

BST02: Using R for Statistics in Medical Research

Part D: Statistics with R

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t-test: `t.test()`

One-sample t-test

- ▶ compares the mean of a sample with a fixed value μ

Two sample / independent samples t-test

- ▶ compares the difference between the means of two samples with a fixed value μ

Related samples t-test

- ▶ compares the mean of the difference between related observations with a fixed value μ (same as one-sample t-test)

Wilcoxon Test: `wilcox.test()`

Wilcoxon Signed Rank Test

- ▶ tests if one sample (or the differences between two paired samples) is/are symmetric about μ

Wilcoxon Rank Sum Test / Mann-Whitney test

- ▶ test for a location shift between the distributions of two independent samples

See also BBR Sections 7.2 & 7.3 (<http://hbiostat.org/doc/bbr.pdf>)

Kruskal-Wallis Rank Sum Test: `kruskal.test()`

- ▶ This is an extension of the Wilcoxon rank sum test for more than two groups
- ▶ Test for a difference in location of a continuous variable between multiple groups
- ▶ The Wilcoxon rank sum test is a special case of the Kruskal-Wallis rank sum test

Other tests for continuous data

- ▶ **Kolmogoriv-Smirnov Test:** `ks.test()`
tests if two samples are drawn from the same continuous distribution
- ▶ **Shapiro-Wilk Normality Test:** `shapiro.test()`
- ▶ **Friedman Rank Sum Test:** `friedman.test()`
non-parametric test for 2 or more related samples
- ▶ ...

Tests for Categorical Data / Proportions

One-sample Proportion Test

- ▶ tests if the proportion in one sample is equal to a fixed value p
- ▶ `prop.test()` and `binom.test()`

Tests for Proportions in Multiple (independent) Groups

- ▶ tests if the proportion in several samples are equal
- ▶ `chisq.test()` and `fisher.test()` (when there are cells with 0)

See also BBR Sections 5.7 & 6 (<http://hbiostat.org/doc/bbr.pdf>)

Tests for Categorical Data / Proportions

Related Samples: McNemar Test

- ▶ Tests for symmetry in a 2×2 table
- ▶ `mcnemar.test()`

3-Dimensional Contingency Table

- ▶ Cochran-Mantel-Haenszel Test
- ▶ χ^2 test for independence of two nominal variables in each stratum
- ▶ `mantelhaen.test()`

Statistical Tests

Demos

- ▶ Name of the demo
- ▶ Name of demo

Practicals

- ▶ Name of practical **html**
- ▶ Name of practical **html**

Statistical Tests

Continuous Outcomes

- ▶ `t.test()`
- ▶ `wilcox.test()`
- ▶ `kruskal.test()`
- ▶ `ks.test()`
- ▶ `friedman.test()`
- ▶ `shapiro.test()`

Categorical Outcomes

- ▶ `prop.test()`
- ▶ `binom.test()`
- ▶ `chisq.test()`
- ▶ `fisher.test()`
- ▶ `mcnemar.test()`
- ▶ `mantelhaen.test()`

Variance and Correlation

- ▶ `cor.test()`
- ▶ `bartlett.test()`
- ▶ `var.test()`

Pairwise tests

- ▶ `pairwise.prop.test()`
- ▶ `pairwise.t.test()`
- ▶ `pairwise.wilcox.test()`

Linear Regression

A standard linear regression model has the form

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p + \varepsilon \quad \text{with } \varepsilon \sim N(0, \sigma^2)$$

where

- ▶ y is the **outcome** variable (“dependent variable”)
- ▶ x_1, \dots, x_p are the **covariates** (“independent variables”)
- ▶ β_0, \dots, β_p are the **regression coefficients**
 - ▶ β_0 is the intercept
 - ▶ β_1, \dots, β_p estimate the effects of the covariates
- ▶ ε is a vector of **residuals**, which we assume to be (approximately) normally distributed.

Linear Regression

To fit a **linear regression** in R we use the function `lm()`.

The most important arguments are

- ▶ **formula:**
a formula object
- ▶ **data:**
a `data.frame` (optional, but usually needed)
- ▶ **subset:**
a vector specifying which observations should be used (optional)

Model Formula

A formula object has the form

```
outcome ~ linear predictor
```

for example

```
y ~ x1 + x2 + x3
```

- ▶ Variables are separated by “+” signs.
- ▶ An intercept is automatically included.
- ▶ one-sided formulas (omitting the outcome) are possible (used for random effects specification)

Model Formula: Interactions

Interaction terms are written using “:” or “*”.

“*” includes the main effects and interaction terms, i.e.,

```
y ~ x1 * x2
```

is equivalent to

```
y ~ x1 + x2 + x1:x2
```

Interactions between multiple variables can be written using “()”, i.e.,

```
y ~ x1 * (x2 + x3)
```

is equivalent to

```
y ~ x1 * x2 + x1 * x3
```

Model Formula: Interactions

To specify a **higher level interaction** (for example a three-way interaction) “^” is used, i.e.,

```
y ~ (x1 + x2 + x3)^3
```

will create all interactions up to 3-way and is equivalent to

```
y ~ x1 * x2 * x3
```

and equivalent to

```
y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3 + x1:x2:x3
```

and

```
y ~ (x1 + x2 + x3)^2
```

will create all two-way interactions and is equivalent to

```
y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3
```

Model Formula: Removing terms

The “-” sign can be used to remove terms from a model formula, for example

```
y ~ x1 * x2 * x3 - x2 - x1:x3
```

is equivalent to

```
y ~ x1 + x3 + x1:x2 + x2:x3 + x1:x2:x3
```

The **intercept** can be removed from a formula by using “-1” or “+0”, i.e.

```
y ~ x1 + x2 - 1
```

```
y ~ x1 + x2 + 0
```

Generalized Linear Regression (GLM)

A **generalized linear regression** model has the form

$$g(\mathbb{E}(y)) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

where $g(\)$ is a link function and y is from the exponential family.

For example **logistic regression** for binary y :

$$\log \left(\frac{P(y = 1)}{1 - P(y = 1)} \right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

$\log \left(\frac{p}{1-p} \right)$ is the **logit** link.

Generalized Linear Regression (GLM)

To fit a **GLM** in R we use the function `glm()`.

The most important arguments are

- ▶ **formula:**
a formula object
- ▶ **family:**
a family object or name of the family function, describing the error distribution and link function
- ▶ **data:**
a `data.frame` (optional, but usually needed)
- ▶ **subset:**
a vector specifying which observations should be used (optional)

Families and Link Functions

Common families & available links in R:

(see also `?family`)

family	link
binomial	logit, probit, cauchit, log, cloglog
gaussian	identity, log, inverse
Gamma	inverse, identity, log
poisson	log, identity, sqrt

The `family` argument in `glm()` can be specified in the following ways:

- ▶ `binomial(link = "logit")`
- ▶ `binomial()`
- ▶ `binomial`
- ▶ `"binomial"`

Note:

When the link is not explicitly specified (i.e. option 1), the default link is used.

Regression

Regression Models

- ▶ `lm()`
- ▶ `glm()`

Regression Results

- ▶ `summary()`
- ▶ `coef()`, `confint()`
- ▶ `fitted()`, `residuals()`
- ▶ `AIC()`, `BIC()`
- ▶ `anova()`

Plots

- ▶ `plot()`
- ▶ `qqnorm()`, `qqline()`, `qqplot()`

Topic

- ▶ `ns()`, `bs()`, `I()`
- ▶ `p.adjust()`
- ▶ `all.vars()`
- ▶ `update()`
- ▶ `as.formula()`