

Excellent

EXAMPLE 12.1 Hypotheses and Data for a Two-Factor Analysis of Variance with Fixed-Effects Factors and Equal Replication

The data are plasma calcium concentrations (in mg/100 ml) of birds of both sexes, half of the birds of each sex being treated with a hormone and half not treated with the hormone.

H_0 : There is no effect of hormone treatment on the mean plasma calcium concentration of birds (i.e., $\mu_{\text{no hormone}} = \mu_{\text{hormone}}$ or $\mu_1 = \mu_2$).

H_A : There is an effect of hormone treatment on the mean plasma calcium concentration of birds (i.e., $\mu_{\text{no hormone}} \neq \mu_{\text{hormone}}$ or $\mu_1 \neq \mu_2$).

H_0 : There is no difference in mean plasma calcium concentration between female and male birds (i.e., $\mu_{\text{female}} = \mu_{\text{male}}$ or $\mu_1 = \mu_2$).

H_A : There is a difference in mean plasma calcium concentration between female and male birds (i.e., $\mu_{\text{female}} \neq \mu_{\text{male}}$ or $\mu_1 \neq \mu_2$).

H_0 : There is no interaction of sex and hormone treatment on the mean plasma calcium concentration of birds.

H_A : There is interaction of sex and hormone treatment on the mean plasma calcium concentration of birds.

$\alpha = 0.05$

No Hormone Treatment		Hormone Treatment	
Female	Male	Female	Male
16.3	15.3	38.1	34.0
20.4	17.4	26.2	22.8
12.4	10.9	32.3	27.8
15.8	10.3	35.8	25.0
9.5	6.7	30.2	29.3

$$\text{Cell totals: } \sum_{l=1}^5 X_{11l} = 74.4 \quad \sum_{l=1}^5 X_{12l} = 60.6 \quad \sum_{l=1}^5 X_{21l} = 162.6 \quad \sum_{l=1}^5 X_{22l} = 138.9$$

$$\text{Cell means: } \bar{X}_{11} = 14.88 \quad \bar{X}_{12} = 12.12 \quad \bar{X}_{21} = 32.52 \quad \bar{X}_{22} = 27.78$$

EXAMPLE 12.2 Two-Factor ANOVA Summary for the Data and Hypotheses of Example 12.1

Analysis of Variance Summary Table			
Source of variation	SS	DF	MS
Total	1762.2175	19	
Cells	1461.3255	3	
Factor A (hormone)	1386.1125	1	1386.1125
Factor B (sex)	70.3125	1	70.3125
$A \times B$	4.9005	1	4.9005
Within-Cells (Error)	301.3920	16	18.8370

For H_0 : There is no effect of hormone treatment on the mean plasma calcium concentration of birds in the population sampled.

$$F = \frac{\text{hormone MS}}{\text{within-cells MS}} = \frac{1386.1125}{18.8370} = 73.6$$

$$F_{0.05(1),1,16} = 4.49$$

Therefore, reject H_0 .

$$P < 0.0005 \quad [P = 0.00000022]$$

For H_0 : There is no difference in mean plasma calcium concentration between male and female birds in the population sampled.

$$F = \frac{\text{sex MS}}{\text{within-cells MS}} = \frac{70.3125}{18.8370} = 3.73$$

$$F_{0.05(1),1,16} = 4.49$$

Therefore, do not reject H_0 .

$$0.05 < P < 0.10 \quad [P = 0.071]$$

For H_0 : There is no interaction of sex and hormone treatment affecting the mean plasma calcium concentration of birds in the population sampled.

$$F = \frac{\text{hormone} \times \text{sex interaction MS}}{\text{within-cells MS}} = \frac{4.9005}{22.8370} = 0.260$$

$$F_{0.05(1),1,16} = 4.49$$

Therefore, do not reject H_0 .

$$P > 0.25 \quad [P = 0.62]$$

R

CODE

#ex12.1-2

hormone=as.factor(c(rep('No',10),rep('Yes',10)))

	<pre>gender=as.factor(rep(c(rep('M',5),rep('F',5)),2)) calcium=c(15.3,17.4,10.9,10.3,6.7,16.3,20.4,12.4, 15.8,9.5,34,22.8,27.8,25,29.3,38.1,26.2,32.3,35.8,30.2) data.frame(hormone,gender,calcium) summary(aov(calcium~hormone+gender+hormone:gender))</pre>																																																								
OUTPUT	<pre>> summary(aov(calcium~hormone+gender+hormone:gender)) Df Sum Sq Mean Sq F value Pr(>F) hormone 1 1386.1 1386.1 73.585 2.22e-07 *** gender 1 70.3 70.3 3.733 0.0713 . hormone:gender 1 4.9 4.9 0.260 0.6170 Residuals 16 301.4 18.8 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</pre>																																																								
SAS																																																									
CODE	<pre>data ex12_1; do hormone= 'No ', 'Yes'; do sex= 'Female', 'Male'; do rep= '1', '2', '3', '4', '5'; input calcium @@; output; end; end; end; cards; 16.3 20.4 12.4 15.8 9.5 15.3 17.4 10.9 10.3 6.7 38.1 26.2 32.3 35.8 30.2 34 22.8 27.8 25 29.3 ; run; proc anova data=ex12_1; class hormone sex; model calcium= hormone sex hormone*sex; run;</pre>																																																								
OUTPUT	<table><tr><th>Source</th><th>DF</th><th>Sum of Squares</th><th>Mean Square</th><th>F Value</th><th>Pr > F</th></tr><tr><td>Model</td><td>3</td><td>1461.325500</td><td>487.108500</td><td>25.86</td><td><.0001</td></tr><tr><td>Error</td><td>16</td><td>301.392000</td><td>18.837000</td><td></td><td></td></tr><tr><td>Corrected Total</td><td>19</td><td>1762.717500</td><td></td><td></td><td></td></tr></table> <div><table><tr><th>R-Square</th><th>Coeff Var</th><th>Root MSE</th><th>calcium Mean</th></tr><tr><td>0.829019</td><td>19.88619</td><td>4.340161</td><td>21.82500</td></tr></table><table><tr><th>Source</th><th>DF</th><th>Anova SS</th><th>Mean Square</th><th>F Value</th><th>Pr > F</th></tr><tr><td>hormone</td><td>1</td><td>1386.112500</td><td>1386.112500</td><td>73.58</td><td><.0001</td></tr><tr><td>sex</td><td>1</td><td>70.312500</td><td>70.312500</td><td>3.73</td><td>0.0713</td></tr><tr><td>hormone*sex</td><td>1</td><td>4.900500</td><td>4.900500</td><td>0.26</td><td>0.6170</td></tr></table></div>	Source	DF	Sum of Squares	Mean Square	F Value	Pr > F	Model	3	1461.325500	487.108500	25.86	<.0001	Error	16	301.392000	18.837000			Corrected Total	19	1762.717500				R-Square	Coeff Var	Root MSE	calcium Mean	0.829019	19.88619	4.340161	21.82500	Source	DF	Anova SS	Mean Square	F Value	Pr > F	hormone	1	1386.112500	1386.112500	73.58	<.0001	sex	1	70.312500	70.312500	3.73	0.0713	hormone*sex	1	4.900500	4.900500	0.26	0.6170
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결과해석	<p>호르몬 치료의 여부에 따라 암컷, 수컷별로 새의 플라즈마 칼슘 농도에 차이가 있는지 확인해보기 위해 암컷 수컷 각각 10마리씩을 호르몬 치료를 한 그룹과 받지 않은 그룹으로 나누었다. 다음과 같이 가설을 세우고 2요인 분산분석을 실시하였</p>																																																								

	<p>다.</p> <p>귀무가설1: 호르몬 치료에 따른 새들의 플라즈마 칼슘 농도의 모평균은 동일하다.</p> <p>대립가설1: 호르몬 치료에 따른 새들의 플라즈마 칼슘 농도의 모평균은 같지 않다.</p> <p>귀무가설2: 새의 성별에 따른 플라즈마 칼슘 농도의 모평균은 동일하다.</p> <p>대립가설2: 새의 성별에 따른 플라즈마 칼슘 농도의 모평균은 같지 않다.</p> <p>귀무가설3: 새의 성별과 호르몬 치료 여부에 따른 교호작용이 없다.</p> <p>대립가설3: 새의 성별과 호르몬 치료 여부에 따른 교호작용은 있다.</p> <p>분석 결과 호르몬 치료에 대한 p-value는 매우 유의하게 나와 귀무가설을 기각하여 호르몬 치료에 따라 새들의 플라즈마 칼슘 농도의 모평균은 다르다고 결론을 내릴 수 있다. 그러나 새의 성별에 대한 p-value는 유의수준 0.05하에서 기각할 만큼의 근거가 부족해 성별에 따라 플라즈마 칼슘 농도의 모평균의 차이가 있다고 보기는 어렵다. 또한 성별과 호르몬 치료 여부의 교호작용 역시 유의하지 않아 교호작용이 있다고 보기 어렵다.</p>
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Example. 12.3

EXAMPLE 12.3 Confidence Limits for the Results of Example 12.2

We concluded that mean plasma calcium concentration is different between birds with the hormone treatment and those without.

$$\bar{X}_1 = \frac{\text{total for nonhormone group}}{\text{number in nonhormone group}} = \frac{135.0 \text{ mg/100 ml}}{10} = 13.50 \text{ mg/100 ml}$$

$$\bar{X}_2 = \frac{\text{total for hormone group}}{\text{number in hormone group}} = \frac{301.5 \text{ mg/100 ml}}{10} = 30.15 \text{ mg/100 ml}$$

$$\begin{aligned} 95\% \text{ CI for } \mu_1 &= \bar{X}_1 \pm t_{0.05(2), 16} \sqrt{\frac{s^2}{bn}} \\ &= 13.50 \pm t_{0.05(2), 16} \sqrt{\frac{18.8370}{(2)(5)}} \\ &= 13.50 \pm (2.120)(0.940) \\ &= 13.50 \text{ mg/100 ml} \pm 1.99 \text{ mg/100 ml} \\ L_1 &= 11.51 \text{ mg/100 ml}; L_2 = 15.49 \text{ mg/100 ml} \end{aligned}$$

$$\begin{aligned} 95\% \text{ CI for } \mu_2 &= \bar{X}_2 \pm t_{0.05(2), 16} \sqrt{\frac{s^2}{bn}} \\ &= 30.15 \pm 1.99 \text{ mg/100 ml} \\ L_1 &= 28.16 \text{ mg/100 ml}; L_2 = 32.14 \text{ mg/100 ml} \end{aligned}$$

$$\begin{aligned} 95\% \text{ CI for } \mu_1 - \mu_2 &= \bar{X}_1 - \bar{X}_2 \pm q_{0.05, 16, 2} \sqrt{\frac{s^2}{bn}} \\ &= 13.50 - 30.15 \pm q_{0.05, 16, 2} \sqrt{\frac{18.8370}{(2)(5)}} \\ &= -16.65 \pm (2.998)(0.940) \\ &= -16.65 \text{ mg/100 ml} \pm 2.82 \text{ mg/100 ml} \\ L_1 &= -19.47 \text{ mg/100 ml}; L_2 = -13.82 \text{ mg/100 ml} \end{aligned}$$

We concluded that mean calcium concentration is not different in males and females. That is, the conclusion is that there is no significant difference between μ_{σ} and μ_{ϕ} ,* and we would not speak of separate confidence intervals for each of these two means or for the difference between the means. If we desired, we could pool the means and speak of a confidence interval for the pooled population mean, μ_p :

$$\begin{aligned} \text{pooled } \bar{X} &= \bar{X}_p = \frac{\text{total for females} + \text{total for males}}{\text{number of females} + \text{number of males}} \\ &= \frac{237.0 + 199.5}{10 + 10} = 21.82 \text{ mg/100 ml} \end{aligned}$$

$$\begin{aligned} 95\% \text{ CI for } \mu_p &= \bar{X}_p \pm t_{0.05(2), 16} \sqrt{\frac{s^2}{20}} \\ &= 21.82 \pm (2.120)(0.970) \\ &= 21.82 \text{ mg/100 ml} \pm 2.06 \text{ mg/100 ml} \\ L_1 &= 19.76 \text{ mg/100 ml}; L_2 = 23.88 \text{ mg/100 ml} \end{aligned}$$

R	
CODE	<pre> #ex12.3 x=aov(calcium~hormone+gender+hormone:gender) sd= anova(x)["Residuals", "Mean Sq"] nohor=subset(ex12.1, hormone=="No") yeshor=subset(ex12.1, hormone=="Yes") nomean = mean(nohor\$calcium) noleng = length(nohor\$calcium) yesmean = mean(yeshor\$calcium) yesleng = length(yeshor\$calcium) t=qt(0.025,16, lower.tail = F) cbind(nomean-t*sqrt(sd/noleng),nomean+t*sqrt(sd/noleng)) cbind(yesmean-t*sqrt(sd/yesleng),yesmean+t*sqrt(sd/yesleng)) q=2.998 cbind(nomean-yesmean - q*sqrt(sd/10),nomean-yesmean + q*sqrt(sd/10)) female=subset(ex12.1, gender=="F") male=subset(ex12.1, gender=="M") pooled=mean(ex12.1\$calcium) cbind(pooled-t*sqrt(sd/20),pooled+t*sqrt(sd/20)) </pre>
OUTPUT	<pre> > cbind(nomean-t*sqrt(sd/noleng),nomean+t*sqrt(sd/noleng)) [,1] [,2] [1,] 10.59047 16.40953 > cbind(yesmean-t*sqrt(sd/yesleng),yesmean+t*sqrt(sd/yesleng)) [,1] [,2] [1,] 27.24047 33.05953 > cbind(nomean-yesmean - q*sqrt(sd/10),nomean-yesmean + q*sqrt(sd/10)) [,1] [,2] [1,] -20.76469 -12.53531 > cbind(pooled-t*sqrt(sd/20),pooled+t*sqrt(sd/20)) [,1] [,2] [1,] 19.76765 23.88235 </pre>
SAS	
CODE	<pre> proc ttest data=ex12_1; class hormone; var calcium; run; proc iml; xp=21.82; s=18.8370; l1 = xp - tinv(0.975,16)*sqrt(s/20) l2 = xp + tinv(0.975,16)*sqrt(s/20); print l1 l2; run; quit; </pre>

OUTPUT	hormone	Method	Mean	95% CL Mean	
	No		13.5000	10.4872	16.5128
	Yes		30.1500	26.6377	33.6623
	Diff (1-2)	Pooled	-16.6500	-20.9477	-12.3523
	I1	I2			
	19.762654	23.877346			
결과해석	<p>예제 12.1-12.2에서의 결과를 바탕으로 호르몬 치료에 따른 새들의 플라즈마 칼슘 농도의 모평균에 대한 95퍼센트 신뢰구간을 구해보았다. 계산한 신뢰구간을 확인해 보면 호르몬 치료를 받은 그룹의 신뢰구간과 받지 않은 신뢰구간이 전혀 겹치지 않는 것을 확인할 수 있다. 또한 성별에 따른 차이는 있다고 보기 어렵다고 결론을 내렸기 때문에 성별로 나누었던 것을 다시 합쳐서 신뢰구간을 구하였다.</p>				

Example. 12.4

EXAMPLE 12.4 A Randomized Complete Block Analysis of Variance (Model III Two-Factor Analysis of Variance) without Within-Cell Replication

H_0 : The mean time for effectiveness is the same for all three anesthetics (i.e., $\mu_1 = \mu_2 = \mu_3$).

H_A : The mean time for effectiveness is not the same for all three anesthetics.

$\alpha = 0.05$

Each block consists of three cats from a single source, and each block is from a different source. Within a block, the cats are assigned one of the anesthetics at random, by numbering the cats 1, 2, and 3 and assigning each of them treatment 1, 2, or 3 at random. For this experiment the randomly designated treatments, from 1 to 3, for each block were as follows, with the anesthetic's time for effect (in minutes) given in parentheses:

	<i>Animal 1</i>	<i>Animal 2</i>	<i>Animal 3</i>
<i>Block 1:</i>	Treatment 3 (10.75)	Treatment 1 (8.25)	Treatment 2 (11.25)
<i>Block 2:</i>	Treatment 1 (10.00)	Treatment 3 (11.75)	Treatment 2 (12.50)
<i>Block 3:</i>	Treatment 3 (11.25)	Treatment 1 (10.25)	Treatment 2 (12.00)
<i>Block 4:</i>	Treatment 1 (9.50)	Treatment 2 (9.75)	Treatment 3 (9.00)
<i>Block 5:</i>	Treatment 2 (11.00)	Treatment 1 (8.75)	Treatment 3 (10.00)

These data are rearranged as follows in order to tabulate the treatment, block, and grand totals (and, if not using the machine formulas, the treatment, block, and grand means).

Block (<i>j</i>)	<i>Treatment (i)</i>			Block Total $\left(\sum_{i=1}^a X_{ij}\right)$	Block Mean (\bar{X}_j)
	1	2	3		
1	8.25	11.25	10.75	30.25	10.08
2	11.00	12.50	11.75	35.25	11.75
3	10.25	12.00	11.25	33.50	11.17
4	9.50	9.75	9.00	28.25	9.42
5	8.75	11.00	10.00	29.75	9.92
<hr/>					
Treatment total: $\sum_{j=1}^b X_{ij}$	47.75	56.50	52.75		
Treatment mean: \bar{X}_i	9.55	11.30	10.55		

Grand total = $\sum_{i=1}^a \sum_{j=1}^b X_{ij} = 157.00$ Grand mean = $\bar{X} = 10.47$

The sums of squares required in the following table may be obtained using the equations in Section 12.3, as referenced in Table 12.4.

Source of variation	SS	DF	MS
Total	21.7333	14	
Treatments	7.7083	2	3.8542
Blocks	11.0667	4	
Remainder	2.9583	8	0.3698

$$F = \frac{\text{treatments MS}}{\text{remainder MS}} = \frac{3.8542}{0.3698} = 10.4$$

$F_{0.05(1),2,8} = 4.46$, so reject H_0 .

$0.005 < P < 0.01$ [$P = 0.0060$]

R

```
CODE #ex12.4
trt=as.factor(rep(c('1','2','3'),5))
block=as.factor(rep(c('1','2','3','4','5'),each=3))
time=c(8.25,11.25,10.75,11,12.5,11.75,10.25,12,11.25,9.5,9.75,9,8.75,11,10)
ex12.4=data.frame(block,trt,time)
library(lme4)
lmer(time ~ trt + block+(1|block))
anova(lmer(time ~ trt + block+(1|block)))[ "trt","F value"]
pf(anova(lmer(time ~ trt + block+(1|block)))[ "trt","F value"],2,8, lower.tail = F)
```

**anova(lmer(time~trt+(1|block),
data=ex12.4)**

```
OUTPUT > anova(lmer(time ~ trt + block+(1|block)))
Analysis of Variance Table
      npar Sum Sq Mean Sq F value
trt      2  7.7083   3.8542 10.4225
block    4  1.3646   0.3412  0.9226
> pf(anova(lmer(time ~ trt + block+(1|block)))[ "trt","F value"],2,8, lower.tail = F)
[1] 0.005916618
```

SAS

```
CODE data ex12_4;
input block$ trt$ time @@;
cards;
1 3 10.75 1 1 8.25 1 2 11.25
2 1 11 2 3 11.75 2 2 12.5
3 3 11.25 3 1 10.25 3 2 12
4 1 9.5 4 2 9.75 4 3 9
5 2 11 5 1 8.75 5 3 10
; run;
proc glm data=ex12_4;
class trt block;
model time= trt block;
random block;
run;
```

OUTPUT	Source	DF	Type I SS	Mean Square	F Value	Pr > F	
	trt	2	7.70833333	3.85416667	10.42	0.0059	
	block	4	11.06666667	2.76666667	7.48	0.0082	
결과해석	<p>세 종류의 마취약의 효과의 차이를 확인해보기 위해 총 5곳으로부터 3마리의 고양이를 데려와 무작위로 세 종류의 마취약을 투여한 후 평균 마취 지속시간을 측정하였다. 5곳을 블록으로 지정하여 Randomized complete block 분산분석을 실시하였다.</p> <p>귀무가설: 세 종류의 마취약의 지속시간의 모평균은 모두 동일하다.</p> <p>대립가설: 적어도 한 종류의 마취약의 지속시간의 모평균은 다른 마취약들과는 다르다.</p> <p>분석결과 마취약에 대한 p-value=0.0059정도로 유의한 결과가 나와 귀무가설을 기각한다. 따라서 모든 마취약의 마취 지속시간의 모평균이 같은 것은 아니라는 결론을 내렸다.</p>						

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Example. 12.5

EXAMPLE 12.5 Friedman's Analysis of Variance by Ranks Applied to the Randomized Block Data of Example 12.4

H_0 : The time for effectiveness is the same for all three anesthetics.

H_A : The time for effectiveness is not the same for all three anesthetics.

$$\alpha = 0.05$$

The data from Example 12.4, for the three treatments and five blocks, are shown here, with ranks (1, 2, and 3) within each block shown in parentheses.

Block (j)	Treatment (i)		
	1	2	3
1	8.25 (1)	11.25 (3)	10.75 (2)
2	11.00 (1)	12.50 (3)	11.75 (2)
3	10.25 (1)	12.00 (3)	11.25 (2)
4	9.50 (2)	9.75 (3)	9.00 (1)
5	8.75 (1)	11.00 (3)	10.00 (2)
Rank sum (R_i)	6	15	9
Mean rank (\bar{R}_i)	1.2	3.0	1.8

$$a = 3, b = 5$$

$$\begin{aligned} \chi_r^2 &= \frac{12}{ba(a+1)} \sum R_i^2 - 2b(a+1) \\ &= \frac{12}{(5)(3)(3+1)} (6^2 + 15^2 + 9^2) - 3(5)(3+1) \\ &= 0.200(342) - 60 = 8.400 \end{aligned}$$

$$(\chi_r^2)_{0.05,3,5} = 6.400$$

Reject H_0 .

$$P < 0.01 \quad [P = 0.0085]$$

$$F_F = \frac{(b-1)\chi_r^2}{b(a-1) - \chi_r^2} = \frac{(5-1)(8.4)}{5(3-1)} = 8.4 = \frac{33.6}{1.6} = 21.0$$

$$F_{0.05(1),2,4} = 6.94$$

Reject H_0 .

$$0.005 < P < 0.01 \quad [P = 0.0076]$$

R

CODE

#ex12.5

	<pre>trt=as.factor(rep(c('1','2','3'),5)) block=as.factor(rep(c('1','2','3','4','5'),each=3)) time=c(8.25,11.25,10.75,10,12.5,11.75,10.25,12,11.25,9.5,9.75,9,8.75,11,10) ex12.5=data.frame(block,trt, time) friedman.test(time~trt block, data=ex12.5) chi=friedman.test(time~trt block, data=ex12.5)\$statistic Ff=((5-1)*chi) /(5*(3-1)-chi) pf(Ff,2,4,lower.tail = F)</pre>																				
OUTPUT	<pre>> friedman.test(time~trt block, data=ex12.5) Friedman rank sum test data: time and trt and block Friedman chi-squared = 8.4, df = 2, p-value = 0.015 > pf(Ff,2,4,lower.tail = F) Friedman chi-squared 0.007561437</pre>																				
SAS																					
CODE	<pre>data ex12_5; input block\$ trt\$ time @@; cards; 1 3 10.75 1 1 8.25 1 2 11.25 2 1 10 2 3 11.75 2 2 12.5 3 3 11.25 3 1 10.25 3 2 12 4 1 9.5 4 2 9.75 4 3 9 5 2 11 5 1 8.75 5 3 10 ; run; proc freq data=ex12_5; tables block*trt*time/cmh2 scores=rank; run;</pre>																				
OUTPUT	<table><tr><th colspan="5">Cochran-Mantel-Haenszel 통계량 (랭크 스코어에 기반)</th></tr><tr><th>통계량</th><th>대립가설</th><th>자유도</th><th>값</th><th>Prob</th></tr><tr><td>1</td><td>영(0)이 아닌 상관계수</td><td>1</td><td>0.9000</td><td>0.3428</td></tr><tr><td>2</td><td>행 평균 스코어 차이</td><td>2</td><td>8.4000</td><td>0.0150</td></tr></table>	Cochran-Mantel-Haenszel 통계량 (랭크 스코어에 기반)					통계량	대립가설	자유도	값	Prob	1	영(0)이 아닌 상관계수	1	0.9000	0.3428	2	행 평균 스코어 차이	2	8.4000	0.0150
Cochran-Mantel-Haenszel 통계량 (랭크 스코어에 기반)																					
통계량	대립가설	자유도	값	Prob																	
1	영(0)이 아닌 상관계수	1	0.9000	0.3428																	
2	행 평균 스코어 차이	2	8.4000	0.0150																	
결과해석	<p>예제 12.4의 내용을 일반 분산분석이 아닌 비모수적 방법인 Friedman의 분산분석을 이용하여 분석하였다.</p> <p>귀무가설: 세 종류의 마취약의 지속시간은 모두 같은 분포를 보인다.</p> <p>대립가설: 적어도 한 종류의 마취약의 지속시간은 다른 분포를 보인다.</p> <p>분석 결과 p-value=0.0076정도로 귀무가설을 기각할 충분한 근거가 된다. 따라서 적어도 한 종류의 마취약의 지속시간은 다른 분포를 보인다고 할 수 있다.</p>																				

EXAMPLE 12.6 Cochran's Q Test

H_0 : The proportion of humans attacked by mosquitoes is the same for all five clothing types.

H_A : The proportion of humans attacked by mosquitoes is not the same for all five clothing types.

$\alpha = 0.05$

A person attacked is scored as a "1"; a person not attacked is scored as a "0."

Person (block)	Clothing Type					Totals (B_j)
	Light, loose	Light, tight	Dark, long	Dark, short	None	
1	0	0	0	1	0	1
2*	1	1	1	1	1	*
3	0	0	0	1	1	2
4	1	1	0	1	0	3
5	0	1	1	1	1	4
6	0	1	0	0	1	2
7	0	0	1	1	1	3
8	0	0	1	1	0	2
Totals* (G_i)	1	3	3	6	4	$\sum_{i=1}^a G_i = \sum_{j=1}^b B_j = 17$

$$a = 5; \quad b = 7^*$$

$$Q = \frac{(a-1) \left[\sum_{i=1}^a G_i^2 - \frac{\left(\sum_{i=1}^a G_i \right)^2}{a} \right]}{\sum_{j=1}^b B_j - \frac{\sum_{j=1}^b B_j^2}{a}}$$

$$= \frac{(5-1) \left[1 + 9 + 9 + 36 + 16 - \frac{17^2}{5} \right]}{17 - \frac{(1 + 4 + 9 + 16 + 4 + 9 + 4)}{5}} = \frac{52.8}{7.6} = 6.947$$

$$\nu = a - 1 = 4$$

$$\chi_{0.05,4}^2 = 9.488$$

Therefore, do not reject H_0 .

$$0.10 < P < 0.25 \quad [P = 0.14]$$

*The data for block 2 are deleted from the analysis, because 1's occur for all clothing. (See test discussion in Section 12.8.)

	<pre>person=rep(seq(1,8),5) attack=c(0,1,0,1,0,0,0,0,1,0,1,1,1,0,0,0,1,0,0,1,0,1,1,1,1,1,1,1,0,1,1,0,1,1,0,1,1,1,0) type=rep(c('ll','lt','dl','ds','no'),each=8) ex12.6=data.frame(person,type, attack) library(RVAideMemoire) cochran.qtest(attack~type person)</pre>	https://cran.r-project.org/web/packages/nonpar/nonpar.pdf																									
OUTPUT	<pre>> cochran.qtest(attack~type person) Cochran's Q test data: attack by type, block = person Q = 6.9474, df = 4, p-value = 0.1387 alternative hypothesis: true difference in probabilities is not equal to 0 sample estimates: proba in group <NA> <NA> <NA> <NA> 0.500 0.875 0.250 0.500 0.625</pre>																										
SAS																											
CODE	<pre>data ex12_6; input person\$ type\$ attack @@; cards; 1 11 0 1 1t 0 1 dl 0 1 ds 1 1 no 0 2 11 1 2 1t 1 2 dl 1 2 ds 1 2 no 1 3 11 0 3 1t 0 3 dl 0 3 ds 1 3 no 1 4 11 1 4 1t 1 4 dl 0 4 ds 1 4 no 0 5 11 0 5 1t 1 5 dl 1 5 ds 1 5 no 1 6 11 0 6 1t 1 6 dl 0 6 ds 0 6 no 1 7 11 0 7 1t 0 7 dl 1 7 ds 1 7 no 1 8 11 0 8 1t 0 8 dl 1 8 ds 1 8 no 0 ;run; proc freq data=ex12_6; tables person *type*attack/cmh; run;</pre>	https://documentation.sas.com/docset/statug_freq_examples10.htm?docsetVersion=14.3&locale=en																									
OUTPUT	<table><tr><th colspan="5">Cochran-Mantel-Haenszel 통계량 (테이블 스코어)</th></tr><tr><th>통계량</th><th>대립가설</th><th>자유도</th><th>값</th><th>Prob</th></tr><tr><td>1</td><td>명(0)이 아닌 상관계수</td><td>1</td><td>0.0526</td><td>0.8185</td></tr><tr><td>2</td><td>행 평균 스코어 차이</td><td>4</td><td>6.9474</td><td>0.1387</td></tr><tr><td>3</td><td>일반 연관성</td><td>4</td><td>6.9474</td><td>0.1387</td></tr></table>	Cochran-Mantel-Haenszel 통계량 (테이블 스코어)					통계량	대립가설	자유도	값	Prob	1	명(0)이 아닌 상관계수	1	0.0526	0.8185	2	행 평균 스코어 차이	4	6.9474	0.1387	3	일반 연관성	4	6.9474	0.1387	
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통계량	대립가설	자유도	값	Prob																							
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3	일반 연관성	4	6.9474	0.1387																							
결과해석	<p>옷의 종류에 따라 모기에 물리는 비율의 차이가 있는지 확인해보려고 한다. 따라서 8명의 사람을 모아 5가지의 옷의 종류에 따라 모기에 물리는지 여부를 측정하여 물리면 1 물리지 않았으면 0으로 기입한 후 결과를 통해 Cochran의 Q test를 실시하였다.</p> <p>귀무가설: 5개의 옷의 종류에 따라 사람들이 모기에 물리는 모비율은 동일하다. 대립가설: 5개의 옷의 종류에 따라 사람들이 모기에 물리는 모비율은 같지 않다.</p> <p>분석결과 p-value=0.1387정도로 귀무가설을 기각하기에 충분한 근거가 되지 못한다. 따라서 옷의 종류에 따라 사람들이 모기에 물리는 모비율에 차이가 있다고 보기 어렵다.</p>																										

Example. 13.1

EXAMPLE 13.1 Additive and Multiplicative Effects

- (a) A hypothetical two-way analysis-of-variance design, where the effects of the factors are additive. (Data are in grams.)

Factor B	Factor A		
	<i>Level 1</i>	<i>Level 2</i>	<i>Level 3</i>
<i>Level 1</i>	10	20	25
<i>Level 2</i>	20	30	35

- (b) A hypothetical two-way analysis-of-variance design, where the effects of the factors are multiplicative. (Data are in grams.)

Factor B	Factor A		
	<i>Level 1</i>	<i>Level 2</i>	<i>Level 3</i>
<i>Level 1</i>	10	30	60
<i>Level 2</i>	20	60	120

- (c) The two-way analysis-of-variance design of Example 13.1b, showing the logarithms (rounded to two decimal places) of the data.

Factor B	Factor A		
	<i>Level 1</i>	<i>Level 2</i>	<i>Level 3</i>
<i>Level 1</i>	1.00	1.48	1.78
<i>Level 2</i>	1.30	1.78	2.08

R

```
CODE
#ex13.1
a= rep(c('1','2','3'),each=2)
b= rep(c('1','2'),3)
x=c(10,20,30,60,60,120)
ex13.1=data.frame(a,b,x)
summary(aov(x~a+b))
logx=log10(x)
ex13.1t=data.frame(a,b,logx)
summary(aov(logx~a+b))
```

```
OUTPUT
> data.frame(a,b,x)
  a b  x
1 1 1 10
2 1 2 20
3 2 1 30
4 2 2 60
5 3 1 60
6 3 2 120
```

	<pre>> summary(aov(x~a+b)) Df Sum Sq Mean Sq F value Pr(>F) a 2 5700 2850.0 9.000 0.100 b 1 1667 1666.7 5.263 0.149 Residuals 2 633 316.7 > data.frame(a,b,logx) a b logx 1 1 1 1.000000 2 1 2 1.301030 3 2 1 1.477121 4 2 2 1.778151 5 3 1 1.778151 6 3 2 2.079181 > summary(aov(logx~a+b)) Df Sum Sq Mean Sq F value Pr(>F) a 2 0.6159 0.3079 1.708e+30 <2e-16 *** b 1 0.1359 0.1359 7.540e+29 <2e-16 *** Residuals 2 0.0000 0.0000 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1</pre>																																																					
SAS																																																						
CODE	<pre>data ex13_1; input a\$ b\$ x @@; cards; 1 1 10 1 2 20 2 1 30 2 2 60 3 1 60 3 2 120 ; run; proc anova data=ex13_1; class a b; model x= a b; run; data ex13_1t; set ex13_1; logx= log10(x); run; proc anova data=ex13_1t; class a b; model logx= a b; run;</pre>																																																					
OUTPUT	<table><tr><th>OBS</th><th>a</th><th>b</th><th>x</th><th>logx</th></tr><tr><td>1</td><td>1</td><td>1</td><td>10</td><td>1.00000</td></tr><tr><td>2</td><td>1</td><td>2</td><td>20</td><td>1.30103</td></tr><tr><td>3</td><td>2</td><td>1</td><td>30</td><td>1.47712</td></tr><tr><td>4</td><td>2</td><td>2</td><td>60</td><td>1.77815</td></tr><tr><td>5</td><td>3</td><td>1</td><td>60</td><td>1.77815</td></tr><tr><td>6</td><td>3</td><td>2</td><td>120</td><td>2.07918</td></tr></table> <table><tr><th>Source</th><th>DF</th><th>Anova SS</th><th>Mean Square</th><th>F Value</th><th>Pr > F</th></tr><tr><td>a</td><td>2</td><td>5700.000000</td><td>2850.000000</td><td>9.00</td><td>0.1000</td></tr><tr><td>b</td><td>1</td><td>1666.666667</td><td>1666.666667</td><td>5.26</td><td>0.1487</td></tr></table>	OBS	a	b	x	logx	1	1	1	10	1.00000	2	1	2	20	1.30103	3	2	1	30	1.47712	4	2	2	60	1.77815	5	3	1	60	1.77815	6	3	2	120	2.07918	Source	DF	Anova SS	Mean Square	F Value	Pr > F	a	2	5700.000000	2850.000000	9.00	0.1000	b	1	1666.666667	1666.666667	5.26	0.1487
OBS	a	b	x	logx																																																		
1	1	1	10	1.00000																																																		
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b	1	1666.666667	1666.666667	5.26	0.1487																																																	

	Source	DF	Anova SS	Mean Square	F Value	Pr > F
	a	2	0.61585541	0.30792771	Infty	<.0001
	b	1	0.13592859	0.13592859	Infty	<.0001

결과해석

기존에 수집한 자료를 로그변환을 통해 분산분석을 해보았더니 유의하지 않게 나왔던 결과가 유의하게 나온 것을 확인할 수 있었다. 따라서 특정 분포를 띄고 있는 자료에 변환을 통해 결과를 바꿀 수 있다는 결론을 내릴 수 있다.

Example. 13.2

EXAMPLE 13.2 The Logarithmic Transformation for Data in Which There Is Heterogeneity of Variance and the Standard Deviations Are Directly Proportional to the Means (i.e., the Coefficients of Variation Are the Same)

A prime symbol on a statistic denotes a quantity obtained using the transformed data (e.g., \bar{X}' , s' , L').

The original data (leaf lengths, in centimeters):

Group 1	Group 2
3.1	7.6
2.9	6.4
3.3	7.5
3.6	6.9
3.5	6.3

$$\begin{array}{ll}
 \bar{X}_1 = 3.28 \text{ cm} & \bar{X}_2 = 6.94 \text{ cm} \\
 s_1^2 = 0.0820 \text{ cm}^2 & s_2^2 = 0.3630 \text{ cm}^2 \\
 s_1 = 0.29 \text{ cm} & s_2 = 0.60 \text{ cm} \\
 V_1 = 0.09 & V_2 = 0.09
 \end{array}$$

The logarithmically transformed data, using Equation (13.1):

Group 1	Group 2
0.61278	0.93450
0.59106	0.86923
0.63347	0.92942
0.66276	0.89763
0.65321	0.86332

$\bar{X}'_1 = 0.63066$	$\bar{X}'_2 = 0.89882$
$(s_1^2)' = 0.0008586657$	$(s_2^2)' = 0.0010866641$
$s'_1 = 0.02930$	$s'_2 = 0.03296$
$V'_1 = 0.04646$	$V'_2 = 0.03667$
$s'_{\bar{X}_1} = 0.01310$	$s'_{\bar{X}_2} = 0.01474$

Calculating confidence limits for the mean, using the transformed data from Group 1:

$$\begin{aligned}
 95\% \text{ confidence interval for } \mu'_1 &= \bar{X}'_1 \pm (t_{0.05(2),4})(0.01310) \\
 &= 0.63066 \pm (2.776)(0.01310) \\
 &= 0.63066 \pm 0.03637
 \end{aligned}$$

$$L'_1 = 0.59429 \text{ and } L'_2 = 0.66703$$

95% confidence limits for μ_1 , in the original units:

$$L_1 = \text{antilog } 0.59429 - 1 = 3.93 - 1 = 2.93 \text{ cm}$$

$$L_2 = \text{antilog } 0.66703 - 1 = 4.65 - 1 = 3.65 \text{ cm}$$

The 95% confidence intervals for μ'_2 and for μ_2 may be calculated in the same manner.

R	
CODE	<pre>#ex13.2 x1=c(3.1,2.9,3.3,3.6,3.5) x2=c(7.6,6.4,7.5,6.9,6.3) logx1=log10(x1+1) logx2=log10(x2+1) t.test(logx1) t.test(x1)</pre>
OUTPUT	<pre>> t.test(logx1) One Sample t-test data: logx1 t = 48.128, df = 4, p-value = 1.115e-06 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 0.5942758 0.6670391 sample estimates: mean of x 0.6306575 > t.test(x1) One Sample t-test data: x1 t = 25.612, df = 4, p-value = 1.38e-05 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 2.924442 3.635558 sample estimates: mean of x 3.28</pre>
SAS	
CODE	<pre>data ex13_2; input x1 x2@@; cards; 3.1 7.6 2.9 6.4 3.3 7.5 3.6 6.9 3.5 6.3 ;run; data ex13_2t; set ex13_2; logx1=log10(x1+1); run; proc ttest data=ex13_2t; var logx1; var x1; run;</pre>

OUTPUT

Variable: logx1

N	Mean	Std Dev	Std Err	Minimum	Maximum
5	0.6307	0.0293	0.0131	0.5911	0.6628

Mean	95% CL Mean	Std Dev	95% CL Std Dev
0.6307	0.5943 0.6670	0.0293	0.0176 0.0842

Variable: x1

N	Mean	Std Dev	Std Err	Minimum	Maximum
5	3.2800	0.2864	0.1281	2.9000	3.6000

Mean	95% CL Mean	Std Dev	95% CL Std Dev
3.2800	2.9244 3.6356	0.2864	0.1716 0.8229

결과해석

그룹 별 나뭇잎의 길이에 대한 자료를 로그변환을 통해 신뢰구간을 구하였다. 로그변환을 한 후 다시 역변환을 하면 원래 자료의 신뢰구간과 같은 결과가 나온다는 것을 확인할 수 있다.

lambda
?
sas transreg .
https://documentation.sas.com/?docsetId=statug&docsetTarget=statug_transreg_examples02.htm&docsetVersion=15.1&locale=en
<https://www.rdocumentation.org/packages/EnvStats/versions/2.3.1/topics/boxcox>

Example. 13.3

EXAMPLE 13.3 The Square Root Transformation for Poisson Data

Original data (number of parasites in the lungs of 20 frogs allocated to four experimental groups):

	<i>Group 1</i>	<i>Group 2</i>	<i>Group 3</i>	<i>Group 4</i>
	2	6	9	2
	0	4	5	4
	2	8	6	1
	3	2	5	0
	0	4	11	2
\bar{X}_i	1.4	4.8	7.2	1.8
s_i^2	1.8	5.2	7.2	2.2

Transformed data; by Equation 13.2:

	<i>Group 1</i>	<i>Group 2</i>	<i>Group 3</i>	<i>Group 4</i>
	1.581	2.550	3.082	1.581
	0.707	2.121	2.345	2.121
	1.581	2.915	2.550	1.225
	1.871	1.581	2.345	0.707
	0.707	2.121	3.391	1.581
\bar{X}'_i	1.289	2.258	2.743	1.443
$(s_i^2)'$	0.297	0.253	0.222	0.272
$s'_{\bar{X}_i}$	0.244	0.225	0.211	0.233
$(L'_1)_i$	0.612	1.633	2.157	0.796
$(L'_2)_i$	1.966	2.883	3.329	2.090

On transforming back to original units [e.g., $\bar{X} = (\bar{X}')^2 - 0.5$]:

	<i>Group 1</i>	<i>Group 2</i>	<i>Group 3</i>	<i>Group 4</i>
\bar{X}_i	1.2	4.6	7.0	1.6
$(L_1)_i$	-0.1	2.2	4.2	0.1
$(L_2)_i$	3.4	7.8	10.6	3.9

R

CODE

```
#ex13.3
g1=c(2,0,2,3,0)
g2=c(6,4,8,2,4)
g3=c(9,5,6,5,11)
g4=c(2,4,1,0,2)
```

	<pre>g1t=sqrt(g1+0.5) g2t=sqrt(g2+0.5) g3t=sqrt(g3+0.5) g4t=sqrt(g4+0.5) data.frame(g1t,g2t,g3t,g4t)</pre>																																																						
OUTPUT	<pre>> data.frame(g1t,g2t,g3t,g4t) g1t g2t g3t g4t 1 1.5811388 2.549510 3.082207 1.5811388 2 0.7071068 2.121320 2.345208 2.1213203 3 1.5811388 2.915476 2.549510 1.2247449 4 1.8708287 1.581139 2.345208 0.7071068 5 0.7071068 2.121320 3.391165 1.5811388</pre>																																																						
SAS																																																							
CODE	<pre>data ex13_3; input g1 g2 g3 g4 @@; cards; 2 6 9 2 0 4 5 4 2 8 6 1 3 2 5 0 0 4 11 2 ;run; data ex13_3t; set ex13_3; g1t=sqrt(g1+0.5); g2t=sqrt(g2+0.5); g3t=sqrt(g3+0.5); g4t=sqrt(g4+0.5); run; proc print data=ex13_3t; run;</pre>																																																						
OUTPUT	<table><tr><th>OBS</th><th>g1</th><th>g2</th><th>g3</th><th>g4</th><th>g1t</th><th>g2t</th><th>g3t</th><th>g4t</th></tr><tr><td>1</td><td>2</td><td>6</td><td>9</td><td>2</td><td>1.58114</td><td>2.54951</td><td>3.08221</td><td>1.58114</td></tr><tr><td>2</td><td>0</td><td>4</td><td>5</td><td>4</td><td>0.70711</td><td>2.12132</td><td>2.34521</td><td>2.12132</td></tr><tr><td>3</td><td>2</td><td>8</td><td>6</td><td>1</td><td>1.58114</td><td>2.91548</td><td>2.54951</td><td>1.22474</td></tr><tr><td>4</td><td>3</td><td>2</td><td>5</td><td>0</td><td>1.87083</td><td>1.58114</td><td>2.34521</td><td>0.70711</td></tr><tr><td>5</td><td>0</td><td>4</td><td>11</td><td>2</td><td>0.70711</td><td>2.12132</td><td>3.39116</td><td>1.58114</td></tr></table>	OBS	g1	g2	g3	g4	g1t	g2t	g3t	g4t	1	2	6	9	2	1.58114	2.54951	3.08221	1.58114	2	0	4	5	4	0.70711	2.12132	2.34521	2.12132	3	2	8	6	1	1.58114	2.91548	2.54951	1.22474	4	3	2	5	0	1.87083	1.58114	2.34521	0.70711	5	0	4	11	2	0.70711	2.12132	3.39116	1.58114
OBS	g1	g2	g3	g4	g1t	g2t	g3t	g4t																																															
1	2	6	9	2	1.58114	2.54951	3.08221	1.58114																																															
2	0	4	5	4	0.70711	2.12132	2.34521	2.12132																																															
3	2	8	6	1	1.58114	2.91548	2.54951	1.22474																																															
4	3	2	5	0	1.87083	1.58114	2.34521	0.70711																																															
5	0	4	11	2	0.70711	2.12132	3.39116	1.58114																																															
결과해석	4개의 실험군에 배정된 20마리의 개구리들의 폐에서 발견된 기생충의 숫자에 대한 자료에 제곱근 변환을 한 결과이다.																																																						

Example. 13.4

EXAMPLE 13.4 The Arcsine Transformation for Percentage Data

Original data (p , the percentage of insects killed in each of seven groups of insects subjected to one of two insecticides):

<i>Insecticide 1 (%)</i>	<i>Insecticide 2 (%)</i>
84.2	92.3
88.9	95.1
89.2	90.3
83.4	88.6
80.1	92.6
81.3	96.0
85.8	93.7
$\bar{p}_1 = 84.7\%$	$\bar{p}_2 = 92.7\%$
$s_1^2 = 12.29(\%)^2$	$s_2^2 = 6.73(\%)^2$
$s_1 = 3.5\%$	$s_2 = 2.6\%$

Transformed data (by using Equation 13.5 or Appendix Table B.24) (p'):

<i>Insecticide 1 (°)</i>	<i>Insecticide 2 (°)</i>
66.58	73.89
70.54	77.21
70.81	71.85
65.96	70.27
63.51	74.21
64.38	78.46
67.86	75.46
$\bar{p}'_1 = 67.09$	$\bar{p}'_2 = 74.48$
$(s_1^2)' = 8.0052$	$(s_2^2)' = 8.2193$
$s'_1 = 2.83$	$s'_2 = 2.87$
$s'_{\bar{X}_1} = 1.07$	$s'_{\bar{X}_2} = 1.08$

Calculating confidence limits:

$$95\% \text{ confidence interval for } \mu'_1 : \bar{p}'_1 \pm (t_{0.05(2),6})(1.07) = 67.09 \pm 2.62$$

$$L'_1 = 64.47^\circ \text{ and } L'_2 = 69.71^\circ$$

By using Appendix Table B.25 to transform backward from L'_1 , L'_2 , and p'_1 :

95% confidence limits for $\mu_1 : L_1 = 81.5\%$ and $L_2 = 88.0\%$.

$$\bar{p}_1 = 84.9\%$$

R

CODE

#ex13.4

in1=c(84.2,88.9,89.2,83.4,80.1,81.3,85.8)

	<pre> in2=c(92.3,95.1,90.3,88.6,92.6,96,93.7) in1t=asin(sqrt(in1/100))*(180/pi) in2t=asin(sqrt(in2/100))*(180/pi) t.test(in1t) back=(sin(in1t*(pi/180))^2)*100 t.test(back) </pre>
OUTPUT	<pre> > t.test(in1t) One Sample t-test data: in1t t = 62.69, df = 6, p-value = 1.108e-09 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 64.47203 69.70942 sample estimates: mean of x 67.09072 > t.test(back) One Sample t-test data: back t = 63.914, df = 6, p-value = 9.864e-10 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 81.45732 87.94268 sample estimates: mean of x 84.7 </pre>
SAS	
CODE	<pre> data ex13_4; input i1 i2 @@; cards; 84.2 92.3 88.9 95.1 89.2 90.3 83.4 88.6 80.1 92.6 81.3 96 85.8 93.7 ;run; data ex13_4t; set ex13_4; pi=constant("pi"); ari1=arsin(sqrt(i1/100))*180/pi; ari2=arsin(sqrt(i2/100))*180/pi; run; proc print data=ex13_4t; run; proc ttest data=ex13_4t; var ari1; var i1; run; </pre>

OUTPUT	OBS	i1	i2	pi	ari1	ari2
	1	84.2	92.3	3.14159	66.5785	73.8896
	2	88.9	95.1	3.14159	70.5389	77.2111
	3	89.2	90.3	3.14159	70.8141	71.8535
	4	83.4	88.6	3.14159	65.9564	70.2669
	5	80.1	92.6	3.14159	63.5066	74.2149
	6	81.3	96.0	3.14159	64.3778	78.4630
	7	85.8	93.7	3.14159	67.8626	75.4634
	Mean	95% CL Mean		Std Dev	95% CL Std Dev	
	67.0907	64.4720	69.7094	2.8315	1.8246	6.2351
결과해석	Mean	95% CL Mean		Std Dev	95% CL Std Dev	
	84.7000	81.4573	87.9427	3.5062	2.2594	7.7209
	7개의 그룹에 대해 두 종류의 살충제로 죽은 벌레들의 백분율을 나타낸 자료에 역사인 변환을 한 것으로 역사인 변환은 값들이 범위 끝 쪽에 있을 때 사용하는 것은 바람직하지 않다고 알려져 있다.					