linear models says being depressed (d) and alcohol (b) are related, but related in a simple way, specifically with the same odds ratio at all values of the other variables, and subject to that condition, the other variables may have any relationship at all? Write in the model, as in 1.1. Give the numerical value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible? (10 points)	Model: [db][damg][bamg] Value: 5.11 df: 7 P: 0.64 Circle One: **Plausible** Not Plausible
1.4 Consider [dm][dg][ba][bg][amg] as the model. Give the value of the likelihood ratio test of fit, its degrees of freedom (df), the P-value (P). Based just on the this test of fit, is this model plausible?	Value: 17.6 df: 18 P: 0.48 Circle One: **Plausible** Not Plausible
1.5 The model [dm][dg][ba][bg][amg] in question 1.4 says being depressed (d) is independent of age (a).	Circle One: TRUE **FALSE**
1.6 The model [dm][dg][ba][bg][amg] in question 1.4 says the odds ratio (in the full nhanesD table) linking being depressed (d) with being married (m) is different for men and women (g).	Circle One: TRUE **FALSE**

Stat 501 S-2013 Final Exam: Answer Page 2 Answers.

See the data page.	Fill in or CIRCLE the correct answer
2.1 Test the null hypothesis that the model [dm][dg][ba][bg][amg] in 1.4 is adequate against the alternative hypothesis that the [dmg] u-term needs to be added to the model. Give the value of chi-square for this test, its degrees of freedom, and indicate whether the null hypothesis is plausible.	Value: 0.166 df: 1 P: 0.68 Circle One: (Plausible) Not Plausible
2.2 Are there any u-terms in the model [dm][dg][ba][bg][amg] that may be removed without a statistically significant degradation in fit at the 0.05 level. If yes, list any and all u-terms that may be removed (one at a time) without degradation of fit. If none, write "none".	none
2.3 In the model [dm][dg][ba][bg][amg], give the fitted odds ratio linking being depressed with being married for men, under 50, who had fewer than 12 alcoholic drinks last year. Repeat for women, under 50, who had fewer than 12 alcoholic drinks last year. See the data page.	Set eps=0.000001 in the loglin call. Report odds ratios to 2 significant digits. Men, <50, <12 drinks: 0.48 Women, <50, <12 drinks: 0.48
2.4 Consider just individuals who are under 50 and had fewer than 12 alcoholic drinks last year. For these individuals, based on your answer to question 2.3, the point estimates of odds ratios suggest that married men are about half as likely as unmarried men to be depressed, but women in this group are twice as likely to be depressed.	Circle One: TRUE (FALSE) Married men are half as likely as unmarried men to be depressed, but the same is true for married women.
2.5 In the model [dm][dg][ba][bg][amg], under age 50, with fewer than 12 alcoholic drinks last year, married men are estimated to be about 5 times more likely than married women to be depressed. (Use fitted odds ratios).	Circle One: TRUE (FALSE) 1/5 as likely, not 5 times as likely.
2.6 In model [dm][dg][ba][bg][amg], married men under age 50 with fewer than 12 drinks last year are estimated to have a probability of depression of about 0.05.	Circle One: (TRUE) FALSE

Doing the Problem Set in R
(Final Spring 2013 Statistics 501)

1.1

```
> loglin(nhanesD,list(1,2,3,4,5))
2 iterations: deviation 9.094947e-13
$lrt
[1] 729.894
$df
[1] 26
> 1-pchisq(729.894,26)
[1] 0
```

1.2

```
> loglin(nhanesD,list(c(1,2,3,5),c(1,3,4,5)))
2 iterations: deviation 1.136868e-13
$lrt
[1] 12.5054
$df
[1] 8
$margin
$margin[[1]]
[1] "depressed" "alcohol"   "age"       "gender"
$margin[[2]]
[1] "depressed" "age"       "married"   "gender"
> 1-pchisq(12.5054,8)
[1] 0.1300384
```

1.3

```
> loglin(nhanesD,list(c(1,2),c(1,3,4,5),c(2,3,4,5)))
4 iterations: deviation 0.03090209
$lrt
[1] 5.111691
$df
[1] 7
$margin
$margin[[1]]
[1] "depressed" "alcohol"
$margin[[2]]
[1] "depressed" "age"       "married"   "gender"
$margin[[3]]
[1] "alcohol" "age"     "married" "gender"
> 1-pchisq(5.111691,7)
[1] 0.6463351
```

1.4

```
> loglin(nhanesD,list(c(1,4),c(1,5),c(2,3),c(2,5),c(3,4,5)))
5 iterations: deviation 0.01719219
$lrt
[1] 17.5982
$df
[1] 18
$margin
$margin[[1]]
[1] "depressed" "married"
$margin[[2]]
[1] "depressed" "gender"
$margin[[3]]
[1] "alcohol" "age"
$margin[[4]]
[1] "alcohol" "gender"
$margin[[5]]
[1] "age"     "married" "gender"
> 1-pchisq(17.5982,18)
[1] 0.4824019
```

2.1 Compare two nested models, the following model and the one in 1.4.

```
> loglin(nhanesD,list(c(1,4,5),c(2,3),c(2,5),c(3,4,5)))
5 iterations: deviation 0.01679229
$lrt
[1] 17.43217
$df
[1] 17
$margin
$margin[[1]]
[1] "depressed" "married"   "gender"
$margin[[2]]
[1] "alcohol" "age"
$margin[[3]]
[1] "alcohol" "gender"
$margin[[4]]
[1] "age"     "married" "gender"
> 17.5982-17.43217
[1] 0.16603
> 18-17
[1] 1
> 1-pchisq(0.16603,1)
[1] 0.6836644
```

2.3 You set eps==0.000001 to ensure you are close to convergence.

```
> ft<-loglin(nhanesD,list(c(1,4),c(1,5),c(2,3),c(2,5),c(3,4,5)),fit=T,
eps=0.000001,iter=30)$fit
10 iterations: deviation 1.730364e-07 (Notice: 10 iterations)
> ft[,1,1,,1]
                married
depressed         married     other
  Depressed      3.500608  7.269726
  Not Depressed 65.192347 71.938623
> or(ft[,1,1,,1])
[1] 0.4815323
> ft[,1,1,,2]
                married
depressed         married     other
  Depressed      17.70299  36.61797
  Not Depressed 185.21136 203.56637
> or(ft[,1,1,,2])
[1] 0.4834511
```

2.6

```
> ft[,1,1,,1]
                married
depressed         married     other
  Depressed      3.500608  7.269726
  Not Depressed 65.192347 71.938623
> 3.500608/(3.500608+65.192347)
[1] 0.05096022
```

Statistics 501, Spring 2012, Midterm: Data Page #1

Due in class, noon, Tuesday March 27, 2012

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. The University often expels students caught cheating on exams. Cheating on an exam is the single dumbest thing a PhD student at Penn can do.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question. **Due in class Tuesday 29 March 2011.**

The data for this problem are at in the latest Rst501.RData for R users as the object bmi501 and in the bmi501 file at http://stat.wharton.upenn.edu/statweb/course/Spring-2008/stat501 The list is case sensitive, so nhanes501.txt is with lower case items.

The data are from the US National Health and Nutrition Examination Survey (NHANES) for 2007-2008. You can obtain the complete survey from ICPSR via the Penn library web page or directly from the CDC, but there is no reason to do this for the current exam. The data consist of 676 matched pairs of one daily smoker and one nonsmoker. A daily smoker reported smoking on every day of the past 30 days (SMD641=30) and having smoked at least 100 cigarettes in his or her lifetime (SMQ020=YES). A nonsmoker reports having smoked fewer than 100 cigarettes in his or her lifetime (SMQ020=NO) and has no reported smoking in the previous 30 days (SMD641=missing). Data for a smoker begins with S, while data for a nonsmoking control begins with C. The pairs were matched for education (Educ, higher=more), Income (ratio to poverty level), Black (1=yes), Female (1=yes), Married (1=yes), and Age. In the first row of bmi501, an unmarried female smoker aged 77 is paired with an unmarried female nonsmoker aged 79.

It is often said that smoking depresses appetite. People sometimes say that they are reluctant to quit smoking for fear of gaining weight. What do data say about this? The dataset also contains BMI for smokers and controls. See http://www.nhlbisupport.com/bmi/ In the first row of bmi501, the smoker weighed a little less, BMI = 19.96 for the smoker versus BMI = 22.71 for the control.

```
> dim(bmi501)
[1] 676  14
> bmi501[1,]
  Seduc Sincome Sblack Sfemale Smarried Sage
1     2    1.57      0       1        0   77
   SBMI Ceduc Cincome Cblack Cfemale Cmarried
1 19.96     2    1.67      0       1        0
  Cage  CBMI
   1  79 22.71
```

You will need to calculate the matched pair difference in BMI

```
>attach(bmi501)
> dif<-SBMI-CBMI
```

You will need the variable grp, which equals the variable grp2. Spend some time to make sure you understand what the levels of grp means and what it means that grp = grp2.

```
> grp<-factor(SMarried):factor(SFemale)
> grp2<-factor(CMarried):factor(CFemale)
> table(grp,grp2)
     grp2
grp   0:0 0:1 1:0 1:1
  0:0 227   0   0   0
  0:1   0 174   0   0
  1:0   0   0 162   0
  1:1   0   0   0 113
```

STATISTICS 501, SPRING 2012, MIDTERM DATA PAGE #2

Due in class, noon, Tuesday March 27, 2012

Please assume that the 676 matched pairs are independent for distinct pairs and that they represent 676 independent draws from a single multivariate (ie many variable) distribution.

The model for **question 2.2-2.4** has the $dif_{ij} = \mu + \tau_j + e_{ij}$ where there are groups j = 1, 2, 3, 4. You are asked to test $H_0: \tau_1 = \tau_2 = \tau_3 = \tau_4$ against a general alternative, and six hypotheses of the form $H_{12}: \tau_1 = \tau_2$, $H_{13}: \tau_1 = \tau_3$, $H_{14}: \tau_1 = \tau_4$, $H_{23}: \tau_2 = \tau_3$, $H_{24}: \tau_2 = \tau_4$, $H_{34}: \tau_3 = \tau_4$.

Question 3 asks you to use the rfit function in the Rfit package to fit and compare two regressions using just data on the 676 controls.

Model 1: $CBMI = \beta_0 + \beta_{age}\ CAge + \beta_{female}\ CFemale + e$ with e iid, symmetric about 0, continuous.

Model 2: $CBMI = \gamma_0 + \gamma_{age}\ CAge + \gamma_{female}\ CFemale + \gamma_{educ}\ CEduc + \gamma_{income}\ CIncome + u$ with u iid, symmetric about 0, continuous.

Print Name **Last name**, then First: _____ ID#_____

Statistics 501, Spring 2012, Midterm, Answer Page #1 Due noon, Tuesday March 27, 2012

This is an exam. Do not discuss it with anyone.

Use bmi501 to answer these questions.	Fill in or CIRCLE the Correct Answer
1.1 The median smoker and the median nonsmoker are both overweight (BMI 25-29.9).	TRUE FALSE
1.2 More than a quarter of smokers and more than a quarter of nonsmokers are obese (BMI of 30 or more).	TRUE FALSE
1.3 In the dataset, men are always paired with men and women are always paired with women.	TRUE FALSE
1.4 Use the Shapiro-Wilk test to test the null hypothesis that the matched pair differences "dif" in BMI are Normally distributed. Give the P-value. Is the null hypothesis plausible?	P-value: _____ Circle one: PLAUSIBLE NOT PLAUSIBLE
1.5 Use the appropriate Wilcoxon procedure to test the null hypothesis that the smoker-minus-control matched pair differences are symmetrically distributed about zero. Give the 2-sided P-value. Is the null hypothesis plausible?	P-value: _____ Circle one: PLAUSIBLE NOT PLAUSIBLE
1.6 For the test you did in 1.5, give the corresponding point estimate of the center of symmetry of the smoker-minus-control matched pair differences. Is this point estimate the median of the `choose(676,2)= 228150` pairwise differences between a smoker and a matched control? (Yes or No).	Point estimate: _____ Circle one: YES NO
1.7 Give the 2-sided 95% confidence interval for the center of symmetry of the smoker-minus-control pair differences based on the test you did in 1.5. Give the interval. Smoking is associated with an increase in BMI. (True or false).	Confidence interval: _____ Circle one: TRUE FALSE
1.8 Use an appropriate t-test to construct the confidence interval for the center of symmetry of the smoker-minus-control pair differences. Give the interval. The t-interval is more than 8% longer than the Wilcoxon interval. (True or false).	Confidence interval: _____ Circle one: TRUE FALSE
1.9 A central limit theorem says t has more power than Wilcoxon in large samples.	Circle one: TRUE FALSE

Print Name Clearly, **Last**, First: _____ ID#_____

Statistics 501, Spring 2012, Midterm, Answer Page #2 Due noon, Tuesday March 27, 2012

This is an exam. Do not discuss it with anyone.

2.1 Use an appropriate Wilcoxon procedure to test the null hypothesis that the smoker-minus-control pair difference "dif" in BMI has the same distribution for men and women. Give the two-sided P-value and the associated point estimate for the difference. Is the hypothesis plausible?	P-value: _____ Point estimate:_____ Circle one: PLAUSIBLE NOT PLAUSIBLE
2.2 Use an appropriate nonparametric analog of the F-test (from H&W) to test the null hypothesis that the four levels of "grp" have the same distribution of "dif". (See the data page for definitions.) What is the name of the test? What is the P-value? Is the null hypothesis plausible?	Name of test:_____ P-value: _____ Circle one: PLAUSIBLE NOT PLAUSIBLE
2.3 Use Holm's procedure with an appropriate Wilcoxon procedure to test all pairwise comparisons in 2.2. What is the smallest of the 6 adjusted P-values from Holm's procedure?	Smallest of 6 pairwise P-values after adjustment using Holms method: P-value: _____
2.4 When using Holm's procedure, it is logically possible that there is exactly one false hypothesis, namely H_{14}: $\tau_1 = \tau_4$.	Circle one: TRUE FALSE
2.5 If one looks at two of the 676 matched pairs picked at random, what is the estimate of the probability that the pair with the higher CEduc also has the higher SEduc?	Estimated probability: _____

Question 3 refers to models 1 and 2 on the data page and asks you to fit them using the rfit function in the Rfit package.	Fill in or CIRCLE the Correct Answer
3.1 In model 1 on the data page, test the null hypothesis H_0: $\beta_{age} = 0$ using the nonparametric analog of the partial t-test in regression. Give the 2-sided P-value. Is H_0 plausible as judged by the conventional 0.05 standard?	P-value: _____ Circle one: PLAUSIBLE NOT PLAUSIBLE
3.2 In model 2 on the data page, test the null hypothesis H_0: $\gamma_{educ} = \gamma_{income} = 0$ using the nonparametric analog of the partial F-test (aka general linear hypothesis). Give the P-value. Is H_0 plausible as judged by the conventional	P-value: _____ Circle one: PLAUSIBLE NOT PLAUSIBLE

0.05 standard?	

Statistics 501, Spring 2012, Midterm, Answer Page #1, ANSWERS

Use bmi501 to answer these questions.	Fill in or CIRCLE (6 points each)
1.1 The median smoker and the median nonsmoker are both overweight (BMI 25-29.9).	(TRUE) FALSE
1.2 More than a quarter of smokers and more than a quarter of nonsmokers are obese (BMI of 30 or more).	(TRUE) FALSE
1.3 In the dataset, men are always paired with men and women are always paired with women.	(TRUE) FALSE
1.4 Use the Shapiro-Wilk test to test the null hypothesis that the matched pair differences "dif" in BMI are Normally distributed. Give the P-value. Is the null hypothesis plausible?	P-value: `1.765e-07` Circle one: PLAUSIBLE (NOT PLAUSIBLE)
1.5 Use the appropriate Wilcoxon procedure to test the null hypothesis that the smoker-minus-control matched pair differences are symmetrically distributed about zero. Give the 2-sided P-value. Is the null hypothesis plausible?	P-value: `9.045e-08` Circle one: PLAUSIBLE (NOT PLAUSIBLE)
1.6 For the test you did in 1.5, give the corresponding point estimate of the center of symmetry of the smoker-minus-control matched pair differences. Is this point estimate the median of the `choose(676,2)= 228150` pairwise differences between a smoker and a matched control? (Yes or No).	Point estimate: -1.92 Circle one: YES (NO) It is the median of the pairwise averages, not the pairwise differences.
1.7 Give the 2-sided 95% confidence interval for the center of symmetry of the smoker-minus-control pair differences based on the test you did in 1.5. Give the interval. Smoking is associated with an increase in BMI. (True or false).	Confidence interval: [-2.60, -1.23] Circle one: TRUE (FALSE)
1.8 Use an appropriate t-test to construct the confidence interval for the center of symmetry of the smoker-minus-control pair differences. Give the interval. The t-interval is more than 8% longer than the Wilcoxon interval. (True or false).	Confidence interval: [-2.77, -1.29] Circle one: (TRUE) FALSE
1.9 A central limit theorem says t has more power than Wilcoxon in large samples.	Circle one: TRUE (FALSE)

For 1.9, t has best power if the data are Normal, but not in general.

2.1 Use an appropriate Wilcoxon procedure to test the null hypothesis that the smoker-minus-control pair difference "dif" in BMI has the same distribution for men and women. Give the two-sided P-value and the associated point estimate for the difference. Is the hypothesis plausible?	P-value: 0.613 Point estimate: 0.360 Circle one: (PLAUSIBLE) NOT PLAUSIBLE
2.2 Use an appropriate nonparametric analog of the F-test (from H&W) to test the null hypothesis that the four levels of "grp" have the same distribution of "dif". (See the data page for definitions.) What is the name of the test? What is the P-value? Is the null hypothesis plausible?	Name of test: Kruskal-Wallis P-value: 0.607 Circle one: (PLAUSIBLE) NOT PLAUSIBLE
2.3 Use Holm's procedure with an appropriate Wilcoxon procedure to test all pairwise comparisons in 2.2. What is the smallest of the 6 adjusted P-values from Holm's procedure?	Smallest of 6 pairwise P-values after adjustment using Holms method: P-value: 1
2.4 When using Holm's procedure, it is logically possible that there is exactly one false hypothesis, namely $H_{14}: \tau_1 = \tau_4$.	TRUE (FALSE) If 1 and 4 are unequal, they can't both equal 2, so there can't just be 1 false hypothesis.
2.5 If one looks at two of the 676 matched pairs picked at random, what is the estimate of the probability that the pair with the higher CEduc also has the higher SEduc?	Estimated probability: 0.972 This is the probability of concordance from Kendall's correlation.

Question 3 refers to models 1 and 2 on the data page and asks you to fit them using the rfit function in the Rfit package.	Fill in or CIRCLE (8 points each)
3.1 In model 1 on the data page, test the null hypothesis $H_0: \beta_{age} = 0$ using the nonparametric analog of the partial t-test in regression. Give the 2-sided P-value. Is H_0 plausible as judged by the conventional 0.05 standard?	P-value: 0.04996 Circle one: PLAUSIBLE (NOT PLAUSIBLE)
3.2 In model 2 on the data page, test the null hypothesis $H_0: \gamma_{educ} = \gamma_{income} = 0$ using the nonparametric analog of the partial F-test (aka general linear hypothesis). Give the P-value. Is H_0 plausible as judged by the conventional 0.05 standard?	P-value: 0.779 Circle one: (PLAUSIBLE) NOT PLAUSIBLE

Doing the Problem Set in R: Spring 2012 Midterm St 501

1.1 and 1.2

```
> attach(bmi501)
> boxplot(SBMI,CBMI)
> summary(SBMI)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  14.20   22.99   26.48   27.63   31.02   63.95
> summary(CBMI)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  15.69   25.31   28.48   29.66   32.64   73.43
```

1.3

```
> table(SFemale,CFemale)
       CFemale
SFemale   0   1
      0 389   0
      1   0 287
```

1.4

```
> dif<-SBMI-CBMI
> shapiro.test(dif)
        Shapiro-Wilk normality test
data:  dif
W = 0.9817, p-value = 1.765e-07
```

1.5-1.7

```
> wilcox.test(dif,conf.int=T)
Wilcoxon signed rank test:  dif
V = 87263.5, p-value = 9.045e-08
95 percent confidence interval:
 -2.600036 -1.230013
sample estimates:
     -1.919962
```

1.8

```
> t.test(dif)
        One Sample t-test  data:  dif
t = -5.3672, df = 675, p-value = 1.101e-07
95 percent confidence interval:
 -2.769503 -1.285911
sample estimates:  mean of x
-2.027707
> (-1.285911)-(-2.769503)
[1] 1.483592
> (-1.230013)-(-2.600036)
[1] 1.370023
> 1.483592/1.370023
[1] 1.082896
> wilcox.test(dif~SFemale,conf.int=T)
Wilcoxon rank sum test data:  dif by SFemale
W = 57091.5, p-value = 0.613
```

```
95 percent confidence interval:
 -1.049956  1.770011
sample estimates: difference in location
             0.3599914
2.2
> kruskal.test(dif~grp)
Kruskal-Wallis rank sum test data:  dif by grp
Kruskal-Wallis chi-squared = 1.8368, df = 3, p-value =
0.607
2.3
> pairwise.wilcox.test(dif,grp)
Pairwise comparisons using Wilcoxon rank sum test
data:  dif and grp P value adjustment method: holm
    0:0 0:1 1:0
0:1 1   -   -
1:0 1   1   -
1:1 1   1   1
2.5
> cor.test(SEduc,CEduc,method="kendall")
Kendall's rank correlation tau data:  SEduc and CEduc
z = 29.5666, p-value < 2.2e-16
sample estimates: tau
0.9446568
> (0.94465685+1)/2
[1] 0.9723284
3.1-2
> out<-rfit(CBMI~CAge+CFemale)
> summary(out)
Coefficients:
         Estimate Std. Error t.value p.value
        26.985321   0.691313 39.0349 < 2e-16 ***
CAge     0.026457   0.013472  1.9638 0.04996 *
CFemale  0.691179   0.441895  1.5641 0.11826
> out2<-rfit(CBMI~CAge+CFemale+CIncome+CEduc)
> summary(out2)
Coefficients:
         Estimate Std. Error t.value p.value
        27.316813   0.921498 29.6439 < 2e-16 ***
CAge     0.025602   0.013506  1.8956 0.05844 .
CFemale  0.734714   0.449071  1.6361 0.10229
CIncome  0.028365   0.164397  0.1725 0.86307
CEduc   -0.151863   0.221289 -0.6863 0.49278
> drop.test(out2,out)
Drop in Dispersion Test
F-Statistic     p-value
    0.25046     0.77851
```

Statistics 501, Spring 2011, Midterm: Data Page #1

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. The University often expels students caught cheating on exams. Cheating on an exam is the single dumbest thing a PhD student at Penn can do.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question. **Due in class Tuesday 29 March 2011.**

The data for this problem are at in the latest Rst501.RData for R users as the object nhanes501 and in nhanes501.txt as a text file at http://stat.wharton.upenn.edu/statweb/course/Spring-2008/stat501 The list is case sensitive, so nhanes501.txt is with lower case items.

The data are from the US National Health and Nutrition Examination Survey (NHANES) for 2007-2008. You can obtain the complete survey from ICPSR via the Penn library web page, but there is no reason to do this for the current exam. The data consist of 250 matched pairs of one daily smoker and one nonsmoker. A daily smoker reported smoking on every day of the past 30 days (SMD641=30) and having smoked at least 100 cigarettes in his or her lifetime (SMQ020=YES). A nonsmoker reports having smoked fewer than 100 cigarettes in his or her lifetime (SMQ020=NO) and has no reported smoking in the previous 30 days (SMD641=missing). The pairs were matched for gender, age, Hispanic or black or other, education level, household income level, and missing value indicators for education and income.

LBXBCD is the blood level of cadmium in μg/dL, and LBXBPB is is the blood level of lead in μg/dL, where LBXBCDsmk is for the smoker in a pair, LBXBCDcont is for the nonsmoker (control) in the pair, and LBXBCDdif is the difference, .82-.37=.45 for pair 1. SMD650smk is for the smoker in the pair: it is the answer to "During the past 30 days, on the days that you smoked, about how many cigarettes did you smoke per day? 1 pack = 20 cigarettes. If >95, enter 95". There is one missing value for SMD650smk – it is an NA. The variable female = 1 if the smoker is female, but in almost all pairs, the two individuals are of the same gender.

```
> dim(nhanes501)
[1] 250   9
> round(nhanes501,2)[1:3,]
  id LBXBCDsmk LBXBCDcont LBXBCDdif LBXBPBsmk LBXBPBcont LBXBPBdif SMD650smk female
1  1      0.82       0.37      0.45      0.86       1.30     -0.44         1      1
2  2      3.00       0.27      2.73      2.60       0.82      1.78         3      1
3  3      0.44       0.53     -0.09      1.71       3.40     -1.69         3      1
```

For problem 1.2, the codes are:

A. The matched pair differences in blood cadmium levels are approximately Normal.
B. The matched pair differences in blood cadmium levels have a thick right tail compared to the Normal (i.e., too many large positive values)
C. The matched pair differences in blood cadmium levels have a thick left tail compared to the Normal (i.e., too many large negative values)
D. The matched pair differences in blood cadmium levels have thick symmetric tails compared to the Normal (i.e., extreme values occur too often for the Normal, but they are equally likely to be positive or negative)
E. There are three large outliers, but otherwise the differences look Normal.

For question 2.
Hypotheses:

I. H_0: Z_i are iid, continuous and symmetric about zero versus H_A: Z_i are iid, continuous but not symmetric about 0.
II. H_0: Z_i are iid, continuous and symmetric about zero versus H_A: Z_i are iid, continuous symmetric about θ.
III. H_0: Z_i are independent, continuous and with median zero versus H_A: Z_i are iid, continuous with common median θ.

For **question 3**, use the model (Z_i, V_i) are iid bivariate observations from a continuous distribution.

Question 4 asks you to construct 3 groups based on the number of cigarettes smoked per day, SMD650smk. The groups are less than 10 (less than half a pack), half a pack to less than a pack (10 to less than 20), and a pack or more. You do this in R with the command cut. Notice that you need to use right=F to exclude 10 from the first interval and exclude 20 from the second. **An easy way to mess up on question 4** is to make the wrong groups. Check that you have the right groups by making sure you have the correct numbers in each group. Remember there is one NA, so 74+82+93 = 249.

```
> pack<-cut(SMD650smk,c(0,10,20,99),right=F)
> table(pack)
pack
 [0,10) [10,20) [20,99)
     74      82      93

as.numeric(pack) makes pack into 1, 2, 3.
> table(as.numeric(pack),pack)
   pack
    [0,10) [10,20) [20,99)
  1     74       0       0
  2      0      82       0
  3      0       0      93
```

The model for **question 4** has the $Z_{ij} = \mu + \tau_j = e_{ij}$ where there are groups j = 1, 2, 3, and i goes from 1 to 74 in group 1, from 1 to 82 in group 2, and from 1 to 93 in group 3, where the e_{ij} are iid from a continuous distribution. Here, j=1 for <half a pack, j=2 for at least half a pack but less than a pack, and j=3 for a pack or more per day. You are asked to test H_0: $\tau_1 = \tau_2 = \tau_3$ against a general alternative, and H_{12}: $\tau_1 = \tau_2$, H_{13}: $\tau_1 = \tau_3$, and H_{23}: $\tau_2 = \tau_3$.

Print Name **Last name**, then First: _____ ID#_____

Statistics 501, Spring 2011, Midterm, Answer Page #1

This is an exam. Do not discuss it with anyone.

1. Question 1 refers to the matched pair differences in blood levels of cadmium, LBXBCDdif.

All parts of question 1 use LBXBCDdif	Fill in or CIRCLE the correct answer
1.1 Test the null hypothesis that the differences in cadmium levels are Normally distributed using the Shapiro-Wilk test. Give the P-value and state whether the null hypothesis is plausible.	P-value: _____ Null hypothesis is: PAUSIBLE NOT PLAUSIBLE
1.2 Do a normal quantile plot of the differences in cadmium levels. Circle the ONE best interpretation of that plot; see the data page for the descriptions. (Do not turn in the plot.)	A B C D E
1.3 Use the appropriate version of Wilcoxon's test to test the null hypothesis that the differences in cadmium levels are symmetric about zero. Give the full name of the test, the two-sided P-value, and state whether the null hypothesis is plausible.	Full name: _____ P-value: _____ PAUSIBLE NOT PLAUSIBLE
1.4 Give the 95% confidence interval for the center of symmetry of the matched pair differences associated with the test in 1.3. Give the 95% confidence interval from the paired t-test. Is it true or false that the t-test interval is about 20% longer than the nonparametric interval?	Nonparametric interval: [,] t-test interval: [,] TRUE FALSE
1.5 What is the Hodges-Lehmann point estimate of the center of symmetry of the differences in cadmium levels.	Estimate: _____

2. Question 2 refers to the analyses you did in question 1 and to the three hypotheses, I, II, and III listed on the data page, where the Z_i are the matched pair differences in cadmium levels, i=1,2,…,250.

	Fill in or CIRCLE the correct answer
2.1 Wilcoxon's test can be used to test hypothesis I, but it will have meaningful power only if Prob($Z_i+Z_j>0$) is not close to ½. Here, "can be used" means that it falsely rejects the null hypothesis at the stated level, conventionally 0.05.	TRUE FALSE
2.2 The Hodges-Lehmann point estimate and confidence interval are not valid under the alternative hypothesis H_A of I but are value under H_A of II. Here, valid means that the point estimate is consistent for the center of symmetry of the Z_i and the 95% confidence interval covers the center of symmetry in 95% of studies.	TRUE FALSE
2.3 You cannot correctly use Wilcoxon's test to test hypothesis III, but you can use the sign test. Here, correctly means that the test falsely rejects a true null hypothesis at the nominal rate, conventionally 0.05.	TRUE FALSE
2.4 For the matched pair differences in cadmium levels in question 1, under the alternative hypothesis H_A of I, give a consistent estimate of Prob($Z_i+Z_j>0$). Give the numerical value of the estimate.	Estimate: _____

Print Name Clearly, **Last**, First: _____ ID#_____

Statistics 501, Spring 2011, Midterm, Answer Page #2

This is an exam. Do not discuss it with anyone.

3. Question 3 asks you to relate the pair differences in cadmium LBXBCDdif to the pair differences in lead LBXBPBdif.

	Fill in or CIRCLE the correct answer
3.1 Use Pearson's Normal theory correlation to test the null hypothesis that cadmium differences are unrelated to lead differences. Give the two-sided P-value and the point estimate of the correlation. By this standard, is it plausible that LBXBCDdif and LBXBPBdif are unrelated?	P-value: _____ Correlation: _____ PLAUSIBLE NOT PLAUSIBLE
3.2 Use Kendall's nonparametric correlation to test the null hypothesis that cadmium differences are unrelated to lead differences. Give the two-sided P-value and the point estimate of the correlation. By this standard, is it plausible that LBXBCDdif and LBXBPBdif are unrelated?	P-value: _____ Correlation: _____ PLAUSIBLE NOT PLAUSIBLE
3.3 Use the results in 3.2 to estimate the probability that, in two pairs, the higher cadmium difference will occur in the same pair as the higher lead difference (ie the probability of concordance.	Estimate: _____

4. Question 4 asks you to relate the pair differences in cadmium LBXBCDdif to the number of packs per day smoked by the smoker in each pair, in three groups, less than half a pack, at least half a pack but less than a pack, and a pack or more. See the data page for construction of the variable `pack`. Do this step carefully, or everything will be wrong – make sure the groups have 74, 82, and 93 pairs. Use the notation on the data page for question 4 (eg. H_0 or H_{12}) to refer to null hypotheses – do not invent a new notation.

	Fill in or CIRCLE the correct answer
4.1 Use an appropriate nonparametric test to test H_0, the hypothesis of no difference against the alternative of any pattern of differences among the τ's. Give the name of the test, the P-value and state whether the null hypothesis is plausible.	P-value: _____ Name of test: _____ PLAUSIBLE NOT PLAUSIBLE
4.2 Use Kendall's correlation to correlate SMD650smk and LBXBCDdif . Use it again to correlate as.numeric(pack) and LBXBCDdif. Give both correlations and two-sided P-values.	SMD650smk: P-value_____ Correlation:_____ as.numeric(pack): P-value_____ Correlation:_____
4.3 As discussed in class, use Holm's method to correct the pairwise Wilcoxon P-values. Give the P-values.	H_{12}: _____ H_{13}: _____ H_{23}:_____
4.4 As discussed in class, use Bonferroni's method to correct the pairwise Wilcoxon P-values. Give the P-values.	H_{12}: _____ H_{13}: _____ H_{23}:_____
4. Extra-credit: As discussed in class, use Shaffer's method to correct the pairwise Wilcoxon P-values. Give the P-values. (R won't do this, so it takes more thinking, although it is not difficult.)	H_{12}: _____ H_{13}: _____ H_{23}:_____

Statistics 501, Spring 2011, Midterm, Answer Page #1 ANSWERS

1. Question 1 refers to the matched pair differences in blood levels of cadmium, LBXBCDdif.

All parts of question 1 use LBXBCDdif	Fill in or CIRCLE the correct answer
1.1 Test the null hypothesis that the differences in cadmium levels are Normally distributed using the Shapiro-Wilk test. Give the P-value and state whether the null hypothesis is plausible. (6 points)	P-value: 1.3×10^{-15} Null hypothesis is: PAUSIBLE (NOT PLAUSIBLE)
1.2 Do a normal quantile plot of the differences in cadmium levels. Circle the ONE best interpretation of that plot; see the data page for the descriptions. (Do not turn in the plot.) (6 points)	A (B) C D E
1.3 Use the appropriate version of Wilcoxon's test to test the null hypothesis that the differences in cadmium levels are symmetric about zero. Give the full name of the test, the two-sided P-value, and state whether the null hypothesis is plausible. (6 points)	Full name: Wilcoxon's signed rank test P-value: 2.2×10^{-16} PAUSIBLE (NOT PLAUSIBLE)
1.4 Give the 95% confidence interval for the center of symmetry of the matched pair differences associated with the test in 1.3. Give the 95% confidence interval from the paired t-test. Is it true or false that the t-test interval is about 20% longer than the nonparametric interval? (10 points)	Nonparametric interval: [0.79, 0.99] t-test interval: [0.92, 1.16] (TRUE) FALSE
1.5 What is the Hodges-Lehmann point estimate of the center of symmetry of the differences in cadmium levels. (6 points)	Estimate: 0.885

2. Question 2 refers to the analyses you did in question 1 and to the three hypotheses, I, II, and III listed on the data page, where the Z_i are the matched pair differences in cadmium levels, i=1,2,…,250.

6 points each	Fill in or CIRCLE the correct answer
2.1 Wilcoxon's test can be used to test hypothesis I, but it will have meaningful power only if Prob($Z_i+Z_j>0$) is not close to ½. Here, "can be used" means that it falsely rejects the null hypothesis at the stated level, conventionally 0.05.	See comment 14, age 49 in H&W. (TRUE) FALSE
2.2 The Hodges-Lehmann point estimate and confidence interval are not valid under the alternative hypothesis H_A of I but are value under H_A of II. Here, valid means that the point estimate is consistent for the center of symmetry of the Z_i and the 95% confidence interval covers the center of symmetry in 95% of studies. (6 points)	You can't estimate the center of symmetry unless the distribution is symmetric. (TRUE) FALSE
2.3 You cannot correctly use Wilcoxon's test to test hypothesis III, but you can use the sign test. Here, correctly means that the test falsely rejects a true null hypothesis at the nominal rate, conventionally 0.05. (6 points)	Contrast the assumptions of the sign test (p60) with those of the signed rank test. (TRUE) FALSE
2.4 For the matched pair differences in cadmium levels in question 1, under the alternative hypothesis H_A of I, give a consistent estimate of Prob($Z_i+Z_j>0$). Give the numerical value of the estimate. (6 points)	Estimate: 0.983 98.3% of the time, when you look at two pairs, the more affected pair (larger $\lvert Z_i \rvert$) is positive, so positive results offset other results 98.3% of the time.

3. Question 3 asks you to relate the pair differences in cadmium LBXBCDdif to the pair differences in lead LBXBPBdif.

	Fill in or CIRCLE the correct answer
3.1 Use Pearson's Normal theory correlation to test the null hypothesis that cadmium differences are unrelated to lead differences. Give the two-sided P-value and the point estimate of the correlation. By this standard, is it plausible that LBXBCDdif and LBXBPBdif are unrelated? (6 points)	P-value: 0.28 Correlation: 0.069 (PLAUSIBLE) NOT PLAUSIBLE
3.2 Use Kendall's nonparametric correlation to test the null hypothesis that cadmium differences are unrelated to lead differences. Give the two-sided P-value and the point estimate of the correlation. By this standard, is it plausible that LBXBCDdif and LBXBPBdif are unrelated? (6 points)	P-value: 0.00037 Correlation: 0.151 PLAUSIBLE (NOT PLAUSIBLE)
3.3 Use the results in 3.2 to estimate the probability that, in two pairs, the higher cadmium difference will occur in the same pair as the higher lead difference (ie the probability of concordance.) (6pts)	Estimate: 0.576 versus 0.500 for chance agreement

4. Question 4 asks you to relate the pair differences in cadmium LBXBCDdif to the number of packs per day smoked by the smoker in each pair, in three groups, less than half a pack, at least half a pack but less than a pack, and a pack or more. See the data page for construction of the variable `pack`. Do this step carefully, or everything will be wrong – make sure the groups have 74, 82, and 93 pairs. Use the notation on the data page for question 4 (eg. H_0 or H_{12}) to refer to null hypotheses – do not invent a new notation.

	Fill in or CIRCLE the correct answer
4.1 Use an appropriate nonparametric test to test H_0, the hypothesis of no difference against the alternative of any pattern of differences among the τ's. Give the name of the test, the P-value and state whether the null hypothesis is plausible. (6 points)	P-value: `0.008776` Name of test: Kruskal-Wallis test PLAUSIBLE (NOT PLAUSIBLE)
4.2 Use Kendall's correlation to correlate SMD650smk and LBXBCDdif . Use it again to correlate as.numeric(pack) and LBXBCDdif. Give both correlations and two-sided P-values. (6 points)	SMD650smk: P-value 0.0003145 Correlation: 0.161 as.numeric(pack): P-value 0.00374 Correlation: 0.142
4.3 As discussed in class, use Holm's method to correct the pairwise Wilcoxon P-values. Give the P-values. (6 points)	H_{12}: 0.0507 H_{13}: 0.0086 H_{23}: 0.4841
4.4 As discussed in class, use Bonferroni's method to correct the pairwise Wilcoxon P-values. Give the P-values. (6 points)	H_{12}: 0.0761 H_{13}: 0.0086 H_{23}: 1.000
4. Extra-credit: As discussed in class, use Shaffer's method to correct the pairwise Wilcoxon P-values. Give the P-values. (R won't do this, so it takes more thinking, although it is not difficult.) (3 points)	H_{12}: 0.0254 H_{13}: 0.0086 H_{23}: 0.4841

STATISTICS 501 SPRING 2011 MIDTERM
DOING THE PROBLEM SET IN R

1.1 and 1.2

```
> par(mfrow=c(1,2))
> boxplot(LBXBCDdif)
> qqnorm(LBXBCDdif)
> shapiro.test(LBXBCDdif)
        Shapiro-Wilk normality test
data:  LBXBCDdif
W = 0.8351, p-value = 1.324e-15
```

1.3-1.5

```
> wilcox.test(LBXBCDdif,conf.int=T)
        Wilcoxon signed rank test with continuity correction
data:  LBXBCDdif
V = 30836.5, p-value < 2.2e-16
alternative hypothesis: true mu is not equal to 0
95 percent confidence interval:
 0.7900248 0.9899250
sample estimates:
(pseudo)median
      0.885041

> t.test(LBXBCDdif)
        One Sample t-test
data:  LBXBCDdif
t = 17.0183, df = 249, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.9162798 1.1561202
sample estimates:
mean of x
   1.0362

> 1.1561202-0.9162798
[1] 0.2398404
> 0.9899250-0.7900248
[1] 0.1999002
> 0.2398404/0.1999002
[1] 1.199801
```

```
2.4
Refer to the output above from wilcox.test.
> 30836.5/(250*(250+1)/2)
[1] 0.9828367

3.1
> cor.test(LBXBCDdif,LBXBPBdif)
        Pearson's product-moment correlation
data:  LBXBCDdif and LBXBPBdif
t = 1.0816, df = 248, p-value = 0.2805
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.05602143  0.19096538
sample estimates:
       cor
0.06852183

3.2
> cor.test(LBXBCDdif,LBXBPBdif,method="kendall")
        Kendall's rank correlation tau
data:  LBXBCDdif and LBXBPBdif
z = 3.5588, p-value = 0.0003725
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1512510

3.2
> (0.1512510+1)/2
[1] 0.5756255

4.1
> kruskal.test(LBXBCDdif,pack)

        Kruskal-Wallis rank sum test

data:  LBXBCDdif and pack
Kruskal-Wallis chi-squared = 9.4715, df = 2, p-value = 0.008776
```

```
4.2
> cor.test(SMD650smk,LBXBCDdif,method="kendall")
        Kendall's rank correlation tau
data:  SMD650smk and LBXBCDdif
z = 3.6031, p-value = 0.0003145
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1614722

> cor.test(LBXBCDdif,as.numeric(pack),method="kendall")
        Kendall's rank correlation tau
data:  LBXBCDdif and as.numeric(pack)
z = 2.8992, p-value = 0.003742
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1421939

4.3
> pairwise.wilcox.test(LBXBCDdif,pack)
        Pairwise comparisons using Wilcoxon rank sum test
data:  LBXBCDdif and pack
        [0,10) [10,20)
[10,20) 0.0507 -
[20,99) 0.0086 0.4841
P value adjustment method: holm

4.4 pairwise.wilcox.test(LBXBCDdif,pack,p.adjust.method="bonf")
        Pairwise comparisons using Wilcoxon rank sum test
data:  LBXBCDdif and pack

        [0,10) [10,20)
[10,20) 0.0761 -
[20,99) 0.0086 1.0000

4. Extra credit
pairwise.wilcox.test(LBXBCDdif,pack,p.adjust.method="none")
        Pairwise comparisons using Wilcoxon rank sum test
data:  LBXBCDdif and pack
        [0,10) [10,20)
[10,20) 0.0254 -
[20,99) 0.0029 0.4841
In Shaffer’s method with 3 groups, 0.0029 is adjusted to 3x0.0029 =
0.0086, but if this is less than 0.05, then the other two p-values are
not adjusted.
```

Statistics 501 Spring 2012 Final Exam: Data Page 1
This is an exam. Do not discuss it with anyone.
Due: Wednesday, May 2, 2012 at 11:00am

Table `MaritalMarijuana` is from a paper by Kazuo Yamaguchi and Denise Kandel, "Marital homophily on illicit drug use among young adults," *Social Forces*, 1993, 72, 505-528. It is in JSTOR if you want to look at it, but there is no need to do that for this exam. The data were extracted from a repeated survey. The table describes illicit drug use before marriage (time 1) and after marriage (time 2) for couples consisting of a husband and a wife. A + indicates use of illicit drugs, including marijuana, psychedelics, cocaine, heroin and nonprescribed pills. A – indicates no use of illicit drugs. For example, in 44 instances, a husband and wife who had both used drugs before marriage (Wife1=+, Husband1=+) were both not using drugs in the final survey when married (Wife2=-, Husband 2=-). MaritalMarijuana is in the R workspace for the course. For other programs, you will have to enter the 16 numbers.

IMPORTANT: Refer to the four variables in this table by their letter/number pairs, W1 = Wife1, H1 = Husband1, W2 = Wife2, H2 = Husband 2. Fit only hierarchical log-linear models and refer to them by the highest order u-terms they contain, so [W1,H1] [W2,H2] has a interaction u-term linking W1 and H1, W2 and H2, and main effect u-terms for W1, H1, W2, H2, separately and a constant term.

```
> MaritalMarijuana
, , Wife1 = +, Husband1 = +
     Husband2
Wife2  +  -
    + 92 16
    - 46 44
, , Wife1 = -, Husband1 = +
     Husband2
Wife2  +  -
    +  5  2
    - 41 66
, , Wife1 = +, Husband1 = -
     Husband2
Wife2 +  -
    + 1 13
    - 0 42
, , Wife1 = -, Husband1 = -
     Husband2
Wife2 +   -
    + 0   4
    - 1 156
```

This is an exam. Do not discuss it with anyone.

Statistics 501 Spring 2012 Final Exam: Data Page 2
This is an exam. Do not discuss it with anyone.

Save yourself some arithmetic by learning to use [ ] in R. See what happens when you type `MaritalMarijuana[,,1,1]`. Also, type `help(margin.table)`

Some questions are "true or false". Such a question says: "blah and blah and blah", where the options as answers are "true" and "false". Circle "true" if "blah and blah and blah" makes sense and is true, but circle false if "blah and blah and not blah" is true. Circle false if "blah and blah and blah" makes no sense.

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question.

Please write your name on both sides of the exam, last name first. Please include your Penn ID number.

This problem set is an exam. If you discuss or communicate with anyone about this exam, then you have cheated on an exam. Cheating on an exam is the single dumbest thing a doctoral student at Penn can do.

Make and keep a photocopy of your answer page. Place the exam in an envelope with 'Paul Rosenbaum, Statistics Department' on it**. The exam is due in my office, 473 Huntsman, on Wednesday, May 2, 2012 at 11:00am.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman or by giving it to Adam at the front desk in statistics, but if you turn in the exam early, place it in an envelope addressed to me. When all of the exams are graded, I will add an **answer key** to the on-line bulk-pack for the course. You can compare the answer key to your photocopy of your exam. Your course grade will be available from the Registrar. I no longer distribute answer keys and graded exams by US Mail, but you may stop in the pick up your graded exam if you wish.

Have a great summer!

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2012 Final Exam: Answer Page 1 This is an exam. Do not discuss it.

Due Wednesday, May 2 at 11:00am	Fill in or CIRCLE the correct answer
1.1 The table `MaritalMarijuana` describes how many people? How many married couples?	People: _____ Couples: _____
1.2 What percent of wives used illicit drugs before marriage? Of husbands before marriage? Of wives after marriage? Of husbands after marriage?	Before After Wife _____% _____% Husband _____% _____%
1.3 Ignoring the data after marriage, what is the odds ratio linking illicit drug use before marriage by people who would later become husband and wife? (This is the W1-H1 odds ratio collapsing over W2-H2.) Give the odds ratio and the two-sided 95% confidence interval (CI). Repeat this for the husband/wife odds ratio after marriage (W2-H2) ignoring data before marriage (i.e., collapsing over W1-H1).	Collapsed Husband/Wife Odds Ratio (OR) **Before Marriage** OR: _____ CI: _____ **After Marriage** OR: _____ CI: _____
1.4 A multinomial model for table `MaritalMarijuana` assumes independence of drug use by all the individual people in the table, including independence of husbands and wives.	True False
1.5 Only 2 husbands switched from not using illicit drugs prior to marriage to using illicit drugs after marriage.	True False

2 Fit the hierarchical log-linear model with all 2-variable interactions and no three-factor or four factor interactions. Use this model for the questions in 2.	Fill in or CIRCLE the correct answer
2.1 What is the likelihood ratio goodness of fit (LRgof) statistic for this model? What are the degrees of freedom (DF)? What is the p-value? Based just on the LRgof: Is this an acceptable fit?	LRgof=_____ DF=_____ P-value: _____ Acceptable Not Acceptable
2.2 Use the fitted counts from this model to estimate the odds ratio linking after marriage drug use by husbands and wives (Husband2 and Wife2) at each level of use before marriage. Write in 4 odds ratios.	W1=+,H1=+:_____W1=-,H1=+:_____ W1=+,H1=-:_____W1=-,H1=-:_____

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2012 Final Exam: Answer Page 2 This is an exam. Do not discuss it.

3.1 The model [W1,H1] [W2,H2] says drug use by husbands and wives may be related at a fixed time, but the couples' patterns of use before marriage are independent of the patterns of use after marriage.	True False
3.2 Test the fit of the model [W1,H1] [W2,H2] using the likelihood ratio goodness of fit statistic (LRgof). What is its value? What are the degrees of freedom (DF)? What is the p-value? Based just on the LRgof: Is this an acceptable fit?	LRgof=_____ DF=_____ P-value: _____ Acceptable Not Acceptable
3.3 The model [W1,W2] [H1,H2] says that, for a person, drug use before marriage may be related to drug use after marriage, but drug use by husbands is independent of drug use by wives. (True/False) Is the fit of this model acceptable?	True False Acceptable Not Acceptable

4 The model (called **mq4**) in question 4 is [W1,W2],[W1,H1],[H1,H2],[W2,H2]	Fill in or CIRCLE the correct answer
4.1 Test the hypothesis that the model mq4 is acceptable against the alternative that the model in question 2 (which adds [W1,H2] and [W2,H1]) is required. What is the likelihood ratio chi square? What are the degrees of freedom? What is the p-value? Is mq4 acceptable by this test?	LR chi square=_____ DF=_____ P-value: _____ Acceptable Not Acceptable
4.2 There are four hierarchical models that delete one two-factor u-term from mq4, but none of these four models is an acceptable fit. (True or false)	True False
4.3 Model mq4 says that a wife's drug use before marriage (W1) is independent of her husband's drug use after marriage (H2).	True False
4.4 Model mq4 says that a wife's drug use before marriage (W1) is conditionally independent of her husband's drug use after marriage (H2) given (W2,H1).	True False
4.5 Use the **fitted counts** from model mq4 to estimate the odds ratio linking W1 and H2 for a couple with (W2=+,H1=+).	Odds ratio = _____

Stat 501 S-2012 Final Exam: Answer Page 1. Answers

All questions 7 points, except 1.4, 2 points.	Fill in or CIRCLE the correct answer
1.1 The table `MaritalMarijuana` describes how many people? How many married couples?	People: 1058 Couples: 529
1.2 What percent of wives used illicit drugs before marriage? Of husbands before marriage? Of wives after marriage? Of husbands after marriage?	Before / After Wife 48.0% 25.1% Husband 59.0% 35.2%
1.3 Ignoring the data after marriage, what is the odds ratio linking illicit drug use before marriage by people who would later become husband and wife? (This is the W1-H1 odds ratio collapsing over W2-H2.) Give the odds ratio and the two-sided 95% confidence interval (CI). Repeat this for the husband/wife odds ratio after marriage (W2-H2) ignoring data before marriage (i.e., collapsing over W1-H1).	Collapsed Husband/Wife Odds Ratio (OR) **Before Marriage** OR: 4.98 CI: [3.35, 7.46] **After Marriage** OR: 9.75 CI: [6.10, 15.87]
1.4 A multinomial model for table `MaritalMarijuana` assumes independence of drug use by all the individual people in the table, including independence of husbands and wives.	True (False)
1.5 Only 2 husbands switched from not using illicit drugs prior to marriage to using illicit drugs after marriage.	(True) False

2 Fit the hierarchical log-linear model with all 2-variable interactions and no three-factor or four factor interactions. Use this model for the questions in 2.	Fill in or CIRCLE the correct answer
2.1 What is the likelihood ratio goodness of fit (LRgof) statistic for this model? What are the degrees of freedom (DF)? What is the p-value? Based just on the LRgof: Is this an acceptable fit?	LRgof= 1.346 DF= 5 P-value: 0.93 (Acceptable) Not Acceptable
2.2 Use the fitted counts from this model to estimate the odds ratio linking after marriage drug use by husbands and wives (Husband2 and Wife2) at each level of use before marriage. Write in 4 odds ratios.	W1=+,H1=+: 5.39 W1=-,H1=+: 5.39 W1=+,H1=-: 5.39 W1=-,H1=-: 5.39

Stat 501 S-2012 Final Exam: Answer Page 2 . Answers

3.1 The model [W1,H1] [W2,H2] says drug use by husbands and wives may be related at a fixed time, but the couples' patterns of use before marriage are independent of the patterns of use after marriage.	(True) False
3.2 Test the fit of the model [W1,H1] [W2,H2] using the likelihood ratio goodness of fit statistic (LRgof). What is its value? What are the degrees of freedom (DF)? What is the p-value? Based just on the LRgof: Is this an acceptable fit?	LRgof= 358.05 DF= 9 P-value: <0.0001 Acceptable (Not Acceptable)
3.3 The model [W1,W2] [H1,H2] says that, for a person, drug use before marriage may be related to drug use after marriage, but drug use by husbands is independent of drug use by wives. (True/False) Is the fit of this model acceptable?	(True) False Acceptable (Not Acceptable)

4 The model (called **mq4**) in question 4 is [W1,W2],[W1,H1],[H1,H2],[W2,H2]	Fill in or CIRCLE the correct answer
4.1 Test the hypothesis that the model mq4 is acceptable against the alternative that the model in question 2 (which adds [W1,H2] and [W2,H1]) is required. What is the likelihood ratio chi square? What are the degrees of freedom? What is the p-value? Is mq4 acceptable by this test?	LR chi square= 4.06 DF= 2 P-value: 0.13 (Acceptable) Not Acceptable
4.2 There are four hierarchical models that delete one two-factor u-term from mq4, but none of these four models is an acceptable fit. (True or false)	(True) False
4.3 Model mq4 says that a wife's drug use before marriage (W1) is independent of her husband's drug use after marriage (H2).	True (False)
4.4 Model mq4 says that a wife's drug use before marriage (W1) is conditionally independent of her husband's drug use after marriage (H2) given (W2,H1).	(True) False
4.5 Use the **fitted counts** from model mq4 to estimate the odds ratio linking W1 and H2 for a couple with (W2=+,H1=+).	Odds ratio = 1.000

```
1.1
> sum(m)
[1] 529
> 2*sum(m)
[1] 1058

1.2
> margin.table(m,1)/529
Wife2
        +         -
0.2514178 0.7485822
> margin.table(m,2)/529
Husband2
        +         -
0.3516068 0.6483932
> margin.table(m,3)/529
Wife1
        +         -
0.4801512 0.5198488
> margin.table(m,4)/529
Husband1
        +         -
0.5897921 0.4102079

1.3
> fisher.test(margin.table(m,c(3,4)))
        Fisher's Exact Test for Count Data
p-value < 2.2e-16
95 percent confidence interval:
 3.353750 7.459505
sample estimates of odds ratio: 4.977578
> fisher.test(margin.table(m,c(1,2)))
        Fisher's Exact Test for Count Data
p-value < 2.2e-16

95 percent confidence interval:
  6.09626 15.87163
sample estimates of odds ratio: 9.745102

2.1
> loglin(m,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)),fit=T)
$lrt
[1] 1.345795
$df
[1] 5
> 1-pchisq(1.345795,5)
[1] 0.9301496

         Doing the Problem Set in R: Spring 2012 Final (Page 1)
2.2
> ft<-
loglin(m,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)),fit=T)$fit
11 iterations: deviation 0.07459749
> or(ft[,,1,1])
[1] 5.389931
> or(ft[,,1,2])
[1] 5.389931
```

```
> or(ft[,,2,1])
[1] 5.389931
> or(ft[,,2,2])
[1] 5.389931

3.2
> loglin(m,list(c(1,2),c(3,4)))
$lrt
[1] 358.0547
$df
[1] 9

3.3
> loglin(m,list(c(1,3),c(2,4)))
$lrt
[1] 152.9353
$df
[1] 9

4.1 Compare two nested models using change in LR chi square.
> loglin(m,list(c(1,2),c(1,3),c(2,4),c(3,4)))

$lrt
[1] 5.405324
$df
[1] 7
> 5.405324-1.345795
[1] 4.059529
> 1-pchisq(5.405324-1.345795,2)
[1] 0.1313665
4.2  Four tests, of which the first is:
> loglin(m,list(c(1,2),c(1,3),c(2,4)))
$lrt
[1] 39.72262
$df
[1] 8
> 1-pchisq(39,8)
[1] 4.915382e-06
> ft<-loglin(m,list(c(1,2),c(1,3),c(2,4),c(3,4)),fit=T)$fit
> or(ft[1,,,1])
[1] 1
```

Statistics 501 Spring 2011 Final Exam: Data Page 1
This is an exam. Do not discuss it with anyone.

The data in the contingency table `smoke` are from the US National Health and Nutrition Examination Survey (NHANES) for 2007-2008. You can obtain the complete survey from ICPSR via the Penn library web page, but there is no reason to do this for the current exam. A daily smoker reported smoking on every day of the past 30 days (SMD641=30) and having smoked at least 100 cigarettes in his or her lifetime (SMQ020=YES). A nonsmoker reports having smoked fewer than 100 cigarettes in his or her lifetime (SMQ020=NO) and has no reported smoking in the previous 30 days (SMD641=missing). The table also classifies individuals by gender (RIAGENDR), whether the individual served in the military (DMQMILIT), and whether family income is at least twice the poverty level (INDFMPIR>=2). During WWII, the military supplied cigarettes to soldiers, which has led to various studies of the relationship between smoking and military service.

The table smoke is now in the Rworkspace for the course available at my web page http://www-stat.wharton.upenn.edu/~rosenbap/index.html . You will need to download it again. You may need to clear your web-browser's memory so it forgets the old version and downloads the new one – if you can't find smoke, that's probably the reason. If you are not using R, you will need to enter the 16 numbers by hand into some other log-linear program.

IMPORTANT: Refer to the four variables in this table by their first letters, S=SmokeDaily, M=Military, T=TwicePoverty, G=Gender. Fit only hierarchical log-linear models and refer to them by the highest order u-terms they contain, so [SM] [TG] has a u-term linking S=SmokeDaily and M=Military, and another linking T=TwicePoverty and G=Gender, contains all four main effects and a constant. This is the **COMPACT NOTATION**.

```
> smoke
, , TwicePoverty = >= 2xPoverty, Gender = Male
             Military
SmokeDaily    Served Did not
  Nonsmoker      149     509
  Smokes Daily    48     147

, , TwicePoverty = < 2xPoverty, Gender = Male
             Military
SmokeDaily    Served Did not
  Nonsmoker       54     376
  Smokes Daily    66     286

, , TwicePoverty = >= 2xPoverty, Gender = Female
             Military
SmokeDaily    Served Did not
  Nonsmoker       16     820
  Smokes Daily     5     123

, , TwicePoverty = < 2xPoverty, Gender = Female
             Military
SmokeDaily    Served Did not
  Nonsmoker        7     780
  Smokes Daily     2     292
```

Statistics 501 Spring 2011 Final Exam: Data Page 2
This is an exam. Do not discuss it with anyone.

Save yourself some arithmetic by learning to use [ ] in R. See what happens when you type `smoke[,,1,1].` Also, type `help(margin.table)`

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question.

Make and keep a photocopy of your answer page. Place the exam in an envelope with 'Paul Rosenbaum, Statistics Department' on it**. The exam is due in my office, 473 Huntsman, on Friday, May 6 at 10:00am.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman or by giving it to Adam at the front desk in statistics. When all of the exams are graded, I will add an **answer key** to the on-line bulk-pack for the course. You can compare the answer key to your photocopy of your exam. Your course grade will be available from the Registrar. I no longer distribute answer keys and graded exams by US Mail, but you may stop in the pick up your graded exam if you wish.

Have a great summer!

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2011 Final Exam: Answer Page 1 This is an exam. Do not discuss it.

1. From the 2x2x2x2 table smoke, compute the 2x2 marginal table relating smoking (S) to military service (M). Give the counts and the marginal totals (fill in 9 numbers).

S x M margin table	Served in Military	Did not serve	Total
Nonsmoker			
Smokes Daily			
Total			

2. Use the marginal table in question 1 to answer question 2. (R-users, please use the fisher.test command in R.) (Fill in or circle the correct answer.)

2a. Test the hypothesis of independence in the 2x2 table in question 1, smoking x military service. Give the p-value. Is the null hypothesis of independence plausible?	P-value: _____ Plausible Not Plausible
2b. What is the (point) estimate of the **odds ratio** of the table in question 1? Are people who served in the military **more likely** than others to smoke daily? Base your answer on the table in question 1.	Odds ratio: _____ More likely Not more likely
2c. What is the 95% confidence interval for the odds ratio in the table in question 1?	Conf. Interval = [,]

3. Questions 3-6 return to the 2x2x2x2 table smoke and asks you to answer by fitting log-linear models. Always **use the likelihood ratio chi-square**, not the Pearson chi-square. Refer to models by the COMPACT NOTATION described on the data page.

You want to test the **null hypothesis** that smoking (S) is independent of the other three variables, allowing the other three variables to have any relationship at all.	Fill in or circle the correct answer
3a. **Circle the one model** which best expresses the null hypothesis (i.e., the null hypothesis is true if the model is true).	[S][M][T][G] [SM][ST][SG] [S][MT][MG][TG] [S][MTG]
3b. Test the goodness of fit of the one selected model in 3a. Give the value of the test statistic, the degrees of freedom (DF), the p-value. Is the null hypothesis of problem 3 that S is independent of M, T, and G plausible?	Value: _____ DF: _____ p-value: _____ Plausible Not Plausible

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2011 Final Exam: Answer Page 2 This is an exam. Do not discuss it.

4. In the 2x2x2x2 table smoke, fit the hierarchical model with all two-variable u-terms and no three-variable u-terms. Use this model to answer the following questions.

4.1 Use the compact notation to express the model.	**Model is**:
4.2 Does this model fit the data reasonably well as judged by the likelihood ratio test of goodness of fit. Give the value of the statistic, its degrees of freedom, p-value and indicate whether this test **alone** suggests the fit is ok.	Value: _____ DF: _____ p-value: _____ CIRCLE ONE: Fit looks OK Definitely not OK
4.3 **Use the fitted counts** from the model in question 4 to estimate four odds ratios linking smoking (S) and military service (M) for the four categories of Twice Poverty and Gender. Fill in the four odds ratios.	<table><tr><td></td><td>Male</td><td>Female</td></tr><tr><td>>=2xPoverty</td><td></td><td></td></tr><tr><td><2xPoverty</td><td></td><td></td></tr></table>
4.3 Test each of the 2-variable u-terms in the model in 4.1 **one at a time** to see if you can simplify the model. That is, test the null hypothesis that each 2-variable u-term is zero in a model that retains all the other 2-variable u-terms. So you are thinking about models that differ from the model in 4.1 by one u-term. **Do not do a goodness of fit test**. **List only** those u-terms for which the null hypothesis is plausible, so that a model without that u-term is plausible. **If none, write none**.	List **only** u-terms that are plausibly zero. Here [MG] is the name of the u-term linking Military service and gender. Give the chi-square, degrees of freedom, p-value. You will lose points if you list u-terms that are not plausibly zero. u-term Chi-Square DF p-value

5.

5.1 Which log-linear model says that S = smoking daily is conditionally independent of M=military service given both of the other variables, G=Gender, T =TwicePoverty. Use the compact notation.	
5.2 Test the goodness of fit of the model in 5.1. Give the likelihood ratio goodness of fit test statistic, degrees of freedom, p-value and state whether the model is rejected at the 0.05 level based on this test.	Value: _____ DF: _____ p-value: _____ CIRCLE ONE: Reject at 0.05 Do not reject

Answers

Stat 501 S-2011 Final Exam: Answer Page 1 This is an exam. Do not discuss it.

1. From the 2x2x2x2 table smoke, compute the 2x2 marginal table relating smoking (S) to military service (M). Give the counts and the marginal totals (fill in 9 numbers).

S x M margin table	Served in Military	Did not serve	Total
Nonsmoker	226	2485	2711
Smokes Daily	121	848	969
Total	347	3333	3680

2. Use the marginal table in question 1 to answer question 2. (R-users, please use the fisher.test command in R.) (Fill in or circle the correct answer.)

2a. Test the hypothesis of independence in the 2x2 table in question 1, smoking x military service. Give the p-value. Is the null hypothesis of independence plausible?	P-value: 0.0002495 Plausible (Not Plausible)
2b. What is the (point) estimate of the **odds ratio** of the table in question 1? Are people who served in the military **more likely** than others to smoke daily? Base your answer on the table in question 1.	Odds ratio: 0.637 (More likely) Not more likely
2c. What is the 95% confidence interval for the odds ratio in the table in question 1?	Conf. Interval = [0.502 , 0.813]

3. Questions 3-6 return to the 2x2x2x2 table smoke and asks you to answer by fitting log-linear models. Always **use the likelihood ratio chi-square**, not the Pearson chi-square. Refer to models by the COMPACT NOTATION described on the data page.

You want to test the **null hypothesis** that smoking (S) is independent of the other three variables, allowing the other three variables to have any relationship at all.	Fill in or circle the correct answer
3a. **Circle the one model** which best expresses the null hypothesis (i.e., the null hypothesis is true if the model is true).	[S][M][T][G] [SM][ST][SG] [S][MT][MG][TG] ([S][MTG])
3b. Test the goodness of fit of the one selected model in 3a. Give the value of the test statistic, the degrees of freedom (DF), the p-value. Is the null hypothesis of problem 3 that S is independent of M, T, and G plausible?	Value: 237.1 DF: 7 p-value: <0.0001 Plausible (Not Plausible)

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2011 Final Exam: Answer Page 2 This is an exam. Do not discuss it.

4. In the 2x2x2x2 table smoke, fit the hierarchical model with all two-variable u-terms and no three-variable u-terms. Use this model to answer the following questions.

4.1 Use the compact notation to express the model.	**Model is**: [S,M][ST][SG][MT][MG][TG]
4.2 Does this model fit the data reasonably well as judged by the likelihood ratio test of goodness of fit. Give the value of the statistic, its degrees of freedom, p-value and indicate whether this test **alone** suggests the fit is ok.	Value: 5.02 DF: 5 p-value: 0.41 CIRCLE ONE: (Fit looks OK) Definitely not OK
4.3 **Use the fitted counts** from the model in question 4 to estimate four odds ratios linking smoking (S) and military service (M) for the four categories of Twice Poverty and Gender. Fill in the four odds ratios.	

	Male	Female
>=2xPoverty	0.752	0.752
<2xPoverty	0.752	0.752

4.3 Test each of the 2-variable u-terms in the model in 4.1 **one at a time** to see if you can simplify the model. That is, test the null hypothesis that each 2-variable u-term is zero in a model that retains all the other 2-variable u-terms. So you are thinking about models that differ from the model in 4.1 by one u-term. **Do not do a goodness of fit test**. **List only** those u-terms for which the null hypothesis is plausible, so that a model without that u-term is plausible. **If none, write none**.	List **only** u-terms that are plausibly zero. Here [MG] is the name of the u-term linking Military service and gender. Give the chi-square, degrees of freedom, p-value. You will lose points if you list u-terms that are not plausibly zero. u-term Chi-Square DF p-value None

5.

5.1 Which log-linear model says that S = smoking daily is conditionally independent of M=military service given both of the other variables, G=Gender, T =TwicePoverty. Use the compact notation.	[SGT] [MGT]
5.2 Test the goodness of fit of the model in 5.1. Give the likelihood ratio goodness of fit test statistic, degrees of freedom, p-value and state whether the model is rejected at the 0.05 level based on this test.	Value: 7.87 DF: 4 p-value: 0.097 CIRCLE ONE: Reject at 0.05 (Do not reject)

Doing the Problem Set in R
Final, Spring 2011

```
Question 1.
> margin.table(smoke,c(1,2))
              Military
SmokeDaily     Served Did not
  Nonsmoker       226    2485
  Smokes Daily    121     848

Question 2.
> fisher.test(margin.table(smoke,c(1,2)))

        Fisher's Exact Test for Count Data

data:  margin.table(smoke, c(1, 2))
p-value = 0.0002495
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.5016968 0.8128271
sample estimates:
odds ratio
  0.637456

Question 3.
> loglin(smoke,list(1,c(2,3,4)))
2 iterations: deviation 1.136868e-13
$lrt
[1] 237.1712
$pearson
[1] 240.0149
$df
[1] 7
> 1-pchisq(237.1712,7)
[1] 0

$margin
$margin[[1]]
[1] "SmokeDaily"
$margin[[2]]
[1] "Military"     "TwicePoverty" "Gender"

Question 4.1
> loglin(smoke,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)))
5 iterations: deviation 0.06586971
$lrt
[1] 5.021628
$pearson
[1] 5.039157
$df
[1] 5
> 1-pchisq(5.021628,5)
[1] 0.4132464
```

Question 4.2

```
ft<-
loglin(smoke,list(c(1,2),c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)),fit=T)$fit
> or(ft[,,1,1])
[1] 0.7522604
> or(ft[,,1,2])
[1] 0.7522604
> or(ft[,,2,1])
[1] 0.7522604
> or(ft[,,2,2])
[1] 0.7522604
```

Question 4.3

None of the terms can be deleted. For example:

```
> loglin(smoke,list(c(1,3),c(1,4),c(2,3),c(2,4),c(3,4)))
5 iterations: deviation 0.02724409
$lrt
[1] 9.778795

$pearson
[1] 10.62873

$df
[1] 6

> 9.778795-5.021628
[1] 4.757167
> 1-pchisq(4.757167,1)
[1] 0.02917653
```

Question 5.

```
> loglin(smoke,list(c(1,3,4),c(2,3,4)))
2 iterations: deviation 1.136868e-13
$lrt
[1] 7.868466

$pearson
[1] 8.222663

$df
[1] 4

$margin
$margin[[1]]
[1] "SmokeDaily"   "TwicePoverty" "Gender"

$margin[[2]]
[1] "Military"     "TwicePoverty" "Gender"


> 1-pchisq(7.868466,4)
[1] 0.09651703
```

Statistics 501, Spring 2010, Midterm: Data Page #1

This is an exam. Do not discuss it with anyone. If you discuss the exam in any way with anyone, then you have cheated on the exam. The University often expels students caught cheating on exams. Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question. Due in class Tuesday 30 March.

The data for this problem are at in the latest Rst501.RData for R users as the object katzkrueger and in katzkrueger.txt as a text file at http://stat.wharton.upenn.edu/statweb/course/Spring-2008/stat501 The list is case sensitive, so katzkrueger.txt is with lower case items.

The data are from a paper by Lawrence Katz and Alan Krueger (1992), The effect of the minimum wage on the fast food industry, *Industrial and Labor Relations Review*, 46, 6-21, specifically the subset of data in Table 5 of that paper. (You do not need to look at the paper to do the problem set. If you wish to look at the paper, it in JSTOR on the UPenn library web page at http://www.jstor.org/stable/2524735.) The paper concerns an increase in the Federal minimum wage from $3.80 to $4.25 per hour that took place on April 1, 1991, and its effects on employment in the fast food industry in Texas. The data are based on two surveys of the same 100 fast food restaurants, one in December 1990 before the increase in the minimum wage, the other in July/August 1991 after the increase in the minimum wage. The restaurant chains were Burger King, KFC and Wendy's (McDonald's refused). Economic theory typically predicts that an increase in the minimum wage will reduce employment essentially because some workers are worth employing at $3.80 per hour but not at $4.25 per hour (e.g., George J. Stigler (1946) The Economics of Minimum Wage Legislation, *American Economic Review*, 36, 358-365, http://www.jstor.org/stable/1801842). Katz and Krueger looked at this in various ways. In particular, they looked at the change in full-time-equivalent (fte) employment, after-minus-before, which is `fte91-fte90`. (Some of the numbers look a little odd – they are survey responses.) They also looked at the gap in starting wages that the restaurant needed to close to comply with the new minimum age. For instance, the first restaurant (`id=1`) below was a Burger King (`bk=1, kfc=0`) that was not company owned (`co_owned=0`) paying $3.85 per hour as a starting wage in December 1990, so to reach the new minimum wage it had to close a `gap` of $4.25-$3.85 = $0.40. Notice that the second restaurant below (`id=3`) had the same `gap`, but raised the starting wage to $4.40, that is, an increase of $0.65, rather than the required $0.40. Notice that the eighth restaurant (`id=27`) was paying $4.60 before the increase, so its `gap` is zero, as the law did not require it to raise wages. Katz and Krueger argued that if conventional theory were correct, the decline in employment should be larger if `gap` is larger. The variable `grp` forms groups using `gap`, while `twogrp` makes just two groups, >$0.40 and <=$0.25 with the rest as missing (NA).

```
> dim(katzkrueger)
[1] 100  11
> katzkrueger[1:10,]
   id bk kfc co_owned paydec payjul  gap fte90 fte91         grp twogrp
1   1  1   0        0   3.85   4.25 0.40 10.13  3.57  (0.25,0.4]     NA
2   3  1   0        0   3.85   4.40 0.40 25.70 23.55  (0.25,0.4]     NA
3   4  0   1        1   4.15   4.25 0.10 11.98 12.70    (0,0.24]      1
4  14  0   0        0   4.00   4.25 0.25 21.66 29.95 (0.24,0.25]      1
5  20  1   0        0   3.80   4.25 0.45 31.40 18.54  (0.4,0.45]      0
6  24  1   0        0   3.80   4.25 0.45 14.25 12.14  (0.4,0.45]      0
7  25  1   0        1   3.80   4.25 0.45 11.40 19.25  (0.4,0.45]      0
8  27  1   0        0   4.60   4.25 0.00 23.55  7.41    (-Inf,0]      1
9  30  1   0        1   4.20   4.25 0.05 26.99 27.00    (0,0.24]      1
10 32  0   0        0   3.80   4.32 0.45  8.55  7.70  (0.4,0.45]      0
…
> table(twogrp,grp)
      grp
twogrp (-Inf,0] (0,0.24] (0.24,0.25] (0.25,0.4] (0.4,0.45]
     1       10       10           23          0          0
     0        0        0            0          0         37
```

Define three new variables as:

```
> attach(katzkrueger)
> dife<-fte91-fte90
> difer<-fte90-fte91
> difp<-payjul-paydec
```

Notice that `difer = -dife`.

Model 1: $X_i = \theta + \delta_i$, $i=1,2,\ldots,m$, $Y_i = \theta + \Delta + \delta_{j+m}$, $j=1,\ldots,n$, where $\delta_k \sim$ iid, $k=1,2,\ldots,n+m$, with a continuous distribution.

Model 2: $(X_1,Y_1), \ldots, (X_n,Y_n)$ are n iid observations from a continuous bivariate distribution.

Model 3: X_i, $i=1,2,\ldots,m$, are iid from one continuous distribution, and Y_i, $j=1,\ldots,n$, are iid from another continuous distribution, and the X's and Y's are independent of each other.

Model 4: X_i, $i=1,2,\ldots,m$, and Y_i, $j=1,\ldots,n$, are $n+m$ *iid* observations from the same continuous distribution.

Model 5: $Y_i - X_i = \Delta + \delta_i$ where $\delta_i \sim$ iid, with a continuous distribution symmetric about 0, i=1,…,n.

Model 6: $Y_i = \theta + \Delta X_i + e_i$, …, where the e_i are n iid observations from a continuous distribution with median zero independent of the X_i which are untied.

Model 7: $Y_i - X_i = \Delta + \delta_i$ where δ_i are independent, with possibly different continuous distributions each having median zero.

Model 8: $X_{ij} = \theta + \tau_j + \delta_{ij}$, $i=1,2,\ldots,n_j$, $j=1,\ldots,K$ where the δ_{ij}'s are iid from a continuous distribution, with $0 = \tau_1+\ldots+\tau_K$.

Model 9 $X_{ij} = \theta + \tau_j + \delta_{ij}$, $i=1,2,\ldots,n_j$, $j=1,\ldots,K$ where the δ_{ij}'s are iid from a continuous distribution, with $0 = \tau_1+\ldots+\tau_K$, with $\tau_j>\tau_{j+1}$ or $\tau_j=\tau_{j+1}$ with at least one strict inequality.

Model 10: $X_{ij} = \theta + \tau_j + \delta_{ij}$, $i=1,2,\ldots,n_j$, $j=1,\ldots,K$ where the δ_{ij}'s are iid from a continuous distribution, with $0 = \tau_1+\ldots+\tau_K$, $\tau_j<\tau_{j+1}$ or $\tau_j=\tau_{j+1}$ with at least one strict inequality.

Model 11: $X_{ij} = \theta + \delta_{ij}$, $i=1,2,\ldots,n_j$, $j=1,\ldots,K$ where the δ_{ij}'s are iid from a continuous distribution.

Print Name Clearly, Last, First: _____ ID#_____

Statistics 501, Spring 2010, Midterm, Answer Page #1

This is an exam. Do not discuss it with anyone. Use abbreviations and model #'s from the data page.

1. Use the 100 observations on `dife` to answer question 1. `dife` is defined on the data page.

1.A. Do a boxplot, a Normal quantile plot and a Shapiro-Wilk test of Normality to determine whether the changes in employment (`dife`) look like observations from a Normal distribution. Do not turn in the plots. What is the P-value for the Shapiro-Wilk test? Do the changes in employment look like observations from a Normal distribution?	Shapiro-Wilk P-value: _____ CIRCLE ONE Looks Normal Does not look Normal
1.B Use Wilcoxon's signed rank test to test the hypothesis that the changes in employment (`dife`) are symmetric about zero difference. What is the value of the test statistic? What is the two-sided P-value? Is the null hypothesis rejected at the conventional 0.05 level?	Test statistic: _____ P-value: _____ CIRCLE ONE Rejected at 0.05 Not rejected at 0.05
1.C Use procedures developed from Wilcoxon's signed rank test to find a two-sided 95% confidence interval and a point estimate for the center of symmetry of the changes in employment (`dife`). Taking the point estimate at naively, at face value, roughly (to the nearest integer) how many fte employees were gained or lost following the increase in the minimum wage?	95% Interval: [_____, _____] Point estimate: _____ Lost _____ or gained _____ employees
1.D Do a two-sided test of the null hypothesis that the center of symmetry of the changes in employment (`dife`) reflect a typical decline of ½ of an full time equivalent (fte) employee. State briefly how you did the test, give the value of the test statistic, the P-value, and say whether an ½ employee decline is plausible.	How you did it: Test statistic _____ P-value: _____ CIRCLE ONE Plausible Not plausible
1.E Of the models on the data page, which one model underlies Wilcoxon's signed rank test as you used it in 1.D? Give one model number.	Model number: _____

2. Use the 100 observations on (`dife, gap`) to answer question 2.

2.A. Test the null hypothesis that `dife` and `gap` are independent using Kendall's correlation. Give: the correlation estimate, the two-sided P-value, and the estimated probability of concordance. Is it plausible that `dife` and `gap` are unrelated? Does this result suggest that declines in employment are typically larger when an increase in the minimum wage requires a larger increase in starting wages to comply with the new minimum wage?	Correlation: _____ P-value: _____ Probability of concordance: _____ CIRCLE ONE Plausible Not plausible CIRCLE ONE Does suggest Does not suggest
2.B. Under which two models on the data page would the test in 2A be appropriate? Write two model numbers.	Model numbers: _____ _____
2C. In model 6, with Y_i=dife, X_i=gap, use Kendall's correlation to test the hypothesis that H_0: β= -1, so that a restaurant with the maximum gap of gap=0.45 would experience about ½ (exactly 0.45) larger decline than a restaurant with gap=0.	Two-sided p-value: _____ CIRCLE ONE H_0: β= -1 is plausible Not plausible

Print Name Clearly, Last, First: _____ ID#_____

Statistics 501, Spring 2010, Midterm, Answer Page #1

This is an exam. Do not discuss it with anyone. Use abbreviations and model #'s from the data page.

3. Question 3 asks you to compare the changes in employment, `dife`, for the restaurants with a large (`gap`>.4) or small (`gap`<=0.25) `gap` as defined by `twogrp`. There are 37 large gaps, and 43 small ones. You are looking at the large-minus-small differences in the change in employment, that is, in a difference-in-differences.

3.A Use an appropriate two-sided nonparametric test to see if the change in employment, after-minus-before, is higher or lower with twogrp=0 versus twogrp=1. What is the name of the test statistic? What is the two-sided P-value? Is the null hypothesis of no difference plausible?	Name of test: _____ P-value: _____ CIRCLE ONE Plausible Not plausible
3.B Give a two-sided 95% confidence interval and point estimate of shift associated with the test in 3A. Orient the difference so it is high gap minus low gap, or twogrp=0 minus twogrp=1. Does this calculation suggest that a large gap to meet the new minimum wage is associated with a larger decline in employment?	95% Confidence Interval: [_____, _____] Point estimate: _____ CIRCLE ONE Does suggest Does not suggest
3C. Which model underlies the procedure in 3B. Give one model number.	Model number: _____
3D. If Y=`dife` for `twogrp`=1 and X=`dife` for `twogrp`=0, give an estimate of Pr(Y>X) based on the procedure in 3A. Does this calculation suggest that a large gap to meet the new minimum wage is associated with a larger decline in employment?	Point estimate: _____ CIRCLE ONE Does suggest Does not suggest
3E. Is the model in 3C needed for the estimate in 3D or could a more general model be used instead? If a more general model would suffice, give its model number.	CIRCLE ONE Needed More general would suffice Model #, if applicable:_____

4. Question 4 asks you to use either `dife` or `difer` with `grp` to compare levels of changes in employment for groups defined by `gap`. There are 100 restaurants in 5 groups.

4A. Test the null hypothesis that the five groups do not differ in level. What is the name of the appropriate nonparametric test? What is the P-value? Which one model is the null hypothesis in this test and which other one model is the alternative hypothesis? (Pick the best choices and give model numbers.)	Name of test: _____ P-value: _____ Null Model: _____ Alternative: _____
4B. Use Holm's procedure with the Wilcoxon test to compare all pairs of groups. List the pairs of groups that differ significantly as (grp1, grp2).	List pairs. If none, write "none".
4C. Stigler's analysis would lead you to expect that a larger gap would lead to a greater decline in employment. Test no difference against Stigler's prediction using the Jonckheere-Terpstra test and the jonck.test function in the course workspace. Give the one-sided p-value. Be careful and think: you must orient the test and calculations so it aims at Stigler's prediction. Is no difference rejected at the 0.05 level in the direction that Stigler predicted?	One-sided p-value: _____ CIRCLE ONE Rejected at 0.05 Not rejected at 0.05

Print Name Clearly, Last, First: _____ ID#_____

Statistics 501, Spring 2010 Midterm Answer Page 1

This is an exam. Do not discuss it with anyone. Use abbreviations and model #'s from the data page.

1. Use the 100 observations on `dife` to answer question 1. `dife` is defined on the data page.

1.A. Do a boxplot, a Normal quantile plot and a Shapiro-Wilk test of Normality to determine whether the changes in employment (`dife`) look like observations from a Normal distribution. Do not turn in the plots. What is the P-value for the Shapiro-Wilk test? Do the changes in employment look like observations from a Normal distribution?	Shapiro-Wilk P-value: 0.0488 CIRCLE ONE Looks Normal (Does not look Normal)
1.B Use Wilcoxon's signed rank test to test the hypothesis that the changes in employment (`dife`) are symmetric about zero difference. What is the value of the test statistic? What is the two-sided P-value? Is the null hypothesis rejected at the conventional 0.05 level?	Test statistic: 2966 P-value: 0.0557 CIRCLE ONE Rejected at 0.05 (Not rejected at 0.05)
1.C Use procedures developed from Wilcoxon's signed rank test to find a two-sided 95% confidence interval and a point estimate for the center of symmetry of the changes in employment (`dife`). Taking the point estimate at naively, at face value, roughly (to the nearest integer) how many fte employees were gained or lost following the increase in the minimum wage?	95% Interval: [-0.015, 2.345] Point estimate: 1.08 Lost _____ or gained 1 employees
1.D Do a two-sided test of the null hypothesis that the center of symmetry of the changes in employment (`dife`) reflect a typical decline of ½ of an full time equivalent (fte) employee. State briefly how you did the test, give the value of the test statistic, the P-value, and say whether an ½ employee decline is plausible.	How you did it: Subtract -1/2 (or add ½) and test no difference. Test statistic 3312.5 P-value: 0.00681 CIRCLE ONE Plausible (Not plausible)
1.E Of the models on the data page, which one model underlies Wilcoxon's signed rank test as you used it in 1.D? Give one model number.	Model number: 5

2. Use the 100 observations on (`dife, gap`) to answer question 2.

2.A. Test the null hypothesis that `dife` and `gap` are independent using Kendall's correlation. Give: the correlation estimate, the two-sided P-value, and the estimated probability of concordance. Is it plausible that `dife` and `gap` are unrelated? Does this result suggest that declines in employment are typically larger when an increase in the minimum wage requires a larger increase in starting wages to comply with the new minimum wage?	Correlation: 0.177 P-value: 0.01664 Probability of concordance: .59 CIRCLE ONE Plausible (Not plausible) CIRCLE ONE Does suggest (Does not suggest)
2.B. Under which two models on the data page would the test in 2A be appropriate? Write two model numbers.	Model numbers: 2 and 6
2C. In model 6, with Y_i=dife, X_i=gap, use Kendall's correlation to test the hypothesis that H_0: = -1, so that a restaurant with the maximum gap of gap=0.45 would experience about ½ (exactly 0.45) larger decline than a restaurant with gap=0.	Two-sided p-value: 0.0087 CIRCLE ONE H_0: = -1 is plausible (Not plausible)

Print Name Clearly, Last, First: _____ ID#_____

Statistics 501, Spring 2010, Midterm, Answer Page #1

This is an exam. Do not discuss it with anyone. Use abbreviations and model #'s from the data page.

3. Question 3 asks you to compare the changes in employment, `dife`, for the restaurants with a large (`gap`>.4) or small (`gap`<=0.25) `gap` as defined by `twogrp`. There are 37 large gaps, and 43 small ones. You are looking at the large-minus-small differences in the change in employment, that is, in a difference-in-differences.

3.A Use an appropriate two-sided nonparametric test to see if the change in employment, after-minus-before, is higher or lower with twogrp=0 or twogrp=1. What is the name of the test statistic? What is the two-sided P-value? Is the null hypothesis of no difference plausible?	Name: Wilcoxon rank sum P-value: 0.0268 CIRCLE ONE Plausible (Not plausible)
3.B Give a two-sided 95% confidence interval and point estimate of shift associated with the test in 3A. Orient the difference so it is high gap minus low gap, or twogrp=0 minus twogrp=1. Does this calculation suggest that a large gap to meet the new minimum wage is associated with a larger decline in employment?	95% Confidence Interval: [0.41 , 5.41] Point estimate: 2.57 CIRCLE ONE Does suggest (Does not suggest)
3C. Which model underlies the procedure in 3B. Give one model number.	Model number: 1
3D. If Y=`dife` for `twogrp`=0 and X=`dife` for `twogrp`=1, give an estimate of Pr(Y>X) based on the procedure in 3A. Does this calculation suggest that a large gap to meet the new minimum wage is associated with a larger decline in employment?	Point estimate: 0.645 (accepted .35 = 1-.645) CIRCLE ONE Does suggest (Does not suggest)
3E. Is the model in 3C needed for the estimate in 3D or could a more general model be used instead? If a more general model would suffice, give its model number.	CIRCLE ONE Needed (More general would suffice) Model #, if applicable: 3

4. Question 4 asks you to use either `dife` or `difer` with `grp` to compare levels of changes in employment for groups defined by `gap`. There are 100 restaurants in 5 groups.

4A. Test the null hypothesis that the five groups do not differ in level. What is the name of the appropriate nonparametric test? What is the P-value? Which one model is the null hypothesis in this test and which other one model is the alternative hypothesis? (Pick the best choices and give model numbers.)	Name of test: Kruskal-Wallis P-value: .135 Null Model: 11 Alternative: 8
4B. Use Holm's procedure with the Wilcoxon test to compare all pairs of groups. List the pairs of groups that differ significantly as (grp1, grp2).	List pairs. If none, write "none". None
4C. Stigler's analysis would lead you to expect that a larger gap would lead to a greater decline in employment. Test no difference against Stigler's prediction using the Jonckheere-Terpstra test and the jonck.test function in the course workspace. Give the one-sided p-value. Be careful and think: you must orient the test and calculations so it aims at Stigler's prediction. Is no difference rejected at the 0.05 level in the direction that Stigler predicted?	One-sided p-value: 0.987 CIRCLE ONE Rejected at 0.05 (Not rejected at 0.05) The direction is backwards, so you do not reject in this direction. Had you predicted the opposite direction, you would have rejected.

Doing the Problem Set in R (Spring 2010)

1.A

```
> par(mfrow=c(1,2))
> boxplot(dife,ylab="change in fte")
> qqnorm(dife,ylab="change in fte")
> qqline(dife)
> shapiro.test(dife)
        Shapiro-Wilk normality test
data:  dife
W = 0.9745, p-value = 0.04888
```

1.B, 1.C

```
> wilcox.test(dife,conf.int=T)
Wilcoxon signed rank test with continuity correction
data:  dife
V = 2966, p-value = 0.05568
alternative hypothesis: true location is not equal to 0
95 percent confidence interval:
 -0.01494096  2.34500504
sample estimates:
(pseudo)median
      1.080024
```

1.D

```
> wilcox.test(dife+.5)
Wilcoxon signed rank test with continuity correction
data:  dife + 0.5
V = 3312.5, p-value = 0.00681
alternative hypothesis: true location is not equal to 0
```

or equivalently

```
> wilcox.test(dife-(-.5))
data:  dife - (-0.5)
V = 3312.5, p-value = 0.00681
alternative hypothesis: true location is not equal to 0
```

2.A

```
> cor.test(dife,gap,method="kendall")
        Kendall's rank correlation tau
data:  dife and gap
z = 2.3945, p-value = 0.01664
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1771132
> (0.1771132+1)/2
[1] 0.5885566
```

2.C

```
> cor.test(dife-(-1*gap),gap,method="kendall")
        Kendall's rank correlation tau
data:  dife - (-1 * gap) and gap
z = 2.6229, p-value = 0.00872
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1939636
```

3A, 3B, 3C.

```
> wilcox.test(dife~twogrp,conf.int=T)
        Wilcoxon rank sum test with continuity correction
data:  dife by twogrp
W = 1025.5, p-value = 0.02678
alternative: true location shift is not equal to 0
95 percent confidence interval:
 0.4100318 5.4100372
sample estimates:
difference in location
              2.57228
```

```
> 1025.5/(43*37)
[1] 0.6445632
```

4A.

```
> kruskal.test(dife,grp)
        Kruskal-Wallis rank sum test
data:  dife and grp
Kruskal-Wallis chi-squared = 7.0116, df = 4, p-value =
0.1353
```

4B.

```
> pairwise.wilcox.test(dife,grp)
        Pairwise comparisons using Wilcoxon rank sum test
data:  dife and grp
            (-Inf,0] (0,0.24] (0.24,0.25] (0.25,0.4]
(0,0.24]    1.00     -        -           -
(0.24,0.25] 1.00     1.00     -           -
(0.25,0.4]  1.00     1.00     1.00        -
(0.4,0.45]  0.62     0.79     1.00        0.62
P value adjustment method: holm
```

4C. *Must use difer to get direction right.*

```
> jonck.test(difer,grp)
$pval
0.986594
```

Statistics 501 Spring 2010 Final Exam: Data Page 1
This is an exam. Do not discuss it with anyone.

The data are from a survey conducted in 2007 by the CDC: "The Youth Risk Behavior Surveillance System (YRBSS) monitors priority health-risk behaviors and the prevalence of obesity and asthma among youth and young adults. The YRBSS includes a national school-based survey conducted by the Centers for Disease Control and Prevention (CDC) and state, territorial, tribal, and local surveys conducted by state, territorial, and local education and health agencies and tribal governments." Strictly speaking, specialized methods should be used for data from complex sample surveys, but for the current exam this issue will be ignored. http://www.cdc.gov/HealthyYouth/yrbs/data/index.htm

The data are a 2^5 contingency table, `yrbs2007`, described kids 15-18, describing smoking (S), cocaine use (C), alcohol use (A), age in years (Y) and gender (G). **Use S, C, A, Y, and G to refer to the variables.** The table `yrbs2007.2` is the same as `yrbs2007` except it uses the letters S, C, A, Y and G; use either table.

```
> yrbs2007
, , alcohol_Q42 = 0 times, age = 15-16, Q2 = Female
          cocaine_Q50
smoke_Q34 0 times >0 times
      No     2318        5
      Yes     111        4

, , alcohol_Q42 = >0 times, age = 15-16, Q2 = Female
          cocaine_Q50
smoke_Q34 0 times >0 times
      No      520       27
      Yes     130       32

, , alcohol_Q42 = 0 times, age = 17-18, Q2 = Female
          cocaine_Q50
smoke_Q34 0 times >0 times
      No     1715        6
      Yes     144        2

, , alcohol_Q42 = >0 times, age = 17-18, Q2 = Female
          cocaine_Q50
smoke_Q34 0 times >0 times
      No      496       29
      Yes     155       44

, , alcohol_Q42 = 0 times, age = 15-16, Q2 = Male
          cocaine_Q50
smoke_Q34 0 times >0 times
      No     2133       15
      Yes      91        2

, , alcohol_Q42 = >0 times, age = 15-16, Q2 = Male
          cocaine_Q50
smoke_Q34 0 times >0 times
      No      508       49
      Yes     142       43

, , alcohol_Q42 = 0 times, age = 17-18, Q2 = Male
          cocaine_Q50
smoke_Q34 0 times >0 times
      No     1520       12
      Yes     118        7

, , alcohol_Q42 = >0 times, age = 17-18, Q2 = Male
          cocaine_Q50
smoke_Q34 0 times >0 times
      No      641       45
      Yes     212       75
```

Statistics 501 Spring 2010 Final Exam: Data Page 2
This is an exam. Do not discuss it with anyone.

```
> dimnames(yrbs2007)
$smoke_Q34
[1] "No"  "Yes"
S = smoke_Q34 is “Have you ever smoked cigarettes daily, that is, at
least one cigarette every day for 30 days?”
$cocaine_Q50
[1] "0 times"  ">0 times"
C = cocaine_Q50 is: “During the past 30 days, how many times did you
use any form of cocaine, including powder, crack or freebase?”
$alcohol_Q42
[1] "0 times"  ">0 times"
A = alcohol_Q42 is: “During the past 30 days, on many days did you have
5 or more drinks of alcohol in a row, that is, within a couple of
hours?
$age
[1] "15-16" "17-18"
Y for years.  (Younger kids are excluded.)
$Q2
[1] "Female" "Male"
G for gender.
```

Save yourself some arithmetic by learning to use [ ] in R. See what happens when you type `yrbs2007[,,1,1,1]` or `yrbs2007[,2,,,]`. Also, type `help(round)`

IMPORTANT

The only log-linear models considered are hierarchical models. Refer to such a model using the **compact notation** that indicates the highest order u-terms that are included. Example: $\log(m_{ijklm}) = u + u_{S(i)} + u_{C(j)} + u_{A(k)} + u_{Y(l)} + u_{G(m)} + u_{SC(ij)} + u_{YG(lm)}$ is [SC] [A] [YG]. Use the S, C, A, Y, G letters and brackets [ ].

Turn in only the answer page. Write answers in the spaces provided: brief answers suffice. If a question asks you to circle the correct answer, then you are correct if you circle the correct answer and incorrect if you circle the incorrect answer. If instead of circling an answer, you cross out an answer, then you are incorrect no matter which answer you cross out. Answer every part of every question.

Make and keep a photocopy of your answer page. Place the exam in an envelope with ‘Paul Rosenbaum, Statistics Department’ on it**. The exam is due in my office, 473 Huntsman, on Tuesday, May 11 at 11:00am.** You may turn in the exam early at my mail box in the Statistics Department, 4th floor, Huntsman. When all of the exams are graded, I will add an answer key to the on-line bulk-pack for the course.

This is an exam. Do not discuss it with anyone.

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2010 Final Exam: Answer Page 1 This is an exam. Do not discuss it.

1 Answer this question using ONLY the likelihood ratio goodness-of-fit chi-square for the one model in this question.	CIRCLE ONE or FILL IN
1.1. Does the hierarchical log-linear model with all 2-factor interactions (and no 3 factor interactions) provide an adequate fit to the data?	adequate not adequate
1.2. What is the value of the likelihood ratio chi-square for the model in 1.1? What are its degrees of freedom? What is the p-value?	chi square: _____ df: _____ p-value: _____

2 Answer this question using ONLY the likelihood ratio goodness-of-fit chi-square for the one model in this question.	CIRCLE ONE or FILL IN
2.1 Which hierarchical log-linear model says smoking (S) is conditionally independent of gender (G) given the other three variables (C & A & Y)? The question asks for the largest or most complex model which has this condition.	
2.2 Does the hierarchical log-linear model in 2.1 provide an adequate fit to the data?	adequate not adequate
2.3. What is the value of the likelihood ratio chi-square for the model in 2.1? What are its degrees of freedom? What is the p-value?	chi square: _____ df: _____ p-value: _____

3 Answer this question using ONLY the likelihood ratio goodness-of-fit (**lrgof**) chi-square for the one model in this question.	CIRCLE ONE or FILL IN
3.1 Does the model [SC] [CA] [CG] [SAY] [AYG] provide an adequate fit based on the **lrgof**?	adequate not adequate
3.2 What is the value of the likelihood ratio chi-square for the model in 3.1? What are its degrees of freedom? What is the p-value?	chi square: _____ df: _____ p-value: _____
3.3. If the model in 3.1 were true, would smoking and gender be conditionally independent give the other three variables?	yes no

Last Name: _____ First Name: _____ ID#: _____

Stat 501 S-2010 Final Exam: Answer Page 2 This is an exam. Do not discuss it.

4 Question 4 asks you to compare the simpler model [SC] [CA] [CG] [SAY] [AYG] and the more complex model [SC] [CA] [CG] [SAY] [AYG] [CAG] to see whether the added complexity is needed.	CIRCLE ONE or FILL IN
4.1 Is the fit of the simpler model adequate or is the CAG term needed. In this question, use the 0.05 level as the basis for your decision.	adequate not adequate
4.2 What is the value of the likelihood ratio chi-square for the test in 4.1? What are its degrees of freedom? What is the p-value?	chi square: _____ df: _____ p-value: _____
4.3. If CAG were needed, would the odds ratio linking cocaine use (C) and alcohol (A) be different for males and females?	yes no

5. Fit the model [SC] [CA] [CG] [SAY] [AYG] setting eps=0.01. Use the fitted counts under this model to estimate the eight odds ratios linking smoking (S) with cocaine (C) for fixed levels of alcohol (A), age (Y) and gender (G). Fill in the following table with the eight fitted odds ratios.

	Male	Male	Female	Female
	Age 15-16	Age 17-18	Age 15-16	Age 17-18
Alcohol = 0				
Alcohol > 0				

6. Fit the model [SC] [CA] [CG] [SAY] [AYG] setting eps=0.01. Use the fitted counts under this model to estimate the 16 conditional probabilities of cocaine use, cocaine>0, given the levels of the other four variables. Put the values in the table. **Round to 2 digits**, so probability 0.501788 rounds to 0.50. The first cell (upper left) is the estimate of the probability of cocaine use for a male, aged 15-16, who neither smokes nor drinks.

		Male	Male	Female	Female
		Age 15-16	Age 17-18	Age 15-16	Age 17-18
Smoke = 0	Alcohol = 0				
Smoke = 0	Alcohol > 0				
Smoke > 0	Alcohol = 0				
Smoke > 0	Alcohol > 0				

1 Answer this question using ONLY the likelihood ratio goodness-of-fit chi-square for the one model in this question.	CIRCLE ONE or FILL IN
1.1. Does the hierarchical log-linear model with all 2-factor interactions (and no 3 factor interactions) provide an adequate fit to the data?	adequate **not adequate**
1.2. What is the value of the likelihood ratio chi-square for the model in 1.1? What are its degrees of freedom? What is the p-value?	chi square: 32.4 df: 16 p-value: 0.00889

2 Answer this question using ONLY the likelihood ratio goodness-of-fit chi-square for the one model in this question.	CIRCLE ONE or FILL IN
2.1 Which hierarchical log-linear model says smoking (S) is conditionally independent of gender (G) given the other three variables (C & A & Y)? The question asks for the largest or most complex model which has this condition.	[SCAY] [CAYG] This is the most complex hierarchical model which has no u-term linking S and G, that is, no $u_{SG(im)}$ etc.
2.2 Does the hierarchical log-linear model in 2.1 provide an adequate fit to the data?	**adequate** not adequate
2.3. What is the value of the likelihood ratio chi-square for the model in 2.1? What are its degrees of freedom? What is the p-value?	chi square: 6.58 df: 8 p-value: 0.58

3 Answer this question using ONLY the likelihood ratio goodness-of-fit (**lrgof**) chi-square for the one model in this question.	CIRCLE ONE or FILL IN
3.1 Does the model [SC] [CA] [CG] [SAY] [AYG] provide an adequate fit based on the **lrgof**?	**adequate** not adequate
3.2 What is the value of the likelihood ratio chi-square for the model in 3.1? What are its degrees of freedom? What is the p-value?	chi square: 13.99 df: 16 p-value: 0.599
3.3. If the model in 3.1 were true, would smoking and gender be conditionally independent give the other three variables?	**yes** no As in 2.1, there are no u-terms linking S and G.

4 Question 4 asks you to compare the simpler model [SC] [CA] [CG] [SAY] [AYG] and the more complex model [SC] [CA] [CG] [SAY] [AYG] [CAG] to see whether the added complexity is needed.	CIRCLE ONE or FILL IN
4.1 Is the fit of the simpler model adequate or is the CAG term needed. In this question, use the 0.05 level as the basis for your decision.	(adequate) not adequate Barely adequate – p-value is 0.089
4.2 What is the value of the likelihood ratio chi-square for the test in 4.1? What are its degrees of freedom? What is the p-value?	chi square: 2.91 df: 1 p-value: 0.089
4.3. If CAG were needed, would the odds ratio linking cocaine use (C) and alcohol (A) be different for males and females?	(yes) no

5. Fit the model [SC] [CA] [CG] [SAY] [AYG] setting eps=0.01. Use the fitted counts under this model to estimate the eight odds ratios linking smoking (S) with cocaine (C) for fixed levels of alcohol (A), age (Y) and gender (G). Fill in the following table with the eight fitted odds ratios.

	Male	Male	Female	Female
	Age 15-16	Age 17-18	Age 15-16	Age 17-18
Alcohol = 0	4.59	4.59	4.59	4.59
Alcohol > 0	4.59	4.59	4.59	4.59

6. Fit the model [SC] [CA] [CG] [SAY] [AYG] setting eps=0.01. Use the fitted counts under this model to estimate the 16 conditional probabilities of cocaine use, cocaine>0, given the levels of the other four variables. Put the values in the table. **Round to 2 digits**, so probability 0.501788 rounds to 0.50. The first cell (upper left) is the estimate of the probability of cocaine use for a male, aged 15-16, who neither smokes nor drinks.

		Male	Male	Female	Female
		Age 15-16	Age 17-18	Age 15-16	Age 17-18
Smoke = 0	Alcohol = 0	0.01	0.01	0.00	0.00
Smoke = 0	Alcohol > 0	0.07	0.07	0.05	0.05
Smoke > 0	Alcohol = 0	0.03	0.03	0.02	0.02
Smoke > 0	Alcohol > 0	0.27	0.27	0.20	0.20

Spring 2010 Final: Doing the Exam in R

Question 1. This model has all 10 = 5x4/2 pairwise interactions.

```
> loglin(yrbs2007.2,list(c(1,2),c(1,3),c(1,4),c(1,5),c(2,3),c(2,4),
c(2,5),c(3,4),c(3,5),c(4,5)))
6 iterations: deviation 0.02655809
$lrt
[1] 32.38944
$df
[1] 16
> 1-pchisq(32.38944,16)
[1] 0.00889451
```

Question 2. This model omits the [S,G] or [4,5] u-term and all higher order u-terms that contain it, but includes all other u-terms.

```
> loglin(yrbs2007.2,list(c(1,2,3,4),c(2,3,4,5)))
2 iterations: deviation 0
$lrt
[1] 6.578771
$df
[1] 8
> 1-pchisq(6.578771,8)
[1] 0.5826842
```

Question 3.

```
> loglin(yrbs2007.2,list(c(1,2),c(2,3),c(2,5),c(1,3,4),c(3,4,5)))
5 iterations: deviation 0.05294906
$lrt
[1] 13.99041
$df
[1] 16
> 1-pchisq(13.99041,16)
[1] 0.5994283

> loglin(yrbs2007.2,list(c(1,2),c(2,3),c(2,5),c(1,3,4),c(3,4,5)))
5 iterations: deviation 0.05294906
$lrt
[1] 13.99041
$df
[1] 16
> loglin(yrbs2007.2,list(c(1,2),c(2,3),c(2,5),c(1,3,4),
c(3,4,5),c(2,3,5)))
6 iterations: deviation 0.01950314
$lrt
[1] 11.07689
$df
[1] 15
> 13.9904108-11.076890
[1] 2.913521
> 1-pchisq(2.914,1)
[1] 0.08781383
```

Question 5.

```
> mhat<-loglin(yrbs2007.2,list(c(1,2),c(2,3),c(2,5),
c(1,3,4),c(3,4,5)),eps=0.01,fit=T)$fit
6 iterations: deviation 0.005120433

> mhat[,,1,1,1]
     C
S       0 times  >0 times
  No  2319.8584 10.135780
  Yes  105.8827  2.123171

> or<-function(tb){tb[1,1]*tb[2,2]/(tb[1,2]*tb[2,1])}
> or(mhat[,,1,1,1])
[1] 4.58949
> or(mhat[,,1,1,2])
[1] 4.58949
> or(mhat[,,1,2,1])
[1] 4.58949
> or(mhat[,,1,2,2])
[1] 4.58949
> or(mhat[,,2,1,1])
[1] 4.58949
> or(mhat[,,2,1,2])
[1] 4.58949
> or(mhat[,,2,2,1])
[1] 4.58949
> or(mhat[,,2,2,2])
[1] 4.58949
```

Question 6.

```
> round( mhat[,2,,,]/( mhat[,1,,,]+ mhat[,2,,,]),2)
, , Y = 15-16, G = Female
     A
S     0 times >0 times
  No     0.00     0.05
  Yes    0.02     0.20

, , Y = 17-18, G = Female
     A
S     0 times >0 times
  No     0.00     0.05
  Yes    0.02     0.20

, , Y = 15-16, G = Male
     A
S     0 times >0 times
  No     0.01     0.07
  Yes    0.03     0.27

, , Y = 17-18, G = Male
     A
S     0 times >0 times
  No     0.01     0.07
  Yes    0.03     0.27
```

Have a great summer!

Some useful articles (available from the Library Web Page)

- The Analysis of Repeated Measures: A Practical Review with Examples
- Author(s): B. S. Everitt
- Source: *Journal of the Royal Statistical Society. Series D (The Statistician)*, Vol. 44, No. 1 (1995), pp. 113-135
- Published by: Blackwell Publishing for the Royal Statistical Society
- Stable URL: http://www.jstor.org/stable/2348622

Abstract

Repeated measures data, in which the same response variable is recorded on each observational unit on several different occasions, occur frequently in many different disciplines. Many methods of analysis have been suggested including t-tests at each separate time point and multivariate analysis of variance. In this paper the application of a number of methods is discussed and illustrated on a variety of data sets. The approach involving the calculation of a small number of relevant summary statistics is considered to have advantages in many circumstances._kw Compound Symmetry

- 328. Note: The Use of Non-Parametric Methods in the Statistical Analysis of the Two-Period Change-Over Design
- Author(s): Gary G. Koch
- Source: *Biometrics*, Vol. 28, No. 2 (Jun., 1972), pp. 577-584
- Published by: International Biometric Society
- Stable URL: http://www.jstor.org/stable/2556170

Abstract

The two-period change-over design is often used in clinical trials in which subjects serve as their own controls. This paper is concerned with the statistical analysis of data arising from such subjects when assumptions like variance homogeneity and normality do not necessarily apply. Test procedures for hypotheses concerning direct effects and residual effects of treatments and period effects are formulated in terms of Wilcoxon statistics as calculated on appropriate within subject linear functions of the observations. Thus they may be readily applied to small sample-data.

- A Distribution-Free Test for Related Correlation Coefficients
- Author(s): Douglas A. Wolfe
- Source: *Technometrics*, Vol. 19, No. 4 (Nov., 1977), pp. 507-509
- Published by: American Statistical Association and American Society for Quality
- Stable URL: http://www.jstor.org/stable/1267893

Abstract

Let (X1,X2,X3) be a continuous, trivariate random vector for which it is of interest to compare the correlation between X2 and X1 with that between X3 and X1. This problem is important, for example, when both X2 and X3 are potential linear predictors for X1 or, more generally, whenever the variable (X1,X2,X3) represents a triplet of measurements on the same individual and correlation comparisons are desired. In this note it is shown that an exact distribution-free test for such problems can be based on a single Kendall correlation coefficient.

- The Analysis of Multidimensional Contingency Tables
- Author(s): Stephen E. Fienberg
- Source: *Ecology*, Vol. 51, No. 3 (May, 1970), pp. 419-433
- Published by: Ecological Society of America
- Stable URL: http://www.jstor.org/stable/1935377

Abstract

Ecological data often come in the form of multidimensional tables of counts, referred to as contingency tables. During the last decade several new methods of analyzing such tables have been proposed. Here, a class of models analogous to those used in the analysis of variance is discussed, and a method for computing the expected cell counts for the different models is presented. Two differenet tests for checking the goodness-of-fit of a particular model are then examined. The first is the simple generalization of the Pearson chi-square test statistic, while the second is referred to as the likelihood-ratio chi-square test statistic. Both have the same asympototic chi-square distribution. The likelihood-ratio statistic can be used in the selection of a suitable model, via the technique of partitioning. All of the methods presented are illustrated using data collected by Schoener on lizards from the West Indies.

Other useful materials available from the library web page:

Shaffer, Juliet Popper. "Multiple hypothesis testing." *Annual Review of Psychology* 46 (1995): 561-584.