

Example.8.4

EXAMPLE 8.4 Estimation of Required Sample Size for a Two-Sample t Test

We desire to test for significant difference between the mean blood-clotting times of persons using two different drugs. We wish to test at the 0.05 level of significance, with a 90% chance of detecting a true difference between population means as small as 0.5 min. The within-population variability, based on a previous study of this type (Example 8.1), is estimated to be 0.52 min^2 .

Let us guess that sample sizes of 100 will be required. Then, $\nu = 2(100 - 1) = 198$, $t_{0.05(2),198} \approx 1.972$, $\beta = 1 - 0.90 = 0.10$, $t_{0.10(1),198} = 1.286$, and we calculate (by Equation 8.22):

$$n \geq \frac{2(0.52)}{(0.5)^2} (1.972 + 1.286)^2 = 44.2.$$

Let us now use $n = 45$ to determine $\nu = 2(n - 1) = 88$, $t_{0.05(2),88} = 1.987$, $t_{0.10(1),88} = 1.291$, and

$$n \geq \frac{2(0.52)}{(0.5)^2} (1.987 + 1.291)^2 = 44.7.$$

Therefore, we conclude that each of the two samples should contain at least 45 data.

If n_1 were constrained to be 30, then, using Equation 8.21, the required n_2 would be

$$n_2 = \frac{(44.7)(30)}{2(30) - 44.7} = 88.$$

R

CODE	<pre> #ex8.4 #method1 size = power.t.test(n=, delta = 0.5, sd = sqrt(0.52), sig.level = 0.05, power = 0.9, type = "two.sample", alternative = "two.sided") size ceiling(size\$n) nn= round(size\$n, 1) n2 = function(n1, n){ n2= ceiling((n*n1)/(2*n1-n)) return(n2) } n2(30, nn) #method2 library(pwr) del=0.5/sqrt(0.52) pwr.t.test(n=, d= del, sig.level = 0.05, power= 0.9, type= "two.sample", alternative = "two.sided") ceiling(pwr.t.test(n=, d= del, sig.level = 0.05, power= 0.9, type= "two.sample", alternative = "two.sided")\$n) n2 = pwr.t2n.test(n1= 30, n2=, d= del, sig.level = 0.05, power= 0.9, alternative = "two.sided") ceiling(n2\$n2) </pre>
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OUTPUT	<pre> > #method1 > size = power.t.test(n=, delta = 0.5, sd = sqrt(0.52), sig.level = 0.05, power = 0.9, ided") > size Two-sample t test power calculation n = 44.69341 delta = 0.5 sd = 0.7211103 sig.level = 0.05 power = 0.9 alternative = two.sided NOTE: n is number in *each* group > ceiling(size\$n) [1] 45 > nn= round(size\$n, 1) > n2 = function(n1, n){ + n2= ceiling((n*n1)/(2*n1-n)) + return(n2) + } > n2(30, nn) [1] 88 > #method2 > library(pwr) > del=0.5/sqrt(0.52) > pwr.t.test(n=, d= del, sig.level = 0.05, power= 0.9, type= "two.sample", alternative = "two.sided") Two-sample t test power calculation n = 44.69342 d = 0.6933752 sig.level = 0.05 power = 0.9 alternative = two.sided NOTE: n is number in *each* group > ceiling(pwr.t.test(n=, d= del, sig.level = 0.05, power= 0.9, type= "two.sample", alternative = "two.sided")\$n) [1] 45 > n2 = pwr.t2n.test(n1= 30, n2=, d= del, sig.level = 0.05, power= 0.9, alternative = "two.sided") > ceiling(n2\$n2) [1] 86 </pre>
SAS	
CODE	<pre> proc power; twosamplemeans meandiff=0.5 stddev= 0.72111 alpha=0.05 power= 0.9 npergroup=.; run; /* n1의 표본 수가 30으로 제한되어 있을 때*/ proc power; twosamplemeans meandiff=0.5 stddev= 0.72111 alpha=0.05 power= 0.9 groupns= 30 .; run; </pre>

while()

[https://
rfriend.tistory.com/90](https://rfriend.tistory.com/90)

OUTPUT	Computed N per Group		Computed N2	
	Actual Power	N per Group	Actual Power	N2
	0.902	45	0.900	86
결과해석	<p>두 가지 약에 따라 혈액이 응고하는 각각의 모평균 시간에 서로 차이가 있는지 검정을 할 때 유의한 결과를 얻기 위해 요구되는 최소 표본 수를 위와 같은 방법으로 구하였더니 각각 최소 45개씩 표본이 필요하다는 것을 알 수 있었다. 만약 집단1에서 구할 수 있는 표본 수가 30개로 제한되어 있다면 집단2에서 요구되는 표본 수는 자연스럽게 더 커질 것이고, 위의 방법을 통해 구해보면 최소 88개의 표본이 필요하다는 것을 알 수 있다. R과 SAS에서 함수를 사용해서 한 집단의 표본 수가 제한되었을 때 다른 집단에서 요구되는 최소 요구 표본 수가 86이 나오는 이유는 공식에 사용되는 n값이 무조건 올림을 사용하기 때문에 약간의 오차가 생긴 것으로 보인다. 따라서 최소 요구되는 표본 수가 86이 나왔지만 말 그대로 유효한 효과를 얻기 위한 최소한의 표본 수이기 때문에 나온 결과보다 실제로 약간 더 많은 수의 표본 수를 선정할 필요가 있다.</p>			

Example.8.5	
<p>EXAMPLE 8.5 Estimation of Minimum Detectable Difference in a Two-Sample t Test</p> <p>In two-tailed testing for significant difference between mean blood-clotting times of persons using two different drugs, we desire to use the 0.05 level of significance and sample sizes of 20. What size difference between means do we have a 90% chance of detecting?</p> <p>Using Equation 8.23 and the sample variance of Example 8.1, we calculate:</p> $\delta = \sqrt{\frac{2(0.5193)}{20}} (t_{0.05(2),38} + t_{0.10(1),38})$ $= (0.2279)(2.024 + 1.304) = 0.76 \text{ min.}$	
R	
CODE	<pre>#ex8.5 dd=power.t.test(n=20, delta =, sd = sqrt(0.52), sig.level = 0.05, power = 0.9, type = "two.sample", alternative = "two.sided") round(dd\$delta, 2)</pre>
OUTPUT	<pre>> #ex8.5 > dd=power.t.test(n=20, delta =, sd = sqrt(0.52), sig.level = 0.05, power = 0.9, type = "two.sample", alternative = "two.sided") > round(dd\$delta, 2) [1] 0.76</pre>
SAS	
CODE	<pre>proc power; twosamplemeans meandiff=, stddev= 0.720624 alpha= 0.05 power= 0.9 ntotal= 40; run;</pre>

OUTPUT	Computed Mean Diff
	Mean Diff
	0.758
결과해석	<p>두 가지 약에 따라 혈액이 응고하는 각각의 모평균 시간에 차이가 있는지 검정을 할 때 0.05의 유의수준과 90%의 검정력 하에서 유의한 정도의 최소 차이값(최소검출차)이 어느정도 되는지 확인해보기 위해 20개의 표본을 가지고 위와 같이 계산해 봤더니 0.76(분)이라는 값이 나왔다. 따라서 표본이 각각 20개씩 주어졌을 때 유의수준 0.05, 검정력 90%하에서 두 약에 따른 혈액응고 모평균 시간의 차이가 0.76까지 유의하다고 할 수 있다. 만약 더 미세한 정도를 확인하고 싶다면 표본 수를 늘려 계산해 볼 수 있다.</p>

Example.8.6	
<p>EXAMPLE 8.6 Estimation of the Power of a Two-Sample t Test</p> <p>What would be the probability of detecting a true difference of 1.0 min between mean blood-clotting times of persons using the two drugs of Example 8.1, if $n_1 = n_2 = 15$, and $\alpha(2) = 0.05$?</p> <p>For $n = 15$, $\nu = 2(n - 1) = 28$ and $t_{0.05(2),28} = 2.048$. Using Equation 8.24:</p> $t_{\beta(1),28} \leq \frac{1.0}{\sqrt{\frac{2(0.5193)}{15}}} - 2.048 = 1.752.$ <p>Consulting Appendix Table B.3, we see that, for one-tailed probabilities and $\nu = 28$: $0.025 < P(t \geq 1.752) < 0.05$, so $0.025 < \beta < 0.05$.</p> <p>Power = $1 - \beta$, so $0.95 < \text{power} < 0.975$.</p> <p>Or, by the normal approximation, we can estimate β by $P(Z \geq 1.752) = 0.04$. So power = 0.96. [The exact figures are $\beta = 0.045$ and power = 0.955.]</p> <p>To use Appendix Figure B.1, we calculate</p> $\phi = \sqrt{\frac{n\delta^2}{4s_p^2}} = \sqrt{\frac{(15)(1.0)}{4(0.5193)}} = 2.69.$ <p>In the first page of Appendix Figure B.1, we find that $\phi = 2.69$ and $\nu (= \nu_2) = 28$ are associated with a power of about 0.96.</p>	
R	
CODE	<pre>#ex8.6 power.t.test(n=15, delta = 1, sd = sqrt(0.52), sig.level = 0.05, power = , type = "two.sample", alternative = "two.sided") # 정규근사를 이용한 power구하기 na = function(n, d,alpha, sp){ v = 2*(n-1) tb = round(d/sqrt(2*sp/n)- qt(alpha/2,v, lower.tail = F),3) z = pnorm(tb) return(z) } na(15,1,0.05,0.5193) # phi</pre>

	<pre>ps = function(n, d, sp){ v = 2*(n -1) phi= round(sqrt((n*d^2)/(4*sp)),2) return(phi) } ps(15,1,0.5193)</pre>			
OUTPUT	<pre>> #ex8.6 > power.t.test(n=15, delta = 1, sd = sqrt(0.52), sig.level = 0.05, power = 0.9558658) Two-sample t test power calculation n = 15 delta = 1 sd = 0.7211103 sig.level = 0.05 power = 0.9558658 alternative = two.sided NOTE: n is number in *each* group > # 정규근사를 이용한 power구하기 > na = function(n, d,alpha, sp){ + v = 2*(n-1) + tb = round(d/sqrt(2*sp/n)- qt(alpha/2,v, lower.tail = F),3) + z = pnorm(tb) + return(z) + } > na(15,1,0.05,0.5193) [1] 0.9601131 > # phi > ps = function(n, d, sp){ + v = 2*(n -1) + phi= round(sqrt((n*d^2)/(4*sp)),2) + return(phi) + } > ps(15,1,0.5193) [1] 2.69</pre>			
SAS				
CODE	<pre>proc power; twosamplemeans meandiff=1 stddev= 0.720624 alpha= 0.05 power= . ntotal= 30; run;</pre>			
OUTPUT	<table><tr><th>Computed Power</th></tr><tr><th>Power</th></tr><tr><td>0.956</td></tr></table>	Computed Power	Power	0.956
Computed Power				
Power				
0.956				
결과해석	위의 예제는 최소검출차가 1, 각 표본의 표본 수가 15개씩 주어졌을 때 유의수준 0.05 하에서의 검정력을 확인해보는 과정이다. 계산되어 나온 검정력 값은 약 0.96으로 두 가			

지 약물에 따른 모평균 혈액 응고시간의 차이를 확인해보기 위해 최소검출차를 1로 설정하고 표본 수를 각각 15개씩 추출했을 때 추정한 검정력이 0.96이라는 의미이다. 다른 방법으로 정규 근사를 시켜 계산할 수도 있고, 아래의 방법처럼 ϕ 값을 계산하여 그래프에서 찾아 검정력을 확인해볼 수도 있다.

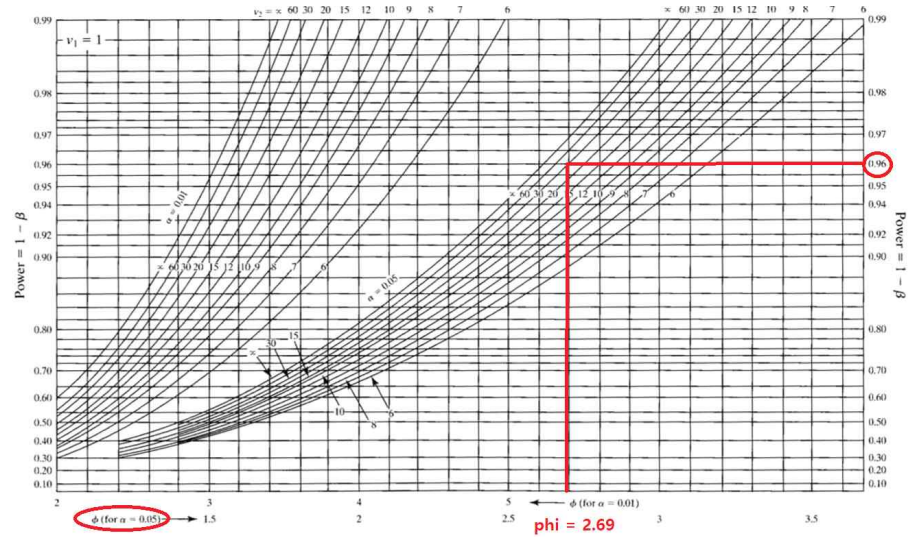


FIGURE B.1a: Power and sample size in analysis of variance; $\nu_1 = 1$.

Note: In this figure (for $\nu_1 = 1$), the curves for $\alpha = 0.05$ and $\alpha = 0.01$ are positioned the reverse of what they are in Figures B.1b–1h.

Example.8.7

EXAMPLE 8.7 The Two-Tailed Variance Ratio Test for the Hypothesis $H_0: \sigma_1^2 = \sigma_2^2$ and $H_A: \sigma_1^2 \neq \sigma_2^2$. The Data Are the Numbers of Moths Caught During the Night by 11 Traps of One Style and 10 Traps of a Second Style

$$H_0: \sigma_1^2 = \sigma_2^2$$

$$H_A: \sigma_1^2 \neq \sigma_2^2$$

$$\alpha = 0.05$$

Trap type 1	Trap type 2
41	52
35	57
33	62
36	55
40	64
46	57
31	56
37	55
34	60
30	59
38	

$$n_1 = 11$$

$$n_2 = 10$$

$$v_1 = 10$$

$$v_2 = 9$$

$$SS_1 = 218.73 \text{ moths}^2$$

$$SS_2 = 116.10 \text{ moths}^2$$

$$s_1^2 = 21.87 \text{ moths}^2$$

$$s_2^2 = 12.90 \text{ moths}^2$$

$$F = \frac{s_1^2}{s_2^2} = \frac{21.87}{12.90} = 1.70$$

$$F_{0.05(2),10,9} = 3.96$$

Therefore, do not reject H_0 .

$$P(0.20 < F < 0.50) [P = 0.44]$$

$$s_p^2 = \frac{218.73 \text{ moths}^2 + 116.10 \text{ moths}^2}{10 + 9} = 17.62 \text{ moths}^2$$

The conclusion is that the variance of numbers of moths caught is the same for the two kinds of traps.

R

CODE

```
# ex8.7
trap1 = c(41, 35, 33, 36, 40, 46, 31, 37, 34, 30, 38)
trap2 = c(52, 57, 62, 55, 64, 57, 56, 55, 60, 59)

# method1
vartest= function(x, y, alpha){
  v1= length(x)-1
  v2= length(y)-1
  s1= var(x)
  s2= var(y)
  if (s1 > s2){
    f= round(s1/s2,2)
  }
  else if (s1 < s2){
    f= round(s2/s1,2)
  }
}
```


	<pre> } fp = qf(alpha/2, v1, v2, lower.tail = F) if (f > fp){ answer= (c("reject H0", "sp=" (s1*v1+s2*v2)/(v1+v2))) } else if (f <= fp){ answer= ("cannot reject H0") } pv= round(pf(f,v1,v2, lower.tail = F)*2,2) return(c(answer, pv)) } vartest(trap1, trap2, 0.05) # method2 var.test(trap1, trap2) </pre>
OUTPUT	<pre> > # ex8.7 > trap1 = c(41, 35, 33, 36, 40, 46, 31, 37, 34, 30, 38) > trap2 = c(52, 57, 62, 55, 64, 57, 56, 55, 60, 59) > # method1 > vartest= function(x, y, alpha){ + v1= length(x)-1 + v2= length(y)-1 + s1= var(x) + s2= var(y) + if (s1 > s2){ + f= round(s1/s2,2) + } + else if (s1 < s2){ + f= round(s2/s1,2) + } + fp = qf(alpha/2, v1, v2, lower.tail = F) + if (f > fp){ + answer= (c("reject H0", "sp=" (s1*v1+s2*v2)/(v1+v2))) + } + else if (f <= fp){ + answer= ("cannot reject H0") + } + pv= round(pf(f,v1,v2, lower.tail = F)*2,2) + return(c(answer, pv)) + } > vartest(trap1, trap2, 0.05) [1] "cannot reject H0" "0.44" </pre>

	<pre>> # method2 > var.test(trap1, trap2) F test to compare two variances data: trap1 and trap2 F = 1.6956, num df = 10, denom df = 9, p-value = 0.4401 alternative hypothesis: true ratio of variances is not equal to 1 95 percent confidence interval: 0.4277543 6.4074588 sample estimates: ratio of variances 1.69556</pre>															
SAS																
CODE	<pre>data ex8_7; input type\$ number@@; cards; 1 41 1 35 1 33 1 36 1 40 1 46 1 31 1 37 1 34 1 30 1 38 2 52 2 57 2 62 2 55 2 64 2 57 2 56 2 55 2 60 2 59 ; run; proc ttest data= ex8_7; class type; var number; run;</pre>															
OUTPUT	<table><tr><th colspan="5">Equality of Variances</th></tr><tr><th>Method</th><th>Num DF</th><th>Den DF</th><th>F Value</th><th>Pr > F</th></tr><tr><td>Folded F</td><td>10</td><td>9</td><td>1.70</td><td>0.4401</td></tr></table>	Equality of Variances					Method	Num DF	Den DF	F Value	Pr > F	Folded F	10	9	1.70	0.4401
Equality of Variances																
Method	Num DF	Den DF	F Value	Pr > F												
Folded F	10	9	1.70	0.4401												
결과해석	<p>덧의 종류에 따라 밤에 잡히는 나방의 수의 산포가 다른지 확인하기 위해 분산비 검정을 실행하였다.</p> <p>귀무가설: 덧의 종류에 따라 덧에 걸리는 나방의 수의 모분산이 같다.</p> <p>대립가설: 덧의 종류에 따라 덧에 걸리는 나방의 수의 모분산에 차이가 있다.</p> <p>분산비 검정을 수행한 결과 p-value가 0.4401로 귀무가설을 기각할 충분한 증거가 되지 못한다. 따라서 현재까지는 덧의 종류에 상관없이 잡히는 나방의 수의 산포가 다르다고 밝히지 못했기 때문에 비슷하다고 판단할 수 있다.</p>															

가 . , 가 .

Example.8.8

EXAMPLE 8.8 A One-Tailed Variance-Ratio Test for the Hypothesis That the Germination Time for Pine Seeds Planted in a Greenhouse Is Less Variable Than for Pine Seeds Planted Outside

$$H_0: \sigma_1^2 \geq \sigma_2^2$$

$$H_A: \sigma_1^2 < \sigma_2^2$$

$$\alpha = 0.05$$

**Germination Time (in Days)
of Pine Seeds**

Greenhouse	Outside
69.3	69.5
75.5	64.6
81.0	74.0
74.7	84.8
72.3	76.0
78.7	93.9
76.4	81.2
	73.4
	88.0
$n_1 = 7$	$n_2 = 9$
$\nu_1 = 6$	$\nu_2 = 8$
$SS_1 = 90.57 \text{ days}^2$	$SS_2 = 700.98 \text{ days}^2$
$s_1^2 = 15.10 \text{ days}^2$	$s_2^2 = 87.62 \text{ days}^2$

$$F = \frac{87.62}{15.10} = 5.80$$

$$F_{0.05(1),8,6} = 4.15$$

Therefore, reject H_0 .

$$0.01 < P(F \geq 5.80) < 0.025 \quad [P = 0.023]$$

The conclusion is that the variance in germination time is less in plants grown in the greenhouse than in those grown outside.

R

CODE

```
# ex8.8
house= c(69.3,75.5,81,74.7,72.3,78.7,76.4)
out= c(69.5,64.6,74,84.8,76,93.9,81.2,73.4,88)
# method1
vartest= function(x, y, alpha){
  v1= length(x)-1
  v2= length(y)-1
  s1= var(x)
  s2= var(y)
  f= round(s2/s1,2)
  fp= qf(0.05,v2,v1, lower.tail = F)
  if (f > fp){
    answer= ("reject H0")
  }
  else if (f <= fp){
    answer= ("cannot reject H0")
  }
}
```

	<pre> } pv= round(pf(f, 8,6, lower.tail = F), 3) return(c(answer, pv)) } vartest(house, out, 0.05) # method2 var.test(house, out, alternative = "less") </pre>
OUTPUT	<pre> > # ex8.8 > house= c(69.3,75.5,81,74.7,72.3,78.7,76.4) > out= c(69.5,64.6,74,84.8,76,93.9,81.2,73.4,88) > # method1 > vartest= function(x, y, alpha){ + v1= length(x)-1 + v2= length(y)-1 + s1= var(x) + s2= var(y) + f= round(s2/s1,2) + fp= qf(0.05,8,6, lower.tail = F) + if (f > fp){ + answer= ("reject H0") + } + else if (f <= fp){ + answer= ("cannot reject H0") + } + pv= round(pf(f, 8,6, lower.tail = F), 3) + return(c(answer, pv)) + } > vartest(house, out, 0.05) [1] "reject H0" "0.023" > # method2 > var.test(house, out, alternative = "less") F test to compare two variances data: house and out F = 0.17227, num df = 6, denom df = 8, p-value = 0.02293 alternative hypothesis: true ratio of variances is less than 1 95 percent confidence interval: 0.0000000 0.7143761 sample estimates: ratio of variances 0.1722715 </pre>
SAS	
CODE	<pre> data ex8_8; input place\$ time@@; cards; H 69.3 H 75.5 H 81 H 74.7 H 72.3 H 78.7 H 76.4 O 69.5 O 64.6 O 74 O 84.8 O 76 O 93.9 O 81.2 O 73.4 O 88 ; run; </pre>

	<pre>proc ttest data= ex8_8; class place; var time; run;</pre>															
OUTPUT	<table><tr><th colspan="5">Equality of Variances</th></tr><tr><th>Method</th><th>Num DF</th><th>Den DF</th><th>F Value</th><th>Pr > F</th></tr><tr><td>Folded F</td><td>8</td><td>6</td><td>5.80</td><td>0.0459</td></tr></table>	Equality of Variances					Method	Num DF	Den DF	F Value	Pr > F	Folded F	8	6	5.80	0.0459
Equality of Variances																
Method	Num DF	Den DF	F Value	Pr > F												
Folded F	8	6	5.80	0.0459												
결과해석	<p>소나무의 씨앗이 발아하는데 걸리는 시간의 산포가 온실에서 키울 때보다 밖에서 키울 때 더 큰지 확인하기 위해 분산비 검정을 실시하였다.</p> <p>귀무가설: 온실에서 소나무를 키우는 것이 밖에서 키울 때 씨앗이 발아하는데 걸리는 시간의 모분산이 더 크거나 같다.</p> <p>대립가설: 밖에서 키우는 것이 온실에서 키울 때보다 소나무 씨가 발아하는데 걸리는 시간의 모분산이 더 크다.</p> <p>검정결과 p-value가 0.023 정도로 어느정도 유의하게 나와 귀무가설을 기각할 수 있다. 따라서 밖에서 키울 때 소나무 씨앗의 발아 시간의 모분산이 더 크다고 판단할 수 있다. SAS에서는 양측검정을 했을 때의 p-value 값이므로 F분포에서 단측검정일 때의 p-value 값은 양측검정의 절반이므로 0.0459를 2로 나눠줘야 한다.</p>															

http://blog.daum.net/_blog/BlogTypeView.do?blogid=0J0n6&articleno=6240787

Example.8.9

EXAMPLE 8.9 The Two-Sample Levene Test for $H_0: \sigma_1^2 = \sigma_2^2$ and $H_A: \sigma_1^2 \neq \sigma_2^2$. The Data Are Those of Example 8.7

$$H_0: \sigma_1^2 = \sigma_2^2$$

$$H_A: \sigma_1^2 \neq \sigma_2^2$$

$$\alpha = 0.05$$

For group 1: $\Sigma X = 401$ moths, $n = 11$, $\nu = 10$, $\bar{X} = 36.45$ moths.

For group 2: $\Sigma X = 577$ moths, $n = 10$, $\nu = 9$, $\bar{X} = 57.70$ moths.

Trap Type 1		Trap Type 2	
X_i	$X'_i = X_i - \bar{X} $	X_i	$X'_i = X_i - \bar{X} $
41	4.55	52	5.70
35	1.45	57	0.70
33	3.45	62	4.30
36	0.45	55	2.70
40	3.55	64	6.30
46	9.55	57	0.70
31	5.45	56	1.70
37	0.55	55	2.70
34	2.45	60	2.30
30	6.45	59	1.30
38	1.55		
$\Sigma X'_i =$		$\Sigma X'_i =$	
ΣX_i	$\Sigma X_i - \bar{X} $	ΣX_i	$\Sigma X_i - \bar{X} $
= 401 moths	= 39.45 moths	= 577 moths	= 28.40 moths

For the absolute values of the deviations from the mean:

$$X'_1 = 39.45 \text{ moths}/11 \quad X'_2 = 28.40 \text{ moths}/10$$

$$= 3.59 \text{ moths} \quad = 2.84 \text{ moths}$$

$$SS'_1 = 77.25 \text{ moths}^2 \quad SS'_2 = 35.44 \text{ moths}^2$$

$$(s_p^2)' = \frac{77.25 \text{ moths}^2 + 35.44 \text{ moths}^2}{10 + 9} = 5.93 \text{ moths}^2$$

$$s'_{\bar{X}_1 - \bar{X}_2} = \sqrt{\frac{5.93 \text{ moths}^2}{11} + \frac{5.93 \text{ moths}^2}{10}} = 1.06 \text{ moths}$$

$$t' = \frac{3.59 \text{ moths} - 2.84 \text{ moths}}{1.06 \text{ moths}} = 0.71$$

$$t_{0.05(2),19} = 2.093$$

Therefore, do not reject H_0 .

$$0.02 < P < 0.50 \quad [P = 0.48]$$

We conclude that the variance of the numbers of moths caught is the same using either kind of trap.

R

CODE

```
# ex8.9
trap1 = c(41, 35, 33, 36, 40, 46, 31, 37, 34, 30, 38)
trap2 = c(52, 57, 62, 55, 64, 57, 56, 55, 60, 59)
# method1
levenetest= function(x, y, alpha){
  n1= length(x)
```

```

n2= length(y)
v1= n1-1
v2= n2-1
xp= round(abs(x-mean(x)),2)
xb= round(mean(xp),2)
yp= round(abs(y-mean(y)),2)
yb= round(mean(yp),2)
ss1= round(sum(xp^2)-(sum(xp))^2/n1,2)
ss2= round(sum(yp^2)-(sum(yp))^2/n2,2)
sp= (ss1+ss2)/(v1+v2)
ssp= round(sqrt(sp/n1+sp/n2),2)
t= (xb-yb)/ssp
tp= round(qt(alpha/2, v1+v2, lower.tail = F),3)
if (abs(t)>tp){
  answer= "reject H0"
}
else if (abs(t)<tp){
  answer= "cannot reject H0"
}
pv= round(pt(t,v1+v2,lower.tail = F)*2,2)
return(c(answer, pv))
}
levenetest(trap1, trap2, 0.05)

# method2
library(lawstat)
time= c(41, 35, 33, 36, 40, 46, 31, 37, 34, 30, 38, 52, 57, 62, 55, 64, 57, 56,
55, 60, 59)
trap= c( 1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2)
levene.test(time,trap, location="mean")

```

OUTPUT	<pre> > # method1 > levenetest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + v1= n1-1 + v2= n2-1 + xp= round(abs(x-mean(x)),2) + xb= round(mean(xp),2) + yp= round(abs(y-mean(y)),2) + yb= round(mean(yp),2) + ss1= round(sum(xp^2)-(sum(xp))^2/n1,2) + ss2= round(sum(yp^2)-(sum(yp))^2/n2,2) + sp= (ss1+ss2)/(v1+v2) + ssp= round(sqrt(sp/n1+sp/n2),2) + t= (xb-yb)/ssp + tp= round(qt(alpha/2, v1+v2, lower.tail = F),3) + if (abs(t)>tp){ + answer= "reject H0" + } + else if (abs(t)<tp){ + answer= "cannot reject H0" + } + pv= round(pt(t,v1+v2,lower.tail = F)*2,2) + return(c(answer, pv)) + } > levenetest(trap1, trap2, 0.05) [1] "cannot reject H0" "0.49" > # method2 > library(lawstat) > time= c(41, 35, 33, 36, 40, 46, 31, 37, 34, 30, 38, 52, 57, 62, 55, 64, 57, 56, 55, 60, 59) > trap= c(1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2) > levene.test(time,trap, location="mean") Classical Levene's test based on the absolute deviations from the mean (none not applied because the location is not set to median) data: time Test Statistic = 0.49267, p-value = 0.4913 </pre>
SAS	
CODE	<pre> data ex8_9; input type\$ number@@; cards; 1 41 1 35 1 33 1 36 1 40 1 46 1 31 1 37 1 34 1 30 1 38 2 52 2 57 2 62 2 55 2 64 2 57 2 56 2 55 2 60 2 59 ; run; proc glm data= ex8_9; class type; model number = type ; means type/ HOVTEST= levene (type=abs); run; </pre>
OUTPUT	

Example.8.10

EXAMPLE 8.10 A Two-Tailed Test for Difference Between Two Coefficients of Variation

H_0 : The intrinsic variability of male weights is the same as the intrinsic variability of male heights (i.e., the population coefficients of variation of weight and height are the same, namely $H_0: \sigma_1/\mu_1 = \sigma_2/\mu_2$).

H_0 : The intrinsic variability of male weight is not the same as the intrinsic variability of male heights (i.e., the population coefficients of variation of weight and height are not the same, namely $H_0: \sigma_1/\mu_1 \neq \sigma_2/\mu_2$).

(a) The variance-ratio test.

Weight (kg)	Log of weight	Height (cm)	Log of height
72.5	1.86034	183.0	2.26245
71.7	1.85552	172.3	2.23629
60.8	1.78390	180.1	2.25551
63.2	1.80072	190.2	2.27921
71.4	1.85370	191.4	2.28194
73.1	1.86392	169.6	2.22943
77.9	1.89154	166.4	2.22115
75.7	1.87910	177.6	2.24944
72.0	1.85733	184.7	2.26647
69.0	1.83885	187.5	2.27300
		179.8	2.25479

$$n_1 = 10$$

$$n_2 = 11$$

$$\nu_1 = 9$$

$$\nu_2 = 10$$

$$\bar{X}_1 = 70.73 \text{ kg}$$

$$\bar{X}_2 = 180.24 \text{ cm}$$

$$SS_1 = 246.1610 \text{ kg}^2$$

$$SS_2 = 678.9455 \text{ cm}^2$$

$$s_1^2 = 27.3512 \text{ kg}^2$$

$$s_2^2 = 67.8946 \text{ cm}^2$$

$$s_1 = 5.23 \text{ kg}$$

$$s_2 = 8.24 \text{ cm}$$

$$V_1 = 0.0739$$

$$V_2 = 0.0457$$

$$(SS_{\log})_1 = 0.00987026$$

$$(SS_{\log})_2 = 0.00400188$$

$$(s_{\log}^2)_1 = 0.0010967$$

$$(s_{\log}^2)_2 = 0.00040019$$

$$F = \frac{0.0010967}{0.00040019} = 2.74$$

$$F_{0.05(2),9,10} = 3.78$$

Therefore, do not reject H_0 .

$$0.10 < P < 0.20 \quad [P = 0.13]$$

It is concluded that the coefficient of variation is the same for the population of weights as it is for the population of heights.

(b) The Z test.

$$V_p = \frac{\nu_1 V_1 + \nu_2 V_2}{\nu_1 + \nu_2} = \frac{9(0.0739) + 10(0.0457)}{9 + 10} = \frac{1.1221}{19} = 0.0591$$

$$V_p^2 = 0.003493$$

$$Z = \frac{V_1 - V_2}{\sqrt{\left(\frac{V_p^2}{\nu_1} + \frac{V_p^2}{\nu_2}\right)(0.5 + V_p^2)}}$$

$$= \frac{0.0739 - 0.0457}{\sqrt{\left(\frac{0.003493}{9} + \frac{0.003493}{10}\right)(0.5 + 0.003493)}}$$

$$= \frac{0.0282}{0.0193} = 1.46$$

$$Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$$

Do not reject H_0 .

$$0.10 < P < 0.20 \quad [P = 0.14]$$

It is concluded that the coefficient of variation is the same for the population of weights as it is for the population of heights.

R

CODE

```
# ex8.10
weight=c(72.5, 71.7, 60.8, 63.2, 71.4, 73.1, 77.9, 75.7, 72, 69)
height=c(183, 172.3, 180.1, 190.2, 191.4, 169.6, 166.4, 177.6, 184.7, 187.5,
179.8)

# 8.10a
vratiotest= function(x, y, alpha){
  n1= length(x)
  n2= length(y)
  v1= n1-1
  v2= n2-1
  logx= log10(x)
  logy= log10(y)
  ss1= round(sum(logx^2)-(sum(logx))^2/n1,2)
  ss2= round(sum(logy^2)-(sum(logy))^2/n2,2)
  vlogx= var(logx)
  vlogy= var(logy)
  f= round(vlogx/vlogy,2)
  fp = qf(alpha/2, 9, 10, lower.tail = F)
  if (f> fp){
    answer= "reject H0"
  }
  else if (f <= fp){
    answer= "cannot reject H0"
  }
  pv= round(pf(2.74, 9, 10, lower.tail = F)*2,2)
  return(c(answer,pv))
}
vratiotest(weight, height, 0.05)

# 8.10b
coeftest= function(x, y, alpha){
  n1= length(x)
  n2= length(y)
```

	<pre> v1= n1-1 v2= n2-1 cf1= sd(x)/mean(x) cf2= sd(y)/mean(y) vp= round((v1*cf1+v2*cf2)/(v1+v2),4) vps= round(vp^2,6) z= round((cf1-cf2)/sqrt((vps/v1+vps/v2)*(0.5+vps)),2) zp= qnorm(alpha/2, lower.tail = F) if (abs(z)> zp){ answer= "reject H0" } else if (abs(z) <= zp){ answer= "cannot reject H0" } pv= round(pnorm(z, lower.tail = F)*2,2) return(c(answer, pv)) } coeftest(weight, height, 0.05) # method2 install.packages("Zar5", repos="http://R-Forge.R-project.org") library("Zar5") CV.test(weight, height, test = "F") CV.test(weight, height, test = "Z") </pre>
OUTPUT	<pre> > # 8.10a > vrtiotest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + v1= n1-1 + v2= n2-1 + logx= log10(x) + logy= log10(y) + ss1= round(sum(logx^2)-(sum(logx))^2/n1,2) + ss2= round(sum(logy^2)-(sum(logy))^2/n2,2) + vlogx= var(logx) + vlogy= var(logy) + f= round(vlogx/vlogy,2) + fp = qf(alpha/2, 9, 10, lower.tail = F) + if (f> fp){ + answer= "reject H0" + } + else if (f <= fp){ + answer= "cannot reject H0" + } + pv= round(pf(2.74, 9, 10, lower.tail = F)*2,2) + return(c(answer,pv)) + } > vrtiotest(weight, height, 0.05) [1] "cannot reject H0" "0.13" ~ </pre>

```

> # 8.10b
> coeftest= function(x, y, alpha){
+   n1= length(x)
+   n2= length(y)
+   v1= n1-1
+   v2= n2-1
+   cf1= sd(x)/mean(x)
+   cf2= sd(y)/mean(y)
+   vp= round((v1*cf1+v2*cf2)/(v1+v2),4)
+   vps= round(vp^2,6)
+   z= round((cf1-cf2)/sqrt((vps/v1+vps/v2)*(0.5+vps)),2)
+   zp= qnorm(alpha/2, lower.tail = F)
+   if (abs(z)> zp){
+     answer= "reject H0"
+   }
+   else if (abs(z) <= zp){
+     answer= "cannot reject H0"
+   }
+   pv= round(pnorm(z, lower.tail = F)*2,2)
+   return(c(answer, pv))
+ }
> coeftest(weight, height, 0.05)
[1] "cannot reject H0" "0.14"
> CV.test(weight, height, test = "F")
$cv1
[1] 0.0739409

$cv2
[1] 0.04571672

$test
[1] "F"

$test.stat
[1] 2.740064

$p
[1] 0.132194

attr(,"class")
[1] "CV.test"

```

	<pre>> CV.test(weight, height, test = "z") \$cv1 [1] 0.0739409 \$cv2 [1] 0.04571672 \$test [1] "z" \$test.stat [1] 1.465159 \$p [1] 0.1428775 attr(,"class") [1] "CV.test"</pre>															
SAS																
CODE	<pre>data ex8_10; input wh\$ nb@@; cards; w 72.5 w 71.7 w 60.8 w 63.2 w 71.4 w 73.1 w 77.9 w 75.7 w 72 w 69 h 183 h 172.3 h 180.1 h 190.2 h 191.4 h 169.6 h 166.4 h 177.6 h 184.7 h 187.5 h 179.8 ; run; proc ttest data= ex8_10 dist= lognormal; class wh; var nb; run;</pre>															
OUTPUT	<table><tr><th colspan="5">Equality of Variances</th></tr><tr><th>Method</th><th>Num DF</th><th>Den DF</th><th>F Value</th><th>Pr > F</th></tr><tr><td>Folded F</td><td>9</td><td>10</td><td>2.74</td><td>0.1322</td></tr></table>	Equality of Variances					Method	Num DF	Den DF	F Value	Pr > F	Folded F	9	10	2.74	0.1322
Equality of Variances																
Method	Num DF	Den DF	F Value	Pr > F												
Folded F	9	10	2.74	0.1322												
결과해석	<p>남성의 몸무게의 변동성과 키의 변동성의 정도의 차이가 있는지 알아보기 위해 변동계수 검정을 실행하였다.</p> <p>귀무가설: 남성의 몸무게의 변동성과 키의 변동성의 정도에 차이가 없다.(키와 몸무게의 모변동계수가 서로 같다.)</p> <p>대립가설: 남성의 몸무게의 변동성과 키의 변동성의 정도에 차이가 있다.(키와 몸무게의 모변동계수가 서로 다르다.)</p> <p>검정결과 p-value가 0.13 정도로 유의하지 않게 나와 귀무가설을 기각할 수 없다. 따라서 모집단 남성의 몸무게의 변동성과 키의 변동성의 정도의 차이가 있다고 볼 수는 없다.</p>															

Example.8.11

EXAMPLE 8.11 The Mann-Whitney Test for Nonparametric Testing of the Two-Tailed Null Hypothesis That There Is No Difference Between the Heights of Male and Female Students

H_0 : Male and female students are the same height.

H_A : Male and female students are not the same height.

$\alpha = 0.05$

Heights of males	Heights of females	Ranks of male heights	Ranks of female heights
193 cm	178 cm	1	6
188	173	2	8
185	168	3	10
183	165	4	11
180	163	5	12
175		7	
170		9	
$n_1 = 7$	$n_2 = 5$	$R_1 = 31$	$R_2 = 47$

$$\begin{aligned}
 U &= n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1 \\
 &= (7)(5) + \frac{(7)(8)}{2} - 31 \\
 &= 35 + 28 - 31 \\
 &= 32
 \end{aligned}$$

$$\begin{aligned}
 U' &= n_1 n_2 - U \\
 &= (7)(5) - 32 \\
 &= 3
 \end{aligned}$$

$$U_{0.05(2),7,5} = U_{0.05(2),5,7} = 30$$

As $32 > 30$, H_0 is rejected.

$$0.01 < P(U \geq 32 \text{ or } U' \leq 3) < 0.02 \quad [P = 0.018]^*$$

Therefore, we conclude that height is different for male and female students.

R

CODE

```
# ex8.11
male= c(193,188,185,183,180,175,170)
female= c(178,173,168,165,163)
mwtest= function(x, y, alpha){
  n1= length(x)
  n2= length(y)
  nr= n1+1
  nn= n1+n2
  rk=rank(-c(x, y), ties.method="average")
  rk
  xrank=rk[1:length(x)]
  yrank=rk[nr:nn]
  r1= sum(xrank)
  r2= sum(yrank)
  u= n1*n2+ n1*(n1+1)/2 - r1
  up= n1*n2 - u
```


	<pre> pu= qwilcox(alpha/2, n1, n2, lower.tail = F)+1 if(max(u, up)>pu){ answer= "reject H0" } else if(max(u, up)<=pu){ answer= "cannot reject H0" } pv= round(pwilcox(u-1, n1,n2, lower.tail = F)+pwilcox(up,n1,n2, lower.tail = T),3) return(c(answer,pv)) } mwtest(male, female, 0.05) # method2 wilcox.test(male, female) </pre>
OUTPUT	<pre> > # ex8.11 > male= c(193,188,185,183,180,175,170) > female= c(178,173,168,165,163) > mwtest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + nr= n1+1 + nn= n1+n2 + rk=rank(-c(x, y), ties.method="average") + rk + xrank=rk[1:length(x)] + yrank=rk[nr:nn] + r1= sum(xrank) + r2= sum(yrank) + u= n1*n2+ n1*(n1+1)/2 - r1 + up= n1*n2 - u + pu= qwilcox(alpha/2, n1, n2, lower.tail = F)+1 + if(max(u, up)>pu){ + answer= "reject H0" + } + else if(max(u, up)<=pu){ + answer= "cannot reject H0" + } + pv= round(pwilcox(u-1, n1,n2, lower.tail = F)+pwilcox(up,n1,n2, lower.tail = T),3) + return(c(answer,pv)) + } > mwtest(male, female, 0.05) [1] "reject H0" "0.018" > # method2 > wilcox.test(male, female) wilcoxon rank sum test data: male and female W = 32, p-value = 0.01768 alternative hypothesis: true location shift is not equal to 0 </pre>
SAS	
CODE	<pre> data ex8_11; input sex\$ height freq@@; cards; m 193 1 m 188 1 m 185 1 m 183 1 m 180 1 m 175 1 m 170 1 f 178 1 f 173 1 f 168 1 f 165 1 f 163 1 ; </pre>

	<pre> run; proc npar1way data= ex8_11 wilcoxon correct=no; class sex; var height; freq freq; run; </pre>																						
OUTPUT	<table border="1"> <thead> <tr> <th colspan="2">Wilcoxon Two-Sample Test</th> </tr> </thead> <tbody> <tr> <td>Statistic</td><td>18.0000</td> </tr> <tr> <td></td><td></td> </tr> <tr> <td>Normal Approximation</td><td></td> </tr> <tr> <td>Z</td><td>-2.3548</td> </tr> <tr> <td>One-Sided Pr < Z</td><td>0.0093</td> </tr> <tr> <td>Two-Sided Pr > Z </td><td>0.0185</td> </tr> <tr> <td></td><td></td> </tr> <tr> <td>t Approximation</td><td></td> </tr> <tr> <td>One-Sided Pr < Z</td><td>0.0191</td> </tr> <tr> <td>Two-Sided Pr > Z </td><td>0.0382</td> </tr> </tbody> </table> <p style="text-align: center;">Distribution of Wilcoxon Scores for height</p>	Wilcoxon Two-Sample Test		Statistic	18.0000			Normal Approximation		Z	-2.3548	One-Sided Pr < Z	0.0093	Two-Sided Pr > Z	0.0185			t Approximation		One-Sided Pr < Z	0.0191	Two-Sided Pr > Z	0.0382
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Two-Sided Pr > Z	0.0382																						
결과해석	<p>남학생과 여학생의 키의 분포에 차이가 있는지 확인해보려고 한다. 그러나 표본 수가 너무 적어 정규성을 만족하지 못한다는 판단을 하여 비모수 검정 방법인 맨-휘트니 검정을 실시하였다.</p> <p>귀무가설: 남학생과 여학생 모집단의 키의 분포는 서로 같다.</p>																						

	<p>대립가설: 남학생과 여학생 모집단의 키의 분포는 서로 다르다.</p> <p>검정 결과 p-value가 약 0.018정도로 유의한 값을 얻었다. 따라서 귀무가설을 기각하는 판단을 하여 남학생과 여학생 모집단의 키의 분포 서로 다르다고 결론을 내릴 수 있다. SAS에서 나온 결과 중 상자그림에서도 확인할 수 있듯이 두 집단의 범위가 전혀 겹치지 않는다는 것을 확인할 수 있다.</p>
--	--

Example.8.12

EXAMPLE 8.12 The One-Tailed Mann-Whitney Test Used to Determine the Effectiveness of High School Training on the Typing Speed of College Students. This Example Also Demonstrates the Assignment of Ranks to Tied Data

H_0 : Typing speed is not greater in college students having had high school typing training.

H_A : Typing speed is greater in college students having had high school typing training.

$\alpha = 0.05$

Typing Speed (words per minute)	
With training (rank in parentheses)	Without training (rank in parentheses)
44 (9)	32 (3.5)
48 (12)	40 (7)
36 (6)	44 (9)
32 (3.5)	44 (9)
51 (13)	34 (5)
45 (11)	30 (2)
54 (14)	26 (1)
56 (15)	
$n_1 = 8$	$n_2 = 7$
$R_1 = 83.5$	$R_2 = 36.5$

Because ranking was done from low to high and the alternate hypothesis states that the data of group one are larger than the data of group two, use U' as the test statistic (as indicated in Table 8.2).

$$\begin{aligned}
 U' &= n_2 n_1 + \frac{n_2(n_2 + 1)}{2} - R_2 \\
 &= (7)(8) + \frac{(7)(8)}{2} - 36.5 \\
 &= 56 + 28 - 36.5 \\
 &= 47.5
 \end{aligned}$$

$$U_{0.05(1),8,7} = U_{0.05(1),7,8} = 43$$

As $47.5 > 43$, reject H_0 .

$$0.01 < P < 0.025 \quad [P = 0.012]$$

Consequently, it is concluded that college-student typing speed is greater for students who had typing training in high school.

R

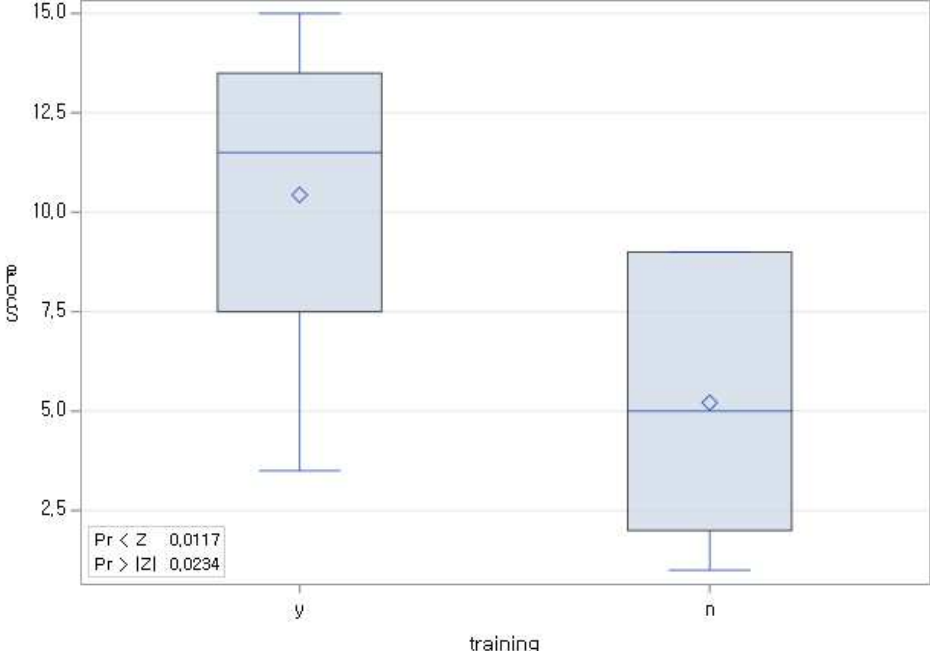
CODE	<pre> # ex8.12 training= c(44,48,36,32,51,45,54,56) notrain= c(32,40,44,44,34,30,26) mwostest= function(x, y, alpha){ n1= length(x) n2= length(y) nr= n1+1 nn= n1+n2 </pre>
------	---

	<pre> rk=rank(c(x, y), ties.method="average") rk xrank=rk[1:length(x)] yrank=rk[nr:nn] r1= sum(xrank) r2= sum(yrank) u= n1*n2+ n1*(n1+1)/2 - r1 up= n1*n2 - u pu= qwilcox(alpha, n1, n2, lower.tail = F)+1 if(max(u,up)>pu){ answer= "reject H0" } else if(max(u,up)<=pu){ answer= "cannot reject H0" } pv= round(pwilcox(max(u,up), n1,n2, lower.tail = F),3) return(c(answer,pv)) } mwostest(training, notrain, 0.05) # method2 wilcox.test(training, notrain, alternative = "greater") </pre>
OUTPUT	<pre> > # ex8.12 > training= c(44,48,36,32,51,45,54,56) > notrain= c(32,40,44,44,34,30,26) > mwostest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + nr= n1+1 + nn= n1+n2 + rk=rank(c(x, y), ties.method="average") + rk + xrank=rk[1:length(x)] + yrank=rk[nr:nn] + r1= sum(xrank) + r2= sum(yrank) + u= n1*n2+ n1*(n1+1)/2 - r1 + up= n1*n2 - u + pu= qwilcox(alpha, n1, n2, lower.tail = F)+1 + if(max(u,up)>pu){ + answer= "reject H0" + } + else if(max(u,up)<=pu){ + answer= "cannot reject H0" + } + pv= round(pwilcox(max(u,up), n1,n2, lower.tail = F),3) + return(c(answer,pv)) + } > mwostest(training, notrain, 0.05) [1] "reject H0" "0.01" </pre>

wilcox.exact()

.

	<pre>> # method2 > wilcox.test(training, notrain, alternative = "greater") Wilcoxon rank sum test with continuity correction data: training and notrain w = 47.5, p-value = 0.0136 alternative hypothesis: true location shift is greater than 0 경고메시지(들): In wilcox.test.default(training, notrain, alternative = "greater") : tie가 있어 정확한 p값을 계산할 수 없습니다</pre>																		
SAS																			
CODE	<pre>data ex8_12; input training\$ speed @@; cards; y 44 y 48 y 36 y 32 y 51 y 45 y 54 y 56 n 32 n 40 n 44 n 44 n 34 n 30 n 26 ; run; proc npar1way data= ex8_12 wilcoxon correct=no; class training; var speed; run;</pre>																		
OUTPUT	<table><tr><th colspan="2">Wilcoxon Two-Sample Test</th></tr><tr><td>Statistic</td><td>36.5000</td></tr><tr><td colspan="2">Normal Approximation</td></tr><tr><td>Z</td><td>-2.2668</td></tr><tr><td>One-Sided Pr < Z</td><td>0.0117</td></tr><tr><td>Two-Sided Pr > Z </td><td>0.0234</td></tr><tr><td colspan="2">t Approximation</td></tr><tr><td>One-Sided Pr < Z</td><td>0.0199</td></tr><tr><td>Two-Sided Pr > Z </td><td>0.0398</td></tr></table>	Wilcoxon Two-Sample Test		Statistic	36.5000	Normal Approximation		Z	-2.2668	One-Sided Pr < Z	0.0117	Two-Sided Pr > Z	0.0234	t Approximation		One-Sided Pr < Z	0.0199	Two-Sided Pr > Z	0.0398
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	<p style="text-align: center;">Distribution of Wilcoxon Scores for speed</p>  <p style="text-align: center;">training</p>
결과해석	<p>고등학교의 타자 연습 교육이 학부생들의 타자속도 향상에 도움이 되는지 확인해보고자 맨-휘트니 검정을 실시하였다.</p> <p>귀무가설: 고등학교 타자 연습 교육을 받은 학부 학생들의 타자속도는 받지 않은 학생들보다 더 빠르지 않다. (고등학교 때 타자 연습 교육을 받은 학생들의 1분에 치는 단어의 수의 분포가 교육을 받지 않은 학생들의 분포와 비슷하거나 왼쪽에 몰려 있다.)</p> <p>대립가설: 고등학교 타자 연습 교육을 받은 학부 학생들의 타자속도는 받지 않은 학생들보다 더 빠르다. (고등학교 때 타자 연습 교육을 받은 학생들의 1분에 치는 단어의 수의 분포가 교육을 받지 않은 학생들의 분포가 오른쪽에 몰려 있다.)</p> <p>검정결과 p-value= 0.01 정도로 유의하게 나왔다. 따라서 귀무가설을 기각하며 고등학교 때 타자 연습 교육을 받는 것이 학부 학생들의 타자속도를 향상시킨다고 결론을 내릴 수 있다. 상자그림에서도 교육을 받은 집단의 타자속도가 더 빠른 것을 확인할 수 있다.</p>

Example.8.13

EXAMPLE 8.13 The Normal Approximation to a One-Tailed Mann-Whitney Test to Determine Whether Animals Raised on a Dietary Supplement Reach a Greater Body Weight Than Those Raised on an Unsupplemented Diet

In the experiment, 22 animals (group 1) were raised on the supplemented diet, and 46 were raised on the unsupplemented diet (group 2). The body weights were ranked from 1 (for the smallest weight) to 68 (for the largest weight), and U was calculated to be 282.

H_0 : Body weight of animals on the supplemented diet are not greater than those on the unsupplemented diet.

H_A : Body weight of animals on the supplemented diet are greater than those on the unsupplemented diet.

$$n_1 = 22, n_2 = 46, N = 68$$

$$U = 282$$

$$U' = n_1 n_2 - U = (22)(46) - 282 = 1012 - 282 = 730$$

$$\mu_U = \frac{n_1 n_2}{2} = \frac{(22)(46)}{2} = 506$$

$$\sigma_U = \sqrt{\frac{n_1 n_2 (N + 1)}{12}} = \sqrt{\frac{(22)(46)(68 + 1)}{12}} = 76.28$$

$$Z = \frac{U' - \mu_U}{\sigma_U} = \frac{224}{76.28} = 2.94$$

For a one-tailed test at $\alpha = 0.05$, $t_{0.05(1), \infty} = Z_{0.05(1)} = 1.6449$.

As $Z = 2.94 > 1.6449$, reject H_0 . [$P = 0.0016$]

So we conclude that the supplemental diet results in greater body weight.

R

CODE

```
# ex8.13
ex13= function(n1, n2, u, alpha){
  n= n1+n2
  up = n1*n2-u
  mu= n1*n2/2
  su= sqrt((n1*n2*(n+1))/12)
  z= (up-mu)/su
  zp= qnorm(alpha, lower.tail = F)
  if(z>zp){
    answer= "reject H0"
  }
  else if(z<=zp){
    answer= "cannot reject H0"
  }
  pv= round(pnorm(z, lower.tail = F),4)
  return(c(answer, pv))
}
ex13(22,46,282,0.05)
```


OUTPUT	<pre> > # ex8.13 > ex13= function(n1, n2, u, alpha){ + n= n1+n2 + up = n1*n2-u + mu= n1*n2/2 + su= sqrt((n1*n2*(n+1))/12) + z= (up-mu)/su + zp= qnorm(alpha, lower.tail = F) + if(z>zp){ + answer= "reject H0" + } + else if(z<=zp){ + answer= "cannot reject H0" + } + pv= round(pnorm(z, lower.tail = F),4) + return(c(answer, pv)) + } > ex13(22,46,282,0.05) [1] "reject H0" "0.0017" </pre>				
SAS					
CODE	<pre> proc iml; n1= 22; n2= 46; n= 68; u= 282; up= n1*n2-u; mu= n1*n2/2; su= sqrt(n1*n2*(n+1)/12); z= (up-mu)/su; zp = -probit(0.05); if z > zp then answer= "reject H0"; else answer= "cannot reject H0"; pv= 1-cdf('normal', z); print answer pv; run; </pre>				
OUTPUT	<table border="1"> <thead> <tr> <th>answer</th><th>pv</th></tr> </thead> <tbody> <tr> <td>reject H0</td><td>0.0016599</td></tr> </tbody> </table>	answer	pv	reject H0	0.0016599
answer	pv				
reject H0	0.0016599				
결과해석	<p>동물들에게 추가의 먹이를 주는 것이 주지 않은 동물들에 비해 몸무게가 더 나가는지 확인해보기 위해 맨-윌트니 검정을 실시하였다.</p> <p>귀무가설: 추가의 먹이를 먹은 동물들의 몸무게가 추가로 먹이를 먹지 않은 동물들의 몸무게보다 더 크지 않다.</p> <p>대립가설: 추가의 먹이를 먹은 동물들의 몸무게가 추가로 먹이를 먹지 않은 동물들의 몸무게보다 더 크다.</p> <p>검정결과 p-value가 0.0016 정도로 매우 유의하게 나와 귀무가설을 기각한다. 따라서 추가의 먹이를 먹은 동물들의 몸무게가 대체적으로 더 많이 나간다고 결론을 내릴 수 있다.</p>				

Example.8.14

EXAMPLE 8.14 The Mann-Whitney Test for Ordinal Data

H_0 : The performance of students is the same under the two teaching assistants.

H_A : Students do not perform equally well under the two teaching assistants.

$\alpha = 0.05$

Teaching Assistant A		Teaching Assistant B	
Grade	Rank of grade	Grade	Rank of grade
A	3	A	3
A	3	A	3
A	3	B+	7.5
A-	6	B+	7.5
B	10	B	10
B	10	B-	12
C+	13.5	C	16.5
C+	13.5	C	16.5
C	16.5	C-	19.5
C	16.5	D	22.5
C-	19.5	D	22.5
		D	22.5
		D-	25
$n_1 = 11$		$n_2 = 14$	
$R_1 = 114.5$		$R_2 = 210.5$	

$$\begin{aligned}
 U &= n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1 \\
 &= (11)(14) + \frac{(11)(12)}{2} - 114.5 \\
 &= 154 + 66 - 114.5 \\
 &= 105.5
 \end{aligned}$$

$$\begin{aligned}
 U' &= n_1 n_2 - U \\
 &= (11)(14) - 105.5 \\
 &= 48.5
 \end{aligned}$$

$$U_{0.05(2),11,14} = 114$$

As $105.5 < 114$, do not reject H_0 .

$$0.10 < P(U \geq 105.5 \text{ or } U \leq 48.5) < 0.20$$

Thus, the conclusion is that student performance is the same under both teaching assistants.

R

CODE

```

# ex8.14
#method1
a= c("a","a","a","b","d","d","f","f","g","g","h")
b= c("a","a","c","c","d","e","g","g","h","j","j","j","j","k")
a= factor(a, levels = letters)
a= as.numeric(a)
b= factor(b, levels = letters)
b= as.numeric(b)
a
b

mwtest= function(x, y, alpha){
  n1= length(x)

```

	<pre> n2= length(y) nr= n1+1 nn= n1+n2 rk=rank(c(x, y), ties.method="average") xrank=rk[1:length(x)] yrank=rk[nr:nn] r1= sum(xrank) r2= sum(yrank) u= n1*n2+ n1*(n1+1)/2 - r1 up= n1*n2 - u pu= qwilcox(alpha/2, n1, n2, lower.tail = F)+1 if(max(u, up)>pu){ answer= "reject H0" } else if(max(u, up)<=pu){ answer= "cannot reject H0" } pv= round(pwilcox(u-1, n1,n2, lower.tail = F)+pwilcox(up,n1,n2, lower.tail = T),3) return(c(answer,pv)) } mwtest(a, b, 0.05) # method2 wilcox.test(a,b) </pre>
OUTPUT	<pre> > # ex8.14 > #method1 > a= c("a","a","a","b","d","d","f","f","g","g","h") > b= c("a","a","c","c","d","e","g","g","h","j","j","j","j","k") > a= factor(a, levels = letters) > a= as.numeric(a) > b= factor(b, levels = letters) > b= as.numeric(b) > a [1] 1 1 1 2 4 4 6 6 7 7 8 > b [1] 1 1 3 3 4 5 7 7 8 10 10 10 10 11 </pre>

	<pre> > mwtest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + nr= n1+1 + nn= n1+n2 + rk=rank(c(x, y), ties.method="average") + xrank=rk[1:length(x)] + yrank=rk[nr:nn] + r1= sum(xrank) + r2= sum(yrank) + u= n1*n2+ n1*(n1+1)/2 - r1 + up= n1*n2 - u + pu= qwilcox(alpha/2, n1, n2, lower.tail = F)+1 + if(max(u, up)>pu){ + answer= "reject H0" + } + else if(max(u, up)<=pu){ + answer= "cannot reject H0" + } + pv= round(pwilcox(u-1, n1,n2, lower.tail = F)+pwilcox(up,n1,n2, lower.tail = T),3) + return(c(answer,pv)) + } > mwtest(a, b, 0.05) [1] "cannot reject H0" "0.127" > # method2 > wilcox.test(a,b) wilcoxon rank sum test with continuity correction data: a and b W = 48.5, p-value = 0.1219 alternative hypothesis: true location shift is not equal to 0 경고메시지(들): In wilcox.test.default(a, b) : tie가 있어 정확한 p값을 계산할 수 없습니다 </pre>
SAS	
CODE	<pre> data ex8_14; input assist\$ grade\$ @@; cards; A A A A A A A- A B A B A C+ A C+ A C A C A C- B A B A B B+ B B+ B B B B- B C B C B C- B D B D B D B D B D- ; run; data trans8_14; set ex8_14; if grade= 'A' then number=1; if grade= 'A-' then number=2; if grade= 'B+' then number=3; if grade= 'B' then number=4; if grade= 'B-' then number=5; if grade= 'C+' then number=6; if grade= 'C' then number=7; if grade= 'C-' then number=8; if grade= 'D+' then number=9; if grade= 'D' then number=10; if grade= 'D-' then number=11; run; proc npar1way data= trans8_14 wilcoxon correct=no; </pre>

wilcox.exact()

	<pre>class assist; var number; run;</pre>																						
OUTPUT	<table border="1"> <thead> <tr> <th colspan="2">Wilcoxon Two-Sample Test</th> </tr> </thead> <tbody> <tr> <td>Statistic</td><td>114.5000</td> </tr> <tr> <td></td><td></td> </tr> <tr> <td>Normal Approximation</td><td></td> </tr> <tr> <td>Z</td><td>-1.5745</td> </tr> <tr> <td>One-Sided Pr < Z</td><td>0.0577</td> </tr> <tr> <td>Two-Sided Pr > Z </td><td>0.1154</td> </tr> <tr> <td></td><td></td> </tr> <tr> <td>t Approximation</td><td></td> </tr> <tr> <td>One-Sided Pr < Z</td><td>0.0642</td> </tr> <tr> <td>Two-Sided Pr > Z </td><td>0.1285</td> </tr> </tbody> </table>	Wilcoxon Two-Sample Test		Statistic	114.5000			Normal Approximation		Z	-1.5745	One-Sided Pr < Z	0.0577	Two-Sided Pr > Z	0.1154			t Approximation		One-Sided Pr < Z	0.0642	Two-Sided Pr > Z	0.1285
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결과해석	<p>보조 교사에 따라 학생들이 받는 평균 성적에 차이가 있는지 확인해 보기 위해 맨-윌트니 검정을 실시했다.</p> <p>귀무가설: 두 보조 교사에 따라 학생들이 받는 성적의 분포에 차이가 없다.</p> <p>대립가설: 두 보조 교사에 따라 학생들이 받는 성적의 분포에 차이가 있다.</p> <p>검정결과 p-value가 약 0.12 정도로 귀무가설을 기각할 수 있는 충분한 증거다 되지 못한다. 따라서 위의 결과를 통해 두 보조 교사에 따라 학생들이 받는 성적의 분포에 차이가 있다고 주장하기는 어렵다.</p>																						

Example.8.15

EXAMPLE 8.15 The Two-Sample Median Test, Using the Data of Example 8.14

H_0 : The two samples came from populations with identical medians (i.e., the median performance is the same under the two teaching assistants).

H_A : The medians of the two sampled populations are not equal.

$\alpha = 0.05$

The median of all 25 measurements in Example 8.14 is $X_{(25+1)/2} = X_{13}$ = grade of C+. The following 2×2 contingency table is then produced:

Number	Sample 1	Sample 2	Total
Above median	6	6	12
Not above median	3	8	11
Total	9	14	23

Analyzing this contingency table (Section 23.3):

$$X_c^2 = \frac{n \left(|f_{11}f_{22} - f_{12}f_{21}| - \frac{n}{2} \right)^2}{(C_1)(C_2)(R_1)(R_2)} \quad (8.59)$$

$$= 0.473.$$

$$X_{0.05,1}^2 = 3.841$$

Therefore, do not reject H_0 .

$$0.25 < P < 0.50 \quad [P = 0.49]$$

So it is concluded that the two samples did not come from populations with different medians.

R

CODE

```
#ex8.15
# method1
mwtest= function(x, y, alpha){
  n1= length(x)
  n2= length(y)
  nr= n1+1
  nn= n1+n2
  rk=rank(c(a, b), ties.method="average")
  xrank=rk[1:length(x)]
  yrank=rk[nr:nn]

  xa= xrank[xrank < median(rk)]
  f11= length(xa)
  xb= xrank[xrank > median(rk)]
  f12= length(xb)
  ya= yrank[yrank < median(rk)]
  f21= length(ya)
  yb= yrank[yrank > median(rk)]
  f22= length(yb)

  c1= f11+f12
```

	<pre> c2= f21+f22 r1= f11+f21 r2= f12+f22 n= f11+f12+f21+f22 chi= (n*(abs(f11*f22-f12*f21)-n/2)^2)/(c1*c2*r1*r2) pchi= qchisq(alpha, 1, lower.tail = F) if(chi>pchi){ answer= "reject H0" } else if(chi<=pchi){ answer= "cannot reject H0" } pv= round(pchisq(chi, 1, lower.tail = F),2) return(c(answer, pv)) } mwtest(a,b,0.05) # method2 mood.test(a,b, alternative = "two.sided") </pre>
OUTPUT	<pre> > #ex8.15 > # method1 > mwtest= function(x, y, alpha){ + n1= length(x) + n2= length(y) + nr= n1+1 + nn= n1+n2 + rk=rank(c(a, b), ties.method="average") + xrank=rk[1:length(x)] + yrank=rk[nr:nn] + + xa= xrank[xrank < median(rk)] + f11= length(xa) + xb= xrank[xrank > median(rk)] + f12= length(xb) + ya= yrank[yrank < median(rk)] + f21= length(ya) + yb= yrank[yrank > median(rk)] + f22= length(yb) + + c1= f11+f12 + c2= f21+f22 + r1= f11+f21 + r2= f12+f22 + n= f11+f12+f21+f22 + chi= (n*(abs(f11*f22-f12*f21)-n/2)^2)/(c1*c2*r1*r2) + pchi= qchisq(alpha, 1, lower.tail = F) + if(chi>pchi){ + answer= "reject H0" + } + else if(chi<=pchi){ + answer= "cannot reject H0" + } + pv= round(pchisq(chi, 1, lower.tail = F),2) + return(c(answer, pv)) + } > mwtest(a,b,0.05) [1] "cannot reject H0" "0.49" </pre>

	<pre>> # method2 > mood.test(a,b, alternative = "two.sided") Mood two-sample test of scale data: a and b Z = -1.2018, p-value = 0.4915 alternative hypothesis: true</pre>	<div>(0.49가 . mood.test</div>																																																						
CODE	<pre>data ex8_15; input sample\$ ud\$ count; cards; 1 above 6 1 below 3 2 above 6 2 below 8 ; run; proc freq data= ex8_15 order=data; weight count; tables sample * ud/ nocol norow nopercnt chisq; run;</pre>	<div>table<- (xtabs(num ~ row + col,data=ex8_15)) table chisq.test(table, correct=T)</div>																																																						
OUTPUT	<div>빈도</div> <table><tr><th colspan="4">테이블 sample * ud</th></tr><tr><th rowspan="2">sample</th><th colspan="2">ud</th><th rowspan="2">합계</th></tr><tr><th>above</th><th>below</th></tr><tr><td>1</td><td>6</td><td>3</td><td>9</td></tr><tr><td>2</td><td>6</td><td>8</td><td>14</td></tr><tr><td>합계</td><td>12</td><td>11</td><td>23</td></tr></table> <div>sample * ud 테이블에 대한 통계량</div> <table><tr><th>통계량</th><th>자유도</th><th>값</th><th>Prob</th></tr><tr><td>카이제곱</td><td>1</td><td>1.2446</td><td>0.2646</td></tr><tr><td>우도비 카이제곱</td><td>1</td><td>1.2626</td><td>0.2612</td></tr><tr><td>연속성 수정 카이제곱</td><td>1</td><td>0.4733</td><td>0.4915</td></tr><tr><td>Mantel-Haenszel 카이제곱</td><td>1</td><td>1.1905</td><td>0.2752</td></tr><tr><td>파이 계수</td><td></td><td>0.2326</td><td></td></tr><tr><td>우발성 계수</td><td></td><td>0.2266</td><td></td></tr><tr><td>크래머의 V</td><td></td><td>0.2326</td><td></td></tr></table> <div>WARNING: 50%개의 셀이 5보다 적은 기대빈도를 가지고 있습니다. 카이제곱 검정은 올바르지 않을 수 있습니다.</div>	테이블 sample * ud				sample	ud		합계	above	below	1	6	3	9	2	6	8	14	합계	12	11	23	통계량	자유도	값	Prob	카이제곱	1	1.2446	0.2646	우도비 카이제곱	1	1.2626	0.2612	연속성 수정 카이제곱	1	0.4733	0.4915	Mantel-Haenszel 카이제곱	1	1.1905	0.2752	파이 계수		0.2326		우발성 계수		0.2266		크래머의 V		0.2326		
테이블 sample * ud																																																								
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연속성 수정 카이제곱	1	0.4733	0.4915																																																					
Mantel-Haenszel 카이제곱	1	1.1905	0.2752																																																					
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우발성 계수		0.2266																																																						
크래머의 V		0.2326																																																						
결과해석	<p>두 보조 교사에 따라 학생들이 받는 성적의 모중위수에 차이가 있는지 확인하기 위해 중위수검정, mood검정을 실시하였다.</p> <p>귀무가설: 보조 교사 A, B에게 학습받은 학생들이 받은 성적의 모중위수가 서로 동일하다.</p>																																																							

	<p>대립가설: 귀무가설: 보조 교사 A, B에게 학습받은 학생들이 받은 성적의 모중위수가 서로 다르다.</p> <p>검정결과 p-value가 0.49 정도로 유의하지 않다. 따라서 귀무가설을 기각할 수 있는 충분한 근거가 되지 못하며 두 보조 교사에 따라 학생들이 받은 성적의 모중위수가 차이가 있다고 보긴 힘들다.</p>
--	---

Example.8.16

EXAMPLE 8.16 Comparing Two Indices of Diversity

H_0 : The diversity of plant food items in the diet of Michigan blue jays is the same as the diversity of plant food items in the diet of Louisiana blue jays.

H_A : The diversity of plant food items in the diet of Michigan blue jays is not the same as in the diet of Louisiana blue jays.

$\alpha = 0.05$

Michigan Blue Jays

Diet item	f_i	$f_i \log f_i$	$f_i \log^2 f_i$
Oak	47	78.5886	131.4078
Corn	35	54.0424	83.4452
Blackberry	7	5.9157	4.9994
Beech	5	3.4949	2.4429
Cherry	3	1.4314	0.6830
Other	2	0.6021	0.1812

$$s_1 = 6 \quad n_1 = \sum f_i = 99 \quad \sum f_i \log f_i = 144.0751 \quad \sum f_i \log^2 f_i = 223.1595$$

$$H'_1 = \frac{n \log n - \sum f_i \log f_i}{n} = \frac{197.5679 - 144.0751}{99} = 0.5403$$

$$s_{H'_1}^2 = \frac{\sum f_i \log^2 f_i - (\sum f_i \log f_i)^2 / n}{n^2} = 0.00137602$$

Louisiana Blue Jays

Diet item	f_i	$f_i \log f_i$	$f_i \log^2 f_i$
Oak	48	80.6996	135.6755
Pine	23	31.3197	42.6489
Grape	11	11.4553	11.9294
Corn	13	14.4813	16.1313
Blueberry	8	7.2247	6.5246
Other	2	0.6021	0.1812

$$s_2 = 6 \quad n_2 = \sum f_i = 105 \quad \sum f_i \log f_i = 145.7827 \quad \sum f_i \log^2 f_i = 213.0909$$

$H'_2 = \frac{n \log n - \sum f_i \log f_i}{n} = \frac{212.2249 - 145.7827}{105} = 0.6328$ $s_{H'_2}^2 = \frac{\sum f_i \log^2 f_i - (\sum f_i \log f_i)^2 / n}{n^2} = 0.00096918$ $s_{H'_1 - H'_2} = \sqrt{s_{H'_1}^2 + s_{H'_2}^2} = \sqrt{0.00137602 + 0.00096918} = 0.0484$ $t = \frac{H'_1 - H'_2}{s_{H'_1 - H'_2}} = \frac{-0.0925}{0.0484} = -1.911$ $v = \frac{\left(\frac{s_{H'_1}^2}{n_1} + \frac{s_{H'_2}^2}{n_2}\right)^2}{\frac{(s_{H'_1}^2)^2}{n_1} + \frac{(s_{H'_2}^2)^2}{n_2}} = \frac{(0.00137602 + 0.00096918)^2}{\frac{(0.00137602)^2}{99} + \frac{(0.00096918)^2}{105}}$ $= \frac{0.000005499963}{0.00000028071} = 196$ $t_{0.05(2),196} = 1.972$ <p>Therefore, do not reject H_0.</p> $0.05 < P < 0.10 \quad [P = 0.057]$ <p>The conclusion is that the diversity of food items is the same in birds from Michigan and Louisiana.</p>	
R	
CODE	<pre> # ex8.16 library(vegan) m= c(47,35,7,5,3,2) l= c(48,23,11,13,8,2) indicetest= function(x,y,alpha){ h1= diversity(x, base= 10) sh1= (sum(x*(log10(x))^2)-((sum(x*log10(x))^2)/sum(x)))/sum(x)^2 h2= diversity(y, base= 10) sh2= (sum(y*(log10(y))^2)-((sum(y*log10(y))^2)/sum(y)))/sum(y)^2 sh= sqrt(sh1+sh2) t= (h1-h2)/sh v= ceiling((sh1+sh2)^2/((sh1^2/sum(x)+(sh2^2)/sum(y))) tp= qt(alpha/2, v, lower.tail = F) if(abs(t)>tp){ answer= "reject H0" } else if(abs(t)<=tp){ answer= "cannot reject H0" } pv= round(pt(abs(t),v, lower.tail = F)*2,3) return(c(answer, pv)) } indicetest(m,l,0.05) </pre>
OUTPUT	

	<pre> > # ex8.16 > library(vegan) > m= c(47,35,7,5,3,2) > l= c(48,23,11,13,8,2) > indicetest= function(x,y,alpha){ + h1= diversity(x, base= 10) + sh1= (sum(x*(log10(x))^2)-((sum(x*log10(x))^2)/sum(x)))/sum(x)^2 + h2= diversity(y, base = 10) + sh2= (sum(y*(log10(y))^2)-((sum(y*log10(y))^2)/sum(y)))/sum(y)^2 + sh= sqrt(sh1+sh2) + t= (h1-h2)/sh + v= ceiling((sh1+sh2)^2/((sh1^2/sum(x)+(sh2^2)/sum(y))) + tp= qt(alpha/2, v, lower.tail = F) + if(abs(t)>tp){ + answer= "reject H0" + } + else if(abs(t)<=tp){ + answer= "cannot reject H0" + } + pv= round(pt(abs(t),v, lower.tail = F)*2,3) + return(c(answer, pv)) + } > indicetest(m,l,0.05) [1] "cannot reject H0" "0.058" </pre>				
	SAS				
CODE	<pre> proc iml; m={ 47, 35, 7, 5, 3, 2 }; h1=(sum(m)*log10(sum(m))-t(m)*log10(m))/sum(m); sh1= (sum(m#log10(m)#log10(m)) -sum(m#log10(m))**2/sum(m))/sum(m)**2; l={ 48, 23, 11, 13, 8, 2 }; h2=(sum(l)*log10(sum(l))-t(l)*log10(l))/sum(l); sh2= (sum(l#log10(l)#log10(l)) -sum(l#log10(l))**2/sum(l))/sum(l)**2; s= sqrt(sh1+sh2); t= (h1-h2)/s; v= ceil((sh1+sh2)**2/(sh1**2/sum(m)+sh2**2/sum(l))); tp= -tinv(0.025, 196); if abs(t) > tp then answer= "reject H0"; else answer= "cannot reject H0"; pv= (1-probt(abs(t),v))*2; print answer pv; run; quit; </pre>				
OUTPUT	<table border="1"> <thead> <tr> <th>answer</th><th>pv</th></tr> </thead> <tbody> <tr> <td>cannot reject H0</td><td>0.0577189</td></tr> </tbody> </table>	answer	pv	cannot reject H0	0.0577189
answer	pv				
cannot reject H0	0.0577189				
결과해석	<p>미시간 주에 서식하는 큰어치(blue jays)와 루이지애나 주에 서식하는 큰어치가 먹는 식물들의 종의 다양성에 차이가 있는지 확인해보기 위해 검정을 실시하였다.</p>				

https://www.allaboutbirds.org/guide/Blue_Jay/sounds
<https://www.youtube.com/watch?v=T--LnIE1nE8>

	<p>귀무가설: 미시간 주에 서식하는 큰어치와 루이지애나 주에 서식하는 큰어치가 먹는 모 집단 식물들의 종의 다양성은 동일하다.</p> <p>대립가설: 미시간 주에 서식하는 큰어치와 루이지애나 주에 서식하는 큰어치가 먹는 모 집단 식물들의 종의 다양성은 차이가 있다.</p> <p>검정결과 p-value가 0.058정도로 유의하지 않다. 따라서 귀무가설을 기각할 증거가 부족하므로 미시간 주와 루이지애나 주에 서식하는 큰어치의 먹이가 되는 모 집단 식물들의 종의 다양성에 차이가 있다고 보긴 어렵다.</p>
--	---

p - value가

가 ?

Example.9.1

EXAMPLE 9.1 The Two-Tailed Paired-Sample t Test

$$H_0: \mu_d = 0$$

$$H_A: \mu_d \neq 0$$

$$\alpha = 0.05$$

Deer (j)	Hindleg length (cm) (X_{1j})	Foreleg length (cm) (X_{2j})	Difference (cm) ($d_j = X_{1j} - X_{2j}$)
1	142	138	4
2	140	136	4
3	144	147	-3
4	144	139	5
5	142	143	-1
6	146	141	5
7	149	143	6
8	150	145	5
9	142	136	6
10	148	146	2

$$n = 10$$

$$\bar{d} = 3.3 \text{ cm}$$

$$s_d^2 = 9.3444 \text{ cm}^2$$

$$s_d = 0.97 \text{ cm}$$

$$v = n - 1 = 9$$

$$t = \frac{\bar{d}}{s_d} = \frac{3.3}{0.97} = 3.402$$

$$t_{0.05(2),9} = 2.262$$

Therefore, reject H_0 .

$$0.005 < P(|t| \geq 3.402) < 0.01 \quad [P = 0.008]$$

R

	# ex9.1
CODE	<pre>hind=c(142,140,144,144,142,146,149,150,142,148) fore=c(138,136,147,139,143,141,143,145,136,146) t.test(hind, fore, alternative = "two.sided", paired = T)</pre>
OUTPUT	<pre>> # ex9.1 > hind=c(142,140,144,144,142,146,149,150,142,148) > fore=c(138,136,147,139,143,141,143,145,136,146) > t.test(hind, fore, alternative = "two.sided", paired = T) Paired t-test data: hind and fore t = 3.4138, df = 9, p-value = 0.007703 alternative hypothesis: true difference in means is not equal to 0 95 percent confidence interval: 1.113248 5.486752 sample estimates: mean of the differences 3.3</pre>

SAS

CODE	<pre>data ex9_1; input hind fore @@; cards; 142 138 140 136 144 147 144 139 142 143 146 141 149 143 150 145 142 136 148 146 ; run; proc ttest data= ex9_1; paired hind * fore; run;</pre>						
OUTPUT	<table border="1"><thead><tr><th>DF</th><th>t Value</th><th>Pr > t </th></tr></thead><tbody><tr><td>9</td><td>3.41</td><td>0.0077</td></tr></tbody></table> <p>The figure is a 'Paired Profiles for (hind, fore)' plot. The x-axis has two categories: 'hind' and 'fore'. The y-axis represents leg length, with values ranging from 137.5 to 150.0. There are 10 blue lines, each representing an individual subject's leg lengths for hind and fore legs. A thick red line represents the mean difference. The red line starts at approximately 144.5 for 'hind' and ends at approximately 141.5 for 'fore', indicating a decrease in mean leg length from hind to fore legs. The legend indicates 'Mean' with a red line.</p>	DF	t Value	Pr > t	9	3.41	0.0077
DF	t Value	Pr > t					
9	3.41	0.0077					
결과해석	<p>사슴의 뒷다리와 앞다리의 다리 길이의 차이가 있는지 확인해보기 위해 10마리의 사슴을 뽑아 paired sample t검정을 실시하였다.</p> <p>귀무가설: 사슴의 앞다리와 뒷다리의 모평균 다리 길이의 차이가 없다.</p> <p>대립가설: 사슴의 앞다리와 뒷다리의 모평균 다리 길이의 차이가 있다.</p> <p>검정결과 p-value= 0.008로 매우 유의한 값이 나왔다. 따라서 귀무가설을 기각하고 사슴의 앞다리와 뒷다리의 평균 다리 길이에 차이가 있다고 결론을 내릴 수 있다.</p> <p>추가적으로 paired profiles에서 대부분의 사슴들이 뒷다리가 더 긴 것을 확인할 수 있다.</p>						

Example.9.2

EXAMPLE 9.2 A One-Tailed Paired-Sample t Test

$$H_0: \mu_d \leq 250 \text{ kg/ha}$$

$$H_A: \mu_d > 250 \text{ kg/ha}$$

$$\alpha = 0.05$$

Plot (j)	Crop Yield (kg/ha)		d_j
	With new fertilizer (X_{1j})	With old fertilizer (X_{2j})	
1	2250	1920	330
2	2410	2020	390
3	2260	2060	200
4	2200	1960	240
5	2360	1960	400
6	2320	2140	180
7	2240	1980	260
8	2300	1940	360
9	2090	1790	300

$$n = 9 \quad \bar{d} = 295.6 \text{ kg/ha}$$

$$s_d^2 = 6502.78 \text{ (kg/ha)}^2 \quad s_d = 26.9 \text{ kg/ha}$$

$$\nu = n - 1 = 8 \quad t = \frac{\bar{d} - 250}{s_d} = 1.695$$

$$t_{0.05(1),8} = 1.860 \quad \text{Therefore, do not reject } H_0.$$

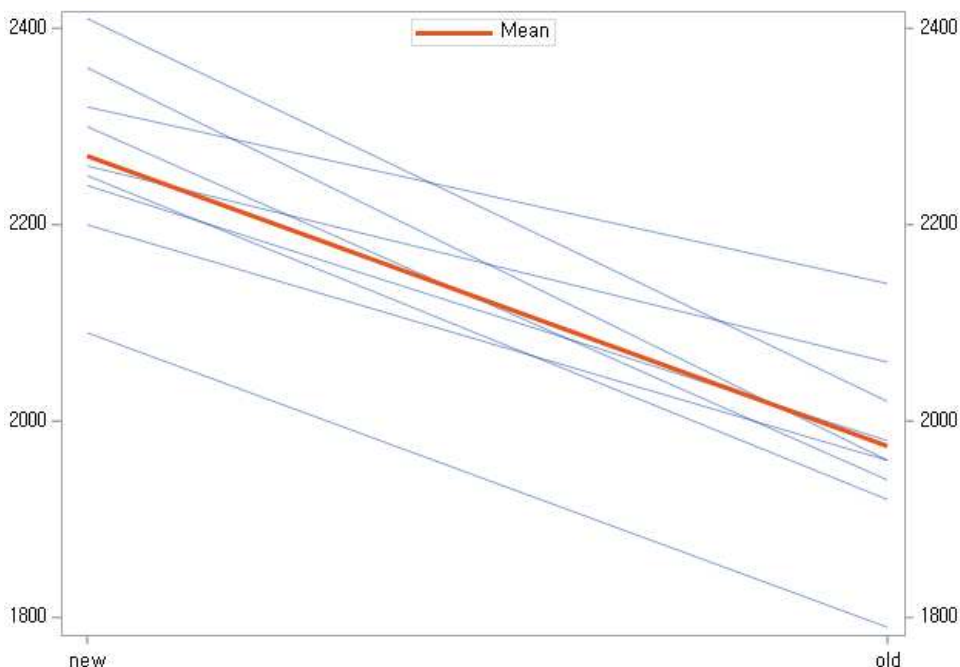
$$0.05 < P < 0.10 \quad [P = 0.064]$$

R

CODE	<pre># ex9.2 new = c(2250,2410,2260,2200,2360,2320,2240,2300,2090) old = c(1920,2020,2060,1960,1960,2140,1980,1940,1790) t.test(new, old, mu=250, alternative = "greater", paired = T)</pre>
	<pre>> # ex9.2 > new = c(2250,2410,2260,2200,2360,2320,2240,2300,2090) > old = c(1920,2020,2060,1960,1960,2140,1980,1940,1790) > t.test(new, old, mu=250, alternative = "greater", paired = T) Paired t-test data: new and old t = 1.6948, df = 8, p-value = 0.06428 alternative hypothesis: true difference in means is greater than 250 95 percent confidence interval: 245.571 Inf sample estimates: mean of the differences 295.5556</pre>

SAS

CODE	<pre>data ex9_2; input new old @@; cards; 2250 1920 2410 2020 2260 2060 2200 1960 2360 1960 2320 2140 2240 1980 2300 1940 2090 1790 ;</pre>
------	---

	<pre>run; proc ttest data= ex9_2 sides=U h0= 250; paired new *old; run;</pre>						
OUTPUT	<div><p>Paired Profiles for (new, old)</p><table><thead><tr><th>DF</th><th>t Value</th><th>Pr > t</th></tr></thead><tbody><tr><td>8</td><td>1.69</td><td>0.0643</td></tr></tbody></table></div>	DF	t Value	Pr > t	8	1.69	0.0643
DF	t Value	Pr > t					
8	1.69	0.0643					
결과해석	<p>이전에 쓰던 비료에 비해 새로 출시된 비료가 평균 작물생산량이 더 많은지 알아보기 위해 one-tailed paired sample t검정을 실시하였다.</p> <p>귀무가설: 새로운 비료를 썼을 때의 모평균 작물생산량이 이전 비료를 썼을 때의 모평균 작물생산량보다 250kg/ha보다 더 적거나 같다.</p> <p>대립가설: 새로운 비료를 썼을 때의 모평균 작물생산량이 이전 비료를 썼을 때의 모평균 작물생산량보다 250kg/ha보다 더 많다.</p> <p>검정결과 p-value= 0.064로 유의수준 0.05 하에서 귀무가설을 기각할 충분한 증거를 확보하지 못했다. 따라서 현재의 표본만으로는 새로운 비료가 작물생산량이 250kg/ha 이상 더 많다고 판단하기는 힘들다. 그러나 SAS의 결과 중 paired profiles에서 확인해보면 새로운 비료를 사용했을 때의 작물생산량이 평균적으로 거의 250kg/ha 정도 많아 보이므로 표본 수를 더 뽑아 검정해 본다면 유의한 결과를 얻을 수 있다고 판단된다.</p>						

Example.9.3

EXAMPLE 9.3 Testing for Difference Between the Variances of Two Paired Samples

$$H_0: \sigma_1^2 = \sigma_2^2$$

$$H_A: \sigma_1^2 \neq \sigma_2^2$$

$$\alpha = 0.05$$

Using the paired-sample data of Example 9.1:

$$n = 10; \nu = 8$$

$$\sum x^2 = 104.10; \sum y^2 = 146.40$$

$$\sum xy = 83.20$$

$$s_1^2 = 11.57 \text{ cm}^2; s_2^2 = 16.27 \text{ cm}^2$$

$$F = 11.57 \text{ cm}^2 / 16.27 \text{ cm}^2 = 0.7111$$

Using Equation 19.1, $r = 0.6739$.

Using Equation 9.3:

$t = -0.656$ and $t_{0.05(2),8} = 2.306$, so H_0 is not rejected.

$$P > 0.50 \quad [P = 0.54]$$

R

CODE	<pre># ex9.3 library(PairedData) hind=c(142,140,144,144,142,146,149,150,142,148) fore=c(138,136,147,139,143,141,143,145,136,146) pitman.morgan.test.default(hind, fore, alternative = "two.sided")</pre>
OUTPUT	<pre>> # ex9.3 > library(PairedData) > hind=c(142,140,144,144,142,146,149,150,142,148) > fore=c(138,136,147,139,143,141,143,145,136,146) > pitman.morgan.test.default(hind, fore, alternative = "two.sided") Paired Pitman-Morgan test data: hind and fore t = -0.65591, df = 8, p-value = 0.5303 alternative hypothesis: true ratio of variances is not equal to 1 95 percent confidence interval: 0.227042 2.226964 sample estimates: variance of x variance of y 11.56667 16.26667</pre>

SAS

CODE	<pre>proc iml; use ex9_1; read all; n= nrow(hind); v= n-2; s1= var(hind); s2= var(fore); f= s1/s2; r= 0.6739;</pre>
------	---

	<pre> t= ((f-1)*sqrt(n-2))/(2*sqrt(f*(1-r**2))); tp= -tinv(0.025, v); if abs(t) > tp then answer= "reject H0"; else answer= "cannot reject H0"; pv= (1-probt(abs(t),v))*2; print answer pv; run; quit; </pre>				
OUTPUT	<table border="1"> <thead> <tr> <th>answer</th><th>pv</th></tr> </thead> <tbody> <tr> <td>cannot reject H0</td><td>0.5303128</td></tr> </tbody> </table>	answer	pv	cannot reject H0	0.5303128
answer	pv				
cannot reject H0	0.5303128				
결과해석	<p>사슴의 앞다리 길이의 모분산과 뒷다리 길이의 모분산의 차이가 있는지 확인해보기 위하여 분산검정을 실시하였다.</p> <p>귀무가설: 모집단 사슴들의 앞다리 길이의 모분산과 뒷다리 길이의 모분산은 동일하다.</p> <p>대립가설: 모집단 사슴들의 앞다리 길이의 모분산과 뒷다리 길이의 모분산은 다르다.</p> <p>검정결과 p-value= 0.54로 유의하지 않다. 따라서 귀무가설을 기각할 증거가 불충분하므로 모집단 사슴들의 앞다리 길이의 모분산과 뒷다리 길이의 모분산은 차이가 있다고 보기는 어렵다.</p>				

Example.9.4																																																																							
<p>EXAMPLE 9.4 The Wilcoxon Paired-Sample Test Applied to the Data of Example 9.1</p> <p>H_0: Deer hindleg length is the same as foreleg length.</p> <p>H_A: Deer hindleg length is not the same as foreleg length.</p> <p>$\alpha = 0.05$</p> <table border="1"> <thead> <tr> <th>Deer (j)</th><th>Hindleg length (cm) (X_{1j})</th><th>Foreleg length (cm) (X_{2j})</th><th>Difference ($d_j = X_{1j} - X_{2j}$)</th><th>Rank of d_j</th><th>Signed rank of d_j</th></tr> </thead> <tbody> <tr><td>1</td><td>142</td><td>138</td><td>4</td><td>4.5</td><td>4.5</td></tr> <tr><td>2</td><td>140</td><td>136</td><td>4</td><td>4.5</td><td>4.5</td></tr> <tr><td>3</td><td>144</td><td>147</td><td>-3</td><td>3</td><td>-3</td></tr> <tr><td>4</td><td>144</td><td>139</td><td>5</td><td>7</td><td>7</td></tr> <tr><td>5</td><td>142</td><td>143</td><td>-1</td><td>1</td><td>-1</td></tr> <tr><td>6</td><td>146</td><td>141</td><td>5</td><td>7</td><td>7</td></tr> <tr><td>7</td><td>149</td><td>143</td><td>6</td><td>9.5</td><td>9.5</td></tr> <tr><td>8</td><td>150</td><td>145</td><td>5</td><td>7</td><td>7</td></tr> <tr><td>9</td><td>142</td><td>136</td><td>6</td><td>9.5</td><td>9.5</td></tr> <tr><td>10</td><td>148</td><td>146</td><td>2</td><td>2</td><td>2</td></tr> </tbody> </table> <p>$n = 10$</p> <p>$T_+ = 4.5 + 4.5 + 7 + 7 + 9.5 + 7 + 9.5 + 2 = 51$</p> <p>$T_- = 3 + 1 = 4$</p> <p>$T_{0.05(2),10} = 8$</p> <p>Since $T_- < T_{0.05(2),10}$, H_0 is rejected.</p> <p>$0.01 < P(T_- \text{ or } T_+ \leq 4) < 0.02$ [$P = 0.014$]</p>						Deer (j)	Hindleg length (cm) (X_{1j})	Foreleg length (cm) (X_{2j})	Difference ($d_j = X_{1j} - X_{2j}$)	Rank of $ d_j $	Signed rank of $ d_j $	1	142	138	4	4.5	4.5	2	140	136	4	4.5	4.5	3	144	147	-3	3	-3	4	144	139	5	7	7	5	142	143	-1	1	-1	6	146	141	5	7	7	7	149	143	6	9.5	9.5	8	150	145	5	7	7	9	142	136	6	9.5	9.5	10	148	146	2	2	2
Deer (j)	Hindleg length (cm) (X_{1j})	Foreleg length (cm) (X_{2j})	Difference ($d_j = X_{1j} - X_{2j}$)	Rank of $ d_j $	Signed rank of $ d_j $																																																																		
1	142	138	4	4.5	4.5																																																																		
2	140	136	4	4.5	4.5																																																																		
3	144	147	-3	3	-3																																																																		
4	144	139	5	7	7																																																																		
5	142	143	-1	1	-1																																																																		
6	146	141	5	7	7																																																																		
7	149	143	6	9.5	9.5																																																																		
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9	142	136	6	9.5	9.5																																																																		
10	148	146	2	2	2																																																																		
R																																																																							
CODE	<pre> # ex9.4 hind=c(142,140,144,144,142,146,149,150,142,148) fore=c(138,136,147,139,143,141,143,145,136,146) </pre>																																																																						

	<pre>diff= paired(hind, fore) wilcox.test.paired(diff)</pre>																									
OUTPUT	<pre>> # ex9.4 > hind=c(142,140,144,144,142,146,149,150,142,148) > fore=c(138,136,147,139,143,141,143,145,136,146) > diff= paired(hind, fore) > wilcox.test.paired(diff)</pre> <div><div>exact test</div><div>.</div></div> <pre> wilcoxon signed rank test with continuity correction data: hind and fore V = 51, p-value = 0.01859 alternative hypothesis: true location shift is not equal to 0 경고메시지(들): In wilcox.test.default(x = c(142, 140, 144, 144, 142, 146, 149, 150, 142, 148), y = c(138, 136, 147, 139, 143, 141, 143, 145, 136, 146), paired = TRUE): cannot compute exact p-value with ties</pre>																									
SAS																										
CODE	<pre>data ex9_4; set ex9_1; diff = hind-fore; run; proc univariate data= ex9_4; var diff; run;</pre>																									
OUTPUT	<table><tr><th colspan="5">위치모수 검정: $\mu_0=0$</th></tr><tr><th>검정</th><th></th><th>통계량</th><th colspan="2">p 값</th></tr><tr><td>스튜던트의 t</td><td>t</td><td>3.413793</td><td>Pr > t </td><td>0.0077</td></tr><tr><td>부호</td><td>M</td><td>3</td><td>Pr >= M </td><td>0.1094</td></tr><tr><td>부호 순위</td><td>S</td><td>23.5</td><td>Pr >= S </td><td>0.0117</td></tr></table>	위치모수 검정: $\mu_0=0$					검정		통계량	p 값		스튜던트의 t	t	3.413793	Pr > t	0.0077	부호	M	3	Pr >= M	0.1094	부호 순위	S	23.5	Pr >= S	0.0117
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결과해석	<p>사슴의 뒷다리와 앞다리의 다리 길이의 차이가 있는지 확인해보기 위해 10마리의 사슴을 뽑아 이번에는 wilcoxon paired sample 검정을 실시하였다.</p> <p>귀무가설: 사슴의 앞다리와 뒷다리의 다리 길이의 대체적인 분포의 차이가 없다.</p> <p>대립가설: 사슴의 앞다리와 뒷다리의 다리 길이의 대체적인 분포의 차이가 있다.</p> <p>검정결과 p-value= 0.008로 매우 유의한 값이 나왔다. 따라서 귀무가설을 기각하고 사슴의 앞다리와 뒷다리의 다리 길이에 대체적으로 차이가 있다고 결론을 내릴 수 있다.</p>																									

