HANDOUT #13: HYPOTHESES TESTING FOR MULTIPLE POPULATIONS

Tests Comparing K Population/Process Parameters

I. Tests about Differences in Population Means/Location Parameter

1. Normal distribution with $\sigma_1 = \sigma_2$:
   - Pooled t-Test
   - Robust of pooled t-Test
2. Normal distributions with $\sigma_1 \neq \sigma_2$:
   - Separate Variance t-Test
3. Nonnormal distributions with small/moderate n_i:
   - Wilcoxon Rank Sum Test
4. Paired Data:
   - Paired t-Test for Normally Distributed Differences
   - Wilcoxon Signed Rank Test for NonNormally Distributed Differences

II. Tests about Differences in Population Proportions

- Chi-squared test of Homogeneity of Proportions
- Chi-squared test of Independence
- Fisher's Exact Test (permutation test)
- Odds Ratio and Relative Risk
- Sensitivity and Specificity
- McNemar's Test for Matched Pairs
- Sets of Tables - Cochran-Mantel-Haenszel Tests
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III. Tests about Differences in Population Standard Deviations

- Sampling from Normal Populations - Hartley's Test
- General Procedure - Brown-Forsythe-Levene's Test

IV. Tests for Correlation in the Data

- For an AR(1) model with normal errors - von Neumann Test
- Distribution-free test - Runs Test

Tests about Differences in Population Location Parameters

Suppose we two populations/processes and we want to test hypotheses about differences in their means. Our parameter of interest is

$$\theta = \mu_1 - \mu_2 \qquad \text{with} \quad \widehat{\theta} = \bar{X} - \bar{Y},$$

where we have $X_1, \ldots, X_n$ iid from Population #1 and
$Y_1, \ldots, Y_m$ iid from Population #2.

In order to make inferences based on $\hat{\theta}$ it is necessary to determine the sampling distribution of $\widehat{\theta}$.

$$E[\widehat{\theta}] = E[\bar{X} - \bar{Y}] = E[\bar{X}] - E[\bar{Y}] = \mu_1 - \mu_2$$

$$Var[\widehat{\theta}] = Var[\bar{X} - \bar{Y}] = Var[\bar{X}] + Var[\bar{Y}] - 2Cov(\bar{X}, \bar{Y}) = \frac{\sigma_1^2}{n} + \frac{\sigma_2^2}{m} - 2Cov(\bar{X}, \bar{Y})$$

We will also need to know the form of the cdf for $\widehat{\theta}$.

Case 1 We will impose the following conditions:

C1. Both populations have a normal distribution

C2. $\sigma_1 = \sigma_2 = \sigma$ with σ unknown

C3. Xs and Ys are independent.

Because Xs and Ys are independent

$$\text{Cov}(\bar{X}, \bar{Y}) = 0 \Rightarrow \quad \text{Var}[\widehat{\theta}] = \frac{\sigma^2}{n} + \frac{\sigma^2}{m} = \sigma^2 \left(\frac{1}{n} + \frac{1}{m} \right).$$

The distribution of $\widehat{\theta} = \bar{X} - \bar{Y}$ is $N\left(\mu_1 - \mu_2, \sigma^2 \left(\frac{1}{n} + \frac{1}{m}\right)\right)$.
Because σ is unknown we need to estimate it. We have two independent unbiased estimates of σ^2: S_1^2 and S_2^2, therefore, we **pool** the two estimates and obtain:

$$\widehat{\sigma} = S_p = \sqrt{\frac{(n-1)S_1^2 + (m-1)S_2^2}{n+m-2}}$$

S_p^2 is a weighted average of the sample variances from the two populations.
If $n = m$, then $\quad S_p^2 = \frac{1}{2}\left(S_1^2 + S_2^2\right), \quad$ the average of the two sample variances.

We can now just use our results about testing a single population mean and apply the t-test to our problem.

To test

$$H_o : \mu_1 \leq \mu_2 + \theta_o \quad \text{vs} \quad H_1 : \mu_1 > \mu_2 + \theta_o$$

just convert the above hypotheses to a hypothesis about $\theta = \mu_1 - \mu_2$, that is, test

$$H_o : \mu_1 - \mu_2 \leq \theta_o \quad \text{vs} \quad H_1 : \mu_1 - \mu_2 > \theta_o$$

That is, test

$$H_o : \theta \leq \theta_o \quad \text{vs} \quad H_1 : \theta > \theta_o$$

Our test statistic would be

$$T = \frac{\widehat{\theta} - \theta_o}{\sqrt{\frac{S_P^2}{n} + \frac{S_P^2}{m}}} = \frac{(\bar{X} - \bar{Y}) - \theta_o}{S_P\sqrt{\frac{1}{n} + \frac{1}{m}}}$$

We next need to determine the sampling distribution of T:

$$T = \frac{(\bar{X} - \bar{Y}) - \theta_o}{\sqrt{\frac{S_P^2}{n} + \frac{S_P^2}{m}}} = \frac{\frac{(\bar{X}-\bar{Y})-\theta}{\sigma\sqrt{\frac{1}{n}+\frac{1}{m}}} + \frac{(\theta-\theta_o)}{\sigma\sqrt{\frac{1}{n}+\frac{1}{m}}}}{\sqrt{\frac{(n+m-2)S_P^2/\sigma^2}{n+m-2}}}$$

$$\stackrel{\mathcal{D}}{=} \frac{N(0,1) + \Delta}{\sqrt{\frac{\chi^2_{n+m-2}}{n+m-2}}}$$

Therefore,

- T has a NonCentral t-distribution with
- $df = n + m - 2$
- noncentrality parameter (ncp)

$$\Delta = \frac{\theta - \theta_o}{\sigma\sqrt{\frac{1}{n} + \frac{1}{m}}}$$

When $\theta = \mu_1 - \mu_2 = \theta_o$,

- t has a Central t distribution
- determine the critical values and p-values using the Central $t-distribution$ cdf with $df = n+m-2$
- In R, $t_{\alpha,df} = qt(1-\alpha, df)$ and $p - value = 1 - pt(t_{cal}, df)$

For the power function we need to use the NonCentral $t - distribution$ cdf with $df = n + m - 2$ and noncentrality parameter

$$\Delta = \frac{\theta - \theta_o}{\sigma\sqrt{\frac{1}{n} + \frac{1}{m}}}$$

We will next consider the forms of the rejection region, p-value, and power function.

Case 1. $\mathbf{H_o}: \mu_\mathbf{1} - \mu_\mathbf{2} \leq \theta_\mathbf{o}$ versus $\mathbf{H_1}: \mu_\mathbf{1} - \mu_\mathbf{2} > \theta_\mathbf{o}$

Let $t_{\alpha,n+m-2}$ be the upper α percentile from a central t-distribution with $df = n + m - 2$, which can be obtained using the R-function: $\mathbf{t_{\alpha,n+m-2} = qt(1-\alpha, n+m-2)}$

- Reject H_o if $T > t_{\alpha,n+m-2}$.
- The power function for $\theta = \mu_1 - \mu_2$ is given by

$$\gamma(\theta) = P_\theta\left(T > t_{\alpha,n+m-2}\right) = 1 - G(t_{\alpha,n+m-2}),$$

where G is the cdf of a noncentral $t - distribution$ with $df = n + m - 2$ and noncentrality parameter

$$\Delta = \frac{\theta - \theta_o}{\sigma\sqrt{\frac{1}{n} + \frac{1}{m}}}$$

- Use the following R-function to calculate power
  $\gamma(\theta) = \mathbf{1 - pt(qt(1-\alpha, n+m-2), n+m-2, \Delta)}$
- p-value is as follows:

$$p - value = P_{\theta_o}(T > T_{obs}) = 1 - G_o(T_{obs})$$

where T_{obs} is the value calculated from the data
G_o is the cdf of a central t-distribution with $df = n + m - 2$,

- Use the following R-function to obtain the p-value:
  $p - value = \mathbf{1 - pt(T_{obs}, n+m-2)}$

Case 2. $\mathbf{H_o}: \mu_\mathbf{1} - \mu_\mathbf{2} \geq \theta_\mathbf{o}$ versus $\mathbf{H_1}: \mu_\mathbf{1} - \mu_\mathbf{2} < \theta_\mathbf{o}$

- Reject H_o if $T < -t_{\alpha,n+m-2}$.
- The power function for $\theta = \mu_1 - \mu_2$ is given by

$$\gamma(\theta) = P_\theta\left(T < -t_{\alpha,n+m-2}\right) = G(-t_{\alpha,n+m-2}),$$

where G is the cdf of a noncentral $t - distribution$ with $df = n + m - 2$ and noncentrality parameter

$$\Delta = \frac{\theta - \theta_o}{\sigma\sqrt{\frac{1}{n} + \frac{1}{m}}}$$

- Use the following R-function to calculate power
  $\gamma(\theta) = \mathbf{pt(-qt(1-\alpha, n+m-2), n+m-2, \Delta)}$
- p-value is as follows:

$$p - value = P_{\theta_o}(T < T_{obs}) = G_o(T_{obs})$$

where T_{obs} is the value calculated from the data
G_o is the cdf of a central t-distribution with $df = n + m - 2$,

- Use the following R-function to obtain the p-value:
  $p - value = \mathbf{pt(T_{obs}, n+m-2)}$

For the two-sided hypotheses, we have

Case 3. $\mathbf{H_o}: \mu_1 - \mu_2 = \theta_o$ versus $\mathbf{H_1}: \mu_1 - \mu_2 \neq \theta_o$

Let $t_{\alpha/2,n+m-2}$ the upper $\alpha/2$ percentile from a central t-distribution with $df = n+m-2$, which can be obtained using the R-function:

$$\mathbf{t_{\alpha/2,n+m-2} = qt(1-\alpha/2, n+m-2)}$$

- Reject H_o if $|T| > t_{\alpha/2,n+m-2}$
- The power function for $\theta = \mu_1 - \mu_2$ is given by

$$\begin{aligned}\gamma(\theta) &= P_\theta\left(|T| > t_{\alpha/2,n+m-2}\right)\\ &= P_\theta\left(T < -t_{\alpha/2,n+m-2}\right) + P_\theta\left(T > t_{\alpha/2,n+m-2}\right)\\ &= G(-t_{\alpha/2,n+m-2}) + 1 - G(t_{\alpha/2,n+m-2})\end{aligned}$$

where G is the cdf of a noncentral t-distribution with $df = n+m-2$ and

noncentrality parameter

$$\Delta = \frac{\theta - \theta_o}{\sigma\sqrt{\frac{1}{n}+\frac{1}{m}}}$$

- Use the following R-function to calculate power:

$$\gamma(\theta) = \mathbf{pt(-qt(1-\alpha/2, n+m-2), n+m-2, \Delta) + 1 - pt(qt(1-\alpha/2, n+m-2), n+m-2, \Delta)}$$

- The p-value is calculated as follows:

$$\begin{aligned}p-value &= P_{\theta_o}(|T| > |T_{obs}|)\\ &= 2P_{\theta_o}(T > |T_{obs}|)\\ &= 2(1 - G_o(|T_{obs}|),\end{aligned}$$

where G_o is the cdf of a central t-distribution with

$df = n+m-2$, and T_{obs} is the value of T calculated from the data.

- Use the following R-function to obtain the p-value:

$$p-value = \mathbf{2(1 - pt(|T_{obs}|, n+m-2))}$$

Example Suppose we wanted to test

$$H_o : \mu_1 \leq \mu_2 + 2 \text{ vs } H_1 : \mu_1 > \mu_2 + 2$$

using independent random samples of sizes $n = 28$ and $m = 31$. The data yields the following summary statistics:

$$\bar{X} = 93.2 \;\; S_1 = 7.5 \qquad \bar{Y} = 88.3 \;\; S_2 = 7.8$$

Test H_o vs H_1 using a size .05 test. Compute the power function for your test.

Solution Based on normal probability plots and the Shapiro-Wilk test, the researcher was relatively certain that the data was from normally distributed populations. The sample standard deviations indicate that the two populations have the same standard deviation. Therefore, we will use the Pooled t-test with

$$S_p = \sqrt{\frac{(28-1)(7.5)^2 + (31-1)(7.8)^2}{28+31-2}} = 7.659 \;\; \text{with} \;\; df = 28 + 31 - 2 = 57$$

Using the pooled t-test with $\alpha = .05$, we have

$$\text{Reject } H_o \text{ if } T > t_{.05,57} = qt(.95, 57) = 1.672$$

$$T = \frac{(93.2 - 88.3) - 2}{7.659\sqrt{\frac{1}{28} + \frac{1}{31}}} = 1.45 \Rightarrow \quad T = 1.45 \not> 1.672 \;\; \text{and}$$

$$p = value = P[T \geq 1.45] = 1 - pt(1.45, 57) = .076 > .05 = \alpha$$

Therefore, we would not reject H_o and conclude that there is not significant evidence (p=value=.076) that μ_1 is 2 units or larger than μ_2.

What is the chance that we have committed a Type I error?

What is the chance that we have committed a Type II error?

The power function (probability of Type II error) will be obtained using the R function

$\mathbf{p}t(qt(1-\alpha, n+m-2, \Delta)$

Because we do not know the value of σ, the power function will be computed in terms of the parameter, Δ. That is,

$$\gamma(\Delta) = P[\text{Reject} \;\; H_o \;\; \text{given} \;\; \Delta] = P[T > t_{\alpha,n+m-2} \;\; \text{given} \;\; \Delta] = 1 - pt(qt(1-\alpha, n+m-2, \Delta)$$

We have df=$n + m - 2 = 28 + 31 - 2 = 57$ and $\gamma(\Delta) = 1 - pt(qt(1 - .05, 57, \Delta)$, for various values of Δ.

Using the following R code, we obtain the table of values for the power:

```
d<- seq(-1,5,.25)
pow<- 1-pt(qt(.95,57),57,d)
pow<- round(pow,3)
output<- cbind(d,pow)
```

Δ	-1.00	-0.75	-0.50	-0.25	0.00	0.25	0.50	0.75	1.00	1.25	1.50	1.75	2.00
$\gamma(\Delta)$	0.004	0.009	0.016	0.029	0.050	0.081	0.125	0.183	0.256	0.341	0.435	0.534	0.630
Δ	2.25	2.50	2.75	3.00	3.25	3.50	3.75	4.00	4.25	4.50	4.75	5.00	
$\gamma(\Delta)$	0.718	0.795	0.858	0.906	0.941	0.965	0.980	0.989	0.995	0.997	0.999	1.000	

What is the chance the test committed a **Type II error**?

Robustness of t-based Procedures - 2 Populations

The t-based confidence intervals and test procedures for comparing two population means require three conditions to be satisfied.

C1. Both population distributions are normally distributed.

- Use Shapiro-Wilk test and normal reference distribution plots to determine if the two samples have been selected from normal populations.
- When the population distributions are either very heavy tailed or highly skewed, the coverage probability for confidence intervals and the level and power of the t test will differ greatly from the stated values. Nonparametric alternatives to the t test which do not require normality should be used.

C2. The population distributions have equal variances: $\sigma_1 = \sigma_2$

- Later in this handout, the BFL-test of equal variances will be described. It can be used to determine if this condition is valid.
- In order to illustrate the effect of unequal variances, a computer simulation was performed in which two independent random samples were generated from normal populations having the same means but unequal variances: $\sigma_1 = k\sigma_2$ with k=.25,.5,1,2 and 4. For each combination of sample sizes and standard deviations, 10,000 simulations were run. For each simulation, a level .05 test was conducted. The proportion of the 10,000 tests that incorrectly rejected H_o are presented in Table 1. If the pooled t test was unaffected by the unequal variances we would expect the proportions to be close to .05, the intended level, in all cases.

Table 1: Effect of Unequal σ's on the Type I Error Rates of the Pooled t-test

		σ_1=$k\sigma_2$				
n_1	n_2	k= .25	.50	1	2	4
10	10	.062	.055	.048	.052	.064
10	20	.012	.019	.051	.113	.161
10	40	.0008	.0057	.050	.181	.295

From the results in Table 1, we can observe that when the sample sizes are equal the proportion of type I errors remains close to .05 (ranged from .048 to .064). When the sample sizes are different, the proportion of type I errors deviated greatly from .05. The more serious case is when the smaller sample size is associated with the larger variance. In this case, the error rates were much larger than .05. For example, when n_1=10, n_2=40, $\sigma_1 = 4\sigma_2$, the error rate was .295. However, when n_1=10, n_2=10 and $\sigma_1 = 4\sigma_2$, the error rate was .064, much closer to .05. This is remarkable and provides a convincing argument to use equal sample sizes unless there are important reasons to assign greater resources to one treatment. The following expressions are an indication of the lack of robustness of the pooled t-test performs poorly when the sample sizes are unequal.

If $\sigma_1 > \sigma_2$ and $n_1 < n_2$ then

$$E[S_p^2] = \frac{(n_1-1)\sigma_1^2 + (n_2-1)\sigma_2^2}{n_1+n_2-2} < \sigma_1^2 \;\Rightarrow\; E\left[\frac{S_p^2}{n_1} + \frac{S_p^2}{n_2}\right] < \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2} \;\Rightarrow$$

Thus, $t = \frac{\bar{X}-\bar{Y}}{\sqrt{\frac{S_p^2}{n_1}+\frac{S_p^2}{n_2}}}$ will be larger than expected and hence will produce excessive number of rejections, i.e., an inflated Type I error rate.

C3. The third condition is that the two random samples are independent.

- At the end of this handout, a test of correlation will be described. It can be used to evaluate the independence condition.
- Practically, we mean that the two samples are randomly selected from two distinct populations and that the elements of one sample are statistically independent of those of the second sample. There are two types of dependencies (data is not independent) that commonly occur in experiments and studies.
- The data may have a *cluster effect* which often results when the data have been collected in subgroups. For example, 50 children are selected from 5 different classrooms for an experiment to compare the effectiveness of two tutoring techniques. The children are randomly assigned to one of the two techniques. Since children from the same classroom have a common teacher and hence may tend to be more similar in their academic achievement than children from different classrooms, the condition of independence between participants in the study may be lacking.
- A second type of dependence is the result of *serial or spatial correlation.* When measurements are taken over time, the observations which are closer together in time tend to be more similar than observations collected at greatly different times, serially correlated. A similar dependence occurs when the data is collected at different locations. For example, water samples taken at various locations in a lake in order to assess whether a chemical plant is discharging pollutants into the lake. Measurements which are physically closer to each other are more likely to be similar than measurements which are taken farther apart. This type of dependence is *spatial correlation.* When the data is dependent, the procedures based on the t distribution will produce confidence intervals having coverage probabilities different from the intended values and tests of hypotheses having type I error rates different from the stated values. There are appropriate statistical procedure for handling this type of data but they are of a more advanced nature. A book on longitudinal or repeated measures data analysis or the analysis of spatial data would provide the details for the analysis of dependent data.

  Also, correlated data is covered in the courses STAT 626-Time Series, STAT 636-Multivariate Analysis, and STAT 647-Spatial Statistics.

Case 2: Both populations are normal, $\sigma_1 \neq \sigma_2$, Xs and Ys are independent.

Separate Variance t-Test - Welch/Satterthwaite Test

We will modify the **Pooled t-Test** by using separate estimators of σ_1 and σ_2 in the t-statistic:

$$t^* = \frac{\bar{X} - \bar{Y}}{\sqrt{\frac{S_1^2}{n} + \frac{S_2^2}{m}}}$$

Suppose the following conditions hold:

C1. Both X_is and Y_is have a normal distributions

C2. X_is and Y_is are independent.

Under the above conditions, Welch and Satterthwaite showed that

t^* had an **approximate** $t-$distribution with $df = \nu$ given by

$$\nu = \frac{(C+1)^2(n-1)(m-1)}{C^2(m-1)+(n-1)} \quad \text{where} \quad C = \frac{S_1^2/n}{S_2^2/m}$$

Consider the following situations:

1. **(Equal Sample Sizes, Equal Variances)**

   Suppose n=m and $\sigma_1 = \sigma_2$, which implies $C \approx 1$, then $\nu = 2(n-1)$, the same value for df as in the pooled t-Test.

   There would be no difference in the two tests.

2. **(Unequal Sample Sizes, Equal Variances)**

   Suppose $m - 1 = k(n-1)$, with $k > 1$ and $\sigma_1 = \sigma_2$, which implies $C \approx k$, then

   $\nu = \frac{(k+1)^2 k}{k^3+1}(n-1)$, $df_{pooled} = k(n-1) + (n-1) = (k+1)(n-1)$ and $\frac{(k+1)^2 k}{k^3+1} < k+1$.

   For example, consider the following samples sizes:

n	m	ν	df_{pooled}
10	10	18	18
10	19	18.3	27
10	28	15.9	36
10	37	14.2	45
10	46	13.2	54

From the above table, we can conclude

- When the population variances are equal, that is, the Pooled t-Test is appropriate, but the sample sizes are very unequal, using the Separate Variance t-Test would yield a test having lower power than the Pooled t-test. (The larger the value for df, the greater the power of the test.)

To illustrate that the separate-variance t test is less affected by unequal variances than is the pooled t test, the data from the computer simulation reported in Table 1 was analyzed using the separate-variance t test.

The proportion of the 10,000 tests that incorrectly rejected H_o are presented in Table 1.

If the separate-variance t test was unaffected by the unequal variances we would expect the proportions to be close to .05, the intended level, in all cases.

Table 2 The Effect of Unequal Variances on the Type I Error Rates of the Separate-Variance t-test

		σ_1=kσ_2				
n_1	n_2	k= .25	.50	1	2	4
10	10	.051	.051	.047	.047	.054
10	20	.051	.051	.052	.053	.053
10	40	.054	.048	.048	.052	.051

From the results in Table 2, we can observe that

1. the separate-variance t test's type I error rates were consistently close to .05 in all cases considered above.

2. Using the values in Table 1, we observe the pooled t test had type I error rates very different from .05 when the sample sizes were unequal and we sampled from populations having very different variances

3. How accurate are the estimated Type I error rates in Tables 1 and 2? That is, how close are the simulated values to the true values for P[Type I error]?

   Let p = P[Type I error]. We have m = 10,000 Bernoulli trials in our simulation. Therefore, our estimate of p, $\hat{p}$, the proportion of Type I errors in the 10,000 trials, has standard error:

$$SE(\hat{p}) = \frac{\sqrt{p(1-p)}}{\sqrt{n}} \approx \frac{\sqrt{.05(1-.05)}}{\sqrt{10,000}} = .0022$$

   Thus, we have greater than two decimal place accuracy in our estimates.

Comparison of Pooled t-test, t and Separate-Variance t-test, t^*

1. The procedure for selecting the critical values and computing the p-values for the Separate Variance t-Test are identical to the procedures for the Pooled t-Test after making the change in degrees of freedom from $df_{pooled} = n + m - 2$ to $df_{sepvar} = \nu$.

2. The power function for the separate variance test is very complex because its degrees of freedom (df) depend on the data. Thus, the derivation of the sampling distribution of the separate variance t-Test under the alternative is only practically accomplished using computer simulation.

3. We developed pooled-variance t methods based on the requirement of independent random samples from normal populations with equal population variances.

   When the variances are not equal, we introduced the separate-variance t^* statistic. Confidence intervals and hypothesis tests based on these procedures (t or t^*) need not give identical results.

4. Standard computer packages often report the results of both t and t^* tests. Which of these results should you use in your statistical analysis?

- If the sample sizes are equal and the population variances are equal, the separate-variance t test and the pooled t test give algebraically identical results, that is, the computed t equals the computed t'.

  Thus, why not always use t^* in place of t when n_1=n_2?

- The reason we would select t over t^* is that the df for t are nearly always larger than the df for t^* and hence the power of the t test is greater than the power of the t^* test when the variances are equal.

- When the sample sizes and variances are very unequal, the results of the t and t^* procedures may differ greatly. The evidence in such cases indicates that the separate-variance methods are somewhat more reliable and more conservative than the results of the pooled t methods.

- However, if the populations have both different means and different variances, an examination of just the size of the difference in their means $\mu_1 - \mu_2$ would be an inadequate description of how the populations differ. We should always examine the size of the differences in both the means and the standard deviations of the populations being compared. The Brown-Forsythe-Levene test procedure can be used to examine the difference in the standard deviations of two populations.

- In many undergraduate textbooks, they do not bother to compute the correct df for the separate variance t-test. Instead they specify the degrees of freedom as $df = min(n - 1, m - 1)$ which produces a test statistic having reduced power and hence greater chance of producing Type II errors. The test is referred to as a a conservative test statistic. Not a good idea!

Case 3: Both populations are nonnormal, but the two distributions belong to same loc-scale family; Xs and Ys are independent.

Wilcoxon Rank Sum Test

Suppose we have two populations/processes distributions which are members of the same location-scale family with the same scale parameter but possibly different location parameters:

- Let $X_1, \ldots, X_n$ be iid with cdf $F_1(x) = F_o(\theta_1 + \nu_1 x)$ and
- Let $Y_1, \ldots, Y_n$ be iid with cdf $F_2(y) = F_o(\theta_2 + \nu_2 y)$,
- where $\nu_1 = \nu_2 = \nu$, with ν unknown and F_o being the standard member of the family of distributions.

The research proposal is to test hypotheses about $\theta_1 - \theta_2$.

The following conditions are placed on the population distributions:

C1. F_1 and F_2 are members of the same location-scale families with the same value for the scale parameter.

C2. The X_is and Y_is are independent

C3. $X_1, \ldots, X_n$ be iid with cdf $F_1(x) = F_o(\theta_1 + \nu x)$

C4. $Y_1, \ldots, Y_n$ be iid with cdf $F_2(y) = F_o(\theta_2 + \nu y)$

1. If F_o was a standard normal cdf then we would have the same conditions as Case 1 and could use the pooled t-Test.

2. The Wilcoxon Rank Sum test is a rank-transform procedure: We replace the data with their ranks in the combined sample and use the Wilcoxon Rank Sum test to evaluate differences in the location parameters: $\theta_1 - \theta_2$.

Implementation of Wilcoxon Rank Sum Test

1. Order the $N = n + m$ observations from smallest to largest
2. Replace the data values with their ranks: 1 to N (In case of ties, assign the average rank to the tied values)
3. Let W_1 be the sum of the ranks for the X_is and let W_2 be the sum of the ranks for the Y_is
4. $W_1 + W_2 = \sum_{i=1}^{N} i = N(N+1)/2$
5. Given the size of the test, α, use Table 11 in the Textbook or the R functions **qwilcox** and **pwilcox** to set the critical value and to compute the p-value for W_1 or W_2

An equivalent test was developed by Mann and Whitney at nearly the same time as the Wilcoxon Rank Sum test. Although the two tests appear to be different they are in fact identical.

Implementation of Mann-Whitney Test:

1. Compare each X_i with each Y_j. Let U_1 be the number of pairs (X_i, Y_j) in which $X_i > Y_j$: $U_1 = \sum_{i,j} I(X_i > Y_j)$
2. Compare each X_i with each Y_j. Let U_2 be the number of pairs (X_i, Y_j) in which $X_i < Y_j$: $U_1 = \sum_{i,j} I(X_i < Y_j)$
3. There are nm pairs and $U_1 + U_2 = nm$.
4. Given the size of the test α use Table 11 to set the critical value (upper $\alpha-$ percentiles) or to compute the p-value

Note: The Wilcoxon Rank Sum Test and the Mann-Whitney U-test are equivalent because:

$$W_1 = U_1 + \frac{n(n+1)}{2} \quad \text{and} \quad W_2 = U_2 + \frac{m(m+1)}{2}$$

Thus, it does not matter which test we use to test hypotheses about $\theta_1 - \theta_2$.

H1. To test $H_o : \theta_1 \leq \theta_2$ versus $H_1 : \theta_1 > \theta_2$

- Reject H_o if $W_1 \geq W_{\alpha,n,m}$ and
- compute $p - value = 1 - G(W_1 - 1)$
  where G is the cdf of W_1 when $\theta_1 = \theta_2$. Table 11 can be used to do both.
- R-function **wilcox** yields both critical value and p-value:
  $W_{\alpha,n,m} = qwilcox(1 - \alpha, n, m) + \frac{n(n+1)}{2}$

  $G(W_1) = pwilcox(W_1 - \frac{n(n+1)}{2}, n, m)$
- Alternatively, the R-function **wilcox.test(x,y,alternative="g",paired=F)** can be used to conduct the Wilcoxon Rank Sum Test, producing both critical value and p-value

H2. To test $H_o : \theta_1 = \theta_2$ versus $H_1 : \theta_1 \neq \theta_2$

Reject H_o if $W_1 \geq W_{\alpha/2,n,m}$ or if $W_1 \leq n(n+m+1) - W_{\alpha/2,n,m}$

$p - value = 2 * min\left(P[W_1 \geq w_1], P[W_1 \leq w_1]\right) = 2 * min(1 - G(w_1 - 1), G(w_1))$

where w_1 is the observed value of w_1 and G is the cdf of W_1 when $\theta_1 = \theta_2$.

- R-function **wilcox** yields both critical value and p-value:
  $W_{\alpha/2,n,m} = qwilcox(1 - \alpha/2, n, m) + \frac{n(n+1)}{2}$

  $G(W_1) = pwilcox(W_1 - \frac{n(n+1)}{2}, n, m)$
- Alternatively, the R-function **wilcox.test(x,y,alternative="t",paired=F)** can be used to conduct the Wilcoxon Rank Sum Test, producing both critical value and p-value

  Note that "g" for greater than was changed to "t" for two-sided test.

EXAMPLE

Many states are considering lowering the blood-alcohol level at which a driver is designated as driving under the influence (DUI) of alcohol. An investigator for a legislative committee designed the following test to study the effect of alcohol on reaction time. Ten subjects consumed a specified amount of alcohol. Another group of ten subjects consumed the same amount of a nonalcoholic drink, a placebo. The two groups did not know whether they were receiving alcohol or the placebo. The twenty subjects' average reaction times (in seconds) to a series of simulated driving situations are reported in the following table. Does it appear that alcohol consumption increases reaction time?

Placebo	0.90	0.37	1.63	0.83	0.95	0.78	0.86	0.61	0.38	1.97
Alcohol	1.46	1.45	1.76	1.44	1.11	3.07	0.98	1.27	2.56	1.32

We want to test the hypotheses:

H_o: The distributions of reaction times for the placebo and alcohol populations are identical.

H_1: The distribution of reaction times for the placebo consumption population is shifted to the left of the distribution for the alcohol population. (That is, larger reaction times are associated with the consumption of alcohol.)

The Shapiro-Wilk test yields p-value = .084 and .022 for the Placebo and Alcohol data, respectively. Therefore, because of the small sample sizes and the non-normality of the data, the Wilcoxon rank sum test will be implemented.

Solution

The Wilcoxon rank sum test will be conducted to evaluate whether alcohol consumption increases reaction time. Let W_1 be the sum of the ranks for the Alcohol group.

Placebo	7	1	16	5	8	4	6	3	2	18
Alcohol	15	14	17	13	10	20	9	11	19	12

1. For $\alpha = .053$, reject H_o if $W_1 \geq 127$,

   using Table 1 in the Appendix with $\alpha = .053$ one-tailed and $n = m = 10$.

2. W_1 is computed by summing the ranks from the Alcohol group,

   $W_1 = 15 + 14 + 17 + 13 + 10 + 20 + 9 + 11 + 19 + 12 = 140.$

3. Since 140 is greater than 127, we reject H_o

   $p - value = 1 - G(W_1 - 1) = 1 - G(140 - 1) = 1 - G(139) < 1 - G(138) < .006$, using Table 11.

4. Using the R-functions:

   $W_{.05,10,10} = qwilcox(.948, 10, 10) + \frac{10(10+1)}{2} = 72 + 55 = 127$

   $p - value = 1 - G(140 - 1) = 1 - pwilcox(139 - \frac{10(10+1)}{2}, 10, 10) = 1 - pwilcox(139 - 55, 10, 10) = .0034$

   The above calculations can be directly obtain using the following R program:

5. Conclude there is significant evidence, p-value=.0034, that the placebo population has shorter reaction times than the population of alcohol consumers.

Program and Output from R

Let x be the vector of values for the X_is and y be the vector of values for the y_is then

The R-function **wilcox.test(x,y,alternative="l",paired=F)** yields

```
x = c(.9,.37,1.63,.83,.95,.78,.86,.61,.38,1.97)

y = c(1.46,1.45,1.76,1.44,1.11,3.07,0.98,1.27,2.56,1.32)

wilcox.test(x,y,alternative="l",paired=F)

        Wilcoxon rank sum test

data:  x and y

W = 15, p-value = 0.003421

alternative hypothesis: true mu is less than 0
```

Note in the above output, R calculates the Mann-Whitney U not the Wilcoxon Rank Sum W:

$W_2 = \frac{N(N+1)}{2} - W_1 = \frac{20(20+1)}{2} - 140 = 70$

$U_2 = W_2 - \frac{n(n+1)}{2} = 70 - 55 = 15$

Approximation using Central Limit Theorem

For large n and m, the distribution of the Wilcoxon Rank Sum test can be approximated by a normal distribution: Let

$$\mu = \frac{n(n+m+1)}{2}$$

$$\sigma = \sqrt{\frac{nm(n+m+1)}{12}}$$

.

Then

$$Z = \frac{W_1 - \mu}{\sigma} \quad \text{is approx. distributed as} \quad N(0,1)$$

We can use the $N(0,1)$ tables to set the critical values and compute p-values for W_1.

In our example on the previous page, we would have

1. $W_1 = 140$
2. $\mu_W = \frac{n(n+m+1)}{2} = \frac{10(20+1)}{2} = 105$
3. $\sigma_W = \sqrt{\frac{nm(n+m+1)}{12}} = \sqrt{\frac{(10)(10)(10+10+1)}{12}} = 13.2288$
4. $W_{.05,10,10} \approx \mu_W + Z_{.05}\sigma_W = 105 + (1.645)(13.2288) = 126.76$
4. $Z = \frac{W_1-\mu}{\sigma} = \frac{140-105}{13.2288} = 2.646 \quad \Rightarrow \quad p - value = P[Z > 2.646] = 1 - \Phi(2.646) = 0.0041$
5. Using the Wilcoxon Tables or R functions we obtained $W_{.053,10,10} = 127$ and p-value = 0.0034.

Comparison of Rank Sum Test to t-Test:

The Wilcoxon Rank Sum test is a distribution-free test in that the critical values and p-value are calculated without having to specify the functional form of F_o.

However, the power function of the Wilcoxon Rank Sum test depends on the size of difference in the location parameter and the population cdf F_o. When the sample sizes are large and the $N(0,1)$ approximation is appropriate, the values of μ and σ when $\theta_1 - \theta_2 \neq 0$ will depend on F_o. This makes it nearly impossible to obtain an analytical form for the power function. Therefore, we will study power of the Wilcoxon Rank Sum test through the following simulation study:

The Wilcoxon rank sum test is an alternative to the two-sample t test with the rank sum test requiring somewhat weaker conditions on the populations from the data is selected than are required for using the t test.

1. The Wilcoxon's test does not require the two populations to have normal distributions, it only requires that the distributions are identical except possibly that one distribution is shifted from the other distribution.

2. When both distributions are normal, the t test will be more likely to detect an existing difference, that is, the t test has greater power than the rank sum test. This is logical since the t test uses the magnitudes of the observations rather than just their relative magnitudes (ranks) as is done in the rank sum test.

3. When the two distributions have long or heavy tails, the Wilcoxon rank sum test has greater power, that is, it is more likely to detect a shift in the population distributions than the t test.

4. Also, the level or probability of a type I error for the Wilcoxon rank sum test will be equal to nominal (stated) level for all population distributions. Whereas, the t test's *actual* level will deviate from its stated value when the population distributions are nonnormal. This is particularly true when nonnormality of the population distributions is present in the form of severe skewness or extreme outliers.

5. Randles and Wolfe (1979) investigated the effect of skewed and heavy tailed distributions on the power of the t test and the Wilcoxon rank sum test.

6. Table 3 contains a portion of the results of their simulation study.

    a. For each set of distributions, sample sizes and shifts in the populations, 5000 samples were drawn and the proportion of times a level $\alpha = .05$ t test or Wilcoxon rank sum test rejected H_0 was recorded.
    b. The distributions considered were Normal, Double Exponential (symmetric, heavy-tailed), Cauchy (symmetric, extremely heavy-tailed), and Weibull (skewed to the right).
    c. Shifts of size 0, $.6\sigma$, and 1.2σ were considered, where σ denotes the standard deviation of the distribution, with the exception of the Cauchy distribution, where σ is a general scale parameter.

Table 3 Power of Pooled t-Test(t) and Wilcoxon Rank Sum Test(W) with $\alpha = .05$

		Distribution F_o											
		Normal			DoubleExp			Cauchy			Weibull		
	Shift:	0	.6	1.2	0	.6	1.2	0	.6	1.2	0	.6	1.2
n,m	Test												
5,5	t	.044	.213	.523	.045	.255	.588	.024	.132	.288	.049	.221	.545
	W	.046	.208	.503	.049	.269	.589	.051	.218	.408	.049	.219	.537
5,15	t	.047	.303	.724	.046	.304	.733	.056	.137	.282	.041	.289	.723
	W	.048	.287	.694	.047	.351	.768	.046	.284	.576	.049	.290	.688
15,15	t	.052	.497	.947	.046	.507	.928	.030	.153	.333	.046	.488	.935
	W	.054	.479	.933	.046	.594	.962	.046	.484	.839	.046	.488	.927

- When the distribution is normal, the t test is only slightly better, greater power values, than the Wilcoxon rank sum test.
- For the double exponential, the Wilcoxon test has greater power than the t test.
- For the Cauchy distribution, the level of the t test deviates significantly from .05 and its power is much lower than the Wilcoxon test.
- When the distribution was somewhat skewed, Weibull distribution, the tests had similar performance. Furthermore, the level and power of the t test were nearly identical to the values when the distribution was normal.
- The t test is quite robust to skewness, except when there are numerous outliers.

The accuracy of the simulated values for the power function are obtained by considering the power as a proportion, p, which we are estimating by running 5000 replications of a Bernoulli trial in which we record

$$Y = \begin{cases} 1 \text{ if} & \text{Tests rejects } H_o \\ 0 \text{ if} & \text{Tests fails to reject } H_o \end{cases}$$

Our estimate of the power is then $\hat{p} = \frac{m}{5000}$ where m is the number of times $Y = 1$.

The estimated standard error of $\hat{p}$ is $\sqrt{\frac{\hat{p}(1-\hat{p})}{5000}}$ which yields the following values:

$$\text{SE(Estimated Power)} = \begin{cases} .0031 & \text{for } \hat{p} \leq .05, \quad \hat{p} \geq .95 \\ .0057 & \text{for } \hat{p} \approx .20, \quad p \approx .80 \\ .0067 & \text{for } \hat{p} \approx .35, \quad \hat{p} \approx .65 \\ .0071 & \text{for } \hat{p} \approx .5 \end{cases}$$

where $\hat{p}$ is the estimated power from the simulation.

Case 4: X's and Y's are Paired

When the experimental units have a high degree of variability prior to being randomly assigned to one of two treatments, the experimental units are paired so as to reduce the variance between $\bar{X}$ and $\bar{Y}$. The two units within a pair are more alike than units in different pairs. This type of design will result in a more precise evaluation of the differences in two populations.

Example 1: Common Attribute to Both Measurements

An experiment was conducted to compare the mean lengths of time required for the bodily absorption of two drugs, D_1 and D_2, used in the treatment of epilepsy. A group of 20 epileptic patients were randomly assigned for inclusion in the study. The 20 patients had very different severity of the disease. The patients were paired so that the patients within a pair were diagnosised as having about the same level of severity of the disease. The two drugs were randomly assigned within each pair of patients. The length of time (in minutes) for the drug to reach a specified level in the blood was recorded for each of the patients. The researchers wanted to know if there was a difference in the performance of the two drugs.

	Disease Severity									
	1	2	3	4	5	6	7	8	9	10
Drug D_1	19.8	45.4	32.0	24.5	47.2	18.1	50.2	47.2	16.8	41.2
Drug D_2	23.0	37.3	11.4	60.6	72.1	41.4	42.6	43.8	42.8	65.3

Example 2: Before and After Study

After strip mining for coal, the mining company is required to restore the land to its condition prior to mining. One of the many factors that is considered is the pH of the soil, which is an important factor in determining what types of plants will survive in a given location. The strip mined area was divided into grids before the mining took place. Twelve grids were randomly selected and the soil pH was measured prior to the mining. When the mining was completed, the mining company attempted to restore the land to its unmined state. The soil pH readings were then taken on the same 12 grids. Is the distribution of pH readings different after mining when compared to the before mining readings?

	Grid Location											
	1	2	3	4	5	6	7	8	9	10	11	12
Before	10.02	10.16	9.96	10.01	9.87	10.05	10.07	10.08	10.05	10.04	10.09	9.92
After	10.21	10.16	10.11	10.10	10.07	10.13	10.08	10.30	10.17	10.10	10.06	10.24

A proper analysis of paired data needs to take into account the lack of independence between the two samples. The sampling distribution for the difference in the sample means, $(\bar{Y}_1 - \bar{Y}_2)$ will have mean and standard error

$$E[\bar{Y}_1 - \bar{Y}_2] = \mu_{\bar{Y}_1 - \bar{Y}_2} = \mu_1 - \mu_2$$

$$SE(\bar{y}_1 - \bar{y}_2) = \sigma_{\bar{y}_1 - \bar{y}_2} = \sqrt{Var(\bar{y}_1 - \bar{y}_2)} = \sqrt{\frac{\sigma_1^2 + \sigma_2^2 - 2\sigma_1\sigma_2\rho}{n}},$$

where ρ measures the amount of correlation (dependence) between the two samples.

When the two samples produce similar measurements, ρ is positive and the standard error of $\bar{Y}_1 - \bar{Y}_2$ will be smaller than what would be obtained using two independent samples.

In this type of situation, the use of paired data will reduce the standard error of the difference in the sample means in comparison to using independent samples for the two populations. The reduction of the variance would lead to a test having greater power if a paired data experiment was conducted

rather than having two independent data sets. However, the reduction in variance is obtained only by a concurrent reduction in the *df* for the $t-$percentiles. That is,

$$t_{\frac{\alpha}{2},n-1} > t_{\frac{\alpha}{2},2(n-1)}$$

Thus, in attempting to decide between using a paired analysis or two independent samples, the trade-off between reduced variability and reduced *df* must be taken into consideration.

Paired Data Analysis

In many cases the sample size, n, is too small to properly estimate the ρ. That is, suppose we have n independent pairs of data values

$$(X_1, Y_1), (X_2, Y_2), \ldots, (X_n, Y_n)$$

an estimator of ρ is given by

$$\hat{\rho} = \frac{\frac{1}{n-1}\sum_{i=1}^{n}(X_i - \bar{x})(Y_i - \bar{Y})}{S_X S_Y}$$

For small n, the above estimator has a large standard error.

An analysis of paired data which eliminates the need to estimate ρ transforms the data to differences in the n pairs of measurements,

$$D_1 = X_1 - Y_1, \quad D_2 = X_2 - Y_2, \quad \ldots, \quad D_n = X_n - Y_n$$

and obtains $\bar{D}$, S_D, the mean and standard deviations in the D_i's.

Also, the hypotheses about μ_1 and μ_2 must be now formulated into hypotheses about the mean of the differences, $\mu_D = \mu_1 - \mu_2$.

With this formulation, it is then possible to apply standard 1-Population procedures to the differences, $D_i's$.

The conditions required to develop t-distribution procedures for testing hypotheses and constructing confidence intervals for μ_x are

Paired Data: Normal Differences

1. The sampling distribution of the D_i's is a normal distribution.
2. The D_i's are independent, that is, the pairs of observations are independent.

The t-Test is then applied to hypotheses framed in terms of $\mu_D = \mu_1 - \mu_2$:

$$T = \frac{\sqrt{n}(\bar{D} - \mu_{Do})}{S_D}$$

The central t-distribution with $df = n - 1$ is then used to set critical values, compute p-values, and construct C.I.'s for the parameter: $\mu_D = \mu_1 - \mu_2$. Power calculations and sample size determinations are made using the noncentral t-distribution with

$$df = n - 1 \quad \text{and noncentrality parameter } \Delta = \frac{\sqrt{n}(\mu_x - \mu_{Do})}{\sigma_x}$$

Paired Data: Non-Normal Differences

1. The sampling distribution of the D_i's is not a normal distribution.
2. The D_i's are independent, that is, the pairs of observations are independent.

Case 1: If the sampling distribution of the D_i's is symmetrically distributed with a continuous cdf, then we would simply apply the **Wilcoxon Signed-Rank** procedure to the differences:

$$D_1 = X_1 - Y_1, \quad D_2 = X_2 - Y_2, \quad \ldots, \quad D_n = X_n - Y_n$$

Case 2: If the sampling distribution of the D_i's is a continuous distribution which is not symmetric then the **sign test** could be used to test hypotheses about $\mu_D = \mu_1 - \mu_2$.

The R-functions **t.test** and **wilcox.test** can be used to conduct the tests for paired data by simply using **paired=T** in both functions.

Sample Size Calculations Based on Power Specifications

The determination of the appropriate samples sizes n and m can be formulated in the same manner as for the 1-sample problem covered in Handout 12:

Case 1: Two Independent Samples from Normal Populations with $\sigma_1 = \sigma_2 = \sigma$

Suppose we want to test $H_1 : \mu_1 - \mu_2 > 0$ (the results for $H_1 : \mu_1 - \mu_2 < 0$ are identical)

1. Suppose we require $n = m$.

   Find the minimum sample size n such that a level α test has power of at least $1 - \beta$ to detect that $\mu_1 - \mu_2 > \delta$.

   If our test statistics is
   $$T = \frac{(\bar{X} - \bar{Y}) - \theta_o}{S_P\sqrt{\frac{1}{n} + \frac{1}{m}}} = \frac{(\bar{X} - \bar{Y}) - \theta_o}{S_P\sqrt{\frac{2}{n}}}$$

   we would need to use a power function based on the non-central t-distribution to determine the appropriate value of n. Many software packages have sample size determination as an option for this type of testing situation.

   A very accurate approximation can be obtained using the test statistic:
   $$Z = \frac{(\bar{X} - \bar{Y}) - \theta_o}{\sigma\sqrt{\frac{2}{n}}}$$

   provided the sample sizes are not too small. Using this test statistic, we have the appropriate sample size is
   $$n = 2\left[\frac{\sigma(z_\alpha + z_\beta)}{\delta}\right]^2$$

   where σ would be a guess at the standard deviation provided by the researcher.

   For a two-sided research hypothesis: $H_1 : \mu_1 - \mu_2 \neq 0$, just replace z_α with $z_{\alpha/2}$.

2. For unequal sample sizes but with the sample sizes being multiples of each other, $m = kn$, then we have
   $$n = \frac{k+1}{k}\left[\frac{\sigma(z_\alpha + z_\beta)}{\delta}\right]^2 \quad \text{and} \quad m = kn = (k+1)\left[\frac{\sigma(z_\alpha + z_\beta)}{\delta}\right]^2$$

Case 2: Paired Samples from Normal Populations

We can directly use our results from the 1-Population situation discussed in Handout 12.

Just consider the data as being $D_i = X_i - Y_i$ with mean $\mu_D = \mu_1 - \mu_2$ and standard deviation σ_D. We can then determine the appropriate sample size n, the number of pairs from either the Table A11 given in Handout 12 or from the formula:
$$n = \left[\frac{\sigma_D(z_\alpha + z_\beta)}{\delta}\right]^2$$

where the researcher would supply a guess at σ_D.

Example 1 Suppose we want to test $H_o : \mu_1 \leq \mu_2$ vs $H_1 : \mu_1 > \mu_2$

based on independent random samples of size n and m.

The researcher wants to determine the values of $n = m$ such that

1. an $\alpha = .05$ test would have
2. a probability of at least 90% of rejecting H_o whenever
3. μ_1 is at least 1.5 units larger than μ_2 .
4. The researcher is fairly certain that $\sigma_1 = \sigma_2 = 3$.

Solution

- $\alpha = .05$ and $\beta = 1 - .9 = .1$, the appropriate sample size would be

$$n = 2\left[\frac{\sigma(z_\alpha + z_\beta)}{\delta}\right]^2 = 2\left[\frac{(3)(1.645 + 1.282)}{1.5}\right]^2 = 68.5$$

- $n = m = 69$ observations would be needed from each of the populations to achieve the desired specifications.

- What is the actual power using the above approximation?

- With $n = m = 69$, $df = n + m - 2 = 136, \alpha = .05$, and

$$\Delta = \frac{\mu_1 - \mu_2}{\sigma\sqrt{\frac{1}{n} + \frac{1}{m}}} = \frac{1.5}{3\sqrt{\frac{1}{69} + \frac{1}{69}}} = 2.936835$$

  we have the following power:

$$\gamma(\mu_1 - \mu_2) = \gamma(1.5) = 1 - pt(qt(.95, 136), 136, 2.936835) = .8992.$$

- The above approximation yielded a power value a bit lower than the specified value,

  $\gamma(2.936835) = 0.8992 < .9$

- Using the sample size/power function in Minitab, the sample sizes should be $n = m = 70$ which yields a power value of .9030.

Example 2 Suppose we want to test $H_o : \mu_1 \leq \mu_2$ vs $H_1 : \mu_1 > \mu_2$ based on n independent pairs of observations.

The researcher wants to determine the values of n such that

1. an $\alpha = .01$ test would have
2. a probability of at least 80% of rejecting H_o
3. whenever μ_1 is at least 1.2 units larger than μ_2 .

Solution

- Suppose the researcher is fairly certain that $\sigma_D = 2$.
- With $\alpha = .01$ and $\beta = 1 - .8 = .2$, we would have that the appropriate sample sizes would be

1. Using Table A11 in Handout 12 with
   $\alpha = .01, \quad \beta = 1 - .8 = .2,$
   $\phi = \frac{\mu_1 - \mu_2}{\sigma_D} = \frac{1.2}{2} = .6$
   We obtain, $n = 31$.
   The power with $\Delta = \frac{\sqrt{n}\mu_D}{\sigma_D} = \frac{\sqrt{31}(1.2)}{2} = 3.34066$ is
   $\gamma(1.2) = 1 - pt(qt(.99, 30), 30, 3.34066) = .8056$

2. The quick and easy approximate formula, yields

$$n = \left[\frac{\sigma_D(z_\alpha + z_\beta)}{\delta}\right]^2 = \left[\frac{(2)(2.326 + .842)}{1.2}\right]^2 = 27.9$$

- Requires $n = 28$ pairs of observations from the populations to achieve the desired specifications.
- What is the actual power using the above approximation?
- With $n = 28, df = n - 1 = 27, \quad \Delta = \frac{\sqrt{n}\mu_D}{\sigma_D} = \frac{\sqrt{28}(1.2)}{2} = 3.1749,$
- The following power of an $\alpha = .01$ test is

$$\gamma(\mu_D) = \gamma(1.2) = 1 - pt(qt(.99, 27), 27, 3.1749) = .7542 < .8.$$

- The above approximation yielded a power value considerably lower than the specified value.

Analysis of Multiple Population (Process) Proportions

MODEL I: Product Multinomial Sampling Model

Pearson Chi-square Test of Homogeneity of Proportions

The data in the following table show the incidence of injuries for 750 accidents involving breakaway light poles. Of interest to the project investigators is whether there are different proportions of injuries in different parts of the country. Let p_i be the proportion of accidents involving breakaway light poles that resulted in an injury. The researcher wanted to test the hypotheses

$$H_o : p_1 = p_2 = p_3 = p_4 = p_5 \text{ vs } H_1 : p_i \neq p_j \text{ for at least one pair}(i, j)$$

A random sample of 150 accidents involving breakaway light poles was taken in each of five geographic locations. The data is given in the following table:

	Geographic Location					
	1	2	3	4	5	Total
Injuries	35	36	46	20	24	161
No Injuries	115	114	104	130	126	589
Total	150	150	150	150	150	750

The product multinomial sampling model involves t populations from which independent random samples of size: $n_1, \cdots, n_t$ are selected. The n_i experimental units are classified into one of two categories: Type A or Type B. The p_i's represent the proportion of units in population i that are of Type A. The sample data can be represented by a $2 \times t$ table:

	Populations					
	1	2	3	$\cdots$	t	Total
Type A	O_{11}	O_{12}	O_{13}	$\cdots$	O_{1t}	R_1
Type B	O_{21}	O_{22}	O_{23}	$\cdots$	O_{2t}	R_2
Total	n_1	n_2	n_3	$\cdots$	n_t	N

The hypotheses to be tested are

$$H_o : p_1 = \cdots = p_t = p_o \text{ vs } H_1 : p_i \neq p_j \text{ for at least one pair}(i, j)$$

where p_o is unknown.

- Under the null hypotheses of no difference in the t proportions, we would expect to observe
  1. $E_{1j} = n_j p_o$ Type A units from the jth population
  2. $E_{2j} = n_j(1 - p_o)$ Type B units from the jth population, where
  - p_o is the proportion of Type A units in each of the t populations.
  3. Since p_o is unknown, we estimate it with
  - $\hat{p}_o = \frac{R_1}{N}$ because
    all t populations have the same proportion under the null hypothesis.

- Under the null hypothesis $p_1 = \cdots = p_t = p_o$, therefore, the *estimated* expected counts are

  1. $\hat{E}_{1j} = n_j \hat{p}_o = n_j R_1 / N$
  2. $\hat{E}_{2j} = n_j (1 - \hat{p}_o) = n_j R_2 / N$

  3. The test statistic compares what was observed in the data, O_{ij}'s to what would be expected under the null hypothesis, E_{ij}:

$$T.S. = \chi^2 = \sum_{i=1}^{2} \sum_{j=1}^{t} (O_{ij} - \hat{E}_{ij})^2 / \hat{E}_{ij}$$

  4. Under H_o, the distribution of the chi-square statistic converges to a Chi-squared distribution with df=t-1.
  5. Reject H_o when
  - $\chi^2 \geq \chi^2_{\alpha, t-1} = qchisq(1 - \alpha, t - 1)$ with
  - $p - value = 1 - F(\chi^2) = 1 - pchisq(\chi^2, t - 1)$, where
  - F is the cdf of a Chi-squared distribution with df=t-1.
  6. If any $\widehat{E}_{ij} < 1$ or more than 20% of the $\widehat{E}_{ij} < 5$, then the asymptotic result does not hold and an exact permutation test is required.
  7. Why are the degrees of freedom t-1?

     With no restrictions, there are t unknown parameters: $p_1, p_2, \ldots, p_t$

     Under the null hypothesis, $H_o : p_1 = \cdots = p_t = p_o$, there is only 1 unknown parameter, p_o

     The asymptotic distribution of the Pearson Chi-squared statistic has degrees of freedom

     df = (# unknown parameters under $H_o \cup H_1$) - (# unknown parameters under H_o) $= t - 1$

The following SAS program and Output will illustrate the above discussion using the accident data.

```
OPTIONS PS=55 LS=75 NOCENTER NODATE;
DATA CAT;
INPUT Injury $ Location $ CNT @@;
CARDS;
I 1  35   NI 1 115
I 2  36   NI 2 114
I 3  46   NI 3 104
I 4  20   NI 4 130
I 5  24   NI 5 126
RUN;
PROC FREQ; TABLES Injury*Location/EXPECTED CELLCHI2 CHISQ;
WEIGHT CNT;
EXACT CHISQ;
RUN;
```

OUTPUT:

Injury Frequency Expected Cell Chi-Square Percent Row Pct Col Pct	Location 1	2	3	4	5	Total
I	35	36	46	20	24	161
	32.2	32.2	32.2	32.2	32.2	
	0.2435	0.4484	5.9143	4.6224	2.0882	
	4.67	4.80	6.13	2.67	3.20	21.47
	21.74	22.36	28.57	12.42	14.91	
	23.33	24.00	30.67	13.33	16.00	
NI	115	114	104	130	126	589
	117.8	117.8	117.8	117.8	117.8	
	0.0666	0.1226	1.6166	1.2635	0.5708	
	15.33	15.20	13.87	17.33	16.80	78.53
	19.52	19.35	17.66	22.07	21.39	
	76.67	76.00	69.33	86.67	84.00	
Total	150	150	150	150	150	750
	20.00	20.00	20.00	20.00	20.00	100.00

Statistic	DF	Value	Prob
Chi-Square	4	16.9568	0.0020
Likelihood Ratio Chi-Square	4	17.1802	0.0018
Mantel-Haenszel Chi-Square	1	5.7027	0.0169
Phi Coefficient		0.1504	
Contingency Coefficient		0.1487	
Cramer's V		0.1504	

Pearson Chi-Square Test

Chi-Square	16.9568
DF	4
Asymptotic Pr > ChiSq	0.0020
Exact Pr >= ChiSq	0.0019

Special Case t=2

When the number of population proportions being compare is two ($t = 2$) and the sample sizes n_1 and n_2 are large, we can test hypotheses about p_1 and p_2 using the following test statistic. This test statistic is equivalent to the Pearson chi-square statistic and will allow us to make power calculations and sample size determinations.

$$Z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

where $\hat{p} = \frac{n_1\hat{p}_1 + n_2\hat{p}_2}{n_1+n_2}$. Using a Central Limit Theorem, with $p_1 - p_2 = 0$, the distribution of Z is approximately $N(0,1)$ for large values of n_1 and n_2.

Consider the following 3 cases:

H1: $H_o : p_1 \leq p_2$ vs $H_1 : p_1 > p_2$

a. Reject H_o if $Z \geq z_\alpha$

b. $p - value = 1 - \Phi(z) = 1 - pnorm(z)$, where z is the value of Z computed from the observed data and Φ is the $N(0,1)$ cdf.

c. The Power function is given by

$$\gamma(p_1, p_2) = P[Z \geq z_\alpha] = 1 - \Phi\left[\frac{z_\alpha\sqrt{p(1-p)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} - (p_1 - p_2)}{\sigma}\right]$$

$$\text{where} \quad \sigma = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}} \quad \text{and} \quad p = \frac{n_1p_1 + n_2p_2}{n_1 + n_2}$$

H2: $H_o : p_1 \geq p_2$ vs $H_1 : p_1 < p_2$

a. Reject H_o if $Z \leq -z_\alpha$

b. $p - value = \Phi(z) = pnorm(z)$, where z is the value of Z computed from the observed data.

c. The Power function is given by

$$\gamma(p_1, p_2) = P[Z \leq -z_\alpha] = \Phi\left[\frac{-z_\alpha\sqrt{p(1-p)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} - (p_1 - p_2)}{\sigma}\right]$$

H3: $H_o : p_1 = p_2$ vs $H_1 : p_1 \neq p_2$

a. Reject H_o if $|Z| \geq z_{\alpha/2}$

b. $p - value = 2\Phi(|z|) = 2(1 - pnorm(z))$, where z is the value of Z computed from the observed data.

c. The Power function is given by

$$\gamma(p_1, p_2) = P[|Z| \geq z_\alpha] = 1 - \Phi\left[\frac{z_{\alpha/2}\sqrt{p(1-p)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} - (p_1 - p_2)}{\sigma}\right] + \Phi\left[\frac{-z_{\alpha/2}\sqrt{p(1-p)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} - (p_1 - p_2)}{\sigma}\right]$$

EXAMPLE The article "Adjuvant Radiotherapy and Chemotherapy in Node-Positive Premenopausal Women with Breast Cancer", *New England Journal of Medicine,* 1997, pp. 956-962, reported on a study designed to evaluate two therapies:

Therapy 1: treating cancer patients with chemotherapy only and Therapy 2: treating cancer patients with chemotherapy and radiation.

There were 154 cancer patients who were treated with chemotherapy only. Of these patients, 76 survived at least 15 years after treatment.

There were 164 cancer patients who were treated with chemotherapy and radiation. Of these patients, 98 survived at least 15 years after treatment.

Is there sufficient evidence at an $\alpha = .01$ level that including radiation provided an increased survival rate over the chemotherapy only treatment?

$H_o : p_1 \geq p_2$ vs $H_1 : p_1 < p_2$

a. Reject H_o if $Z \leq -z_{.05} = -2.326$

$\hat{p}_1 = 76/154 = .494$ and $\hat{p}_2 = 98/164 = .598 \quad \Rightarrow \hat{p} = (76 + 98)/(154 + 164) = .547$

$Z = \frac{.494-.598}{\sqrt{.547(1-.547)\left(\frac{1}{154}+\frac{1}{164}\right)}} = -1.86 > -2.326$

Thus we fail to reject H_o and conclude there is not significant evidence (p-value=.0314) that including radiation in the treatment has increased the survival rate.

b. $p - value = P[Z \leq -1.86] = pnorm(-1.86) = .0314 > .01.$

c. A 99% C.I. on $p_1 - p_2$ is given by

$\hat{p}_1 - \hat{p}_2 \pm z_{\alpha/2}\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}} \Rightarrow$

$.494 - .598 \pm (2.576)\sqrt{\frac{.494(1-.494)}{154} + \frac{.598(1-.598)}{164}} = -.104 \pm .143 = (-.247, .039)$

Multiple Comparisons of t Proportions

We can use the results for $t = 2$ to further investigate the accident data example. Based on the test of homogeneity of proportions, we found there was significant evidence that the proportion of accidents resulting in an injury differed over the four locations. To further investigate this data, we would want to determine which pairs of locations had significantly different proportions. There are $\binom{5}{2} = 10$ pairs of locations. It would be necessary to conduct 10 tests of $H_o : p_k = p_m$ vs $H_1 : p_k \neq p_m$ for $k \neq m = 1, 2, 3, 4, 5$.

Just as in the case of simultaneous confidence intervals which was discussed in Handout 11, it is necessary to account for multiple testing of the five location proportions. Thus, each of the 10 tests of hypotheses will be conducted using a per comparison (PC) Type I error rate of $\alpha_{pc} = \alpha_{Exp}/M$ where α_{Exp} is the desired overall Type I error rate and M is the number tests conducted. In our accident example, if we want $\alpha_{Exp} = .05$ then is necessary to conduct each of the 10 tests at a level of $\alpha_{pc} = .05/10 = .005$. This may result in an inflated Type II error rate due to the very low level at which each of the 10 tests is conducted.

The proportion of accidents resulting in an injury are given below:

	Location				
	1	2	3	4	5
Proportion Injured	.233	.240	.307	.133	.160

Using the p-values from $Z = \dfrac{\hat{p}_i - \hat{p}_j}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}}$,

conduct the 10 pairwise comparisons of the proportions (p_k vs p_m) we obtain the following results:

	Comparison									
Comparison	1 vs 2	1 vs 3	1 vs 4	1 vs 5	2 vs 3	2 vs 4	2 vs 5	3 vs 4	3 vs 5	4 vs 5
p-value	.892	.153	.025	.110	.195	.018	.083	.0003	.0027	.514

Using a per comparison error rate of .05/10 = .005, there are two pairs having p-value $\leq .005$,

"Loc. 3 vs Loc. 4" and "Loc. 3 vs Loc. 5".

Thus, there was not significant evidence that the locations (1, 2, 3) had significantly different proportions of accidents resulting in injuries.

Also, there was not significant evidence that the locations (1, 2, 4, 5) had significantly different proportions of accidents resulting in injuries.

Thus, we have now gained considerably more insight about the relationship between proportion of accidents resulting in injuries and the type of location where the accident occurs. Using the test of homogeneity of proportions, it was determined that there was a difference in the five proportions but the test did not specify which locations were similar and which were different.

Sample Size Calculations

To determine the appropriate sample sizes, we will only consider the case $n_1 = n_2 = n$:

Specifications:

1. Level of Test: α
2. Type II error rate, β at a specified set of values for p_1 and p_2.

   That is, we want to determine the minimum sample size n, such that, an α level test will have a probability of Type II error of at most β if the true proportions are the given values of p_1 and p_2.
3. Let $p_1 - p_2 = D$
4. The appropriate sample size for a 1-sided test ($H_1 : p_1 > p_2$ or $H_1 : p_1 < p_2$) is given by

$$n = \frac{\left[z_\alpha \sqrt{(p_1 + p_2)(2 - p_1 - p_2)/2} + z_\beta \sqrt{p_1(1 - p_1) + p_2(1 - p_2)}\right]^2}{D^2}$$

5. The appropriate sample size for a 2-sided test ($H_1 : p_1 \neq p_2$) is given by

$$n = \frac{\left[z_{\alpha/2} \sqrt{(p_1 + p_2)(2 - p_1 - p_2)/2} + z_\beta \sqrt{p_1(1 - p_1) + p_2(1 - p_2)}\right]^2}{D^2}$$

EXAMPLE A researcher wants to determine the minimum sample sizes $n_1 = n_2 = n$ such that an $\alpha = .05$ test of $H_1 : p_1 > p_2$ would have maximum probability of Type II error of at most $\beta = .1$ if the true values of p_1 and p_2 are $p_1 = .0003$ and $p_2 = .00015$.

Using the above formula we obtain

$$n = \frac{\left[z_{.05} \sqrt{(.0003 + .00015)(2 - .0003 - .00015)/2} + z_{.1} \sqrt{.0003(1 - .0003) + .00015(1 - .00015)}\right]^2}{(.0003 - .00015)^2} = 171072.1$$

Thus, we would need $n_1 = n_2 = 171072$ experimental units for each of the two sets of Bernoulli trials.

The power of the test at these values: $\alpha = .05$, $n_1 = n_2 = 171072$, $p_1 = .0003$ and $p_2 = .00015$ would be calculated as follows:

$p = \frac{n_1 p_1 + n_2 p_2}{n_1 + n_2} = .000225 \Rightarrow \sigma = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}} = .000036262$

$$\gamma(p_1, p_2) = \gamma(.0003, .00015) = P[Z \geq z_{.05}] = P[Z \geq 1.645] = 1 - \Phi\left[\frac{z_\alpha \sqrt{p(1-p)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} - (p_1 - p_2)}{\sigma}\right] \Rightarrow$$

$$\gamma(.0003, .00015) = 1 - \Phi\left[\frac{1.645\sqrt{.000225(1 - .000225)\left(\frac{2}{171072}\right)} - (.0003 - .00015)}{.000036262}\right] \Rightarrow$$

$$\gamma(.0003, .00015) = 1 - pnorm(-1.279999) = .8997272 \approx .9 = 1 - .1$$

Fisher Exact Test - Permutation Test for Small Sample Sizes

When the condition for using the Chi-square approximation to the distribution of the Test Statistic is invalid, an inference will be derived which depends on an exact distribution rather than applying an asymptotic result that was required in the Chi-square test.

We will illustrate these methods using the comparison of two population proportions. This test is refered to as the *Fisher Exact Test.* The hypotheses to be tested are $H_o : p_1 \leq p_2$ versus $H_1 : p_1 > p_2$, where p_i is the probability of "success" for populaton i, i=1,2. In developing a small-sample test of hypotheses, we need to develop the exact probability distribution for the cell counts in all 2X2 tables having the same row and column totals as the 2×2 table from the observed table:

	Outcome		
Population	Success	Failure	Total
1	X	$n_1 - X$	n_1
2	Y	$n_2 - Y$	n_2
Total	m	$n - m$	n

For tables having the same row and column totals: $n_1, n_2, m, n-m$, the value of X determines the counts for the remaining three cells.

Thus, we can use the hypergeometric distribution to express the distribution that applies to the sets of 2X2 tables having fixed row and column totals. When $p_1 = p_2$, the probability of observing a particular value for x, that is, the probability of a particular table being observed, is given by

$$P(X = x|X + Y = m) = \frac{\binom{n_1}{x}\binom{n_2}{m-x}}{\binom{n}{m}}$$

To test the difference in the two population proportions, the p-value of the test is the sum of hypergeometric probabilities for outcomes at least as in support of the alternative hypothesis as the observed table. For $H_1 : p_1 > p_2$, we need to determine which other possible 2X2 tables would provide stronger support of H_1 than the observed table. Given the marginal totals, $n_1, n_2, m, n-m$, tables having larger X values will have larger values for $\hat{p}_1$
and hence provide stronger evidence in favor of $p_1 > p_2$.

Let x be the observed value of X. Then, any integer greater than x would provide even greater evidence that $p_1 > p_2$. The possible values of x are $0, 1, \ldots, min(n_1, m)$. Therefore, we have that

$$\text{p-value} = P[X \geq x] = \sum_{k=x}^{min(n_1,m)} \frac{\binom{n_1}{k}\binom{n_2}{m-k}}{\binom{n}{m}}$$

Using R we obtain: $p - value = 1 - phyper(x - 1, n_1, n_2, m)$

For the two sided alternative: $H_1 : p_1 \neq p_2$, the p-value is defined as the sum of the probabilities of tables no more likely than the observed table. Thus, the p-value is the sum of the probabilities of all values of $X = k$ for which $P(k) \leq P(x)$ where x is the observed value of X.

Note: The textbook has a formula for p-value but it is only valid if $n_1 = n_2$ and $n = m$.

The power function for the Fisher Exact test (with $n_1 = n_2$) is given by

$$\gamma(n, p_1, p_2) = \sum_{r=0}^{2n} \sum_{x \in C_r} \binom{n}{x}\binom{n}{r-x} p_1^x (1-p_1)^{n-x} p_2^{r-x} (1-p_2)^{n-r+x}$$

where r is the total number of observed successes in the two groups, x is the number of observed success in Group 1, and C_r is the critical region of the Fisher Exact Test.

Example of Applying Fisher Exact Test

Example 9.6 in the textbook considers the results from a clinical trial for comparing two drug therapies for leukemia: P and PV. Twenty-one patients were assigned to drug P and forty-two patients to drug PV. The following table summaries the success of both drugs:

	Outcome		
Drug	Success	Failure	Total
PV	38	4	42
P	14	7	21
Total	52	11	63

1. Compute the p-value for testing $H_o : p_1 \geq p_2$ vs $H_1 : p_1 < p_2$,

   where p_1, p_2 are the probabilities patient under Drug P, PV, respectively, goes into remission.

   The probability of the observed table is

   $$P(X = x) = \frac{\binom{42}{38}\binom{21}{14}}{\binom{63}{52}} = .0211 = dhyper(38, 42, 21, 52)$$

   Thus, the one-sided p-value is the sum of the probabilities for all tables having 38 or more successes:

   $$\begin{aligned} \text{p-value} = P[X \geq 38] &= \sum_{k=38}^{min(42,52)} \frac{\binom{42}{k}\binom{21}{52-k}}{\binom{63}{52}} \\ &= .02114 + .00379 + .00041 + .00002 + 0 = .02536 \end{aligned}$$

   Using R: $p - value = 1 - phyper(x - 1, n_1, n_2, m) = 1 - phyper(38 - 1, 42, 21, 52) = .02536501$

2. Compute the p-value for testing $H_o : p_1 = p_2$ vs $H_1 : p_1 \neq p_2$

   The p-value for the two-sided alternative hypothesis is the sum of the probabilities for all tables having probability of occurring that are less than the probability of the observed table: $P(38) = .0211$:

k	0	1	·	30	31	32	33	34	35	36
P(k)	.000000	.000000	·	.000000	.006951	.050180	.152060	.254925	.262208	.173349
k	37	38	39	40	41	42	43	·	51	52
P(k)	.074962	.021136	.003794	.000411	.000024	.000001	.000000	·	.000000	.000000

Thus, the two-sided p-value is .021136+.006951+.003794+.000411+.000024+.000001=.032317.

The following SAS program will compute the Chi-square test for the example and the value of the Fisher's Exact Test:

```
DATA CAT;
INPUT Result $ Drug $ CNT @@;
CARDS;
S P  14   F P  7
S PV 38   F PV 4
RUN;
PROC FREQ; TABLES Result*Drug/EXPECTED CELLCHI2 CHISQ;
WEIGHT CNT;
EXACT CHISQ;
RUN;
```

OUTPUT FROM SAS: EXAMPLE 2: RESULTS BY DRUG

Result Drug

Frequency Expected Cell Chi-Square Percent Row Pct Col Pct	P	PV	Total
F	7 3.6667 3.0303 11.11 63.64 33.33	4 7.3333 1.5152 6.35 36.36 9.52	11 17.46
S	14 17.333 0.641 22.22 26.92 66.67	38 34.667 0.3205 60.32 73.08 90.48	52 82.54
Total	21 33.33	42 66.67	63 100.00

Statistics for Table of Result by Drug

Statistic	DF	Value	Prob
Chi-Square	1	5.5070	0.0189
Likelihood Ratio Chi-Square	1	5.2010	0.0226
Continuity Adj. Chi-Square	1	3.9788	0.0461
Mantel-Haenszel Chi-Square	1	5.4196	0.0199
Phi Coefficient		0.2957	
Contingency Coefficient		0.2835	
Cramer's V		0.2957	

WARNING: 25% of the cells have expected counts less than 5.
(Asymptotic) Chi-Square may not be a valid test.

Fisher's Exact Test

Cell (1,1) Frequency (F)	7
Left-sided Pr <= F	0.9958
Right-sided Pr >= F	0.0254
Table Probability (P)	0.0211
Two-sided Pr <= P	0.0323

Model II: Multinomial Sampling

Pearson Chi-squared Test of Independence

A social scientist wants to determine if there is an association between political affiliation and annual income level. A random sample of 592 registered voters is selected and each of the selected individuals was asked their political affiliation and their annual income. These values were then summarized in the following table:

	Income Level				
	(0, 30K)	[30K, 50K)	[50K, 100K)	[100K, ∞)	Total
Republican	20	84	17	94	215
Democrat	68	119	26	7	220
Independent	5	29	14	16	64
Other	15	54	14	10	93
Total	108	286	71	127	592

Note the difference between the research question posed above and the research question posed in the Homogeneity of Proportions research question. Also, there is a difference between the sampling schemes in the two settings.

In the test of Independence of two variables setting, a random sample of N units is selected from a population and two characteristics are measured on each unit, Party Affiliation and Income. In the test of Homogeneity of Proportions, there were t populations and a random sample of N_i units was selected from the ith population, $i = 1, 2, \ldots, t$.

In the test of Independence problem, we have two categorical random variables, X and Y having r and c levels, respectively.

Let $p_{ij} = P[X = X_i,\ Y = Y_j]$ be the probability that a randomly selected unit falls in the (i, j) cell of the $r \times c$ contingency table.

Let $p_{i.} = P[X = X_i]$ and $p_{.j} = P[Y = Y_j]$ be the **marginal** probabilities associated with X and Y, respectively.

The null hypothesis is that X and Y are independent, that is,

$$P[X = X_i,\ Y = Y_j] = P[X = X_i]P[Y = Y_j] \text{ that is, } p_{ij} = p_{i.}p_{.j} \text{ for all pairs } (i, j)$$

The alternative hypothesis is X and Y are not independent, :

$$H_o : p_{ij} = p_{i.}p_{.j} \text{ for all } (i, j) \text{ vs } H_1 : p_{ij} \neq p_{i.}p_{.j} \text{ at least one pair } (i, j)$$

Randomly select N units from the population and classify them into the $r \times c$ cells according the their values of (X, Y), yielding the following contingency table:

	Populations					
	Y_1	Y_2	Y_3	$\cdots$	Y_c	Total
X_1	O_{11}	O_{12}	O_{13}	$\cdots$	O_{1c}	$n_{1.}$
X_2	O_{21}	O_{22}	O_{23}	$\cdots$	O_{2c}	$n_{2.}$
X_3	O_{31}	O_{32}	O_{33}	$\cdots$	O_{3c}	$n_{3.}$
$\cdots$	$\cdots$	$\cdots$	$\cdots$	$\cdots$	$\cdots$	$\cdots$
X_r	O_{r1}	O_{r2}	O_{r3}	$\cdots$	O_{rc}	$n_{r.}$
Total	$n_{.1}$	$n_{.2}$	$n_{.3}$	$\cdots$	$n_{.c}$	N

The expected counts would need to be computed next in order to apply the Chi-square test:

- Under the null hypothesis that X_i and Y_j are independent, we have

$$p_{ij} = p_{i.}p_{.j}, \text{ for all } (i,j) \text{ pairs}$$

Therefore, the expected counts are computed under H_o as follows:

1. $E_{ij} = Np_{ij} = Np_{i.}p_{.j}$, which are unknown
2. Estimate $p_{i.}$ and $p_{.j}$ by
   $\hat{p}_{i.} = n_{i.}/N$ and $\hat{p}_{.j} = n_{.j}/N$
3. Estimate E_{ij} by $\hat{E}_{ij}$ =N$\hat{p}_{i.}\hat{p}_{.j} = N\frac{n_{i.}}{N}\frac{n_{.j}}{N} = \frac{n_{i.}n_{.j}}{N} = \frac{\text{(ith row total)(jth column total)}}{N}$
4. The test statistic compares what was observed in the data, O_{ij}'s to what would be expected under the null hypothesis, $\hat{E}_{ij}$:

$$T.S. = \chi^2 = \sum_{i=1}^{r}\sum_{j=1}^{c}(O_{ij} - \hat{E}_{ij})^2/\hat{E}_{ij}$$

4. Under H_o, the distribution of the chi-square statistic converges to a Chi-squared distribution with df=(r-1)(c-1)
5. Reject H_o when
   - $\chi^2 \geq \chi^2_{\alpha,df}$ with
   - $p - value = 1 - F(\chi^2)$, where
   - F is the cdf of a Chi-squared distribution with df=(r-1)(c-1)
6. If any $E_{ij} < 1$ or more than 20% of the $E_{ij} < 5$, then the asymptotic result does not hold and an exact permutation test is required.
7. Why are the degrees of freedom (r-1)(c-1)?

   With no restrictions, there are $rc - 1$ unknown parameters:

   $rc - 1$ unknown proportions: $p_{ij}, i = 1, \cdots, r; \quad j = 1, \ldots, c$ because $\sum_{i=1}^{r}\sum_{l=1}^{c} p_{ij} = 1$

   Under the null hypothesis, $H_o : p_{ij} = p_{i.}p_{.j}$, and therefore there are (r-1+c-1) unknown parameters because

   (r-1) unknown $p_{i.}$ because $\sum_{i=1}^{r} p_{i.} = 1$ and

   (c-1) unknown $p_{.j}$ because $\sum_{j=1}^{c} p_{.j} = 1$

   Therefore, df = (# parameters under $H_o \cup H_1$) - (# parameters under H_o)

   = (rc - 1) - (r-1 + c-1) = (r-1)(c-1)

   Thus the asymptotic distribution of the Pearson Chi-squared statistic has degrees of freedom, df=(r-1)(c-1)

The calculations are very similar for the Pearson Chi-square Test of Homogeneity of Proportions and the Pearson Chi-square Test of Independence. However, the data collection design and the hypotheses being tested are quite different.

In the Test of Homogeneity of Proportions: $H_o : p_1 = p_2 = \cdots = p_t$ vs $H_o : p_i$ not all the same, whereas in Test of Independence: $H_o : p_{ij} = p_{i.}p_{.j}$ for all (i,j) vs $H_o : p_{ij} \neq p_{i.}p_{.j}$ for some (i,j)

The same SAS program that was used to analyze the accident data would be used for the Political Affiliation study:

```
OPTIONS PS=55 LS=75 NOCENTER NODATE;
DATA POL;
INPUT Party $ Income $ CNT @@;
CARDS;
Rep  I1  20      Dem  I1   68   Ind I1  5   Other I1 15
Rep  I2  84      Dem  I2  119   Ind I2 29   Other I2 54
Rep  I3  17      Dem  I3   26   Ind I3 14   Other I3 14
Rep  I4  94      Dem  I4    7   Ind I4 16   Other I4 10
RUN;
PROC FREQ; TABLES Party*Income/EXPECTED CELLCHI2 CHISQ;
WEIGHT CNT;
*EXACT CHISQ;
RUN;
```

SAS Output is given next:

```
The FREQ Procedure
Table of Party by Income
Party           Income
Frequency
Expected
Cell Chi-Square
Percent
Row Pct
Col Pct        I1      I2      I3      I4        Total
---------------------------------------------------------
Dem                68     119      26       7     220
               40.135  106.28  26.385  47.196
               19.346  1.5214  0.0056  34.234
                11.49   20.10    4.39    1.18   37.16
                30.91   54.09   11.82    3.18
                62.96   41.61   36.62    5.51
---------------------------------------------------------
Ind                 5      29      14      16      64
               11.676  30.919  7.6757   13.73
               3.8169  0.1191  5.2109  0.3754
                 0.84    4.90    2.36    2.70   10.81
                 7.81   45.31   21.88   25.00
                 4.63   10.14   19.72   12.60
---------------------------------------------------------
Other              15      54      14      10      93
               16.966  44.929  11.154  19.951
               0.2279  1.8314  0.7263  4.9633
                 2.53    9.12    2.36    1.69   15.71
                16.13   58.06   15.05   10.75
                13.89   18.88   19.72    7.87
---------------------------------------------------------
Rep                20      84      17      94     215
               39.223  103.87  25.785  46.123
               9.4211  3.8005  2.9933  49.697
                 3.38   14.19    2.87   15.88   36.32
                 9.30   39.07    7.91   43.72
                18.52   29.37   23.94   74.02
---------------------------------------------------------
Total             108      286       71      127      592
                18.24    48.31    11.99    21.45   100.00
```

```
Statistics for Table of Party by Income

Statistic                     DF       Value      Prob

Chi-Square                     9    138.2898    <.0001
Likelihood Ratio Chi-Square    9    146.4436    <.0001
Mantel-Haenszel Chi-Square     1     89.4571    <.0001
Phi Coefficient                      0.4833
Contingency Coefficient              0.4352
Cramer's V                           0.2790

Sample Size = 592
```

From the above results, we have that there is significant evidence (p-value$<$.0001) that Party Affiliation and Income level are not independent. Thus, the Income distribution for one party may be quite different from the Income distribution for a second party. In particular, Republicans have over 40% of their member in the upper two income levels, whereas Democrats have approximately 15% in the upper two income levels.

Odds Ratio and Relative Risk

The are numerous measures of association which are used to evaluate the strength of association in a contingency table. In particular, for 2×2 tables, the most widely used measure is the **Odds Ratio**, and a related measure of association, the **Relative Risk**.

Suppose we have two breeds of dogs and want to compare the frequency of occurrence of disease in the two breeds. Random sample of size $n_{1.}$ and $n_{2.}$ are selected from a registry of the two breeds. Suppose we obtain the following table:

	Has Disease			
	Yes	No	Total	Proportion with Disease
Breed 1	n_{11}	n_{12}	$n_{1.}$	$p_1 = n_{11}/n_{1.}$
Breed 2	n_{21}	n_{22}	$n_{2.}$	$p_2 = n_{21}/n_{2.}$
Total	$n_{.1}$	$n_{.2}$	n	

Suppose that p_1 and p_2 are the population proportion of dogs having the disease from breed 1 and breed 2, respectively.

DEFINITION The **odds** compares the proportion of the population having a trait (the probability that an event occurs) to the proportion of the population not having the trait (probability that an event does not occur). That is, if p is the proportion of a population having a given trait (P[Event Occurs]) then

$$\text{Odds of Trait} = \frac{p}{1-p} = \frac{\text{P[Event Occurs]}}{\text{P[Event Does Not Occur]}}$$

In our example, we would estimate the odds of Breed 1 having the disease by

$$\widehat{\text{Odds}} = \frac{p_1}{1-p_1} = \frac{n_{11}/n_{1.}}{1-n_{11}/n_{1.}} = \frac{n_{11}/n_{1.}}{n_{12}/n_{1.}} = \frac{n_{11}}{n_{12}}$$

DEFINITION The **odds ratio** compares the odds of having the trait in one group to the odds of having the trait in a second group That is, if p_1 and p_2 are the proportions in population 1 and population 2, respectively, having a given trait then

$$\text{Odds Ratio} = \frac{p_1/(1-p_1)}{p_2/(1-p_2)} = \frac{\text{Odds in Population 1}}{\text{Odds in Population 2}}$$

In our example, we would estimate the odds ratio of having the disease for the two breeds as follows

$$\widehat{\text{OR}} = \frac{p_1/(1-p_1)}{p_2/(1-p_2)} = \frac{n_{11}n_{22}}{n_{12}n_{21}}$$

A few facts about Odds Ratios:

1. If any of the $n_{ij} = 0$ then add .5 to all the n_{ij} prior to computing the OR. However, use the n_{ij} without .5 added to them in performing the Fisher Exact test.
2. Odds ratio range from 0 to ∞
3. When OR=1, then $p_1 = p_2$, that is, there is no difference between the two groups wrt to occurrence of trait.
4. When OR$<$ 1, then $p_1 < p_2$, that is, Group 1 is less likely than Group 2 to have the trait.
5. When OR$>$ 1, then $p_1 > p_2$, that is, Group 1 is more likely than Group 2 to have the trait.

An alternative representation of the Odds and Odds Ratio is used in logistic regression:

DEFINITION The *logit* for the proportion p is given by

$$logit(p) = log\left(\frac{p}{1-p}\right) = log(\text{Odds})$$

The log of the Odds Ratio can be represented as the difference between logit(p_1) and logit(p_2):

$$\begin{aligned} L &= log\,(\text{OR}) \\ &= log\left(\frac{p_1/(1-p_1)}{p_2/(1-p_2)}\right) \\ &= log\left(\frac{p_1}{(1-p_1)}\right) - log\left(\frac{p_2}{(1-p_2)}\right) \\ &= logit(p_1) - logit(p_2) \end{aligned}$$

In the courses STAT 659, STAT 608, and STAT 645, the logistic regression model will be developed in detail. This is a method to model categorical data as a function of explanatory variables. There are many models other than the logit model. See STAT 659 or the book, *Categorical Data Analysis*, by Alan Agresti for further details.

For example, suppose we wanted to study the proportion, p of dogs having contracted heart worms as a function the dog's breed, age, weight, and sex. We evaluate a randomly selected group of n dogs and record

Y=1 if dog has heart worms and Y=0 if dog does not have heart worms.

Also, the values of X_1 = breed, X_2 = age, X_3 = weight, and X_4 = sex are recorded for each dog.

The data could be modeled using the logit model:

$$log\left(\frac{p}{1-p}\right) = \beta_o + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4$$

or equivalently as

$$\frac{p}{1-p} = e^{\beta_o+\beta_1 X_1+\beta_2 X_2+\beta_3 X_3+\beta_4 X_4}$$

which implies

$$p = \frac{e^{\beta_o+\beta_1 X_1+\beta_2 X_2+\beta_3 X_3+\beta_4 X_4}}{1+e^{\beta_o+\beta_1 X_1+\beta_2 X_2+\beta_3 X_3+\beta_4 X_4}}$$

Using non-linear regression, estimates of the coefficients, β_i are obtained.

The results we obtain from observational data using statistical testing and estimation methodology should be interpreted with great care. See the cartoon on next page.


SOMEONE SENT ME ANOTHER ANONYMOUS EMAIL WITH A LINK TO AN ARTICLE ABOUT THE WORLD'S WORST BOSSES.
I GET ONE OF THOSE EMAILS EVERY TIME I LEAVE YOUR CUBICLE. DID YOU THINK I WOULDN'T NOTICE THE CORRELATION?
CORRELATION DOES NOT IMPLY CAUSATION.
SIGH
Dilbert.com DilbertCartoonist@gmail.com
11-28-11 ©2011 Scott Adams, Inc./Dist. by Universal Uclick

From a Central Limit Theorem, we have that $\hat{L} = log(\widehat{OR})$ has an asymptotic normal distribution with asymptotic mean and variance:

$$\hat{\mu}_L = log(OR) \quad \text{and} \quad \text{AVAR(L)} = \hat{\sigma}_L^2 = \left(\frac{1}{n_{11}} + \frac{1}{n_{12}} + \frac{1}{n_{21}} + \frac{1}{n_{22}}\right)$$

That is, $\hat{L} = log(\widehat{OR})$ has approximately a $N(\hat{\mu}_L,\ \hat{\sigma}_L^2)$ distribution for large n.

Thus, an approximate $100(1-\alpha)\%$ C.I. for the Odds Ratio is obtained as follows:

$$\left[e^{\left(\hat{\mu}_L - z_{\alpha/2}\sqrt{\hat{\sigma}_L^2}\right)}, e^{\left(\hat{\mu}_L + z_{\alpha/2}\sqrt{\hat{\sigma}_L^2}\right)}\right]$$

where $\hat{L} = logit(\hat{p}_1) - logit(\hat{p}_2)$ and $\hat{p}_1$, $\hat{p}_2$ are the sample estimators of p_1 and p_2, respectively.

For **retrospective or prospective studies**, often the type of study used in epidemiological studies, it is often more meaningful to use the parameter *Relative Risk*

$$RR = \frac{p_1}{p_2}$$

to compare the risk of developing a particular condition (often disease) for one group in comparison to a second group. The estimate of RR can be expressed as a function of the estimated value of the odds ratio:

$$\widehat{RR} = \widehat{OR} \times \frac{1 + n_{21}/n_{22}}{1 + n_{11}/n_{12}}$$

Note that OR and RR are nearly equal when the outcome (condition, disease) is a *rare outcome*. That is, when n_{11} and n_{21} are small relative to n_{12} and n_{22}, respectively.

When we are dealing with **cross-sectional** data, the RR is often referred to as the *prevalence ratio*. In this type of data, RR is not assessing the risk of a disease, because the disease and risk factor are assessed at the same time, but RR provides an assessment of the prevalence of a disease (or condition or opinion) in one group compared to a second group.

EXAMPLE In the article, "A multiple testing procedure for clinical trials," *Biometrics*, **35**, pp. 549-556, the data for a randomized clinical trial for comparing Prednisone and Prednisone+VCR drug therapies for treating patients with leukemia is presented. The data is given in the following table:

Drug Type	Success	Failure	Total
Prednisone	13	8	21
Prednisone+VCR	38	4	42
Total	52	11	63

The following SAS code was used to analyze the data:

```
*The following program will calculate the ;
*Chi-square Homogeneity of Proportions Test and
*CI for difference
*for Example 9.6 from the Textbook;
*EX9-6HAND13.sas

ods html;
ods graphics on;
*The following program will calculate the;
*Chi-square Homogeneity of Proportions Test;
*for Example 9.6 from the Textbook;
OPTIONS PS=55 LS=75 NOCENTER NODATE;
TITLE 'TWO LEUKEMIA THERAPIES';

DATA LEU;
INPUT DRUG $ OUTCOME $ CNT @@;
CARDS;
PVCR S  38
PVCR F  4
P    S  13
P    F  8
RUN;

PROC FREQ ORDER=DATA;

TABLES DRUG*OUTCOME/CHISQ EXPECTED CELLCHI2  RISKDIFF MEASURES;

    WEIGHT CNT;

EXACT RISKDIFF ;

RUN;
ods graphics off;
ods html close;
```

The output from the above program is given on the next page.

TWO LEUKEMIA THERAPIES

The FREQ Procedure

Frequency Expected Cell Chi-Square Percent Row Pct Col Pct

Table of DRUG by OUTCOME

DRUG	OUTCOME		
	S	F	Total
PVCR	38 34 0.4706 60.32 90.48 74.51	4 8 2 6.35 9.52 33.33	42 66.67
P	13 17 0.9412 20.63 61.90 25.49	8 4 4 12.70 38.10 66.67	21 33.33
Total	51 80.95	12 19.05	63 100.00

Statistics for Table of DRUG by OUTCOME

Statistic	DF	Value	Prob
Chi-Square	1	7.4118	0.0065
Likelihood Ratio Chi-Square	1	7.0235	0.0080
Continuity Adj. Chi-Square	1	5.6746	0.0172
Mantel-Haenszel Chi-Square	1	7.2941	0.0069
Phi Coefficient		0.3430	
Contingency Coefficient		0.3244	
Cramer's V		0.3430	

WARNING: 25% of the cells have expected counts less than 5. Chi-Square may not be a valid test.

Fisher's Exact Test	
Cell (1,1) Frequency (F)	38
Left-sided Pr <= F	0.9986
Right-sided Pr >= F	0.0099
Table Probability (P)	0.0085
Two-sided Pr <= P	0.0141

Column 1 Risk Estimates						
	Risk	ASE	(Asymptotic) 95% Confidence Limits		(Exact) 95% Confidence Limits	
Row 1	0.9048	0.0453	0.8160	0.9935	0.7738	0.9734
Row 2	0.6190	0.1060	0.4113	0.8267	0.3844	0.8189
Total	0.8095	0.0495	0.7126	0.9065	0.6909	0.8975
Difference	0.2857	0.1152	0.0598	0.5116	0.0126	0.5316
Difference is (Row 1 - Row 2)						

Column 2 Risk Estimates						
	Risk	ASE	(Asymptotic) 95% Confidence Limits		(Exact) 95% Confidence Limits	
Row 1	0.0952	0.0453	0.0065	0.1840	0.0266	0.2262
Row 2	0.3810	0.1060	0.1733	0.5887	0.1811	0.6156
Total	0.1905	0.0495	0.0935	0.2874	0.1025	0.3091
Difference	-0.2857	0.1152	-0.5116	-0.0598	-0.5316	-0.0126
Difference is (Row 1 - Row 2)						

Estimates of the Relative Risk (Row1/Row2)			
Type of Study	Value	95% Confidence Limits	
Case-Control (Odds Ratio)	5.8462	1.5074	22.6734
Cohort (Col1 Risk)	1.4615	1.0304	2.0731
Cohort (Col2 Risk)	0.2500	0.0849	0.7361

Sample Size = 63

The Output from SAS has the following interpretation. The Pearson chi-squared p-value=0.0065 indicates there is substantial evidence of a difference in the success proportions for the two treatments. However, this result cannot be taken as valid because the small sample sizes, 42 and 21, have resulted in one of the four cells (25% of the cells) having expected count less than 5. Thus, the Fisher's exact test should be used. From the Fisher's exact test the p-value is .0141 which is considerably larger than the value from the Pearson chi-squared p-value but it is still less than .05 so we can still conclude that there is substantial evidence of a difference in the success proportions for the two treatments.

Next, we would investigate the size of the difference, the effect size. From the SAS output, 95% confidence intervals on the success probabilies are obtained:

(.774, .973) for p_1, PVCR and (.384, .819) for p_2, Prednisone.

Note that these two C.I.'s overlap which would seem to indicate that there is not significant evidence of a difference in p_1 and p_2.

However, the 95% confidence interval on the difference, $p_1 - p_2$ is (.013, .532) which does not contain 0 which is consistent with the conclusion obtained from the Fisher's Exact test. That is, there is significant evidence of a difference in p_1 and p_2.

This type of result often occurs. A test of the difference in two parameters using individual C.I.'s on the two parameters will often not detect a difference by overlapping. However, when a test of the difference in the two parameters is conducted or a C.I. is placed on the difference in the two parameters, significant evidence will be found of a difference in the two parameters. The individual C.I.'s are not as sensitive (powerful) in detecting differences in comparison to procedures which are based on the difference in the two parameters.

The Odds Ratio is given as 5.8462 with a 95% C.I. of (1.5074, 22.6734). We would interpret the OR as indicating that the odds of Success for the drug therapy Prednisone+VCR is much higher than the odds of Success using Prednisone. That is, Prednisone+VCR has odds of about 5.8 times the odds of Prednisone by itself.

The value 1.4615 is the ratio (RR) of the Success probability for Prednisone+VCR to the Success probability for Prednisone. This would indicate that Prednisone+VCR is providing a larger Success probability than the drug therapy consisting of just Prednisone. Note that the C.I. for RR, (1.0304, 2.0731), does not contain 1.0 and hence we would conclude that with $\alpha = .05$ there is substantial evidence that RR differs from 1.0.

You can alter the level of coverage for the C.I. for the individual probabilities and the OR by including the ALPHA = option in the TABLES statement.

Sensitivity - Specificity - Bayes Theorem

Two measures often used when determining the efficacy of screening tests for pathogens, diseases, or dangerous materials, are sensitivity and specificity. Suppose we are evaluating a diagnostic test for detecting a particular event (disease, hazardous compound, pathogen). A positive result from the test (+) indicates that the event is present and a negative result from the test (-) indicates that the event is not present. Therefore, we have four possibilities:

(Test=+, Event Present), (Test=+, Event Absent), (Test=-, Event Present), (Test=-, Event Absent).

The terms Prevalence, Sensitivity, and Specificity are defined as follows:

DEFINITION

- The **Prevalence** of an Event is proportion of the population possessing the trait:

  Prevalence = P[Event]

- The **Sensitivity** of a screening test is proportion of tests which result in a positive test result given the Event is present : Sensitivity = P$[Test = +|EventPresent]$

- The **Specificity** of a screening test is proportion of tests which result in a negative test result given the Event is not present : Specificity = P$[Test = -|EventAbsent]$

Suppose a screening test is newly developed to determine if *e. coli* is present in a meat sample. In order to determine the sensitivity and specificity of the test, n_1 meat samples have a specified amount of *e. coli* placed in them and n_2 meat samples are treated so that *e. coli* is absolutely not present in the meat samples. The screening test is applied to the $n = n_1 + n_2$ meat samples resulting in the following

	Test Result		
e.coli Status	Test +	Test -	Total
Present	n_{11}	n_{12}	n_1
Absent	n_{21}	n_{22}	n_2

Sensitivity of the test is estimated as

$$\text{Sensitivity} = P[\text{Test } = +|e.coliPresent] \approx \frac{n_{11}}{n_1}$$

Specificity of the test is estimated as

$$\text{Specificity} = P[\text{Test } = -|e.coliAbsent] \approx \frac{n_{22}}{n_2}$$

The sensitivity and specificity are important parameters for any screening test but a more important quantity is the probability that the Event is present given that the test result is positive. That is, what is the chance *e.coli* is in fact present in the meat sample when the screening test yields a positive test result. This probability can be computed using Bayes Theorem once the prevalence of the Event is known. Using Bayes theorem we have

$$\begin{aligned} P[\text{Present}|Test+] &= \frac{P[Test+|\text{ Present}]P[\text{ Present}]}{P[Test+|\text{Present}]P[\text{Present}] + P[Test+|\text{ Absent}]P[\text{ Absent}]} \\ &= \frac{\text{(Sensitivity)(Prevalence)}}{\text{(Sensitivity)(Prevalence)} + \text{(1-Specificity)(1-Prevalence)}} \end{aligned}$$

When the prevalence is small and the disease is present, the probability of a positive test result is often very small. That is, a large proportion of positive test results are false positives. How can we improve the performance of the test? Should we concentrate on increasing the sensitivity or specificity of the test? The following table displays the performance of nine tests for detecting the presence of a pathogen which has a prevelance of .001.

Test	Sensitivity	Specificity	$Pr(Pathogen\|Positive)$
1	.90	.90	.0089
2	.90	.95	.0177
3	.90	.999	.4739
4	.95	.90	.0094
5	.95	.95	.0187
6	.95	.999	.4874
7	.99	.90	.0098
8	.99	.95	.0194
9	.99	.999	.4977

Based on the values given in the above table, which factor, sensitivity or specificity, is more crucial in obtaining an improved test?

Also, how can tests which seem to have relatively high values for Sensitivity and Specificity yield higher values for $Pr(Pathogen|Positive)$?

One way is to run the tests multiple times on independent samples of meat from the same batch.

Declare the pathogen is present if k independent tests of the product ALL yield a positive result.

$$P[\text{pathogen present}|k \text{ independent tests are all } +] =$$

$$\frac{(sensitivity)^k(prevalence)}{(sensitivity)^k(prevalence) + (1 - specificity)^k(1 - prevalence)}$$

For example, in the above table with Prevalence=.001, we have if Sensitivity = .99 and Specificity=.95, then

$$P[\text{pathogen present}|\text{test result is } +] = .0194$$

If we run k tests, how will this probability change:

Number of Tests(k)	Sensitivity	Specificity	$Pr(Pathogen\|kPositives)$
1	.99	.95	.0194
2	.99	.95	.2818
3	.99	.95	.8860
4	.99	.95	.9935
5	.99	.95	.9997

McNemar's Test for Matched Pairs

In some situations the information in a 2×2 contingency table is collected from experimental units for which two related responses are obtained. There is no longer n independent responses categorized into the four cells but rather a pair of responses from related units. For example, responses from the same individual at two different times (before and after an intervention) or from two individuals who are physically related (husband-wife or twins) or from body parts of the same experimental unit (right hand-left hand or right eye-left eye).

The data from a study involving matched pairs has the same form as the 2×2 tables we discussed previously except now the response is recorded in such a manner that the pairing is identified. Consider the following table:

	Response 1		
Response 2	Yes	No	Total
Yes	n_{11}	n_{12}	$n_{1.}$
No	n_{21}	n_{22}	$n_{2.}$
Total	$n_{.1}$	$n_{.2}$	n

The interpretation of the data in the table is as follows: n_{11} is the number of pairs with Yes for both Responses, n_{21} is the number of pairs with Yes for Response 1 but No for Response 2, n_{12} is the number of pairs with No for Response 1 but Yes for Response 2, n_{22} is the number of pairs with No for both Responses.

Suppose the population of responses for all such pairs has proportions given in the following table:

Population Proportions

	Response 1		
Response 2	Yes	No	Total
Yes	p_{11}	p_{12}	$p_{1.}$
No	p_{21}	p_{22}	$p_{2.}$
Total	$p_{.1}$	$p_{.2}$	1

The research question in this situation is whether the proportion of pairs responding Yes for Response 1 is the same as the proportion of pairs responding Yes for Response 2. The Pearson Chi-square test is not a valid test statistic because the cell counts may be correlated due to pairing of the two responses. We want to test the hypotheses:

$$H_o : p_{1.} = p_{.1} \text{ versus } H_1 : p_{1.} \neq p_{.1},$$

or a corresponding 1-sided hypotheses: $H_o : p_{1.} \geq p_{.1}$ versus $H_1 : p_{1.} < p_{.1}$.

First note that

$$p_{1.} - p_{.1} = (p_{11} + p_{12}) - (p_{11} + p_{21}) = p_{12} - p_{21}$$

Therefore, a test of the marginal homogeneity for the matched pairs $H_o : p_{1.} = p_{.1}$ is equivalent to a test of $H_o : p_{12} = p_{21}$.

That is, are the proportions of switches from Yes to No and from No to Yes equal.

When H_o is true, the expected values for the counts n_{12} and n_{21} should be equal. Let $m = n_{12} + n_{21}$ be the total count in the off-diagonal cells in the 2×2 table. Under H_o, the allocation of the m observations to the (1,2) and (2,1) cells is a binomial experiment with $\frac{1}{2}$ chance for each of the two cells.

Let B have a Bin(m,.5) distribution then the p-value for the test is given as follows:

1. For testing $H_1 : p_{1.} > p_{.1}$, p-value=$P[B \geq n_{12}]$, where B has a Bin(m,.5) distribution.
2. For testing $H_1 : p_{1.} < p_{.1}$, p-value=$P[B \leq n_{12}]$, where B has a Bin(m,.5) distribution.
3. For testing $H_1 : p_{1.} \neq p_{.1}$, p-value=$2 \cdot min\left(P[B \geq n_{12}], P[B \leq n_{12}]\right)$, where B has a Bin($m$,.5) distribution.

In all three sets of hypotheses, we reject H_o when p-value$\leq \alpha$. Also, note the hypotheses are equivalent to a test comparing p_{12} to $\frac{1}{2}$.

Alternative Approach

For $m > 15$, we could use the normal approximation to the binomial distribution, and use the test statistic:

$$Z = \frac{\hat{p}_{12} - .5}{\sqrt{\frac{(.5)(1-.5)}{m}}} = \frac{\frac{n_{12}}{m} - .5}{\sqrt{\frac{(.5)(1-.5)}{m}}} = \frac{n_{12} - .5m}{\sqrt{(.5)(1-.5)m}} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}$$

McNemar in a 1947 article proposed

$$Q_{MN} = \frac{(n_{12} - n_{21})^2}{(n_{12} + n_{21})} \qquad \text{under} \quad H_o \quad Q_{MN} \quad \text{is approximately chi-square with df=1}$$

as the test statistic to evaluate these hypotheses. Note, that

$$Q_{NM} = Z^2 \quad \text{and} \quad Z^2 \quad \text{is approximately distributed chi-square with df=1}$$

Thus McNemar's test is a large sample version of the exact binomial test but McNemar's test is applicable only to 2-sided alternatives.

An approximate $100(1-\alpha)\%$ confidence interval on $p_{1.} - p_{.1}$ is

$$(\hat{p}_{1.} - \hat{p}_{.1}) \pm Z_{\alpha/2}\sqrt{\frac{\hat{p}_{1.}(1-\hat{p}_{1.}) + \hat{p}_{.1}(1-\hat{p}_{.1}) - 2(\hat{p}_{11}\hat{p}_{22} + \hat{p}_{12}\hat{p}_{21})}{n}}$$

which simplifies to

$$(\hat{\pi}_{1.} - \hat{\pi}_{.1}) \pm Z_{\alpha/2}\frac{1}{n}\sqrt{(n_{12} + n_{21}) + \frac{1}{n}(n_{12} - n_{21})^2}$$

EXAMPLE A case-control study was conducted in which the researchers were interested in determining if there was a relationship between diabetes and chronic circulatory problems. The 180 patients having chronic circulatory problems were matched by age, gender, occupation, and ethnicity with 180 patients without chronic circulatory problems. The 180 pairs of subjects were then asked whether they had been diagnosed as having diabetes. The data is given in the following table:

	With Circulatory Problems		
Without Circulatory Problems	Diabetes	No Diabetes	Total
Diabetes	79	21	100
No Diabetes	39	41	80
Total	118	62	180

The 180 pairs of subjects in the study consist of four groups:

Group	With Circulatory Problems	Without Circulatory Problems	Count
1	Diabetes Y	Diabetes Y	79
2	Diabetes Y	Diabetes N	39
3	Diabetes N	Diabetes Y	21
4	Diabetes N	Diabetes N	41

We want to test the research hypothesis that the proportion of Without Circulatory problems patients having diabetes is less than the proportion of With Circulatory problems patients having diabetes. That is, test $H_1 : p_{1\cdot} < p_{\cdot 1}$ or equivalently, test $H_1 : p_{12} < p_{21}$

From the data we have $\hat{p}_{1\cdot} = 100/180 = .556$ and $\hat{p}_{\cdot 1} = 118/180 = .656$

Therefore, $\hat{p}_{1\cdot} - \hat{p}_{\cdot 1} = .556 - .656 = -.1$. The proportion of diabetic patients Without Circulatory problems is 10% less than the proportion of diabetic patients With Circulatory problems.

The p-value $= P[B \leq 21]$ where $m = 21 + 39 = 60$ and B is Bin(60,.5).

Thus, p-value$=P[B \leq 21] = 0.014$.

Hence, conclude there is substantial evidence that the proportion of Without Circulatory problems patients having diabetes is less than the proportion of With Circulatory problems patients having diabetes.

Using McNemar's Test, we have $Q_{NM} = \frac{(21-39)^2}{(21+39)} = 5.4$ with p-value$=P[\chi^2_1 \geq 5.4] = 0.020$. However, this p-value is for a two-sided alternative hypothesis. From the following SAS program, we obtain both the Asymptotic and Exact p-values. Once again, these values are computed for a two-sided alternative. The Exact p-value $= .0273 \approx 2(.01367)$, our 1-sided p-value.

The following is an approximate 95% C.I. on $p_{1\cdot} - p_{\cdot 1}$

$$\left(\frac{100}{180} - \frac{118}{180}\right) \pm 1.96\frac{1}{180}\sqrt{(21+39) + \frac{1}{180}(21-39)^2}$$

That is, $-.10 \pm .0856 = (-.186,\ -.014)$

The following SAS program will analyze the data for the above example:

```
*The following program will calculate the ;
*McNemar Test;
*for Example in Handout 13;

OPTIONS PS=55 LS=75 NOCENTER NODATE;
TITLE 'Circulatory Problem - McNemar Test';
DATA CIRC;
INPUT DIABWITHOUTCIR $ DIABWITHCIR $ CNT @@;
CARDS;
YES  YES   79
YES  NO    21
NO   YES   39
NO   NO    41
RUN;
PROC FREQ ORDER=DATA;
TABLES DIABWITHOUTCIR*DIABWITHCIR;
WEIGHT CNT;
EXACT MCNEM;
RUN;
```

From SAS, we obtain the following output. Note that the p-value from the EXACT option is for a two-sided alternative and is twice the value we obtained.

Circulatory Problem - McNemar Test

The FREQ Procedure

Table of DIABWITHOUTCIR by DIABWITHCIR

DIABWITHOUTCIR DIABWITHCIR

Frequency Percent Row Pct Col Pct	YES	NO	Total
YES	79 43.89 79.00 66.95	21 11.67 21.00 33.87	100 55.56
NO	39 21.67 48.75 33.05	41 22.78 51.25 66.13	80 44.44
Total	118 65.56	62 34.44	180 100.00

Statistics for Table of DIABWITHOUTCIR by DIABWITHCIR

McNemar's Test

Statistic (S)	5.4000
DF	1
Asymptotic Pr > S	0.0201
Exact Pr >= S	0.0273

Simple Kappa Coefficient

Kappa	0.3095
ASE	0.0704
95% Lower Conf Limit	0.1715
95% Upper Conf Limit	0.4474

Sample Size = 180

Design Study Without Pairing

Suppose there exists a pool of 360 subjects which are very similar with respect to age, occupation, gender, ethnicity, etc. How could we design the study to obtain a more effective evaluation of the association between the two diseases? We would not need to pair the subjects so the 360 subjects would be examined and the following table would be obtained:

	Diabetes		
Circulatory Problems	Yes	No	Total
Yes	n_{11}	n_{12}	$n_{1.}$
No	n_{21}	n_{22}	$n_{2.}$
Total	$n_{.1}$	$n_{.2}$	360

We would then use the Pearson chi-square test to evaluate the degree association between subjects having circulatory problems and diabetes. This test would be a more sensitive test than the McNemar's test in determining associations provided the subjects are relatively homogeneous with respect to all characteristics other than the two characteristics for which association is being examined.

Cochran-Mantel-Haenszel Test for Sets of Contingency Tables

The following example will illustrate the problems that may arise when we have sets of contingency tables which are often combined into a single table.

The results from a large survey are described in *American Statistician*, 50, pp. 340-341 (1996). The 1314 women in the survey were asked whether they smoked. Twenty years later, the women were again contacted and determined if they were alive or dead. The data is summarized as follows:

Smoking Status and Survival Status

	Survival Status			
Smoking Status	Dead	Alive	Total	Odds of Death
Yes	139	443	582	.314
No	230	502	732	.458
Total	369	945	1314	OR=.658

From the above table, 139/582=24% of the smokers had died during the twenty years but even a larger percentage of the nonsmokers 230/732=31% had died. Thus, smokers have a higher survival rate. The odds ratio of smokers versus nonsmokers for death is $OR = .658 < 1$, odds of death are considerably less for smokers than nonsmokers. Furthermore, the Pearson chi-square test comparing the survival rates for smokers vs nonsmokers has a p-value of 0.0025. Thus, there is substantial evidence that the survival rate for smokers is higher than for nonsmokers.

What could possibly explain this relationship? Another crucial variable is the age of the participant. It may be that older women are less likely to be smokers and this may help explain the differential in survival rate. The following table includes the explanatory variable, age of participant, when survey was initially conducted in 1975.

Smoking Status and Survival Status, Separated by Women's Age

	Age Group							
	18-34		35-54		55-65		65+	
Smoking Status	Dead	Alive	Dead	Alive	Dead	Alive	Dead	Alive
Yes	5	174	41	198	51	64	42	7
No	6	213	19	180	40	81	165	28
OR	1.02		1.96		1.61		1.02	

Note that OR is the odds ratio of Smokers to NonSmokers for death and has a value greater than 1 for all four groups. That is, when considered separately within each of four age groups, the smokers are more likely to die than the non-smokers. Why is there a contradiction between the two tables?

The following table has the conditional probabilities of Death for Smokers and Nonsmokers, conditioning on Age:

Percentage of Deaths Conditioning on Women's Age

	Age Group				
Smoking Status	18-34	35-54	55-65	65+	Overall
Yes	2.8%	17.2%	44.3%	85.7%	23.9%
No	2.7%	9.5%	33.1%	85.5%	31.4%
OR	1.02	1.96	1.61	1.02	

From the above table, we can observe that

1. For the youngest and oldest age groups, the difference in the proportion of respondents who were dead twenty years later for Smokers is nearly equal to the proportion of deaths for nonsmokers.
2. For the middle two groups, the proportion of deaths is much higher for smokers.
3. For each of the four age groups, the proportion of women who smoked had a higher death rate than the death rate for nonsmokers.
4. There appears to be a contradiction between the death rates in the overall table and the death rates observed conditional on the age of the respondent. This contradiction is often is referred to as the **Simpson Paradox**.

An explanation of this apparent contradiction is as follows:

- The proportion of women who smoked tended to be higher for younger women:

  45% of 18-34 smoked whereas, 20% of 65+ smoked.

- However, the proportion of 18-34 who were died 20 years later was 3% but

  the proportion of 65+ women who were dead 20 years later was 86%.

- Thus, the difference in survival rates between smokers and nonsmokers in the overall table is most likely due to the fact that younger women are more likely to be smokers but they are also less likely to die twenty years after the survey was taken.
- The opposite is true for the oldest age group.
- Also, note that the four age groups are not equally represented in the overall table:

  The percentage of respondents in the four age groups was 30.3%, 33.3%, 51.3%, and 18.4%.

This example illustrates how ignoring potential explanatory variables can often lead to very misleading conclusions in studies. The variable Age in this example in some sense explains why the conclusion that smokers have a lower death rate than nonsmokers is not true when other factors are taken into account. We will consider in STAT 642 a similar type of situation in trying to reach conclusions concerning design factors when there exists an interaction effect between two factors.

Conditional and Marginal Analysis

The analysis using the table pooled over Age is called a marginal analysis and the analysis taking into account Age is called a conditional analysis conditioning on the variable Age.

The following test referred to as the Cochran-Mantel-Haenszel (CMH) Test is a test of conditional independence given the values of a third variable.

In our example, CMH tests the conditional independence of the variables Smoking and Survival given the values of the variable Age.

In general, suppose we have K levels of a variable Z and at each level of Z we have two variables X and Y each with two levels, that is, we have K 2×2 tables.

The null hypothesis is that X and Y are independent given Z:

$$p_{ijk} = p_{i.k}p_{.jk} \quad \text{for all} \quad k = 1, \ldots, K$$

This hypothesis can be interpreted as the conditional odds ratio $\theta_{XY(k)}$ between X and Y equals 1 in each of the K 2×2 tables.

Given the the row totals, $(n_{1.k}, n_{2.k})$, and column totals, $(n_{.1k}, n_{.2k})$ in the kth table, the count n_{11k} determines all other counts in this table.

Under the null hypothesis, the mean and variance of n_{11k} are given by

$$\mu_{11k} = E(n_{11k}) = \frac{n_{1.k}n_{.1k}}{n_{..k}} \qquad Var(n_{11k}) = \frac{n_{1.k}n_{2.k}n_{.1k}n_{.2k}}{n_{..k}^2(n_{..k} - 1)}$$

When the true odds ratio θ_{XYk} exceeds 1.0 in the kth table, the expectation is that $(n_{11k} - \mu_{11k}) > 0$.

When the true odds ratio θ_{XYk} is less than 1.0 in the kth table, the expectation is that $(n_{11k} - \mu_{11k}) < 0$.

The CMH test statistic sums these differences over the K tables:

$$CMH = \frac{\left[\sum_{k=1}^{K}(n_{11k} - \mu_{11k})\right]^2}{\sum_{k=1}^{K} Var(n_{11k})}$$

Under the null hypothesis, CMH asymptotically has a chi-squared distribution with $df = 1$.

The CMH statistic combines the information about the association between X and Y across the K tables. The CMH will be *large* when $(n_{11k} - \mu_{11k})$ is consistently positive or consistently negative for all K tables, rather than varying from positive in some tables and then negative for the remaining tables.

When an association exists between the variables X and Y and this association is relatively homogeneous across the K tables, it is informative to estimate this common value of the K true odds ratios.

Suppose $\theta_{XY(1)} = \theta_{XY(2)} = \cdots = \theta_{XY(K)}$, the CMH estimator of the common value is given by

$$\hat{\theta}_{CMH} = \frac{\sum_{k=1}^{K}(n_{11k}n_{22k}/n_{..k})}{\sum_{k=1}^{K}(n_{12k}n_{21k}/n_{..k})}$$

The standard error of the estimator is an extremely complex formula but can be obtained from SAS.

The CMH test is a powerful test for detecting association against the null hypothesis of conditional independence in the K tables. However, the CMH test loses its power to detect overall association between the variables X and Y when the associations vary from a positive association to a negative association across the K tables. Thus, the CMH test should be applied to situations in which $OR_1 = OR_2 = \cdots = OR_k = OR_o$, where OR_o is the common odds ratio. Use Breslow-Day to evaluate this condition. The CMH procedure is then testing $H_o : OR_o = 1$ versus $H_o : OR_o \neq 1$.

Breslow-Day Test

A test of common odds ratio between X and Y for the K 2×2 tables:

$$H_o : \theta_{XY(1)} = \theta_{XY(2)} = \cdots = \theta_{XY(K)} \quad \text{versus} \quad H_1 : \text{ not all } \theta_{XY(k)}s \text{ are equal}$$

The Breslow-Day Test tests the above hypotheses. The computation of this statistic is relatively complex but can be obtained using SAS. When the Breslow-Day test fails to reject H_o, there is justification in summarizing the conditional association between X and Y by a single odds ratio, the CMH odds ratio, for all K tables. If the Breslow-Day test rejects H_o, then separate tests should be run for each of the k tables.

1. First test $H_o : \theta_{XY(1)} = \theta_{XY(2)} = \cdots = \theta_{XY(k)}$ using the Breslow-Day test.
2. If H_o is not rejected then test the Conditional Independence of $(X,\ Y)$ using the Cochran-Mantel-Haenszel test.
3. If H_o is rejected then test the K 2x2 tables separately for each of the K levels of the confounding variable using $\alpha_{pc} = \frac{\alpha}{K}$, where α is the chance of a Type I error across all K tests.

The following SAS code and output completes our analysis of the survival data of women smokers versus nonsmokers.

```
*The following program will calculate the ;
*General Cochran-Mantel-Haenszel Statistic for the situation;
*where there is a third variable over which the original;
*counts were aggregated.;
*Age refers to the age of the respondent;
*Smoker refers to whether or not respondent was a smoker when survived;
*Surv refers to the Survival Status of the respondent 20 years later;

OPTIONS PS=55 LS=75 NOCENTER NODATE;
DATA ByAge;
INPUT Age $ Smoker $ Surv $ CNT @@;
CARDS;
18-34 Y D 5    18-34 Y A 174
18-34 N D 6    18-34 N A 213
35-54 Y D 41   35-54 Y A 198
35-54 N D 19   35-54 N A 180
55-64 Y D 51   55-64 Y A  64
55-64 N D 40   55-64 N A  81
65+ Y D 42   65+ Y A   7
65+ N D 165  65+ N A  28
RUN;

PROC FREQ ORDER=DATA;

TABLES SMOKER*SURV/EXPECTED CELLCHI2 CHISQ;

WEIGHT CNT;

EXACT CHISQ;

RUN;

PROC FREQ ORDER=DATA;

TABLES AGE*SMOKER*SURV/CMH;

WEIGHT CNT;

RUN;
```

The FREQ Procedure

Table of Smoker by Surv

Smoker	Surv		
Frequency			
Expected			
Cell Chi-Square			
Percent			
Row Pct			
Col Pct	D	A	Total
Y	139	443	582
	163.44	418.56	
	3.6542	1.4269	
	10.58	33.71	44.29
	23.88	76.12	
	37.67	46.88	
N	230	502	732
	205.56	526.44	
	2.9054	1.1345	
	17.50	38.20	55.71
	31.42	68.58	
	62.33	53.12	
Total	369	945	1314
	28.08	71.92	100.00

Statistics for Table of Smoker by Surv

Statistic	DF	Value	Prob
Chi-Square	1	9.1209	0.0025
Likelihood Ratio Chi-Square	1	9.2003	0.0024
Continuity Adj. Chi-Square	1	8.7515	0.0031
Mantel-Haenszel Chi-Square	1	9.1140	0.0025
Phi Coefficient		-0.0833	
Contingency Coefficient		0.0830	
Cramer's V		-0.0833	

Pearson Chi-Square Test

Chi-Square	9.1209
DF	1
Asymptotic Pr > ChiSq	0.0025
Exact Pr >= ChiSq	0.0030

Statistics for Table of Smoker by Surv

Likelihood Ratio Chi-Square Test

Chi-Square	9.2003
DF	1
Asymptotic Pr > ChiSq	0.0024
Exact Pr >= ChiSq	0.0025

Mantel-Haenszel Chi-Square Test

Chi-Square	9.1140
DF	1
Asymptotic Pr > ChiSq	0.0025
Exact Pr >= ChiSq	0.0030

Fisher's Exact Test

Cell (1,1) Frequency (F)	139
Left-sided Pr <= F	0.0015
Right-sided Pr >= F	0.9990
Table Probability (P)	5.052E-04
Two-sided Pr <= P	0.0030

Sample Size = 1314

Table 1 of Smoker by Surv
Controlling for Age=18-34

Smoker	Surv		
Frequency			
Percent			
Row Pct			
Col Pct	D	A	Total
Y	5	174	179
	1.26	43.72	44.97
	2.79	97.21	
	45.45	44.96	
N	6	213	219
	1.51	53.52	55.03
	2.74	97.26	
	54.55	55.04	
Total	11	387	398
	2.76	97.24	100.00

Table 2 of Smoker by Surv
Controlling for Age=35-54

Smoker	Surv		
Frequency			
Percent			
Row Pct			
Col Pct	D	A	Total
Y	41	198	239
	9.36	45.21	54.57
	17.15	82.85	
	68.33	52.38	
N	19	180	199
	4.34	41.10	45.43
	9.55	90.45	
	31.67	47.62	
Total	60	378	438
	13.70	86.30	100.00

Table 3 of Smoker by Surv
Controlling for Age=55-64

Smoker	Surv		
Frequency			
Percent			
Row Pct			
Col Pct	D	A	Total
Y	51	64	115
	21.61	27.12	48.73
	44.35	55.65	
	56.04	44.14	
N	40	81	121
	16.95	34.32	51.27
	33.06	66.94	
	43.96	55.86	
Total	91	145	236
	38.56	61.44	100.00

Table 4 of Smoker by Surv
Controlling for Age=65+

Smoker	Surv		
Frequency			
Percent			
Row Pct			
Col Pct	D	A	Total
Y	42	7	49
	17.36	2.89	20.25
	85.71	14.29	
	20.29	20.00	
N	165	28	193
	68.18	11.57	79.75
	85.49	14.51	
	79.71	80.00	
Total	207	35	242
	85.54	14.46	100.00

```
Summary Statistics for Smoker by Surv
Controlling for Age

  Cochran-Mantel-Haenszel Statistics (Based on Table Scores)

Statistic    Alternative Hypothesis    DF       Value      Prob

    1        Nonzero Correlation        1      6.5896    0.0103
    2        Row Mean Scores Differ     1      6.5896    0.0103
    3        General Association        1      6.5896    0.0103


            Estimates of the Common Relative Risk (Row1/Row2)

Type of Study     Method                  Value     95% Confidence Limits

Case-Control      Mantel-Haenszel        1.5611       1.1081       2.1994
  (Odds Ratio)    Logit                  1.5556       1.1038       2.1922

Cohort            Mantel-Haenszel        1.2282       1.0490       1.4381
  (Col1 Risk)     Logit                  1.0718       0.9548       1.2032

Cohort            Mantel-Haenszel        0.9370       0.8918       0.9845
  (Col2 Risk)     Logit                  0.9811       0.9521       1.0109


     Breslow-Day Test for
Homogeneity of the Odds Ratios

Chi-Square              1.9862
DF                           3
Pr > ChiSq              0.5753


Total Sample Size = 1314
```

Breslow-Day test fails to reject the hypothesis that the four Age-Groups have different odds-ratios. We would next want to estimate the common odds-ratio amongst the k groups:

$$\widehat{OR} = \frac{\sum_k n_{11k} n_{22k}/n_{..k}}{\sum_k n_{12k} n_{21k}/n_{..k}}$$

For the four Age-Groups in the Smoking example, we would obtain the following estimate of the common OR:

$$\widehat{OR} = \frac{(5)(213)/398 + (41)(180)/438 + (51)(81)/236 + (42)(28)/242}{(6)(174)/398 + (19)(198)/438 + (40)(64)?236 + (165)(7)/242} = 1.56 < 1$$

We would thus conclude that the odds of death during the 20 years is 56% higher for Smokers than for Non-Smokers.

TESTS FOR COMPARING SEVERAL POPULATION VARIANCES

We have discussed a method for comparing variances from two normally distributed populations based on taking independent random samples from the populations. In many situations, we will need to compare more than two populations. For example, we may want to compare the variability in the level of nutrients of five different suppliers of a feed supplement or the variability in scores of the students using SAT preparatory materials from the three major publishers of those materials. Thus, we need to develop a statistical test which will allow us to compare $t > 2$ population variances. We will consider two procedures.

The first procedure, Hartley's test is very simple to apply but has the restriction that the population distributions must be normally distributed and the sample sizes equal.

The second procedure, Brown-Forsythe-Levene (BFL) test, is more complex in its computations but does not restrict the population distributions or the sample sizes. The BFL test can be obtained from many of the statistical software packages. For example, *SAS* and *Mintab* both use BFL test for comparing population variances. This test is available in the R package "lawstat" as the function **levene.test**.

Hartley F_{max}:

H. O. Hartley (1950) developed a test for the evaluating the hypotheses

$$H_o : \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_t^2 \quad \text{vs} \quad H_a : \sigma_i^2\text{'s not all equal.}$$

The Hartley F_{max} requires that we have independent random samples of the same size n from t normally distributed populations. With the exception that we require $n_1 = n_2 = \cdots = n_t = n$, the Hartley test is a logical extension of the F test from the previous section for testing $t = 2$ variances. With s_i^2 denoting the sample variance computed from the ith sample: $s_1^2,\ s_2^2,\ \ldots,\ s_t^2$

Let $s_{min}^2 = \min(s_1^2,\ s_2^2,\ \ldots,\ s_t^2)$ and $s_{max}^2 = \min(s_1^2,\ s_2^2,\ \ldots,\ s_t^2)$.

The Hartley F_{max} test statistic is

$$F_{max} = \frac{s_{max}^2}{s_{min}^2}.$$

The test procedure is summarized here.

Hartley's F_{max} Test for
Homogeneity of
Population Variances

$H_o : \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_t^2$ homogeneity of variances

H_a : Population variances are not all equal

T.S.: $F_{max} = \dfrac{s_{max}^2}{s_{min}^2}$

R.R. Reject H_o if $F_{max} \geq F_{max,\alpha,t,n-1}$

the value of $F_{max,\alpha,t,n-1}$ for specified values of α,t,and df_2=n-1, where n is the common sample size for the t random samples is given in the table on the next page. Note that this is not the standard F-tables.

Percentage points of $F_{max} = s^2_{max}/s^2_{min}$

Upper 5% Points

df_2 \ t	2	3	4	5	6	7	8	9	10	11	12
2	39.0	87.5	142	202	266	333	403	475	550	626	704
3	15.4	27.8	39.2	50.7	62.0	72.9	83.5	93.9	104	114	124
4	9.60	15.5	20.6	25.2	29.5	33.6	37.5	41.1	44.6	48.0	51.4
5	7.15	10.8	13.7	16.3	18.7	20.8	22.9	24.7	26.5	28.2	29.9
6	5.82	8.38	10.4	12.1	13.7	15.0	16.3	17.5	18.6	19.7	20.7
7	4.99	6.94	8.44	9.70	10.8	11.8	12.7	13.5	14.3	15.1	15.8
8	4.43	6.00	7.18	8.12	9.03	9.78	10.5	11.1	11.7	12.2	12.7
9	4.03	5.34	6.31	7.11	7.80	8.41	8.95	9.45	9.91	10.3	10.7
10	3.72	4.85	5.67	6.34	6.92	7.42	7.87	8.28	8.66	9.01	9.34
12	3.28	4.16	4.79	5.30	5.72	6.09	6.42	6.72	7.00	7.25	7.48
15	2.86	3.54	4.01	4.37	4.68	4.95	5.19	5.40	5.59	5.77	5.93
20	2.46	2.95	3.29	3.54	3.76	3.94	4.10	4.24	4.37	4.49	4.59
30	2.07	2.40	2.61	2.78	2.91	3.02	3.12	3.21	3.29	3.36	3.39
60	1.67	1.85	1.96	2.04	2.11	2.17	2.22	2.26	2.30	2.33	2.36
∞	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Upper 1% Points

df_2 \ t	2	3	4	5	6	7	8	9	10	11	12
2	199	448	729	1036	1362	1705	2063	2432	2813	3204	3605
3	47.5	85	120	151	184	21(6)	24(9)	28(1)	31(0)	33(7)	36(1)
4	23.2	37	49	59	69	79	89	97	106	113	120
5	14.9	22	28	33	38	42	46	50	54	57	60
6	11.1	15.5	19.1	22	25	27	30	32	34	36	37
7	8.89	12.1	14.5	16.5	18.4	20	22	23	24	26	27
8	7.50	9.9	11.7	13.2	14.5	15.8	16.6	17.9	18.9	19.8	21
9	6.54	8.5	9.9	11.1	12.1	13.1	13.9	14.7	15.3	16.0	16.6
10	5.85	7.4	8.6	9.6	10.4	11.1	11.8	12.4	12.9	13.4	13.9
12	4.91	6.1	6.9	7.6	8.2	8.7	9.1	9.5	9.9	10.2	10.6
15	4.07	4.9	5.5	6.0	6.4	6.7	7.1	7.3	7.5	7.8	8.0
20	3.32	3.8	4.3	4.6	4.9	5.1	5.3	5.5	5.6	5.8	5.9
30	2.63	3.0	3.3	3.4	3.6	3.7	3.8	3.9	4.0	4.1	4.2
60	1.96	2.2	2.3	2.4	2.4	2.5	2.5	2.6	2.6	2.7	2.7
∞	1.00	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0

Note: s^2_{max} is the largest and s^2_{min} the smallest in a set of t independent mean squares, each based on $df_2 = n - 1$ degrees of freedom. Values in the column $t = 2$ and in the rows $df_2 = 2$ and ∞ are exact. Elsewhere, the third digit may be in error by a few units for the 5% points and several units for the 1% points. The third-digit figures in parentheses for $df_2 = 3$ are the most uncertain.

Source: From *Biometrika Tables for Statisticians*, 3rd ed., Vol. 1; edited by E. S. Pearson and H. O. Hartley (New York: Cambridge University Press, 1966), Table, p. 202. Reproduced by permission of the *Biometrika Trustees*.

We will illustrate the application of the Hartley test with the following example.

EXAMPLE

Wludyka and Nelson(1997), *Technometrics*, Vol. 39, pp. 274-285 describe the following experiment. In the manufacture of soft contact lenses, a monomer is injected into a plastic frame, the monomer is subjected to ultraviolet light and heated (the time, temperature, and light intensity are varied), the frame is removed, and the lens is hydrated. It is thought that temperature can be manipulated to target the power (the strength of the lens), so interest is in comparing the variability in power. The data are coded deviations from target power using monomers from three different suppliers. We wish to test $H_o : \sigma_1^2 = \sigma_2^2 = \sigma_3^2$.

Deviations from Target Power for Three Suppliers

	Sample										
Supplier	1	2	3	4	5	6	7	8	9	n	s_i^2
1	191.9	189.1	190.9	183.8	185.5	190.9	192.8	188.4	189.0	9	8.69
2	178.2	174.1	170.3	171.6	171.7	174.7	176.0	176.6	172.8	9	6.89
3	218.6	208.4	187.1	199.5	202.0	211.1	197.6	204.4	206.8	9	80.22

Solution Prior to conducting the Hartley test we must check the normality condition. The data are evaluated for normality using the normal probability plots and box plots. All three data sets appear to be from normally distributed populations. Thus, we will apply the Hartley F_{max} test to the data sets. From F-max Percentile Table, with a=.05, t=3, and df_2=9-1=8, we have $F_{max,.05} = 6.00$. Thus, our rejection region will be

R.R.: Reject H_o if $F_{max} \geq F_{max,.05,3,8} = 6.00$.

$$s^2_{min} = \min(8.69, 6.89, 80.22) = 6.89 \quad \text{and} \quad s^2_{max} = \max(8.69, 6.89, 80.22) = 80.22$$

Thus,

$$F_{max} = \frac{s^2_{max}}{s^2_{min}} = \frac{80.22}{6.89} = 11.64 > 6.00$$

Thus, we reject H_o and conclude that the variances are not all equal.

If the sample sizes are not all equal, we can take $n = n_{max}$, where n_{max} is the largest sample size. The F_{max} no longer has an exact level α. In fact, the test is liberal in the sense that the probability of type I error is slightly more than the nominal value α. Thus, the test is more likely to falsely reject H_o than the test having all n_i's equal when sampling from normal populations with the variances all equal.

A simulation study was conducted to investigate the effect on the level of the F test of sampling from heavy tailed and skewed distributions rather than the required normal distribution.

For each pair of sample sizes (n_1, n_2) = (10,10), (10,20) or (20,20), random samples of the specified sizes were selected from one of the five distributions. A test of $H_o : \sigma_1^2 = \sigma_2^2$ vs $H_a : \sigma_1^2 \neq \sigma_2^2$ was conducted using an F test with $\alpha = .05$. This proces was repeated 2500 times for each of the five distributions and three sets of sample sizes. The results are given in the following Table.

Proportion of Times $H_o : \sigma_1^2 = \sigma_2^2$ Was Rejected ($\alpha = .05$)

	Distribution				
Sample Sizes	Normal	Uniform	t (df=5)	Gamma (shape=1)	Gamma (shape=.1)
(10,10)	.054	.010	.121	.225	.693
(10,20)	.056	.0068	.140	.236	.671
(20,20)	.050	.0044	.150	.264	.673

The Hartley F_{max} test is quite sensitive to departures from normality. Thus, if the population distributions we are sampling from have a somewhat nonnormal distribution but the variances are equal, the F_{max} will reject H_o and declare the variances to be unequal. The test is detecting the nonnormality of the population distributions not the unequal variances. Thus, when the population distributions are nonnormal, the F_{max} is not recommended as a test of homogeneity of variances. An alternative approach which does not require the populations to have normal distributions is the Brown-Forsythe-Levene (BFL) test. However, the BFL test involves considerably more calculations than the Hartley test. Also, when the populations have a normal distribution, the Hartley test is more powerful than the BFL test. Conover, Johnson, and Johnson (1981), *Technometrics*, Vol. 23, pp. 351-361, conducted a simulation study of a variety of tests of homongeneity of variance including the Hartley and BFL test. The demonstrated the inflated α levels of the Hartley test when the populations have highly skewed distributions and recommended the BFL test as one of several alternative procedures.

Note: If there are only two populations being compared using samples of size n and m , then the Hartley F-max test has exactly an F-distribution with $df = n - 1, m - 1$.

Brown-Forsythe-Levene (BFL) Test for Homogeneity of Population Variances

When one or more of the population distributions is not normally distributed, a much more powerful procedure for evaluating the differences in the population variances is the Brown-Forsythe-Levene (BFL) test for homogeneity of variance.

The BFL test involves replacing the jth observation from sample i, y_{ij}, with the random variable $z_{ij} = |y_{ij} - \tilde{y}_i|$, where $\tilde{y}_i$ is the sample median of the ith sample. We then compute the BFL test statistic on the z_{ij}'s.

$H_o : \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_t^2$ homogeneity of variances

H_a : Population variances are not all equal

T.S.: $L = \dfrac{\sum_{i=1}^{t} n_i(\bar{z}_{i.} - \bar{z}_{..})^2/(t-1)}{\sum_{i=1}^{t}\sum_{j=1}^{n_i}(z_{ij} - \bar{z}_{i.})^2/(N-t)}$

R.R. For a specified value of α, reject H_o if L $\geq F_{\alpha,df_1,df_2}$, where $df_1 = t-1$, $df_2 = N-t$, $N = \sum_{i=1}^{t} n_i$, and F_{α,df_1,df_2} is the upper α percentile from the F-distribution.

The following modification is suggested in the book *Theory of Rank Tests* by Hajek and Sidak:

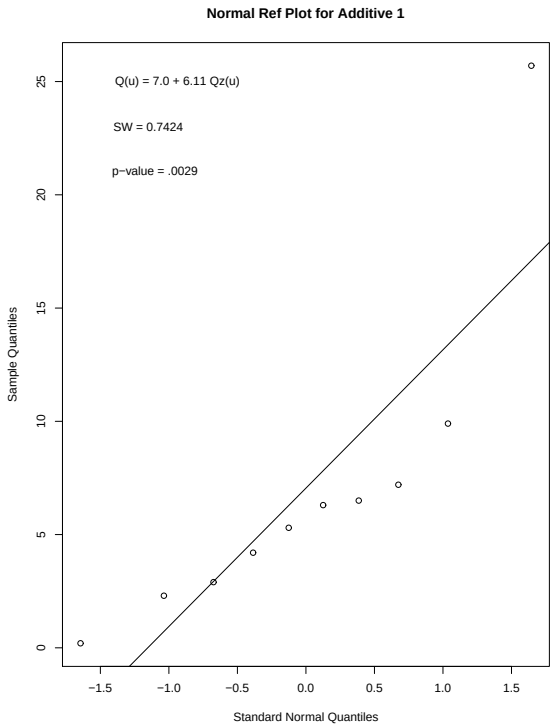
When the sample sizes within the levels of the groups are odd, at least one value of $z_{ij} = |y_{ij} - \tilde{y}_i|$ will always be zero. This artificially dampens the variance estimate for that group. Thus, Hajek-Sidak recommend replacing the zero with the minimum non-zero value if there is only one z_{ij} which is zero. If more than one z_{ij} within a given group is zero, the zeros are kept.

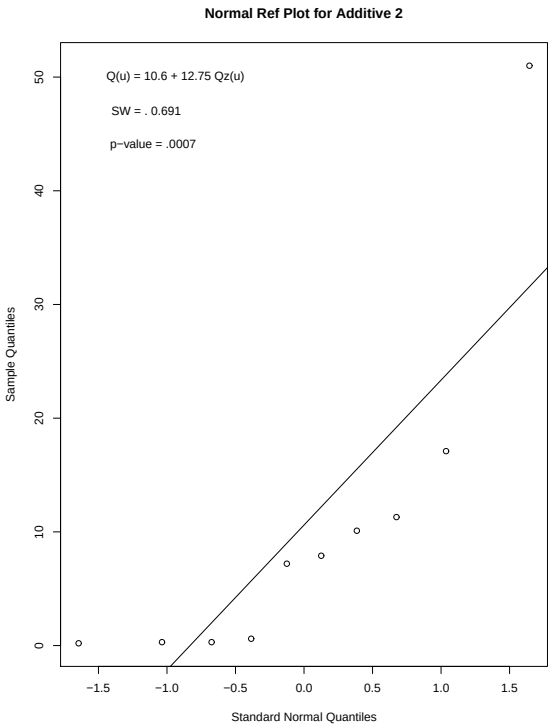
We will illustrate the computations for the BFL test in the following example. The packages *R*, under "lawstat", *SAS* and *Minitab* have functions for conducting the BFL test.

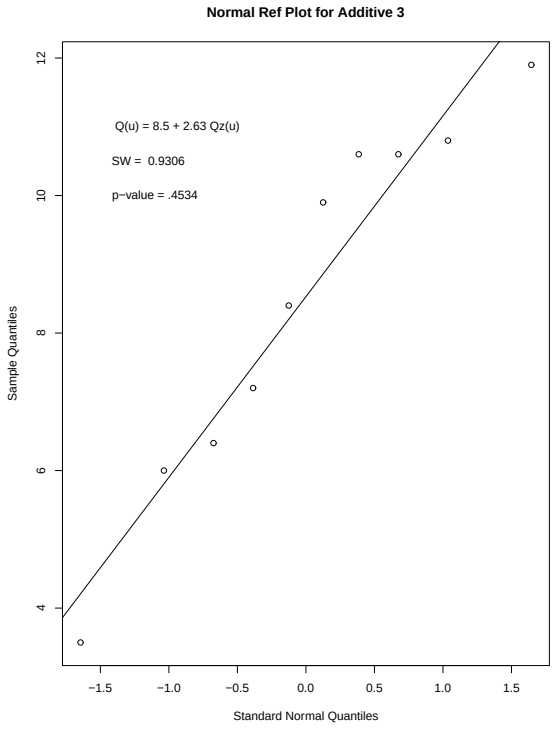
Percent Increase in MPG from Cars Driven Using Three Additives
Three different additives which are marketed for increasing the miles per gallon (mpg) for automobiles were evaluated by a consumer testing agency. Past studies have shown that an average increase of 8% in mpg for economy automobiles after using the product for 250 miles. The testing agency wants to evaluate the variability in the increase in mileage over a variety of brands of cars within the economy class. They randomly selected 30 economy cars of similar age, number of miles on their odometer, and overall condition of the power train to be used in the study. They then randomly assigned 10 cars to each additive. The percentage increase in mpg obtained by each car was recorded for a 250 miles test drive. The testing agency wanted to evaluate whether there was a difference between the three additives with respect to their variability in the increase in mpg. The data is give here along with the intermediate calculations needed to compute the BFL test statistic.

	Percent Increase in MPG for Car i											
Additive	1	2	3	4	5	6	7	8	9	10	n	s_i^2
1	4.2	2.9	0.2	25.7	6.3	7.2	2.3	9.9	5.3	6.5	10	50.525
2	0.2	11.3	0.3	17.1	51.0	10.1	0.3	0.6	7.9	7.2	10	234.927
3	7.2	6.4	9.9	3.5	10.6	10.8	10.6	8.4	6.0	11.9	10	7.220

Using the three normal reference distribution plots on the next page along with the values from the Shapiro-Wilks test, we can observe that the samples from Additive 1 and Additive 2 do not appear to be samples from normally distributed populations.







Therefore, we should not use the Hartley's F_{max} test for evaluating differences in the variances in this example.

The information in Table 5 on the next page will assist us in calculating the value of the BFL test statistic.

The medians of the percent increase in mileage, y_{ij}'s, for the three additives are 5.80, 7.55, and 9.15.

We then calculate the absolute deviations of the data values about their respective medians, namely,

$z_{1j} = |y_{1j} - 5.80|, z_{2j} = |y_{2j} - 7.55|$, and

$z_{3j} = |y_{3j} - 9.15|$ for $j = 1, \ldots, 10$.

These values are given in column 3 of Table 5.

Next, we calculate the three means of these values, $\bar{z}_{1.} = 4.07, \bar{z}_{2.} = 8.88$, and $\bar{z}_{3.} = 2.23$.

Next, we calculate the squared deviations of the z_{ij}'s about their respective means, namely, $(z_{ij} - \bar{z}_{i.})^2$, that is,

$(z_{1j} - 4.07)^2, (z_{2j} - 8.88)^2$, and $(z_{3j} - 2.23)^2$.

These values are contained in column 6 of Table 5.

Then we calculate the squared deviations of the z_{ij}'s about the overall mean,

$\bar{z}_{..} = 5.06$, that is, $(z_{ij} - \bar{z}_{i.})^2 = (z_{ij} - 5.06)^2$.

The last column in Table 5 contains these values.

The final step is to sum columns 6 and 7 in Table 5 yielding

$$T_1 = \sum_{i=1}^{3}\sum_{j=1}^{n_i}(z_{ij} - \bar{z}_{i.})^2 = 1742.6 \quad \text{and} \quad T_2 = \sum_{i=1}^{3}\sum_{j=1}^{n_i}(z_{ij} - \bar{z}_{..})^2 = 1978.4$$

The value of BFL test statistics, in an alternative form, is given by

$$L = \frac{(T_2 - T_1)/(t-1)}{T_1/(N-t)} = \frac{(1978.4 - 1742.6)/(3-1)}{1742.6/(30-3)} = 1.827$$

The rejection region for BFL test is reject H_o if $L \geq F_{\alpha,t-1,N-t} = F_{.05,3-1,30-3} = 3.35$.

Since L = 1.827, we fail to reject $H_o : \sigma_1^2 = \sigma_2^2 = \sigma_3^2$ and conclude that there is insufficient evidence of a difference in the population variances of the percent increase in mpg for the three additives.

Note that if we would have used the Hartley F_{max} test, our conclusion would have been changed.

$s_1^2 = 50.525 \quad s_2^2 = 234.927 \quad s_1^2 = 7.220$

$F_{max} = \frac{234.927}{7.220} = 32.54 > 8.5 = F_{max,.01,3,9}$

Using the Hartley Test, we would conclude there is significant evidence that the three population variances are different.

The Hartley test is distorted by the outliers in the data sets for Additive 1 and Additive 2.

Table 5. Steps in Calculating BFL Test

Additive	y_{1j}	$\tilde{y}_1$	$z_{1j} =$	$\lvert y_{1j} - 5.80 \rvert$	$\bar{z}_{1.}$	$(z_{1j} - 4.07)^2$	$(z_{1j} - 5.06)^2$
1	4.2	5.80		1.60	4.07	6.1009	11.9716
1	2.9			2.90		1.3689	4.6656
1	0.2			5.60		2.3409	0.2916
1	25.7			19.90		250.5889	220.2256
1	6.3			0.50		12.7449	20.7936
1	7.2			1.40		7.1289	13.3956
1	2.3			3.50		0.3249	2.4336
1	9.9			4.10		0.0009	0.9216
1	5.3			0.50		12.7449	20.7936
1	6.5			0.70		11.3569	19.0096
Additive	y_{2j}	$\tilde{y}_2$	$z_{2j} =$	$\lvert y_{2j} - 7.55 \rvert$	$\bar{z}_{2.}$	$(z_{2j} - 8.88)^2$	$(z_{2j} - 5.06)^2$
2	0.2	7.55		7.35	8.88	2.3409	5.2441
2	11.3			3.75		26.3169	1.7161
2	0.3			7.25		2.6569	4.7961
2	17.1			9.55		0.4489	20.1601
2	51.0			43.45		1195.0849	1473.7921
2	10.1			2.55		40.0689	6.3001
2	0.3			7.25		2.6569	4.7961
2	0.6			6.95		3.7249	3.5721
2	7.9			0.35		72.7609	22.1841
2	7.2			0.35		72.7609	22.1841
Additive	y_{3j}	$\tilde{y}_3$	$z_{3j} =$	$\lvert y_{3j} - 9.15 \rvert$	$\bar{z}_{3.}$	$(z_{3j} - 2.23)^2$	$(z_{3j} - 5.06)^2$
3	7.2	9.15		1.95	2.23	0.0784	9.6721
3	6.4			2.75		0.2704	5.3361
3	9.9			0.75		2.1904	18.5761
3	3.5			5.65		11.6964	0.3481
3	10.6			1.45		0.6084	13.0321
3	10.8			1.65		0.3364	11.6281
3	10.6			1.45		0.6084	13.0321
3	8.4			0.75		2.1904	18.5761
3	6.0			3.15		0.8464	3.6481
3	11.9			2.75		0.2704	5.3361
Total					5.06	1742.6	1978.4

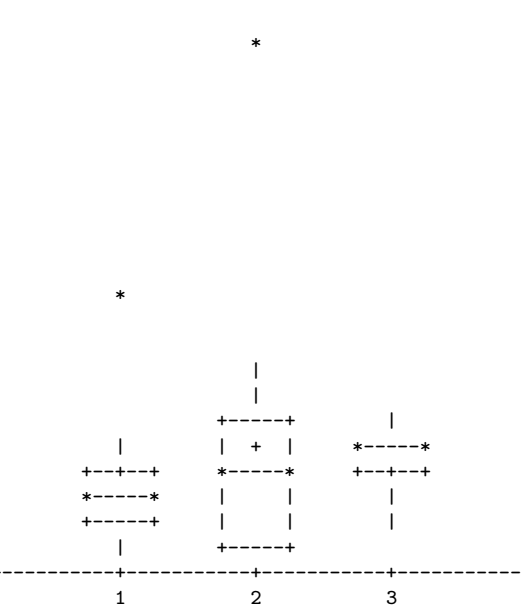
A SAS program to compute BFL test is given next:

```
option ls=70 ps=50 nocenter nodate;
title ' BFL Test of Homogeneity of Variance';
data mpg;
infile '~longneck/meth1/levene.dat';
input Add Y;
label Y = 'Percent Increase in MPG';

*generate Box Plots and Tests of Normality;
proc sort;by Add;
proc univariate def=5 plot normal; by Add;

* BFL Test of Equal Variances;
proc glm data=mpg;
class Add;
model  Y = Add;
means Add/hovtest=bf;
run;
```

BFLTest of Homogeneity of Variance



BFL Test of Homogeneity of Variance

The GLM Procedure

Dependent Variable: Y Percent Increase in MPG

Source	DF	Sum of Squares	Mean Square	F Value
Model	2	63.592667	31.796333	0.33
Error	27	2634.046000	97.557259	
Corrected Total	29	2697.638667		

Brown and Forsythe's Test for Homogeneity of Y Variance
ANOVA of Absolute Deviations from Group Medians

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Add	2	235.8	117.9	1.83	0.1803
Error	27	1742.6	64.5414		

The following R code will compute the Brown-Forsythe Levene test:

```
install.packages("car")
library(car)

y1=c(4.2,2.9,.2,25.7,6.3,7.2,2.3,9.9,5.3,6.5)
y2=c(.2,11.3,.3,17.1,51,10.1,.3,.6,7.9,7.2)
y3=c(7.2,6.4,9.9,3.5,10.6,10.8,10.6,8.4,6,11.9)
y=c(y1,y2,y3)
n1=length(y1)
n2=length(y2)
n3=length(y3)
grp=c(rep(1,n1),rep(2,n2),rep(3,n3))
grp=factor(grp)

leveneTest(y, grp)

Output from leveneTest:

 Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  2  1.8268 0.1803
      27
```

The value of the p-value is identical to the value we obtained from SAS.

Longnecker RCode to compute BFL test for the Example:

```
BFL_HO13Example.R

y1=c(4.2,2.9,.2,25.7,6.3,7.2,2.3,9.9,5.3,6.5)
y2=c(.2,11.3,.3,17.1,51,10.1,.3,.6,7.9,7.2)
y3=c(7.2,6.4,9.9,3.5,10.6,10.8,10.6,8.4,6,11.9)
n1=length(y1)
n2=length(y2)
n3=length(y3)
y=c(y1,y2,y3)
grp=c(rep(1,n1),rep(2,n2),rep(3,n3))
grp = as.factor(grp)

 m1 = median(y1)
 z1 = abs(y1-m1)
 m2 = median(y2)
 z2 = abs(y2-m2)
 m3 = median(y3)
 z3 = abs(y3-m3)
 z = c(z1,z2,z3)

#BFL's Median Test on Raw Data

 BFL  =  aov(z~grp)

 summary(BFL)

            Df Sum Sq Mean Sq F value Pr(>F)
grp          2  235.8  117.91   1.827   0.18
Residuals   27 1742.6   64.54
```

von Neumann Test for Autocorrelation

If the **data values have a normal distribution**, it is often of interest to test if the correlation is of a specific form or pattern. A pattern which is often encountered is first-order autocorrelation, that is, the data values $X_t, \quad t = 1, \cdots, n$ have a time relationship: $X_t = \theta + \rho X_{t-1} + e_t$, where X_t is related to a constant θ, X_{t-1}, the previous value, ρ, the first-order autocorrelation coefficient, and e_t a random normal random variable which is independent of X_{t-1}. An estimate of ρ is given by

$$\hat{\rho} = \frac{\sum_{t=2}^{n}(X_t - \bar{X})(X_{t-1} - \bar{X})}{\sum_{t=1}^{n}(X_t - \bar{X})^2}$$

If $\rho = 0$ then the $X_t's$ are independent. Thus, we want a test of $H_o : \rho = 0$ vs $H_a : \rho \neq 0$. The von Neumann test is given here:

1. Calculate $Q = \frac{\frac{1}{n-1}\sum_{t=2}^{n}(X_t - X_{t-1})^2}{\frac{1}{n}\sum_{t=1}^{n}(X_t - \bar{X})^2}$

- Q large implies Negative correlation and Q small indicates positive correlation

2. Determine $Q_{P,\alpha}$ and $Q_{N,\alpha}$ critical values for Q from the attached table for $n \leq 60$. For $n > 60$, we have the following asymptotic approximation:

   $Q_{P,\alpha} \approx \frac{2n}{n-1} - z_\alpha \frac{2}{\sqrt{n}}$ and $Q_{N,\alpha} \approx \frac{2n}{n-1} + z_\alpha \frac{2}{\sqrt{n}}$ and

3. To test $H_o : \rho = 0$ vs $H_a : \rho > 0$:

   Reject H_o if $Q < Q_{P,\alpha}$

4. To test $H_o : \rho = 0$ vs $H_a : \rho < 0$:

   Reject H_o if $Q > Q_{N,\alpha}$

If the data $X_1, X_2, \ldots, X_n$ is positively correlated, then C.I.'s and tests of hypotheses constructed under the assumption that the data was independent will have the following flaws:

1. The coverage probability will be less than the nominal value for the C.I., i.e.,

$$P[\theta \epsilon C.I.] \leq 1 - \alpha$$

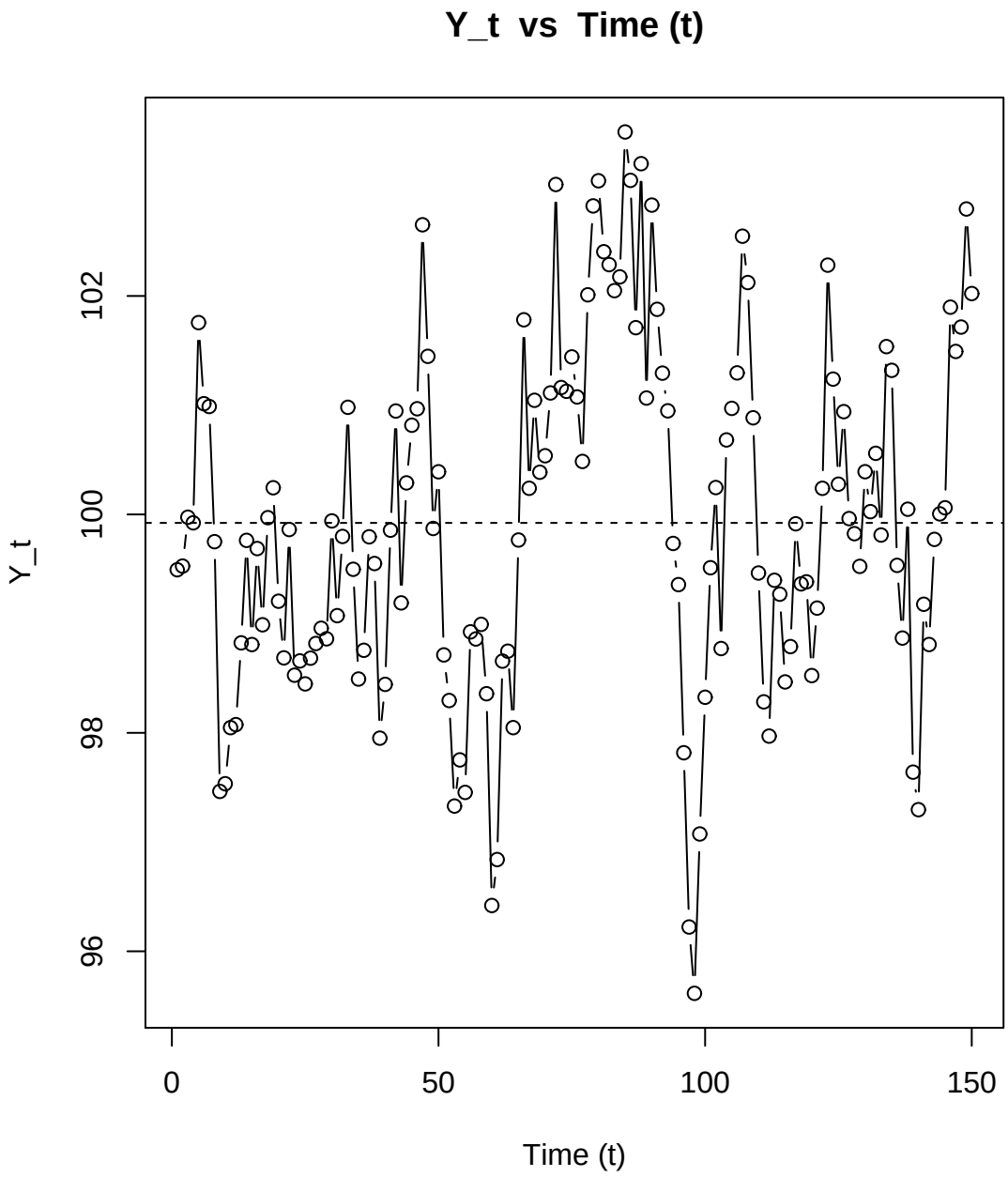
2. Tests of hypotheses will have inflated Type I error rates, i.e.,

$$\alpha_{Pos.Corr} \geq \alpha_{Independence}$$

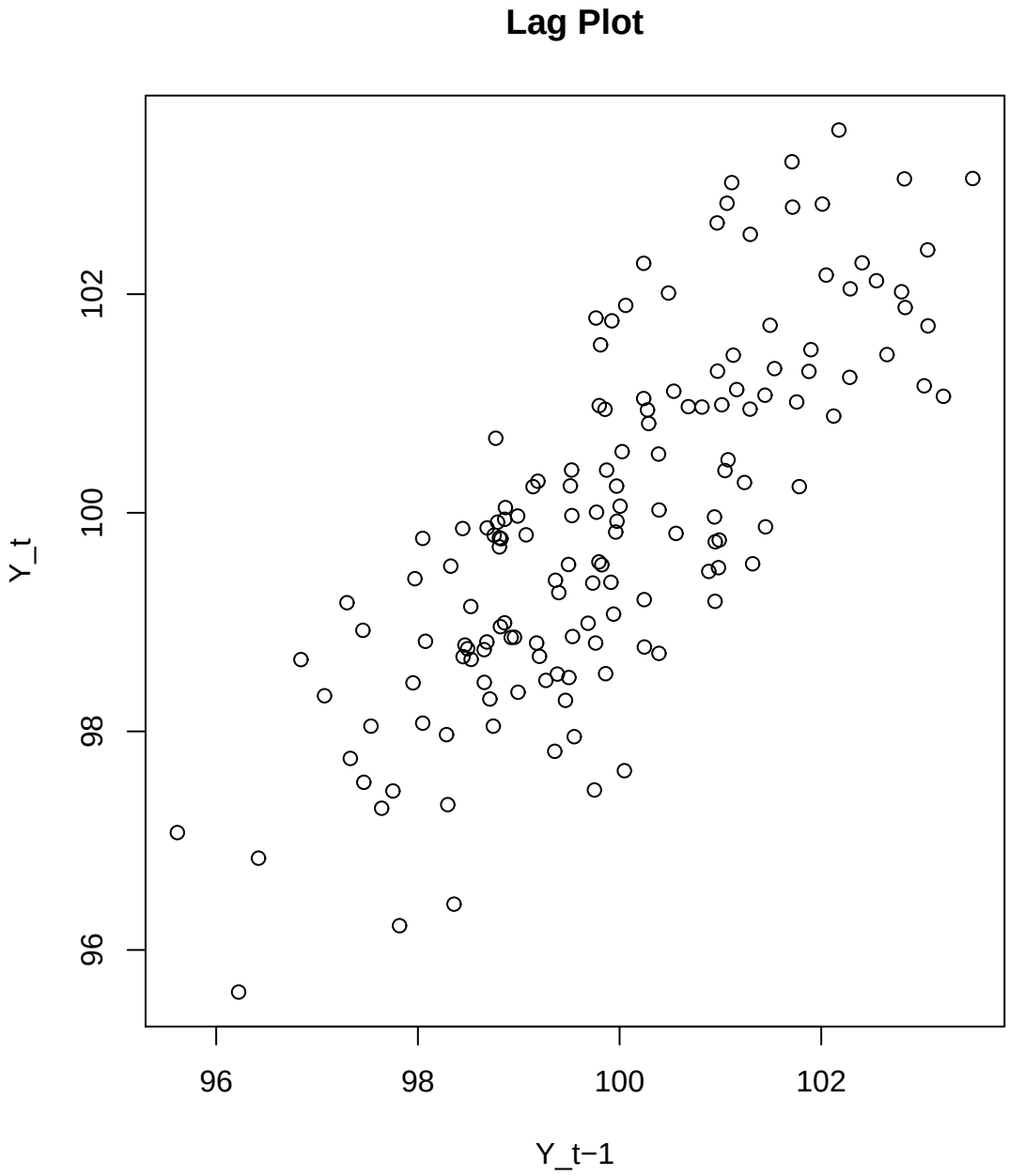
5%, 1%, and .1% Points of the Von Neumann Ratio[a]

Number of Observations	5%	1%	.1%	5%	1%	.1%
	One-tailed test against positive correlation			*One-tailed test against negative correlation*		
4	1.0406	.8341	.7864	4.2927	4.4992	4.5469
5	1.0255	.6724	.5201	3.9745	4.3276	4.4799
6	1.0682	.6738	.4361	3.7318	4.1262	4.3639
7	1.0919	.7163	.4311	3.5748	3.9504	4.2356
8	1.1228	.7575	.4612	3.4486	3.8139	4.1102
9	1.1524	.7974	.4973	3.3476	3.7025	4.0027
10	1.1803	.8353	.5351	3.2642	3.6091	3.9093
11	1.2962	.8706	.5717	3.1938	3.5294	3.8283
12	1.2301	.9033	.6062	3.1335	3.4603	3.7574
13	1.2521	.9336	.6390	3.0812	3.3996	3.6944
14	1.2725	.9618	.6702	3.0352	3.3458	3.6375
15	1.2914	.9880	.6999	2.9943	3.2977	3.5858
16	1.3090	1.0124	.7281	2.9577	3.2543	3.5386
17	1.3253	1.0352	.7548	2.9247	3.2148	3.4952
18	1.3405	1.0566	.7801	2.8948	3.1787	3.4552
19	1.3547	1.0766	.8040	2.8675	3.1456	3.4182
20	1.3680	1.0954	.8265	2.8425	3.1151	3.3840
21	1.3805	1.1131	.8477	2.8195	3.0869	3.3523
22	1.3923	1.1298	.8677	2.7982	3.0607	3.3228
23	1.4035	1.1456	.8866	2.7784	3.0362	3.2953
24	1.4141	1.1606	.9045	2.7599	3.0133	3.2695
25	1.4241	1.1748	.9215	2.7426	2.9919	3.2452
26	1.4336	1.1883	.9378	2.7264	2.9718	3.2222
27	1.4426	1.2012	.9535	2.7112	2.9528	3.2003
28	1.4512	1.2135	.9687	2.6969	2.9348	3.1794
29	1.4594	1.2252	.9835	2.6834	2.9177	3.1594
30	1.4672	1.2363	.9978	2.6707	2.9016	3.1402
31	1.4746	1.2469	1.0115	2.6587	2.8864	3.1219
32	1.4817	1.2570	1.0245	2.6473	2.8720	3.1046
33	1.4885	1.2667	1.0369	2.6365	2.8583	3.0882
34	1.4951	1.2761	1.0488	2.6262	2.8451	3.0725
35	1.5014	1.2852	1.0603	2.6163	2.8324	3.0574
36	1.5075	1.2940	1.0714	2.6068	2.8202	3.0429
37	1.5135	1.3025	1.0822	2.5977	2.8085	3.0289
38	1.5193	1.3108	1.0927	2.5889	2.7973	3.0154
39	1.5249	1.3188	1.1029	2.5804	2.7865	3.0024
40	1.5304	1.3266	1.1128	2.5722	2.7760	2.9898
41	1.5357	1.3342	1.1224	2.5643	2.7658	2.9776
42	1.5408	1.3415	1.1317	2.5567	2.7560	2.9658
43	1.5458	1.3486	1.1407	2.5494	2.7466	2.9545
44	1.5506	1.3554	1.1494	2.5424	2.7376	2.9436
45	1.5552	1.3620	1.1577	2.5357	2.7289	2.9332
46	1.5596	1.3684	1.1657	2.5293	2.7205	2.9232
47	1.5638	1.3745	1.1734	2.5232	2.7125	2.9136
48	1.5678	1.3802	1.1807	2.5173	2.7049	2.9044
49	1.5716	1.3856	1.1877	2.5117	2.6977	2.8956
50	1.5752	1.3907	1.1944	2.5064	2.6908	2.8872
51	1.5787	1.3957	1.2010	2.5013	2.6842	2.8790
52	1.5822	1.4007	1.2075	2.4963	2.6777	2.8709
53	1.5856	1.4057	1.2139	2.4914	2.6712	2.8630
54	1.5890	1.4107	1.2202	2.4866	2.6648	2.8553
55	1.5923	1.4156	1.2264	2.4819	2.6585	2.8477
56	1.5955	1.4203	1.2324	2.4773	2.6524	2.8403
57	1.5987	1.4249	1.2383	2.4728	2.6465	2.8331
58	1.6019	1.4294	1.2442	2.4684	2.6407	2.8260
59	1.6051	1.4339	1.2500	2.4640	2.6350	2.8190
60	1.6082	1.4384	1.2558	2.4596	2.6294	2.8120

The following plot displays a time series of 150 data values. We want to determine if the data is correlated over time. From the plot, the data appears to be positively correlated.



The following lag plot displays the positive correlation in the 150 data values.



The following R code plots the data and computes the von Neumann:

```
 R CODE FOR DISPLAYING CORRELATION PLOTS FOR DATA:

 postscript("u:/meth1/psfiles/corr,p1.ps",height=7,width=6,horizontal=F)

 y  = matrix(0,150,1)
 y  = scan("u:/meth1/Rfiles/corr.dat")


 n  = length(y)
 ytime1  = ts(y,start=1,frequency=1)
 plot.ts(ytime1,type="b",ylab="Y_t",xlab="t",main="Y_t  vs  t")
 ymean  = mean(y)
 abline(h=ymean,lty=2)

postscript("u:/meth1/psfiles/corr,p2.ps",height=7,width=6,horizontal=F)


 yt  = y[2:150]
 ytlag1  = y[1:149]
 plot(ytlag1,yt,main="Lag Plot",ylab="Y_t",xlab="Y_t-1")

#Calculation of von Neumann Statistics

dif1  = (yt-ytlag1)^2
num1  = sum(dif1)
y2  = (y-ymean)^2
den1  = sum(y2)
Q  = (num1/(n-1))/(den1/n)
prd1  = (yt-ymean)*(ytlag1-ymean)
prdsum1  = sum(prd1)
rho1  = prdsum1/den1
rho1
Q

graphics.off()

#Output from Corrplot.s:

#[1] 0.7746074

#[1] 0.441409
```

Runs Test for Correlation

When the **data is nonnormal distributed**, the von Neumann test is invalid. An alternative distribution-free procedure, the Runs Test, will be presented. Let $X_1, X_2, \ldots, X_T$ be T equally spaced observations on a random process. To test if the t observations are correlated:

1. Center the observations: $Y_t = X_t - \bar{X}$, where $\bar{X} = \frac{1}{T}\sum_{t=1}^{T} X_t$
2. Count the number of runs (R), where a run is defined as a sequence of observations of all positive values or all negative values
3. Count the number of positive Y_ts (n_1) and the number of negative Y_ts (n_2)
4. If $n_1 \leq 20$ and $n_2 \leq 20$, then the data indicates that X_t is correlated if $R \leq R_L$ or $R \geq R_U$, where R_L and R_U are values given in the table given in *Annals of Mathematical Statistics,* **14**, pp. 66-87.
5. Large sample size critical values are obtained by declaring that the data indicates that X_t is correlated if $Z > Z_{\alpha/2}$, where

$$Z = \frac{|R - \mu| - 0.5}{\sigma}, \quad \mu = 1 + \frac{2n_1 n_2}{n_1 + n_2}, \quad \sigma^2 = \frac{2n_1 n_2(2n_1 n_2 - n_1 - n_2)}{(n_1 + n_2)^2(n_1 + n_2 - 1)}$$

where $Z_{\alpha/2}$ is the upper $\alpha/2$ percentile of the $N(0,1)$ distribution.

Table A30(*a*) Lower Critical Values of *r* for the Runs Test* ($\alpha = 0.05$)

	Lower Critical Value																		
n_1	$n_2 = 2$	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2											2	2	2	2	2	2	2	2	2
3					2	2	2	2	2	2	2	2	2	3	3	3	3	3	3
4				2	2	2	3	3	3	3	3	3	3	3	4	4	4	4	4
5			2	2	3	3	3	3	3	4	4	4	4	4	4	4	5	5	5
6		2	2	3	3	3	3	4	4	4	4	5	5	5	5	5	5	6	6
7		2	2	3	3	3	4	4	5	5	5	5	5	6	6	6	6	6	6
8		2	3	3	3	4	4	5	5	5	6	6	6	6	6	7	7	7	7
9		2	3	3	4	4	5	5	5	6	6	6	7	7	7	7	8	8	8
10		2	3	3	4	5	5	5	6	6	7	7	7	7	8	8	8	8	9
11		2	3	4	4	5	5	6	6	7	7	7	8	8	8	9	9	9	9
12	2	2	3	4	4	5	6	6	7	8	8	9	9	9	9	9	9	10	10
13	2	2	3	4	5	5	6	6	7	7	8	8	9	9	9	10	10	10	10
14	2	2	3	4	5	5	6	7	7	8	8	8	8	8	10	10	10	11	11
15	2	3	3	4	5	6	6	7	7	8	8	9	9	10	10	11	11	11	12
16	2	3	4	4	5	6	6	7	8	8	9	9	10	10	11	11	11	12	12
17	2	3	4	4	5	6	7	7	8	9	9	10	10	11	11	11	12	12	12
18	2	3	4	5	5	6	7	8	8	9	9	10	10	11	11	12	12	13	13
19	2	3	4	5	6	6	7	8	8	9	10	10	11	11	12	12	13	13	13
20	2	3	4	5	6	6	7	8	9	9	10	10	11	12	12	13	13	13	14

*Any value of *r* that is equal to or smaller than that shown in the body of this table for given values of n_1 and n_2 is significant at the 0.05 level. Tabled values are appropriate for one-tailed test at stated significance level or two-tailed test at twice the significance level.

Source: Adapted from Swed, F. S. and Eisenhart, C. (1943). "Tables for Testing Randomness of Grouping in a Sequence of Alternatives," *Annals of Mathematical Statistics*, **14**, 66–87. Used by permission of the Institute of Mathematical Statistics.

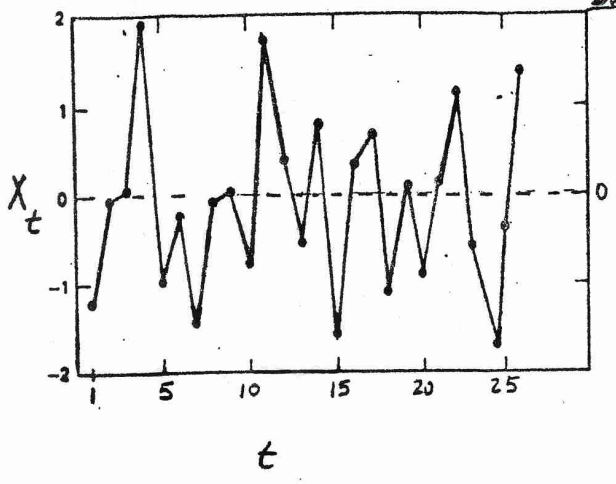
Table A30(*b*) Upper Critical Values of *r* for the Runs Test* ($\alpha = 0.05$)

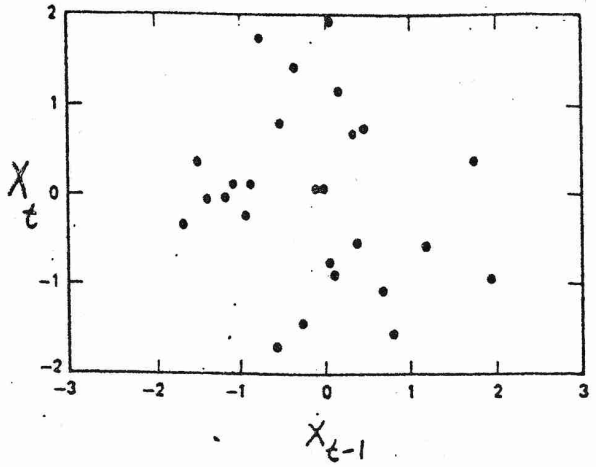
	Upper Critical Value																		
n_1	$n_2 = 2$	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2																			
3																			
4					9	9													
5				9	10	10	11	11											
6				9	10	11	12	12	13	13	13								
7					11	12	13	13	14	14	14	15	15	15					
8					11	12	13	14	14	15	15	16	16	16	16	17	17	17	17
9						13	14	14	15	16	16	16	17	17	18	18	18	18	18
10						13	14	15	16	16	17	17	18	18	18	19	19	19	20
11						13	14	15	16	17	17	18	19	19	19	20	20	20	21
12						13	14	16	16	17	18	19	19	20	20	21	21	21	22
13							15	16	17	18	19	19	20	20	21	21	22	22	23
14							15	16	17	18	19	20	20	21	22	22	23	23	23
15							15	16	18	18	19	20	21	22	22	23	23	24	24
16								17	18	19	20	21	21	22	23	23	24	25	25
17								17	18	19	20	21	22	23	23	24	25	25	26
18								17	18	19	20	21	22	23	24	25	25	26	26
19								17	18	20	21	22	23	23	24	25	26	26	27
20								17	18	20	21	22	23	24	25	25	26	27	27

*Any value of *r* that is equal to or greater than that shown in the body of this table for given values of n_1 and n_2 is significant at the 0.05 level. Tabled values are appropriate for one-tailed test at stated significance level or two-tailed test at twice the significance level.

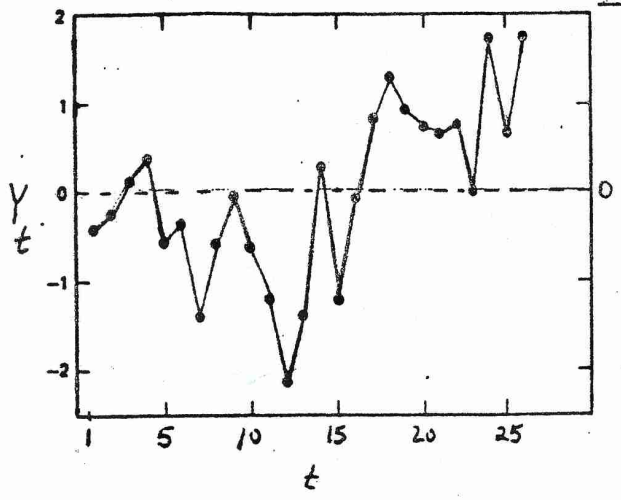
Source: Adapted from Swed, F. S. and Eisenhart, C. (1943). "Tables for Testing Randomness of Grouping in a Sequence of Alternatives," *Annals of Mathematical Statistics*, **14**, 66–87. Used by permission of the Institute of Mathematical Statistics.

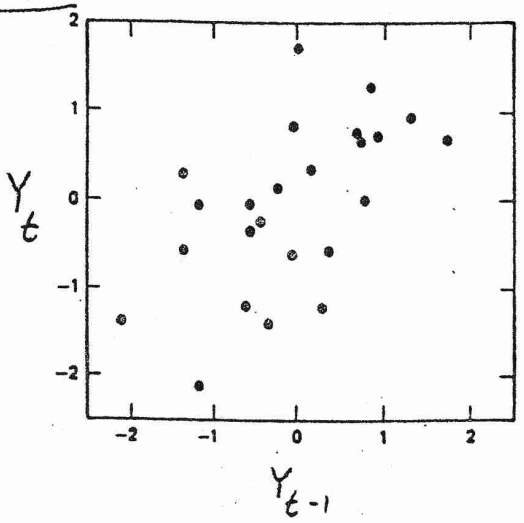
Data Set #1



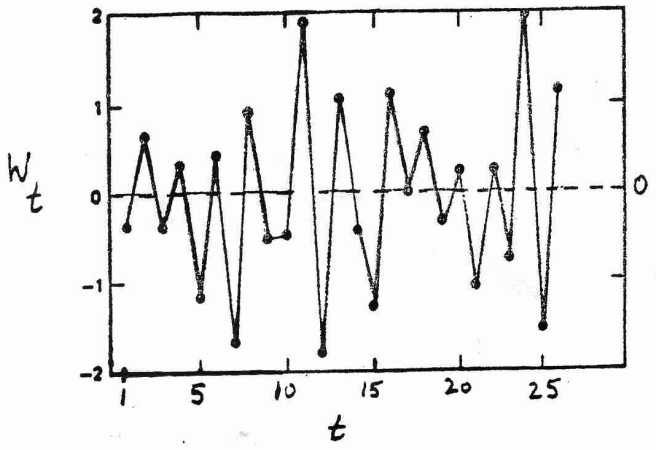


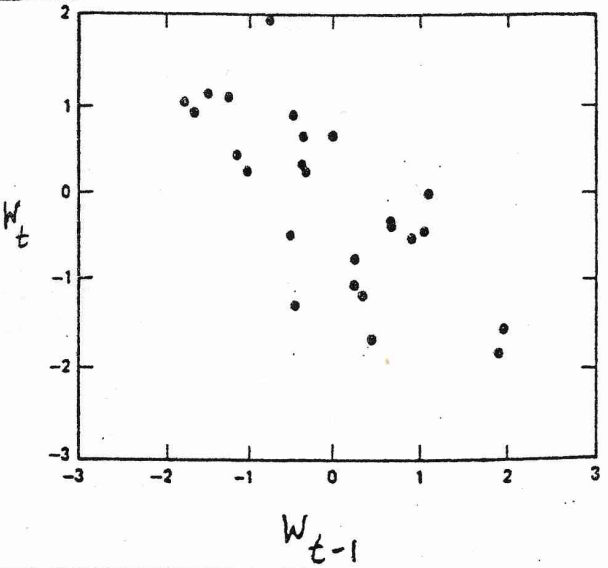
Data Set #2





Data Set #3





Three Time Series from Applied Regression Analysis, 3rd Ed, Draper - Smith

Refer to the data plotted on pages 75-76 and conduct a runs test for correlated data using the following R code:

```
y  = rep(0,150)
y  =  scan("u:/meth1/Rfiles/corr.dat")
n=length(y)
means  =  mean(y)
diff  =  y-means

n.neg  =  rep(0,n)
n.pos  =  rep(0,n)
n.neg  =  length(diff[diff<0])
n.pos  =  length(diff[diff>0])



numb.runs  =  0
  for (j in 2:n) {
    if (sign(diff[j]) != sign(diff[j-1])) {numb.runs  =  numb.runs + 1}
    }


runs.result  =  as.data.frame(cbind(numb.runs, n.pos, n.neg))
names(runs.result)  =  c("No. runs", "N+", "N-")
runs.result

# No. runs  N+   N-
#    29     70   80

mu = 1 + (2*n.neg*n.pos)/(n.neg + n.pos)
sig2 = (2*n.neg*n.pos*(2*n.neg*n.pos - n.neg - n.pos))/((n.neg + n.pos)^2*(n.neg + n.pos-1))

z = (abs(numb.runs-mu)-.5)/sqrt(sig2)
pvalue = 2*(1-pnorm(abs(z)))

results = cbind(mu,sig2,z,pvalue)
results

#           mu        sig2        z       pvalue
#       75.66667   36.91573   7.59841   2.997602e-14
```

Using the formulas on page 78, we have

$$\mu = 1 + \frac{2n_1n_2}{n_1+n_2} = 1 + \frac{2(70)(80)}{70+80} = 75.66667$$

$$\sigma^2 = \frac{2n_1n_2(2n_1n_2 - n_1 - n_2)}{(n_1+n_2)^2(n_1+n_2-1)} = \frac{2(70)(80)(2(70)(80) - 70 - 80)}{(70+80)^2(70+80-1)} = 36.91573$$

$$Z = \frac{|R-\mu| - 0.5}{\sigma} = \frac{|29 - 75.66667| - 0.5}{\sqrt{36.91573}} = 7.59841$$

p-value $= 2P[Z > 7.59841] = 2(1 - pnorm(7.59841)) = 2.997602e-14$

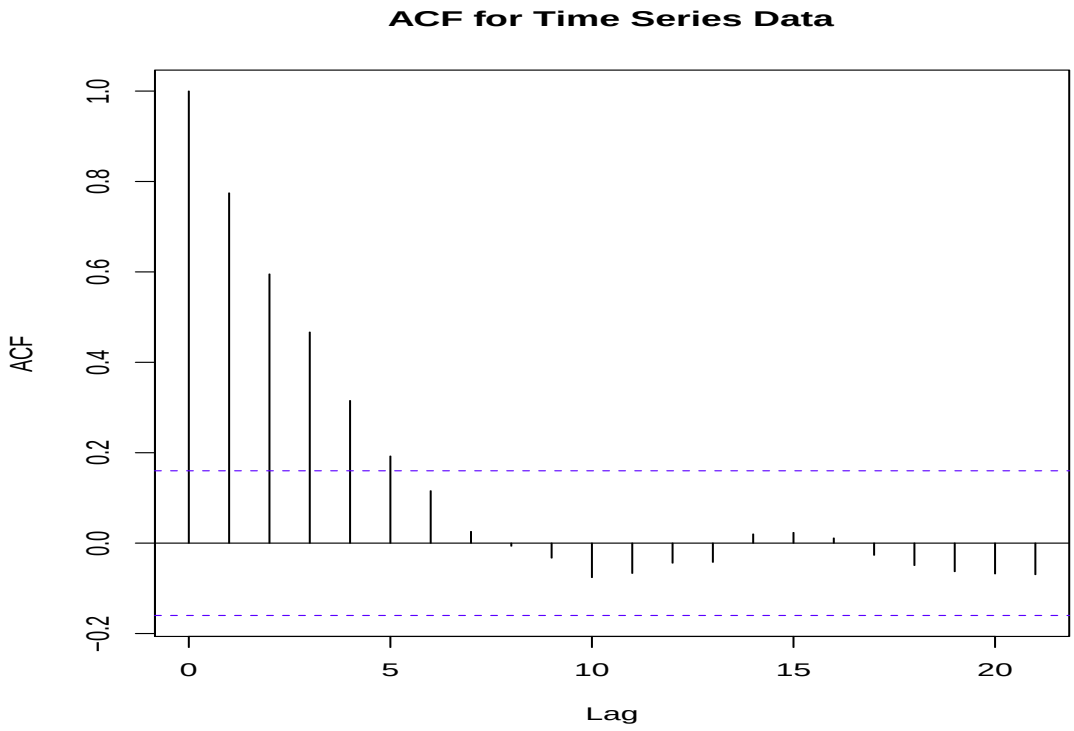
There is substantial evidence that the 150 data values are correlated.

Auto Correlation Function

Using the autocorrelation function from R:

```
acf(y,main="ACF for Time Series Data")
```

The following plot of the lag k correlations can be obtained with 95% C.I.'s:



Thus, we can determine that there is a strong positive correlation in the data because $\rho_1,\ \rho_2,\ \rho_3,\ \rho_4,\ \rho_5$ all have values outside the limits.

The estimated values of $\rho_k = corr(Y_t, Y_{t+k})$ are as follows:

Estimated lag k correlations:

lag	1	2	3	4	5	6	7
$\widehat{\rho}_k$	0.775	0.595	0.467	0.315	0.193	0.116	0.026

Pairwise Comparisons of Population Means

A large percentage of the dietary energy in the bodies of infants is provided by lipids. Lipids are a class of hydrocarbon-containing organic compounds. The following data on total polyunsaturated fats(%) was reported for infants who were randomized to four different feeding regimens: BM (breast milk), CO corn-oil-based formula, SO (soy-oil-based formula), or SMO (soy-marine-oil based formula).

Regimen	n	$\bar{X}$	S	95% C.I. on μ_i
BM	18	43.0	3.5	(41.27, 44.73)
CO	13	40.4	3.3	(38.42, 42.38)
SO	17	43.1	3.2	(41.46, 44.74)
SMO	14	47.1	3.2	(45.27, 48.93)

The researcher wanted to determine if there was significant evidence at the $\alpha = .05$ level that the four Regimens produced different mean percentages of polyunsaturated fat in the infants.

The appropriate analysis would be to construct simultaneous confidence intervals on the difference in the six pairs of treatment means, $\mu_i - \mu_j$.

To test if there is a difference in the pairs of means, the rejection region would be to reject $H_o : \mu_i = \mu_j$ if 0 was not contained in the confidence interval for $\mu_i - \mu_j$.

In order to achieve an overall probability of Type I error across all six comparisons of at most .05, the confidence intervals would need to have individual levels of confidence equal to

$$100(1 - .05/6)\% = 100(1 - .0083)\% = 99.17\%$$

Thus, in the construction of the confidence intervals use, $\alpha/2 = \frac{.05/6}{2} = .00417$

Because there is little difference in the four sample standard deviations, a pooled estimator of their common standard deviation, σ, will be computed:

$$S_p = \sqrt{\frac{\sum_{i=1}^{4}(n_i-1)S^2}{n_1+n_2+n_3+n_4-4)}} = \sqrt{\frac{(18-1)(3.5)^2+(13-1)(3.3)^2+(17-1)(3.2)^2+(14-1)(3.2)^2}{18+17+14+14-4}} = 3.311$$

The confidence intervals on the differences in the six pairs of means $\mu_i - \mu_j$ will be computed as follows:

$$\left(\bar{X}_i - \bar{X}_j\right) \pm t_{58,.05/12} \; S_p \sqrt{\frac{1}{n_i} + \frac{1}{n_j}} = \left(\bar{X}_i - \bar{X}_j\right) \pm (2.732)(3.311)\sqrt{\frac{1}{n_i} + \frac{1}{n_j}}$$

Thus, producing the results given in the following table:

Pair	$(n_i,\ n_j)$	$\lvert\bar{X}_i - \bar{X}_j\rvert$	C.I. on $\mu_i - \mu_j$	Significant Evidence of a Diff. in $\mu_i - \mu_j$?
BM-CO	(18, 13)	2.6	(-0.69, 5.89)	No
BM-SO	(18, 17)	0.1	(-3.16, 2.96)	No
BM-SMO	(18, 14)	4.1	(-7.32, -0.88)	Yes
CO-SO	(13, 17)	2.7	(-6.03, 0.63)	No
CO-SMO	(13, 14)	6.7	(-10.18, -3.22)	Yes
SO-SMO	(17, 14)	4.0	(-7.26, -0.74)	Yes

Thus, we have significant evidence that the SMO regimen produces higher mean lipids than the other three regimens.