

# Package ‘DanielBiostatistics10th’

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DanielBiostatistics10th-package

*Functions for Wayne W. Daniel's Biostatistics (Tenth Edition)*

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### Description

Functions and examples to accompany Wayne W. Daniel's *Biostatistics: A Foundation for Analysis in the Health Sciences*, Tenth Edition, Wiley, ISBN: 978-1-119-62550-6.

<https://www.wiley.com/en-us/Biostatistics:+A+Foundation+for+Analysis+in+the+Health+Sciences,+10th+Edition-p-9781119625506>

Data sets from 10th edition <https://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=7849&itemId=1118302796&resourceId=30373>.

Resources from 11th edition <https://bcs.wiley.com/he-bcs/Books?action=index&bcsId=11491&itemId=1119496578>, with errata of data.

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Chapter01

*Chapter 1: Introduction to Biostatistics*

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### Description

Functions and examples for Chapter 1, *Introduction to Biostatistics*.

### Usage

```
sampleRow(x, size, replace = FALSE, prob = NULL)
```

**Arguments**

x	a <a href="#">data.frame</a>
size	positive <a href="#">integer</a> scalar, number of rows to be selected
replace	<a href="#">logical</a> scalar, whether sampling should be with replacement (default FALSE)
prob	<a href="#">numeric</a> vector of probability weights for each row of input x being sampled. Default NULL indicates simple random sampling

**Value**

Function [sampleRow](#) returns a [data.frame](#), a simple random sample from the input.

**See Also**

[sample.int](#)

**Examples**

```
library(DanielBiostatistics10th)
# To run a line of code, use shortcut
# Command + Enter: Mac and RStudio Cloud
# Control + Enter: Windows, Mac and RStudio Cloud
# To clear the console
# Control + L: Windows, Mac and RStudio Cloud

# Example 1.4.1; Page 8 (10th ed), Page 7 (11th ed)
class(EXA_C01_S04_01) # `EXA_C01_S04_01` is a 'data.frame' (a specific class defined in R)
dim(EXA_C01_S04_01) # dimension, number-row and number-column
head(EXA_C01_S04_01, n = 8L) # first `n` rows of a 'data.frame'
names(EXA_C01_S04_01) # column names of a 'data.frame'
EXA_C01_S04_01$AGE # use `$` to obtain one column from a 'data.frame'
sampleRow(EXA_C01_S04_01, size = 10L, replace = FALSE) # to answer Example 1.4.1

# Example 1.4.2; Page 11 (10th ed), Page 10 (11th ed)
EXA_C01_S04_01[seq.int(from = 4L, to = 166L, by = 18L), ]
```

**Description**

Functions and examples for Chapter 2, *Descriptive Statistics*.

**Usage**

```
print_stats(x, na.rm = TRUE)
```

```
print_freqs(x, breaks, include.lowest = TRUE, right = TRUE)
```

**Arguments**

x	numeric vector, the observations. In function <code>print_freqs</code> , this argument can also be a <code>factor</code>
na.rm	logical scalar, whether to remove the missing observations (default TRUE)
breaks	numeric vector, see <code>cut.default</code>
include.lowest	logical scalar, default TRUE. See <code>cut.default</code>
right	logical scalar, see <code>cut.default</code>

**Details**

Function `print_freqs` prints the (relative) frequencies and cumulative (relative) frequencies, from a numeric input vector, specified interval breaks as well as open/close status of the ends of the intervals.

Function `print_stats` prints the simple statistics of the input observations, such as sample size, mean, median, (smallest) mode, variance, standard deviation, coefficient of variation (if all observations are non-negative), quartiles, inter-quartile range (IQR), range, skewness and kurtosis. A histogram is also printed.

**Value**

Function `print_freqs` returns a `freqs` object, for which a `show` method is defined.

Function `print_stats` does not have a returned value.

**See Also**

[cut.default](#) [table](#) [cumsum](#) [mean.default](#) [median.default](#) [Mode](#) [var](#) [sd](#) [quantile](#) [skewness](#) [kurtosis](#)

**Examples**

```
library(DanielBiostatistics10th)

# Example 2.2.1; Page 20 (10th ed), Page 19 (11th ed)
head(EXA_C01_S04_01)
class(age <- EXA_C01_S04_01$AGE) # 'integer'
sort(age) # Table 2.2.1

# Example 2.3.1; Page 23 (10th ed); Page 22 (11th ed)
(r231 = print_freqs(age, breaks = seq.int(from=30, to=90, by=10), right = FALSE)) # Table 2.3.2
# The open/close of interval ends is determined by textbook using 30-39, 40-49, etc.

# Example 2.4.1-2.4.6; Page 38-42 (10th ed); Page 30-34 (11th ed)
# Example 2.5.1-2.5.3; Page 44-46 (10th ed); Page 35-41 (11th ed)
print_stats(age)

# Example 2.5.4 (omitted); Page 49 (10th ed), Page 41 (11th ed)

# Example 2.5.5; Page 50 (10th ed)
head(EXA_C02_S05_05)
boxplot(EXA_C02_S05_05$GRF, main = c('Example 2.5.5 (10th ed)'))
```

```
print_stats(EXA_C02_S05_05$GRF)
print_freqs(EXA_C02_S05_05$GRF, breaks = seq.int(10, 45, by = 5))
```

**Description**

Examples in Chapter 3, *Some Basic Probability Concepts*.

**Value**

No function defined for Chapter 3.

**Examples**

```
library(DanielBiostatistics10th)

# Example 3.4.1-3.4.9; Page 69-75 (10th ed), Page 61-67 (11th ed)
(d341 = matrix(c(28L, 19L, 41L, 53L, 35L, 38L, 44L, 60L), ncol = 2L, dimnames = list(
  FamilyHx = c('none', 'Bipolar', 'Unipolar', 'UniBipolar'), Onset = c('Early', 'Late'))))
class(d341) # 'matrix', i.e., a two-dimensional 'array'
addProbs(d341)
addProbs(d341, margin = 2L)
addProbs(d341, margin = 1L)

# Example 3.5.1; Page 81 (10th ed), Page 72 (11th ed)
(d351 = matrix(c(495L, 14L, 5L, 436L), nrow = 2L, dimnames = list(
  Alzheimer = c('No', 'Yes'), Test = c('Negative', 'Positive'))))
print(binTab(d351), prevalence = .113)
```

**Description**

Examples in Chapter 4, *Probability Distributions*.

**Value**

No function defined for Chapter 4.

**Examples**

```

library(DanielBiostatistics10th)

# Example 4.2.1-4.2.7; Page 93-97 (10th ed), Page 81-85 (11th ed)
(d421 = rep(1:8, times = c(62L, 47L, 39L, 39L, 58L, 37L, 4L, 11L)))
print_freqs(d421) # Table 4.2.1, 4.2.2, Table 4.2.3

# Example 4.2.8; Page 98 (10th ed), Page 85 (11th ed)
mean(d421)
sd(d421)
var(d421)

# ?dbinom # 'd' for binomial 'density'; calculate Prob(X = x)
# ?pbinom # 'p' for binomial 'probability'
# `lower.tail = TRUE` (default), calculate Prob(X <= x)
# `lower.tail = FALSE`, calculate Prob(X > x)

# Example 4.3.1; Page 99 (10th ed)
dbinom(x = 3L, size = 5L, prob = .858)
# Example 4.3.1; Page 87 (11th ed)
dbinom(x = 3L, size = 5L, prob = .899)

# Example 4.3.2; Page 103 (10th ed), Page 90 (11th ed)
dbinom(x = 4L, size = 10L, prob = .14)

# Example 4.3.3; Page 103 (10th ed), Page 91 (11th ed)
(pL = pbinom(q = 5L, size = 25L, prob = .1, lower.tail = TRUE)) # (a) P(X <= 5L)
(pU = pbinom(q = 5L, size = 25L, prob = .1, lower.tail = FALSE)) # (b) P(X > 5L)
pL + pU # = 1

# Example 4.3.4; Page 105 (10th ed), Page 92 (11th ed)
dbinom(x = 7L, size = 12L, prob = .55)
pbinom(q = 5L, size = 12L, prob = .55)
pbinom(q = 7L, size = 12L, prob = .55, lower.tail = FALSE)

# Example 4.4.1; Page 110 (10th ed), Page 97 (11th ed)
dpois(x = 3L, lambda = 12)

# Example 4.4.2; Page 110 (10th ed), Page 98 (11th ed)
ppois(q = 2L, lambda = 12, lower.tail = FALSE)

# Example 4.4.3; Page 110 (10th ed), Page 98 (11th ed)
ppois(q = 1L, lambda = 2)

# Example 4.4.4; Page 111 (10th ed), Page 98 (11th ed)
dpois(x = 3L, lambda = 2)

# Example 4.4.5; Page 112 (10th ed), Page 98 (11th ed)
ppois(q = 5L, lambda = 2, lower.tail = FALSE)

# Example 4.6.1; Page 119 (10th ed), Page 106 (11th ed)
pnorm(q = 2)

```

```

# Example 4.6.2; Page 120 (10th ed), Page 106 (11th ed)
pnorm(2.55) - pnorm(-2.55)
1 - 2 * pnorm(-2.55) # alternative solution

# Example 4.6.3; Page 121 (10th ed), Page 107 (11th ed)
pnorm(1.53) - pnorm(-2.74)

# Example 4.6.4; Page 121 (10th ed), Page 107 (11th ed)
pnorm(2.71, lower.tail = FALSE)

# Example 4.6.5; Page 122 (10th ed), Page 107 (11th ed)
pnorm(2.45) - pnorm(.84)

# Example 4.7.1; Page 122 (10th ed), Page 109 (11th ed)
pnorm(q = 3, mean = 5.4, sd = 1.3)
pnorm(q = (3-5.4)/1.3) # manual solution

# Example 4.7.2; Page 125 (10th ed), Page 111 (11th ed)
pnorm(q = 649, mean = 491, sd = 119) - pnorm(q = 292, mean = 491, sd = 119)

# Example 4.7.3; Page 122 (10th ed), Page 111 (11th ed)
1e4L * pnorm(q = 8.5, mean = 5.4, sd = 1.3, lower.tail = FALSE)

```

## Description

Functions for Chapter 5, *Some Important Sampling Distributions*, Chapter 6, *Estimation* and Chapter 7, *Hypothesis Testing*.

## Usage

```

aggregated_z(
  xbar,
  n,
  sd,
  null.value,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  ...
)

```

```

aggregated_t(
  xbar,
  xsd,
  n,
  null.value,

```

```

var.equal = FALSE,
alternative = c("two.sided", "less", "greater"),
conf.level = 0.95,
...
)

prop_CLT(
  x,
  n,
  obs,
  xbar = x/n,
  null.value,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  ...
)

aggregated_var(
  xsd,
  n,
  null.value,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  ...
)

```

### Arguments

xbar	<b>numeric</b> scalar or <b>length-2 vector</b> . Sample mean(s) for <b>numeric</b> variable(s) $\bar{x}$ or $(\bar{x}_1, \bar{x}_2)$ . Sample proportion(s) for binary (i.e., <b>logical</b> ) variable(s) $\hat{p}$ or $(\hat{p}_1, \hat{p}_2)$ . In the case of two-sample tests, this could also be a <b>numeric</b> scalar indicating the difference in sample means $\bar{x}_1 - \bar{x}_2$ or sample proportions $\hat{p}_1 - \hat{p}_2$
n	<b>integer</b> scalar $n$ or <b>length-2 vector</b> $(n_1, n_2)$ , sample size(s)
sd	<b>numeric</b> scalar $\sigma$ or <b>length-2 vector</b> $(\sigma_1, \sigma_2)$ , population standard deviation(s)
null.value	(optional) <b>numeric</b> scalar or <b>length-2 vector</b> . Null value(s) of the population mean(s) $(\mu_0, (\mu_{10}, \mu_{20}),$ or $\mu_{10} - \mu_{20})$ for functions <a href="#">aggregated_z</a> and <a href="#">aggregated_t</a> . Null value(s) of the population proportion(s) $(p_0, (p_{10}, p_{20}),$ or $p_{10} - p_{20})$ for <a href="#">prop_CLT</a> . Null value(s) of the population variance(s) (ratio) $(\sigma_0^2, (\sigma_{10}^2, \sigma_{20}^2),$ or $\sigma_{10}^2/\sigma_{20}^2)$ for function <a href="#">aggregated_var</a> . If missing, only the confidence intervals will be computed.
alternative	<b>character</b> scalar, alternative hypothesis, either 'two.sided' (default), 'greater' or 'less'
conf.level	<b>numeric</b> scalar $(1 - \alpha)$ , confidence level, default 0.95
...	potential arguments, not in use currently
xsd	<b>numeric</b> scalar $s$ or <b>length-2 vector</b> $(s_1, s_2)$ , sample standard deviation(s)
var.equal	<b>logical</b> scalar, whether to treat the two population variances as being equal (default FALSE) in function <a href="#">aggregated_t</a>



x	<a href="#">integer</a> scalar or <a href="#">length-2 vector</a> , number of positive count(s) of binary (i.e., <a href="#">logical</a> ) variable(s)
obs	<a href="#">vector</a> , observations, currently used only in one-sample $z$ -test on proportion <a href="#">prop_CLT</a>

### Details

Function [aggregated\\_z](#) performs one- or two-sample  $z$ -test using the aggregated statistics of sample mean(s) and sample size(s) when `null.value` is provided. Otherwise, only the confidence interval based on  $z$ -distribution is computed.

Function [aggregated\\_t](#) performs one- or two-sample  $t$ -test using the aggregated statistics of sample mean(s), sample standard deviation(s) and sample size(s) when `null.value` is provided. Otherwise, only the confidence interval based on  $t$ -distribution is computed.

Function [prop\\_CLT](#) performs one- or two-sample  $z$ -test on proportion(s), using Central Limit Theorem when `null.value` is provided. Otherwise, only the confidence interval based on  $z$ -distribution is computed.

Function [aggregated\\_var](#) performs one-sample  $\chi^2$ -test on variance, or two-sample  $F$ -test on variances, using the aggregated statistics of sample standard deviation(s) and sample size(s) when `null.value` is provided. Otherwise, only the confidence interval based on  $\chi^2$ - or  $F$ -distribution is computed.

### Value

Function [aggregated\\_z](#) returns an 'htest' object when `null.value` is provided, otherwise returns a length-two [numeric](#) vector.

Function [aggregated\\_t](#) returns an [htest](#) object when `null.value` is provided, otherwise returns a length-two [numeric](#) vector.

Function [prop\\_CLT](#) returns an [htest](#) object when `null.value` is provided, otherwise returns a length-two [numeric](#) vector.

Function [aggregated\\_var](#) returns an [htest](#) object when `null.value` is provided, otherwise returns a length-two [numeric](#) vector.

### See Also

[t.test](#) [prop.test](#) [var.test](#)

### Examples

```
library(DanielBiostatistics10th)

# Example 5.3.2; Page 142 (10th ed)
aggregated_z(xbar = 190, sd = 12.7, n = 10L, null.value = 185.6, alternative = 'greater')

# Example 5.3.3;
# Page 143 (10th ed)
pnorm(125, mean = 120, sd = 15/sqrt(50)) - pnorm(115, mean = 120, sd = 15/sqrt(50))
aggregated_z(125, sd = 15, n = 50L, null.value = 120, alternative = 'less')$p.value -
  aggregated_z(115, sd = 15, n = 50L, null.value = 120, alternative = 'less')$p.value
```

```
# Page 127 (11th ed)
aggregated_z(110, sd = 20, n = 50L, null.value = 100, alternative = 'less')$p.value -
  aggregated_z(95, sd = 20, n = 50L, null.value = 100, alternative = 'less')$p.value

# Example 5.4.1; Page 145 (10th ed), Page 129 (11th ed)
aggregated_z(xbar = c(92, 105), sd = 20, n = 15L, null.value = 0, alternative = 'less')

# Example 5.4.2; Page 148 (10th ed),
aggregated_z(xbar = 20, sd = c(15, 20), n = c(35L, 40L), null.value = c(45, 30),
  alternative = 'greater')

# Example 5.5.1; Page 150 (10th ed),
prop_CLT(xbar = .4, n = 150L, null.value = .357, alternative = 'greater')

# Example 5.5.2; Page 152 (10th ed),
prop_CLT(xbar = .45, n = 200L, null.value = .51, alternative = 'less')

# Example 5.6.1; Page 155 (10th ed),
prop_CLT(xbar = .1, null.value = c(.28, .21), n = c(100L, 100L), alternative = 'greater')

# Example 5.6.2; Page 155 (10th ed),
prop_CLT(xbar = .05, null.value = c(.34, .26), n = c(250L, 200L), alternative = 'less')

# Example 6.2.1; Page 166 (10th ed), Page 147 (11th ed)
aggregated_z(xbar = 22, n = 10L, sd = sqrt(45))

# Example 6.2.2; Page 168 (10th ed), Page 149 (11th ed)
aggregated_z(xbar = 84.3, n = 15L, sd = sqrt(144), conf.level = .99)

# Example 6.2.3; Page 168 (10th ed), Page 150 (11th ed)
aggregated_z(xbar = 17.2, n = 35L, sd = 8, conf.level = .9)

# Example 6.2.4; Page 169 (10th ed), Page 150 (11th ed)
head(EXA_C06_S02_04)
aggregated_z(xbar = mean(EXA_C06_S02_04$ACTIVITY), n = nrow(EXA_C06_S02_04), sd = sqrt(.36))

# Example 6.3.1; Page 173 (10th ed),
aggregated_t(xbar = 250.8, xsd = 130.9, n = 19L)

# Example 6.4.1; Page 177 (10th ed),
aggregated_z(xbar = c(4.5, 3.4), sd = sqrt(c(1, 1.5)), n = c(12L, 15L))

# Example 6.4.2; Page 178 (10th ed),
aggregated_z(xbar = c(4.3, 13), sd = c(5.22, 8.97), n = c(328L, 64L), conf.level = .99)

# Example 6.4.3; Page 180 (10th ed),
aggregated_t(xbar = c(4.7, 8.8), xsd = c(9.3, 11.5), n = c(18L, 10L), var.equal = TRUE)

# Example 6.4.4; Page 181 (10th ed),
aggregated_t(xbar = c(4.7, 8.8), xsd = c(9.3, 11.5), n = c(18L, 10L))
# Welch slightly different from Cochran; textbook explained on Page 182

# Example 6.5.1; Page 185 (10th ed),
```

```

prop_CLT(xbar = .18, n = 1220L)

# Example 6.6.1; Page 187 (10th ed),
prop_CLT(x = c(31L, 53L), n = c(68L, 255L), conf.level = .99)

# Example 6.7.1; Page 190 (10th ed),
(n_671 = uniroot(f = function(n, sd, level = .95) {
  qnorm(1-(1-level)/2) * sd/sqrt(n) - 5 # half-width of CI <= 5 grams
}, interval = c(0, 2e2), sd = 20)$root)
ceiling(n_671)

# Example 6.8.1; Page 192 (10th ed),
(n_681 = uniroot(f = function(n, p, level = .95) {
  qnorm(1-(1-level)/2) * sqrt(p*(1-p)/n) - .05
}, interval = c(0, 1e3), p = .35)$root)
ceiling(n_681)

# Example 6.9.1; Page 196 (10th ed),
d691 = c(9.7, 12.3, 11.2, 5.1, 24.8, 14.8, 17.7)
sqrt(aggregated_var(xsd = sd(d691), n = length(d691)))

# Example 6.10.1; Page 200 (10th ed),
aggregated_var(xsd = c(8.1, 5.9), n = c(16L, 4L))

# Example 7.2.1; Page 222 (10th ed); Page 201 (11th ed)
aggregated_z(xbar = 27, sd = sqrt(20), n = 10L, null.value = 30)

# Example 7.2.2; Page 226 (10th ed); Page 204 (11th ed)
aggregated_z(xbar = 27, sd = sqrt(20), n = 10L, null.value = 30, alternative = 'less')

# Example 7.2.3; Page 228 (10th ed); Page 206 (11th ed)
head(EXA_C07_S02_03)
t.test(EXA_C07_S02_03$DAYS, mu = 15)

# Example 7.2.4; Page 231 (10th ed); Page 209 (11th ed)
aggregated_z(xbar = 146, sd = 27, n = 157L, null.value = 140, alternative = 'greater')

# Example 7.2.5; Page 232 (10th ed); Page 210 (11th ed)
d725 = c(33.38, 32.15, 34.34, 33.95, 33.46, 34.13, 33.99, 34.10, 33.85,
  34.23, 34.45, 34.19, 33.97, 32.73, 34.05)
t.test(d725, mu = 34.5)

# Example 7.3.1; Page 237 (10th ed), Page 213 (11th ed)
aggregated_z(xbar = c(4.5, 3.4), sd = sqrt(c(1, 1.5)), n = c(12L, 15L), null.value = 0)

# Example 7.3.2; Page 239 (10th ed), Page 215 (11th ed)
head(EXA_C07_S03_02)
with(EXA_C07_S03_02, t.test(x = CONTROL, y = SCI, alternative = 'less', var.equal = TRUE))

# Example 7.3.3; Page 240 (10th ed), Page 217 (11th ed)
aggregated_t(xbar = c(19.16, 9.53), xsd = c(5.29, 2.69), n = c(15L, 30L), null.value = 0)

# Example 7.3.4; Page 242 (10th ed), Page 219 (11th ed)

```

```

aggregated_z(xbar = c(59.01, 46.61), sd = c(44.89, 34.85), n = c(53L, 54L), null.value = 0,
  alternative = 'greater')

# Example 7.4.1; Page 251 (10th ed), Page 226 (11th ed)
head(EXA_C07_S04_01)
with(EXA_C07_S04_01, t.test(x = POSTOP, y = PREOP, alternative = 'greater', paired = TRUE))

# Example 7.5.1; Page 258 (10th ed), Page 232 (11th ed)
prop_CLT(x = 24L, n = 301L, null.value = .063, alternative = 'greater')

# Example 7.6.1; Page 261 (10th ed), Page 235 (11th ed)
prop_CLT(x = c(24L, 11L), n = c(44L, 29L), null.value = 0, alternative = 'greater')

# Example 7.7.1; Page 264 (10th ed), Page 238 (11th ed)
head(EXA_C07_S07_01)
aggregated_var(xsd = sd(EXA_C07_S07_01$mass), n = 16L, null.value = 600)

# Example 7.8.1; Page 268 (10th ed), Page 242 (11th ed)
aggregated_var(xsd = c(30.62, 11.37), n = 6L, null.value = 1, alternative = 'greater')

# Example 7.8.2; Page 270 (10th ed),
with(EXA_C07_S03_02, var.test(x = CONTROL, y = SCI))

```

---

Chapter07\_power

Chapter 7: Power Curve

---

## Description

Functions for Chapter 7, *Hypothesis Testing*.

## Usage

```

power_z(
  x,
  null.value,
  sd,
  n,
  alternative = c("two.sided", "less", "greater"),
  sig.level = 0.05
)

```

## Arguments

x	<b>numeric vector</b> , mean parameter(s) $\mu_1$ in the alternative hypothesis
null.value	<b>numeric scalar</b> , mean parameter $\mu_0$ in the null hypothesis
sd	<b>numeric scalar</b> , population standard deviation $\sigma$
n	<b>integer scalar</b> , sample size $n$

alternative     **character** scalar, alternative hypothesis, either 'two.sided' (default), 'greater' or 'less'

sig.level        **numeric** scalar, significance level (i.e., Type-I-error rate), default .05

### Details

Function `power_z` calculates the powers at each element of the alternative parameters  $\mu_1$ , for one-sample  $z$ -test

- $H_0 : \mu = \mu_0$  vs.  $H_A : \mu \neq \mu_0$ , if `alternative = 'two.sided'`
- $H_0 : \mu \leq \mu_0$  vs.  $H_A : \mu > \mu_0$ , if `alternative = 'greater'`
- $H_0 : \mu \geq \mu_0$  vs.  $H_A : \mu < \mu_0$ , if `alternative = 'less'`

### Value

Function `power_z` returns a 'power\_z' object, which inherits from 'power.htest' class.

### See Also

[power.t.test](#)

### Examples

```
library(DanielBiostatistics10th)

# Example 7.9.1; Page 272 (10th ed), Page 245 (11th ed)
(p791 = power_z(seq.int(from = 16, to = 19, by = .5), null.value = 17.5, sd = 3.6, n = 100L))
# Table 7.9.1

# Example 7.9.2; Page 276 (10th ed), Page 248 (11th ed)
(p792 = power_z(seq.int(from = 50, to = 70, by = 5), null.value = 65, sd = 15, n = 20L,
  sig.level = .01, alternative = 'less'))

# Example 7.10.1; Page 278 (10th ed),
(n_d7101 <- uniroot(f = function(x) {
  power_z(55, null.value = 65, sd = 15, n = x, sig.level = .01, alternative = 'less')$power - .95
}, interval = c(0, 50))$root)
power_z(55, null.value = 65, sd = 15, n = ceiling(n_d7101), sig.level = .01, alternative = 'less')
```

### Description

Examples for Chapter 8, *Analysis of Variance*.

### Value

No function defined for Chapter 8.

**Examples**

```

library(DanielBiostatistics10th)

# Example 8.2.1; Page 318 (10th ed), Page 280 (11th ed)
head(EXA_C08_S02_01)
boxplot(selenium ~ type, data = EXA_C08_S02_01, main = 'Figure 8.2.7')
(aov_d821 = aov(selenium ~ type, data = EXA_C08_S02_01))
# ?stats::aov # analysis-of-variance model
anova(aov_d821)
# ?stats::anova # ANOVA table

# Example 8.2.2; Page 325 (10th ed), Page 286 (11th ed)
(tukey_d822 <- TukeyHSD(aov_d821, conf.level = 0.95)) # Figure 8.2.8
plot(tukey_d822)

# Example 8.3.1; Page 339 (10th ed), Page 298 (11th ed)
head(EXA_C08_S03_01)
head(d831 <- within(EXA_C08_S03_01, expr = {
  ageGroup = structure(ageGroup, levels = c('<20', '20s', '30s', '40s', '>50'), class = 'factor')
}))
(aov_831 = aov(time ~ method + ageGroup, data = d831))
anova(aov_831)

# Example 8.4.1; Page 348 (10th ed), Page 307 (11th ed)
head(EXA_C08_S04_01)
head(d841 <- within(EXA_C08_S04_01, expr = {
  SUBJ = factor(SUBJ)
  TIME = structure(TIME, levels = c('Baseline', '1-Mon', '3-Mon', '6-Mon'), class = 'factor')
}))
(aov_841 = aov(FUNC ~ SUBJ + TIME, data = d841))
anova(aov_841)

# Example 8.4.2; Page 352 (10th ed), Page 310 (11th ed)
# (optional; out of the scope of this course)
head(EXA_C08_S04_02)
names(EXA_C08_S04_02)[3:6] = c('baseline', '2wk', '4wk', '6wk')
head(d842a <- within(EXA_C08_S04_02, expr = {
  subject = factor(subject)
  treatment = structure(treatment, levels = c('placebo', 'aloe_juice'), class = 'factor')
}))
head(d842b <- reshape2::melt(d842a, id.vars = c('subject', 'treatment'),
  variable.name = 'time', value.name = 'OralScores'))

# Hypothesis:
# Main effect of 'treatment';
# Main effect of 'time';
# Interaction between 'treatment' and 'time'
(aov_842 = aov(OralScores ~ treatment * time + Error(subject), data = d842b))
class(aov_842)
summary(aov_842)
# Section 'Error: subject' in R output
# .. is Figure 8.4.4 'Tests of Between-Subjects Effects' (without the row of 'Intercept')
# .. 'treatment' row: effect of treatment at **baseline** (i.e. reference time),

```

```

# ... degree-of-freedom (dof) = 2-1 = 1
# .. 'Residuals' row: residual at baseline, dof = (25-1) - (2-1) = 23
# .. It's important to note that 'treatment' is a between-subject factor.
# Section 'Error: Within' in R output
# .. is Figure 8.4.4 'Tests of Within-Subjects Effects'
# .. 'time' row: effect of time within subject for placebo (i.e. reference treatment), dof = 4-1 = 3
# .. 'treatment:time' row: interaction of treatment and time, dof = (2-1)*(4-1) = 3
# .. 'Residuals' row: residual at 2wk, 4wk and 6wk, dof = (4-1)*23 = 69
# ... [(4-1) timepoints, 23 dof at each timepoints]
# Analysis Interpretation
# .. No signif. diff. detected between placebo vs. aloe at baseline (p = .815)
# .. No signif. diff. detected in the trends over time between placebo vs. aloe (p = .974)
# .. Signif. diff. detected among the four timepoints, for either placebo or aloe pts (p = 3e-7)
# R code below creates an equivalent ANOVA model
anova(aov(OralScores ~ treatment * time + subject, data = d842b))
# .. 'subject' is considered as a block factor

# Example 8.5.2; Page 364 (10th ed), Page 321 (11th ed)
head(EXA_C08_S05_02)
head(d852 <- within(EXA_C08_S05_02, expr = {
  A = structure(A, levels = c('Cardiac', 'Cancer', 'CVA', 'Tuberculosis'), class = 'factor')
  B = structure(B, levels = c('20s', '30s', '40s', '50+'), class = 'factor')
}))
(aov_852 = aov(HOME ~ A * B, data = d852))
anova(aov_852)
summary(lm(HOME ~ A * B, data = d852))
# produces alpha, beta and (alpha beta)'s in the formulation

```

**Description**

Examples in Chapter 9, *Simple Linear Regression and Correlation*.

**Value**

No function defined for Chapter 9.

**Examples**

```

library(DanielBiostatistics10th)

# Example 9.3.1; Page 417 (10th ed), Page 358 (11th ed)
head(EXA_C09_S03_01)
names(EXA_C09_S03_01)[2:3] = c('Waist', 'AT')
plot(AT ~ Waist, data = EXA_C09_S03_01,
      xlab = 'Waist circumference (cm), X',
      ylab = 'Deep abdominal AT area (cm2), Y',

```

```

    main = 'Figure 9.3.1')
m931 = lm(AT ~ Waist, data = EXA_C09_S03_01)
plot(AT ~ Waist, data = EXA_C09_S03_01,
     xlab = 'Waist circumference (cm), X',
     ylab = 'Deep abdominal AT area (cm2), Y',
     main = 'Figure 9.3.3'); abline(m931, col = 'red', lty = 2)

# Example 9.4.1; Page 432 (10th ed), Page 372 (11th ed)
anova(m931) # Table 9.4.1. Page 434 (10th ed)

# Example 9.4.2; Page 436 (10th ed), Page 375 (11th ed)
summary(m931)
confint(m931) # Page 438 (10th ed)

# (omitted) Example 9.4.3; Page 376 (11th ed)

# (optional)
# Example 9.4.3; Page 440 (10th ed)
# Example 9.4.4; Page 379 (11th ed)
plot(m931, which = 1, main = 'Figure 9.4.8 (10th) or 9.4.9 (11th)')

# Example 9.7.1; Page 447 (10th ed), Page 386 (11th ed)
head(EXA_C09_S07_01)
plot(CV ~ HEIGHT, data = EXA_C09_S07_01,
     xlab = 'Height (cm)',
     ylab = 'Cv (units)',
     main = 'Figure 9.7.2')
m971 = lm(CV ~ HEIGHT, data = EXA_C09_S07_01)
summary(m971); anova(m971) # Figure 9.7.3; Page 450 (10th ed)

# Example 9.7.2; Page 452 (10th ed), Page 390 (11th ed)
cor(EXA_C09_S07_01);
cor.test(~ CV + HEIGHT, data = EXA_C09_S07_01) # Figure 9.7.4, 9.7.5

# Page 453, When the Hypothesized rho Is a Nonzero Value
# R does not have a function to do this

```

**Description**

Examples for Chapter 10, *Multiple Regression and Correlation*.

**Value**

No function defined for Chapter 10.



**Examples**

```

library(DanielBiostatistics10th)

# Example 10.3.1; Page 493 (10th ed), Page 419 (11th ed)
head(EXA_C10_S03_01)
pairs(EXA_C10_S03_01, main = 'Figure 10.3.1')
m1031 = lm(CDA ~ AGE + EDLEVEL, data = EXA_C10_S03_01)
summary(m1031)

# Example 10.4.1; Page 502 (10th ed), Page 428 (11th ed)
# .. see 'Multiple R-squared' (not 'Adjusted R-squared')

# Example 10.4.2; Page 504 (10th ed), Page 429 (11th ed)
# .. see 'F-statistic'

# Example 10.4.3; Page 505 (10th ed), Page 430 (11th ed)
# .. see 'Coefficients:'

# confidence interval for beta's; Page 506 (10th ed), Page 431 (11th ed)
confint(m1031)

# Example 10.5.1; Page 509 (10th ed), Page 434 (11th ed)
(newd_1031 = data.frame(AGE = 68, EDLEVEL = 12))
predict(m1031, newdata = newd_1031, interval = 'prediction')
predict(m1031, newdata = newd_1031, interval = 'confidence')

# Example 10.6.1; Page 511 (10th ed), Page 436 (11th ed)
head(EXA_C10_S06_01)
pairs(EXA_C10_S06_01, main = 'Scatter Plot Matrix, Example 10.6.1')
m1061 = lm(W ~ P + S, data = EXA_C10_S06_01)
summary(m1061)
confint(m1061)
anova(m1061)

# (optional)
# Example 10.6.2; Page 515 (10th ed), Page 440 (11th ed)
psych::partial.r(EXA_C10_S06_01, x = 2:3, y = 1L)

```

**Description**

Examples in Chapter 11, *Regression Analysis: Some Additional Techniques*.

**Value**

No function defined for Chapter 11.

**Examples**

```

library(DanielBiostatistics10th)

# Example 11.1.1; Page 540,
head(EXA_C11_S01_01)
head(log(EXA_C11_S01_01$conc, base = 10))
head(EXA_C11_S01_01$logConc)

# Example 11.1.2; Page 542,
head(EXA_C11_S01_02)
cor.test(~ sbp + weight, data = EXA_C11_S01_02)
cor.test(~ sbp + bmi, data = EXA_C11_S01_02)

# Example 11.2.1; Page 545,
head(EXA_C11_S02_01)
d1121 = within(EXA_C11_S02_01, expr = {
  SMOKE = as.logical(SMOKE)
})
xlab1121 = 'Length of gestation (weeks)'; ylab1121 = 'Birth weight (grams)'
car::scatterplot(GRAMS ~ WEEKS | SMOKE, data = d1121, regLine = FALSE, smooth = FALSE,
  xlab = xlab1121, ylab = ylab1121, main = 'Figure 11.2.1')
m1121 = lm(GRAMS ~ WEEKS + SMOKE, data = d1121)
summary(m1121) # Figure 11.2.2
confint(m1121)
car::scatterplot(GRAMS ~ WEEKS | SMOKE, data = d1121, regLine = FALSE, smooth = FALSE,
  xlab = xlab1121, ylab = ylab1121, main = 'Figure 11.2.3')
(cf1121 = m1121$coefficients)
abline(a = cf1121[1L], b = cf1121[2L], col = 'blue') # regression line for non-smoking mothers
abline(a = cf1121[1L] + cf1121[3L], b = cf1121[2L], col = 'magenta')

# Example 11.2.3; Page 551,
d1123 = within(EXA_C11_S02_03, expr = {
  METHOD = factor(METHOD, levels = c('C', 'A', 'B')) # textbook designated 'C' as reference level
})
summary(m1123 <- lm(EFFECT ~ AGE * METHOD, data = d1123)) # Figure 11.2.5
confint(m1123)
car::scatterplot(EFFECT ~ AGE | METHOD, data = d1123, smooth = FALSE,
  xlab = 'Age', ylab = 'Treatment effectiveness', main = 'Figure 11.2.6')

# Example 11.3.1; Page 561,
head(EXA_C11_S03_01)
names(EXA_C11_S03_01) = c('JOBPER', 'ASRV', 'ENTH', 'AMB', 'COMM', 'PROB', 'INIT')
summary(m1131_raw <- lm(JOBPER ~ ASRV + ENTH + AMB + COMM + PROB + INIT, data = EXA_C11_S03_01))
# summary(m1131 <- MASS::stepAIC(m1131_raw, direction = 'backward'))
# the stepwise selection criterion used in MINITAB is not necessarily AIC

# Example 11.4.1; Page 572,
addmargins(d1141 <- array(c(92L, 21L, 15L, 20L), dim = c(2L, 2L), dimnames = list(
  OCAD = c('Present', 'Absent'), Sex = c('Male', 'Female')))) # Table 11.4.2
(d1141a = within(as.data.frame.table(as.table(d1141)), expr = {
  OCAD = (OCAD == 'Present')
  Sex = factor(Sex, levels = c('Female', 'Male'))
})

```

```

}))
m1141 = glm(OCAD ~ Sex, family = binomial, weights = Freq, data = d1141a)
summary(m1141) # Figure 11.4.1
exp(m1141$coefficients[2L]) # exp(beta_M)
exp(confint(m1141)) # confidence interval of exp(beta)
predict(m1141, newdata = data.frame(Sex = setNames(nm = c('Male', 'Female'))), type = 'response')

# Example 11.4.2; Page 573,
head(EXA_C11_S04_02)
summary(m1142 <- glm(ATT ~ AGE, family = binomial, data = EXA_C11_S04_02)) # Figure 11.4.2
exp(m1142$coefficients[2L])
exp(confint(m1142))
car::Anova(m1142) # Optional

# Example 11.4.3; Page 576,
head(REV_C11_24)
summary(glm(ONSET ~ HIAA + TRYPT, family = binomial, data = REV_C11_24)) # Figure 11.4.4
# Predictor TRYPT should be removed from model due to p-value \approx 1
summary(glm(ONSET ~ HIAA, family = binomial, data = REV_C11_24))

# Example 11.4.4-11.4.5; Page 578-579
DescTools::PseudoR2(m1142, which = 'CoxSnell')
DescTools::PseudoR2(m1142, which = 'Nagelkerke')

```

## Description

Functions for Chapter 12, *The Chi-Square Distribution and the Analysis of Frequencies*.

## Usage

```
print_OE(0, prob)
```

## Arguments

0	<b>integer</b> vector, observed counts
prob	<b>numeric</b> vector, anticipated probability. If missing (default), an uniform distribution across all categories are used.

## Value

Function `print_OE` prints a table with observed and expected frequencies, as well as the category-wise  $\chi^2$  statistics. A **double** vector of the category-wise  $\chi^2$  statistics is returned invisibly.

## Examples

```

library(DanielBiostatistics10th)

# Example 12.3.1; Page 605 (10th ed)
d1231_b = c(-Inf, seq.int(from = 125, to = 275, by = 25), Inf)
(d1231 = setNames( # Table 12.3.1
  c(1L, 3L, 8L, 18L, 6L, 4L, 4L, 3L),
  nm = levels(cut(double(), breaks = d1231_b, right = FALSE, include.lowest = TRUE))))
chi1231 = print_OE(d1231, prob = diff.default(pnorm(q = d1231_b, mean = 198.67, sd = 41.31)))
pchisq(sum(chi1231), df = length(d1231) - 3L, lower.tail = FALSE)
# -3L: three restrictions (explained on Page 608)
# (1) making sum(xo) == sum(xe)
# (2) estimating mean
# (3) estimating sd

# Example 12.3.2; Page 609 (10th ed),
# 100 doctors, 25 patients per doctor
d1232 = c(5L, 6L, 8L, 10L, 10L, 15L, 17L, 10L, 10L, 9L, 0L)
o1232 = setNames(c(sum(d1232[1:2]), d1232[-(1:2)]), nm = c('0-1', 2:9, '10 or more'))
(p1232 = sum((0:10) * d1232) / (25 * 100)) # binomial `prob`
chi1232 = print_OE(o1232, prob = c(
  pbinom(1L, size = 25L, prob = p1232),
  dbinom(2:9, size = 25L, prob = p1232),
  pbinom(9, size = 25L, prob = p1232, lower.tail = FALSE)))
pchisq(sum(chi1232), df = length(o1232) - 2L, lower.tail = FALSE)
# -2L: two restrictions (explained on Page 611)
# (1) making sum(o) == sum(e)
# (2) estimating p1232

# Example 12.3.3; Page 611 (10th ed),
d1233 = c(5L, 14L, 15L, 23L, 16L, 9L, 3L, 3L, 1L, 1L, 0L)
o_1233 = setNames(c(d1233[1:8], sum(d1233[-(1:8)])), nm = c(0:7, '8 or more'))
p_1233 = c(dpois(0:7, lambda = 3), # lambda = 3 is provided by the textbook
  ppois(7L, lambda = 3, lower.tail = FALSE))
chi1233 = print_OE(o_1233, prob = p_1233)
pchisq(sum(chi1233), df = length(o_1233) - 1L, lower.tail = FALSE)
# -1L: one restrictions
# (1) making sum(xo) == sum(xe)
chisq.test(o_1233, p = p_1233) # equivalent # warning on any(E < 5)

# Example 12.3.4; Page 614 (10th ed), Page 531 (11th ed)
d1234 = c('Dec 05' = 62L, 'Jan 06' = 84L, 'Feb 06' = 17L, 'Mar 06' = 16L, 'Apr 06' = 21L)
print_OE(d1234) # Figure 12.3.2
chisq.test(d1234)

# Example 12.3.5; Page 616 (10th ed), Page 533 (11th ed)
d1235 = c(dominant = 43L, heterozygous = 125L, recessive = 32L)
print_OE(d1235, prob = c(1, 2, 1))
chisq.test(d1235, p = c(1, 2, 1), rescale.p = TRUE)

# Example 12.4.1; Page 621 (10th ed)
addmargins(d1241 <- array(c(260L, 15L, 7L, 299L, 41L, 14L), dim = c(3L, 2L), dimnames = list(

```

```

Race = c('White', 'Black', 'Other'), FolicAcid = c('TRUE', 'FALSE'))))
chisq.test(d1241) # ?stats::chisq.test

# Example 12.4.2; Page 626 (10th ed),
addmargins(d1242 <- array(c(131L, 14L, 52L, 36L), dim = c(2L, 2L), dimnames = list(
  Type = c('Faller', 'Non-Faller'), LifestyleChange = c('TRUE', 'FALSE'))))
chisq.test(d1242, correct = FALSE)
chisq.test(d1242, correct = TRUE) # Yates's Correction

# Example 12.5.1; Page 631 (10th ed),
addmargins(d1251 <- array(c(21L, 19L, 75L, 77L), dim = c(2L, 2L), dimnames = list(
  Group = c('Narcoleptic', 'Healthy'), Migraine = c('TRUE', 'FALSE'))))
(chisq_1251 = chisq.test(d1251, correct = FALSE))
if (FALSE) {
  # (optional) using test on two proportions
  # only equivalent for 2*2 contingency table
  (clt_1251 = prop_CLT(x = c(21L, 19L), n = 96L, null.value = 0))
  all.equal.numeric(unnamed(clt_1251$statistic^2), unnamed(chisq_1251$statistic))
}

# Example 12.6.1; Page 638 (10th ed),
addmargins(d1262 <- array(c(2L, 8L, 7L, 4L), dim = c(2L, 2L), dimnames = list(
  Group = c('PI Naive', 'PA Experienced'), Regimen2yr = c('TRUE', 'FALSE'))))
fisher.test(d1262)

# Example 12.7.1; Page 644 (10th ed),
addmargins(d1271 <- array(c(22L, 18L, 216L, 199L), dim = c(2L, 2L), dimnames = list(
  Exercising = c('Extreme', 'No'), PretermLabor = c('Cases', 'Noncases'))))
DescTools::RelRisk(d1271, conf.level = .95) # 95% CI for relative risk
fisher.test(d1271) # 95% CI for odds ratio

# Example 12.7.2; Page 647 (10th ed),
addmargins(d1272 <- array(c(64L, 68L, 342L, 3496L), dim = c(2L, 2L), dimnames = list(
  SmkPregnancy = c('Smoked Throughout', 'Never Smoked'), Obesity = c('Cases', 'Noncases'))))
fisher.test(d1272)

# Example 12.7.3-12.7.4; Page 650-652 (10th ed),
(d1273 <- array(c(21L, 16L, 11L, 6L, 50L, 18L, 14L, 6L), dim = c(2L, 2L, 2L), dimnames = list(
  HTN = c('Present', 'Absent'), OCAD = c('Cases', 'Controls'), Age = c('<=55', '>55'))))
addmargins(d1273, margin = 1:2) # Table 12.7.6
mantelhaen.test(d1273)

```

## Description

Examples for Chapter 13, *Nonparametric and Distribution-Free Statistics*.

**Value**

No function defined for Chapter 13.

**Examples**

```
library(DanielBiostatistics10th)

# Example 13.3.1; Page 673,
d1331 = c(4, 5, 8, 8, 9, 6, 10, 7, 6, 6)
BSDA::SIGN.test(d1331, md = 5)

# Example 13.3.2; Page 677,
head(EXA_C13_S03_02)
with(EXA_C13_S03_02, BSDA::SIGN.test(x = X, y = Y, alternative = 'less'))

# Example 13.4.1; Page 683,
d1341 = c(4.91, 4.10, 6.74, 7.27, 7.42, 7.50, 6.56, 4.64, 5.98, 3.14, 3.23, 5.80, 6.17, 5.39, 5.77)
wilcox.test(d1341, mu = 5.05)

# Example 13.5.1; Page 686,
head(EXA_C13_S05_01)
(med1351 = median(unlist(EXA_C13_S05_01), na.rm = TRUE)) # common median
addmargins(t1351 <- with(EXA_C13_S05_01, expr = {
  tmp <- cbind(Urban = table(URBAN < med1351), Rural = table(RURAL < med1351, useNA = 'no'))
  rownames(tmp) <- paste('Number of scores', c('above', 'below'), 'median')
  tmp
})) # Table 13.5.2
chisq.test(t1351, correct = FALSE)

# Example 13.6.1; Page 691,
head(EXA_C13_S06_01)
with(EXA_C13_S06_01, wilcox.test(X, Y, exact = FALSE, alternative = 'less'))

# Example 13.7.1; Page 699,
head(EXA_C13_S07_01)
ks.test(EXA_C13_S07_01$GLUCOSE, y = pnorm, mean = 80, sd = 6)

# Example 13.8.1; Page 705 (10th ed), Page 611 (11th ed)
(d1381 = data.frame(Air = c(12.22, 28.44, 28.13, 38.69, 54.91),
  Benzaldehyde = c(3.68, 4.05, 6.47, 21.12, 3.33),
  Acetaldehyde = c(54.36, 27.87, 66.81, 46.27, 30.19))) # Table 13.8.1
with(data = reshape2::melt(
  data = d1381,
  id.vars = NULL,
  value.name = 'Eosinophil',
  variable.name = 'Exposure'
), expr = kruskal.test(x = Eosinophil, g = Exposure))

# Example 13.8.2; Page 708 (10th ed), Page 613 (11th ed)
head(EXA_C13_S08_02)
with(data = reshape2::melt(
  data = EXA_C13_S08_02,
```

```

    id.vars = NULL,
    value.name = 'Value',
    variable.name = 'Hospital'
), expr = kruskal.test(x = Value, g = Hospital))

# Example 13.9.1; Page 713 (10th ed); Page 618 (11th ed)
head(EXA_C13_S09_01)
m1391 = as.matrix(EXA_C13_S09_01[LETTERS[1:3]], rownames.force = TRUE)
names(dimnames(m1391)) = c('Therapist', 'Model')
m1391 # Table 13.9.1
friedman.test(m1391)

# Example 13.9.2; Page 715 (10th ed); Page 620 (11th ed)
head(EXA_C13_S09_02)
m1392 = as.matrix(EXA_C13_S09_02[LETTERS[1:4]], rownames.force = TRUE)
names(dimnames(m1392)) = c('Animal', 'Dose')
m1392 # Table 13.9.2
friedman.test(m1392)

# Example 13.10.1; Page 720,
head(EXA_C13_S10_01)
with(EXA_C13_S10_01, cor.test(X, Y, method = 'spearman'))

# Example 13.10.2; Page 722,
head(EXA_C13_S10_02)
with(EXA_C13_S10_02, cor.test(V2, V3, method = 'spearman', exact = FALSE))

# Example 13.11.1-13.11.2; Page 728-729,
testosterone <- c(230, 175, 315, 290, 275, 150, 360, 425)
citricAcid <- c(421, 278, 618, 482, 465, 105, 550, 750)
robslopes::TheilSen(x = citricAcid, y = testosterone)
# textbook uses *central* median of ordered pairs, while ?robslopes::TheilSen uses *upper* median
summary(mblm::mblm(testosterone ~ citricAcid, repeated = FALSE)) # Figure 13.11.1 (11th ed)

```

**Description**

Examples for Chapter 14, *Survival Analysis*.

**Value**

No function defined for Chapter 14.

**Examples**

```
library(DanielBiostatistics10th)
```

```

# Example 14.3.1; Page 756 (10th ed), Page 652 (11th ed)
head(EXA_C14_S03_01)
head(d1431 <- within(EXA_C14_S03_01, expr = {
  TIME = .difftime(TIME, units = 'months')
  OS = survival::Surv(time = TIME, event = (VITAL != 'ned'))
}))
class(d1431$OS) # 'Surv'
head(d1431$OS)
summary(sf_1431 <- survival::survfit(OS ~ TUMOR, data = d1431)) # Table 14.3.2
plot(sf_1431, lty = 2:3, xlab = 'month', ylab = 'OS', main = 'Figure 14.3.1'); legend(
  x = 250, y = .9, legend = c('High', 'Low'), lty = 2:3)

# Example 14.4.1; Page 764 (10th ed), Page 659 (11th ed)
survival::survdiff(OS ~ TUMOR, data = d1431)

# Example 14.5.1; Page 769 (10th ed), Page 663 (11th ed)
head(EXA_C14_S05_01)
head(d1451 <- within(EXA_C14_S05_01, expr = {
  time = .difftime(time, units = 'weeks')
  PFS = survival::Surv(time, status)
  drug = relevel(structure(drug, levels = c('Opiate', 'Other'), class = 'factor'), ref = 'Other')
}))
summary(model1_1451 <- survival::coxph(PFS ~ drug + age, data = d1451))
# 'Opiate' has higher hazard compared to Drug='Other' (hazard ratio (HR) = 9.407, p < .001)
# With 'proportional hazard' assumption,
# ... we don't need to discuss Opiate vs. Other at any specific time point
confint(model1_1451)
# 'age' is not significant (p = .772), so it should be removed from the model
summary(model2_1451 <- survival::coxph(PFS ~ drug, data = d1451))
confint(model2_1451)
# 'Opiate' has higher hazard compared to Drug='Other' (hazard ratio (HR) = 9.923, p < .001)
plot(survival::survfit(PFS ~ drug, data = d1451), lty = 2:3,
  xlab = 'weeks', ylab = 'PFS', main = 'Figure 14.5.1'); legend(
  x = 35, y = .9, legend = c('Other', 'Opiate'), lty = 2:3)

```



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