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Basic statistical tests in R

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Outline

- Example: Tea testing
 - Hypotese testing, type I and type II error
- More tests and how to find and read help files for different tests in R
-

Famous hypotheses test example:

The Design of Experiments (1935), Sir Ronald A. Fisher

- A tea party in Cambridge in the 1920ties
- A lady claims that she can taste whether milk is poured in cup before or after the tea
- All professors agree: impossible
- Fisher: this is statistically interesting!
He organized a test

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The lady tasting tea

- Test with 8 trials, 2 cups in each trial
 - In each trial: guess which cup had the milk poured in first
- Binomial experiment
 - Independent trials
 - Two possible outcomes, she guesses right cup (success), wrong cup (failure)
 - Constant probability of success in each trial
- X = number of correct guesses in 8 trials, each with probability of success p
 - X is Binomially $(8, p)$ distributed $P(X = x) = \binom{8}{x} p^x (1 - p)^{(8-x)}$

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The lady tasting tea cont.

- The null (conservative) hypothesis
 - The one we initially believe in
- The alternative hypothesis
 - The new claim we wish to test
- She has no special ability to taste the difference
 - $p = 0.5$
- She has a special ability to taste the difference
 - $p > 0.5$

How many right to be convinced

We expect maybe 3, 4 or 5 correct guesses if she has no special ability

- Assume 7 correct guesses
 - Is there enough evidence to claim that she has a special ability? If 8 correct guesses this would have been even more obvious!
- What if only 6 correct guesses?
 - Then it is not so easy to answer YES or NO
- Need a rule that says something about what it takes to be convinced.

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How many right to be convinced?

- Rule: We reject H_0 if the observed data have a small probability under H_0 (given H_0 is true).
- Compute the p-value.
 - The probability to obtain the observed value or something more extreme, given that is true
 - **NB!** The p-value is NOT the probability that is true

Small p-value: reject the null hypothesis
Large p-value: keep the null hypothesis

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The lady tasting tea, cont.

- Say: she identified 6 cups correctly
- P-value
 - The probability to obtain the observed value or something more extreme, given that H_0 is true

$$P(X \geq 6 | H_0 \text{ true}) =$$

$$P(X = 6 | p = 0.5) + P(X = 7 | p = 0.5) + P(X = 8 | p = 0.5) = \\ \text{dbinom}(6, 8, 0.5) + \text{dbinom}(7, 8, 0.5) + \text{dbinom}(8, 8, 0.5) = \\ \text{sum}(\text{dbinom}(6:8, 8, 0.5)) = 0.1445$$

- Is this enough to be convinced?
- Need a limit.
 - we must know about the types of errors we can make.

Two types of error

| | H_0 true | H_1 true |
|--------------|--------------|---------------|
| Accept H_0 | OK | Type II error |
| Accept H_1 | Type I error | OK |

- Type I error most serious
 - Wrongly reject the null hypothesis
 - Example:
 - person is not guilty
 - person is guilty
 - To say a person is guilty when he is not is far more serious than to say he is not guilty when he is.

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When to reject

- Decide on the hypothesis' level of significance
 - Choose a level of significance α
 - This guarantees $P(\text{type I error}) \leq \alpha$
 - Example
 - Level of significance at 0.05 gives 5 % probability to reject a true
- Reject H_0 if P-value is less than α

Important parameters in hypothesis testing

- Null hypothesis
- Alternative hypothesis
- Level of significance

Must be decided upon **before** we know the results of the experiment

The lady tasting tea, cont.

- Choose 5 % level of significance Conduct the experiment
 - Say: she identified 6 cups correctly
 - Is this evidence enough?
- P-value
 - The probability to obtain the observed value or something more extreme, given that H_0 is true
$$P(X \geq 6 | H_0 \text{ true}) = \text{sum}(\text{dbinom}(6:8, 8, 0.5))$$
$$= 0.1445$$

The lady tasting tea, cont.

- We obtained a p-value of 0.1443
- The rejection rule says
 - Reject H_0 if p-value is less than the level of significance α
 - Since $\alpha = 0.05$ we do NOT H_0 reject

Small p-value: reject the null hypothesis
Large p-value: keep the null hypothesis

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The lady tasting tea, cont.

- In the tea party in Cambridge:
 - The lady got every trial correct!
- Comment:
 - Why does it taste different?
 - Pouring hot tea into cold milk makes the milk curdle, but not so pouring cold milk into hot tea*

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*<http://binomial.csuhayward.edu/applets/appletNullHyp.html> Curdle = å skille seg

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Area of rejection

- Reject H_0 if p-value $\leq \alpha$
 - Reject H_0 if observed value (x) \geq critical value (x_c)
 - $P(\text{type I error}) = P(\text{reject } H_0 \mid H_0 \text{ true}) = P(X \geq x_c \mid p = 0.5)$
 - $x_c = 7 \rightarrow \text{sum}(\text{dbinom}(7:8, 8, 0.5)) = 0.035 \leq 0.05$
 - $x_c = 6 \rightarrow \text{sum}(\text{dbinom}(6:8, 8, 0.5)) = 0.145 > 0.05$
- Area of rejection: $\{x: x \geq x_c\} \rightarrow \{x: x \geq 7\}$

Type II error

$$P(\text{type I error}) \leq \alpha$$

$$P(\text{type II error}) = \beta$$

- Want both errors as small as possible
 - especially type I.
- β is not explicitly given, depends on H_1
- There is one β for each possible value of p under H_1

| | H_0 true | H_1 true |
|--------------|--------------|---------------|
| Accept H_0 | OK | Type II error |
| Accept H_1 | Type I error | OK |

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Example: type II error

- $P(\text{type II error}) = P(\text{not reject } H_0 \mid H_1 \text{ true})$

– $p = 0.7$:

$$P(\text{not reject } H_0 \mid p = 0.7) = 1 - P(\text{reject } H_0 \mid p = 0.7) =$$

$$1 - P(X \geq 7 \mid p = 0.7) = 1 - (1 - P(X < 7 \mid p = 0.7)) =$$

$$P(X \leq 6 \mid p = 0.7) = \text{sum}(\text{dbinom}(1:6, 8, 0.7)) = 0.745$$

$p = 0.7$: H_0 will wrongly be accepted in 74.5% of the tests

Power of the test

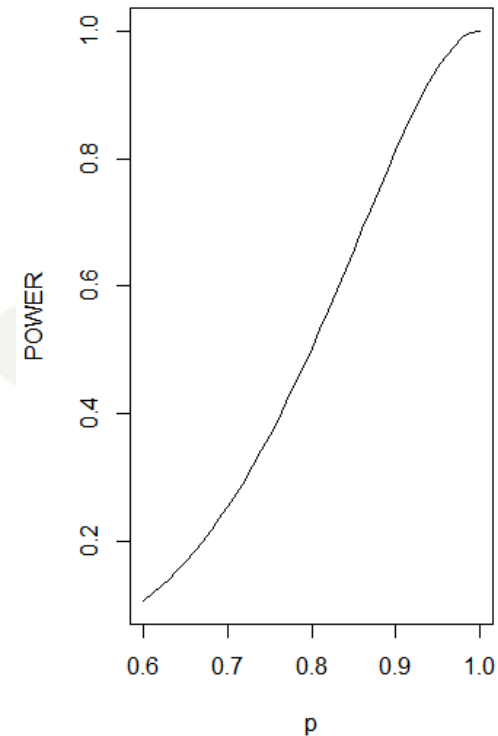
- The probability that a false H_0 is rejected
 $P(\text{reject } H_0 \mid H_1 \text{ true}) = 1 - P(\text{accept } H_0 \mid H_1 \text{ true}) = 1 - \beta$
- A test with large power has:
 - larger probability to draw the right conclusion
 - larger probability to reject a false null hypothesisthen a test with low power.
- α and β is connected:
 - Decreasing α will give an increased β which again will decrease the power of the test

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Example: power function

```
p <- seq(0.6, 1, 0.01)
antall <- length(p)
beta8 <- rep(NA, antall)
for(i in 1:antall){
  beta8[i] <- sum(dbinom(1:6, 8, p[i]))
}
power8 <- 1 - beta8
plot(p, power8, type = "l")
```



<http://www.stanford.edu/~stephsus/basic-stats-tests.pdf>

Summary of Basic Statistical Tests in R

| Type of data | What you want to know... | If data are... | then, in R, do... |
|--------------------------------|--------------------------------|--|---|
| 1 numerical vector | normal distribution? | | <code>shapiro.test()</code> , <code>ks.test()</code> |
| | equal probabilities? | counts | <code>chisq.test()</code> |
| | location of mean? | normal | <code>t.test()</code> |
| | | non-normal | <code>wilcox.test()</code> |
| 2 independent vectors | same distribution? | | <code>ks.test()</code> , <code>w.jitter</code> |
| | same means? | normal | <code>t.test()</code> |
| | | non-normal | <code>wilcox.test()</code> |
| | same variances? | normal | <code>var.test()</code> |
| 2 paired vectors | same means? | normal | <code>t.test(paired = T)</code> |
| | | non-normal | <code>wilcox.test(paired = T)</code> |
| | functional relation? | normal | <code>lm()</code> ¹ |
| | correlated? | normal | <code>cor.test()</code> |
| non-normal | | <code>cor.test(method='spearman')</code> | |
| 1 numerical vector + 1 factor | different group means? | normal, same variances | <code>lm()</code> ¹ , <code>anova()</code> ² , <code>aov()</code> |
| | | different variances | <code>kruskal.test()</code> |
| 2 numerical vectors + 1 factor | different means? interactions? | normal | <code>lm()</code> |
| 2 vectors of counts | different proportions? | | <code>chisq.test()</code> , <code>fischer.test()</code> |

¹In linear regression, watch out for outliers and nonlinear covariates.

²In anova with factor levels > 2, multiple comparisons inflate chances of a significant result; use Bonferroni correction or Tukey's HSD.

(adapted from Lab Syntax lecture on Bayes ch. 4 by Joan Bresnan, February 2011)

help(shapiro.test)

shapiro.test {stats}

R Documentation

Shapiro-Wilk Normality Test

Description

Performs the Shapiro-Wilk test of normality.

Usage

```
shapiro.test(x)
```

Arguments

`x` a numeric vector of data values. Missing values are allowed, but the number of non-missing values must be between 3 and 5000.

Value

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Value

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

`statistic` the value of the Shapiro-Wilk statistic.
`p.value` an approximate p-value for the test. This is said in Royston (1995) to be adequate for `p.value < 0.1`.
`method` the character string "Shapiro-Wilk normality test".
`data.name` a character string giving the name(s) of the data.

Source

The algorithm used is a C translation of the Fortran code described in Royston (1995) and found at <http://lib.stat.cmu.edu/apstat/R94>. The calculation of the p value is exact for $n = 3$, otherwise approximations are used, separately for $4 \leq n \leq 11$ and $n \geq 12$.

References

Patrick Royston (1982) An extension of Shapiro and Wilk's W test for normality to large samples. *Applied Statistics*, **31**, 115–124.

Patrick Royston (1982) Algorithm AS 181: The W test for Normality. *Applied Statistics*, **31**, 176–180.

Patrick Royston (1995) Remark AS R94: A remark on Algorithm AS 181: The W test for normality. *Applied Statistics*, **44**, 547–551.

See Also

[qgnorm](#) for producing a normal quantile-quantile plot.

Examples

```
shapiro.test(rnorm(100, mean = 5, sd = 3))
shapiro.test(runif(100, min = 2, max = 4))
```

shapiro.test()

```
> shapiro.test(rnorm(100, mean = 5, sd = 3))

      Shapiro-Wilk normality test

data:  rnorm(100, mean = 5, sd = 3)
W = 0.984, p-value = 0.2676

> shapiro.test(runif(100, min = 2, max = 4))

      Shapiro-Wilk normality test

data:  runif(100, min = 2, max = 4)
W = 0.9349, p-value = 9.553e-05

>
> |
```

chisq.test()

```
> M <- as.table(rbind(c(762, 327, 468), c(484,239,477)))
> dimnames(M) <- list(gender=c("M","F"), party=c("Democrat","Independent", "Republican"))
> M
      party
gender Democrat Independent Republican
M      762      327      468
F      484      239      477
> (Xsq <- chisq.test(M)) # Prints test summary

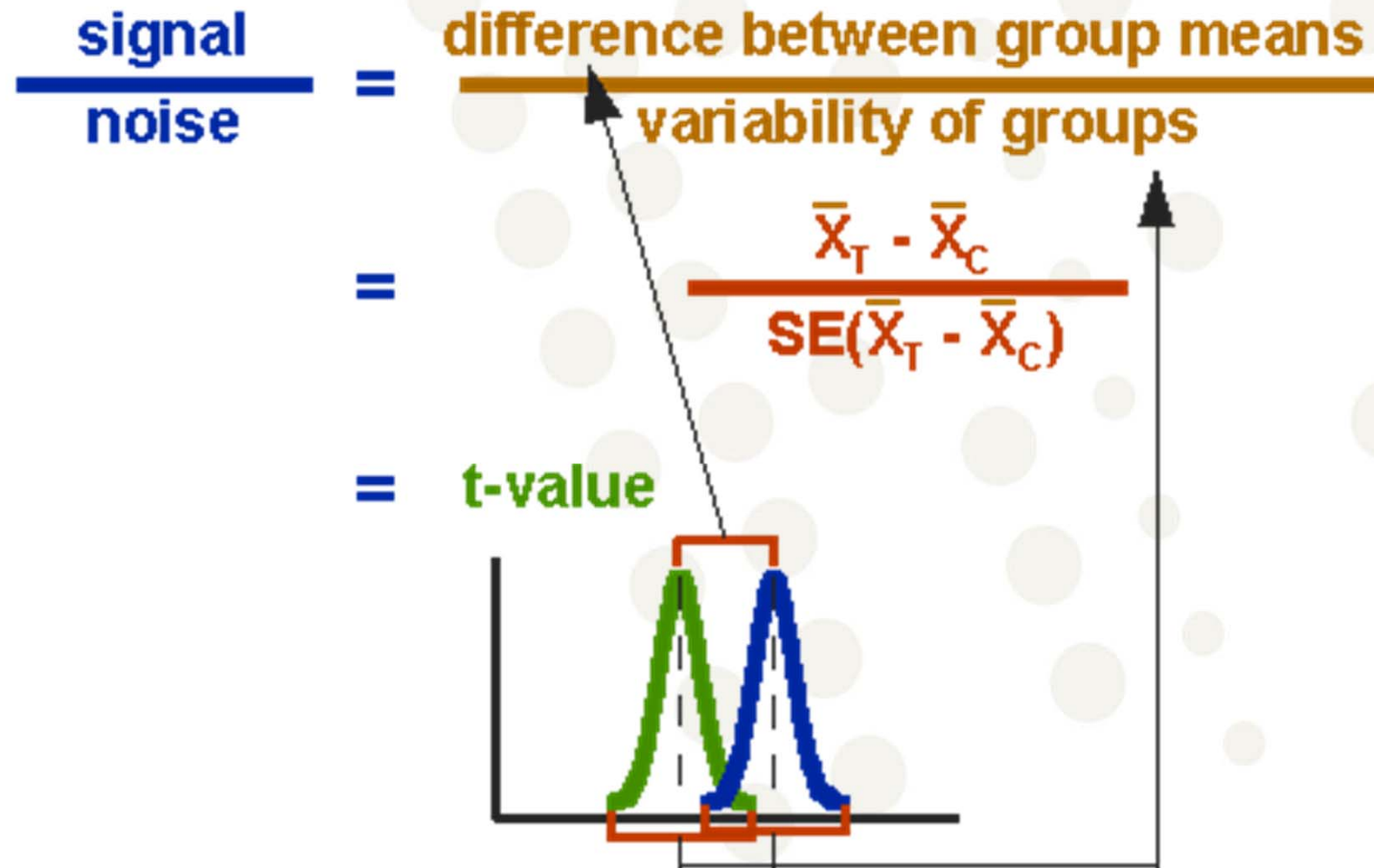
      Pearson's Chi-squared test

data:  M
X-squared = 30.0701, df = 2, p-value = 2.954e-07

> names(Xsq)
[1] "statistic" "parameter" "p.value"  "method"  "data.name" "observed"  "expected"  "residuals"
[9] "stdres"
> Xsq$observed # observed counts (same as M)
      party
gender Democrat Independent Republican
M      762      327      468
F      484      239      477
> Xsq$expected # expected counts under the null
      party
gender Democrat Independent Republican
M 703.6714      319.6453      533.6834
F 542.3286      246.3547      411.3166
> |
```

Reject the null hypotheses and assume that there are differences between the groups

t.test()



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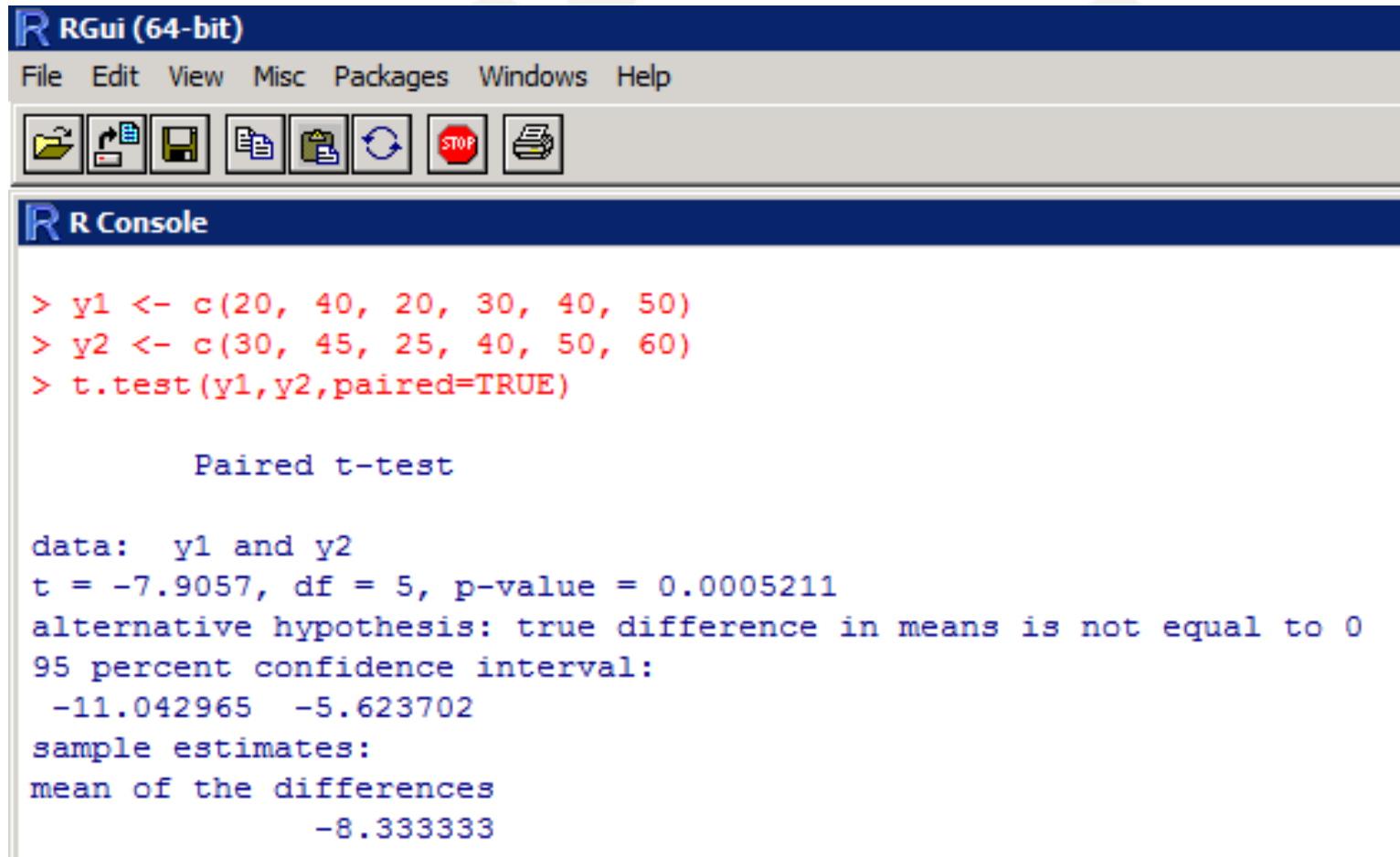
t.test()

```
R RGui (64-bit)
File Edit View Misc Packages Windows Help

Welch Two Sample t-test

data:  y1 and y2
t = -1.1532, df = 9.959, p-value = 0.2758
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -24.443863  7.777196
sample estimates:
mean of x mean of y
 33.33333  41.66667
```

t.test(, paired = TRUE)



```
RGui (64-bit)
File Edit View Misc Packages Windows Help

> y1 <- c(20, 40, 20, 30, 40, 50)
> y2 <- c(30, 45, 25, 40, 50, 60)
> t.test(y1,y2,paired=TRUE)

      Paired t-test

data:  y1 and y2
t = -7.9057, df = 5, p-value = 0.0005211
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -11.042965  -5.623702
sample estimates:
mean of the differences
                -8.333333
```

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wilcox.test()

- Same mean? But not normally distributed data.

```
R RGui (64-bit)
File Edit View Misc Packages Windows Help

[Icons: File Explorer, R, Save, Print, Refresh, Stop, Print]

R Console

> y1 <- c(20, 40, 20, 30, 40, 50)
> y2 <- c(30, 45, 25, 40, 50, 60)
> wilcox.test(y1,y2)

      Wilcoxon rank sum test with continuity correction

data:  y1 and y2
W = 11, p-value = 0.292
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(y1, y2) : cannot compute exact p-value with ties
^
```

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wilcox.test(, paired = TRUE)

```
R RGui (64-bit)
File Edit View Misc Packages Windows Help

[Icons: File Explorer, Copy, Paste, Save, Print, Refresh, Stop, Help]

R Console

> y1 <- c(20, 40, 20, 30, 40, 50)
> y2 <- c(30, 45, 25, 40, 50, 60)
> wilcox.test(y1,y2, paired = TRUE)

      Wilcoxon signed rank test with continuity correction

data:  y1 and y2
V = 0, p-value = 0.03054
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(y1, y2, paired = TRUE) :
  cannot compute exact p-value with ties
```

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help(cor.test)

cor.test {stats}

R Documentation

Test for Association/Correlation Between Paired Samples

Description

Test for association between paired samples, using one of Pearson's product moment correlation coefficient, Kendall's *tau* or Spearman's *rho*.

Usage

```
cor.test(x, ...)

## Default S3 method:
cor.test(x, y,
         alternative = c("two.sided", "less", "greater"),
         method = c("pearson", "kendall", "spearman"),
         exact = NULL, conf.level = 0.95, continuity = FALSE, ...)

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

Arguments

x, y numeric vectors of data values. **x** and **y** must have the same length.

alternative indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.

method a character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.

If `method` is "kendall" or "spearman", Kendall's *tau* or Spearman's *rho* statistic is used to estimate a rank-based measure of association. These tests may be used if the data do not necessarily come from a bivariate normal distribution.

For Kendall's test, by default (if `exact` is NULL), an exact p-value is computed if there are less than 50 paired samples containing finite values and there are no ties. Otherwise, the test statistic is the estimate scaled to zero mean and unit variance, and is approximately normally distributed.

For Spearman's test, p-values are computed using algorithm AS 89 for $n < 1290$ and `exact = TRUE`, otherwise via the asymptotic *t* approximation. Note that these are 'exact' for $n < 10$, and use an Edgeworth series approximation for larger sample sizes (the cutoff has been changed from the original paper).

Value

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

| | |
|--------------------------|---|
| <code>statistic</code> | the value of the test statistic. |
| <code>parameter</code> | the degrees of freedom of the test statistic in the case that it follows a t distribution. |
| <code>p.value</code> | the p-value of the test. |
| <code>estimate</code> | the estimated measure of association, with name "cor", "tau", or "rho" corresponding to the method employed. |
| <code>null.value</code> | the value of the association measure under the null hypothesis, always 0. |
| <code>alternative</code> | a character string describing the alternative hypothesis. |
| <code>method</code> | a character string indicating how the association was measured. |
| <code>data.name</code> | a character string giving the names of the data. |
| <code>conf.int</code> | a confidence interval for the measure of association. Currently only given for Pearson's product moment correlation coefficient in case of at least 4 complete pairs of observations. |

References

D. J. Best & D. E. Roberts (1975), Algorithm AS 89: The Upper Tail Probabilities of Spearman's *rho*. *Applied Statistics*, **24**, 377–379.

Myles Hollander & Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 185–194 (Kendall and Spearman tests).

Arguments

| | |
|--------------------------|--|
| <code>x, y</code> | numeric vectors of data values. <code>x</code> and <code>y</code> must have the same length. |
| <code>alternative</code> | indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association. |
| <code>method</code> | a character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated. |
| <code>exact</code> | a logical indicating whether an exact p-value should be computed. Used for Kendall's <i>tau</i> and Spearman's <i>rho</i> . See 'Details' for the meaning of <code>NULL</code> (the default). |
| <code>conf.level</code> | confidence level for the returned confidence interval. Currently only used for the Pearson product moment correlation coefficient if there are at least 4 complete pairs of observations. |
| <code>continuity</code> | logical: if true, a continuity correction is used for Kendall's <i>tau</i> and Spearman's <i>rho</i> when not computed exactly. |
| <code>formula</code> | a formula of the form $\sim u + v$, where each of <code>u</code> and <code>v</code> are numeric variables giving the data values for one sample. The samples must be of the same length. |
| <code>data</code> | an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> . |
| <code>subset</code> | an optional vector specifying a subset of observations to be used. |
| <code>na.action</code> | a function which indicates what should happen when the data contain <code>NA</code> s. Defaults to <code>getOption("na.action")</code> . |
| <code>...</code> | further arguments to be passed to or from methods. |

Details

The three methods each estimate the association between paired samples and compute a test of the value being zero. They use different measures of association, all in the range $[-1, 1]$ with 0 indicating no association. These are sometimes referred to as tests of no *correlation*, but that term is often confined to the default method.

If `method` is "pearson", the test statistic is based on Pearson's product moment correlation coefficient `cor(x, y)` and follows a t distribution with `length(x) - 2` degrees of freedom if the samples follow independent normal distributions. If there are at least 4 complete pairs of observation, an asymptotic confidence interval is given based on Fisher's Z transform.

See Also

[Kendall](#) in package [Kendall](#).

[pKendall](#) and [pSpearman](#) in package [SuppDists](#), [spearman.test](#) in package [pspearman](#), which supply different (and often more accurate) approximations.

Examples

```
## Hollander & Wolfe (1973), p. 187f.
## Assessment of tuna quality. We compare the Hunter L measure of
## lightness to the averages of consumer panel scores (recoded as
## integer values from 1 to 6 and averaged over 80 such values) in
## 9 lots of canned tuna.

x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
y <- c( 2.6,  3.1,  2.5,  5.0,  3.6,  4.0,  5.2,  2.8,  3.8)

## The alternative hypothesis of interest is that the
## Hunter L value is positively associated with the panel score.

cor.test(x, y, method = "kendall", alternative = "greater")
## => p=0.05972

cor.test(x, y, method = "kendall", alternative = "greater",
         exact = FALSE) # using large sample approximation
## => p=0.04765

## Compare this to
cor.test(x, y, method = "spearm", alternative = "g")
cor.test(x, y,                alternative = "g")

## Formula interface.
require(graphics)
pairs(USJudgeRatings)
cor.test(~ CONT + INTG, data = USJudgeRatings)
```

```
>  
> x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)  
> y <- c( 2.6,  3.1,  2.5,  5.0,  3.6,  4.0,  5.2,  2.8,  3.8)  
>  
> cor.test(x, y, method = "spearm", alternative = "g")
```

Spearman's rank correlation rho

```
data:  x and y  
S = 48, p-value = 0.0484  
alternative hypothesis: true rho is greater than 0  
sample estimates:  
rho  
0.6
```

```
> cor.test(x, y,                      alternative = "g")
```

Pearson's product-moment correlation

```
data:  x and y  
t = 1.8411, df = 7, p-value = 0.05409  
alternative hypothesis: true correlation is greater than 0  
95 percent confidence interval:  
-0.02223023  1.00000000  
sample estimates:  
      cor  
0.5711816
```



Multiple hypothesis testing

- Tests are designed such that it has an expected proportion of incorrectly rejected null hypotheses, most often this level is 5%.
- When many tests are done the probability of rejecting a null hypotheses falsely increase, hence we can correct the probabilities according to how many tests that are done.

Example 10000 genes

- Q: is gene g , $g = 1, \dots, 10\,000$, differentially expressed?
- Gives 10 000 null hypothesis: $H_0^1, H_0^2, \dots, H_0^{10000}$
 - H_0^1 : gene 1 not differentially expressed
 - ...
- Assume: no genes differentially expressed
 - H_0^g true for all g
- Significance level $\alpha \leq 0.01$
 - The probability to incorrectly conclude that one gene is differentially expressed is 0.01. e.g. $0.01 * 10000 = 100$ expected wrong rejections of H_0^g

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Need to control the risk of false positive Type I error

- Corrected p-value:
 - The original p-values do not tell the full story.
 - Instead of using the original p-values for decision making, we should use corrected ones.

Different correction methods

- Bonferroni (1935)
 - Just multiply all the p-values by the number of tests
 - Too conservative
 - need very small p-value to reject H_0
 - give very little power
- Methods that control the family-wise error rate (FWER).
- Methods that control the false discovery rate (FDR).

Family-Wise Error Rate (FWER)

- Control type I errors at a level α
 - Bonferroni
 - Sidak
 - Bonferroni-Holm
 - Westfall & Young
- Use one of these if you are most afraid of getting stuff on your significant list that should not have been there

False Discovery Rate (FDR)

- Calculate the expected proportion of type I error among the rejected hypotheses
- Technique that applies to a set of p-values
 - Benjamini & Hochberg
 - Different newer variants of Benjamini & Hochberg
- Use one of these if you are you most afraid of missing out on interesting stuff

help(p.adjust)

p.adjust {stats}

R Docu

Adjust P-values for Multiple Comparisons

Description

Given a set of p-values, returns p-values adjusted using one of several methods.

Usage

```
p.adjust(p, method = p.adjust.methods, n = length(p))
```

```
p.adjust.methods  
# c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",  
#   "fdr", "none")
```

Arguments

p numeric vector of p-values (possibly with [NAs](#)). Any other R is coerced by [as.numeric](#).

method correction method

n number of comparisons, must be at least `length(p)`; only set this (to non-default) when you know what you are doing!

False discovery rate (fdr)

```
> x <- rnorm(50, mean=c(rep(0,25),rep(3,25)))
> round(x, 3)
 [1]  1.431 -0.302 -0.607 -2.164  0.381  0.227 -1.140  1.658 -0.720 -1.298
[11]  1.587 -0.245  1.722  1.135 -0.806 -1.838 -1.332 -0.830 -2.034  0.800
[21] -0.301  0.692  0.391  0.050  0.892  2.067  3.490  2.833  3.567  2.861
[31]  1.138  3.056 -0.044  3.471  2.617  3.064  2.270  3.828  3.004  2.929
[41]  3.877  2.243  2.726  2.783  3.683  3.883  2.945  2.156  5.059  3.996
> p <- 2*pnorm( sort(-abs(x)) )
> round(p, 3)
 [1] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.001 0.002 0.002 0.003
[13] 0.003 0.003 0.004 0.005 0.005 0.006 0.009 0.023 0.025 0.030 0.031 0.039
[25] 0.042 0.066 0.085 0.097 0.113 0.153 0.183 0.194 0.254 0.255 0.256 0.372
[37] 0.406 0.420 0.424 0.471 0.489 0.544 0.696 0.703 0.763 0.763 0.806 0.821
[49] 0.960 0.965
> round(p.adjust(p, "fdr"), 3)
 [1] 0.000 0.001 0.001 0.001 0.001 0.002 0.003 0.003 0.003 0.010 0.010 0.011
[13] 0.012 0.012 0.014 0.014 0.016 0.018 0.023 0.058 0.059 0.068 0.068 0.081
[25] 0.084 0.127 0.158 0.174 0.194 0.254 0.295 0.304 0.366 0.366 0.366 0.517
[37] 0.543 0.543 0.543 0.589 0.596 0.647 0.799 0.799 0.830 0.830 0.855 0.855
[49] 0.965 0.965
```

regression

- Next lecture!

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