

Package ‘lucid’

March 3, 2026

Title Printing Floating Point Numbers in a Human-Friendly Format

Version 1.11

Description Print vectors (and data frames) of floating point numbers using a non-scientific format optimized for human readers. Vectors of numbers are rounded using significant digits, aligned at the decimal point, and all zeros trailing the decimal point are dropped. See: Wright (2016). Lucid: An R Package for Pretty-Printing Floating Point Numbers. In JSM Proceedings, Statistical Computing Section. Alexandria, VA: American Statistical Association. 2270-2279.

License MIT + file LICENSE

URL <https://kwstat.github.io/lucid/>, <http://kwstat.github.io/lucid/>

BugReports <https://github.com/kwstat/lucid/issues>

Imports nlme

Suggests broom, dplyr, knitr, lattice, lme4, rjags, rmarkdown, sommer, testthat

VignetteBuilder knitr

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

NeedsCompilation no

Author Kevin Wright [aut, cre, cph] (ORCID:
<<https://orcid.org/0000-0002-0617-8673>>)

Maintainer Kevin Wright <kw.stat@gmail.com>

Repository CRAN

Date/Publication 2026-03-03 21:20:37 UTC

Contents

antibiotic	2
lucid	3
vc	5

Index**7**

antibiotic

*Effectiveness of 3 antibiotics against 16 bacterial species.***Description**

Effectiveness of 3 antibiotics against 16 bacterial species.

Format

A data frame with 16 observations on the following 5 variables.

bacteria bacterial species, 16 levels

penicillin MIC for penicillin

streptomycin MIC for streptomycin

neomycin MIC for neomycin

gramstain Gram staining (positive or negative)

Details

The values reported are the minimum inhibitory concentration (MIC) in micrograms/milliliter, which represents the concentration of antibiotic required to prevent growth in vitro.

Source

Will Burtin (1951). *Scope*. Fall, 1951.

References

Wainer, H. (2009). A Centenary Celebration for Will Burtin: A Pioneer of Scientific Visualization. *Chance*, 22(1), 51-55. <https://chance.amstat.org/2009/02/visrev221/>

Wainer, H. (2009). Visual Revelations: Pictures at an Exhibition. *Chance*, 22(2), 46–54. <https://chance.amstat.org/2009/04/vi>

Wainer, H. (2014). *Medical Illuminations: Using Evidence, Visualization and Statistical Thinking to Improve Healthcare*.

Examples

```
data(antibiotic)
lucid(antibiotic)
```

```
## Not run:
```

```
# Plot the data similar to Fig 2.14 of Wainer's book, "Medical Illuminations"
```

```
require(lattice)
require(reshape2)
```

```
# Use log10 transform
```

```

dat <- transform(antibiotic,
                 penicillin=log10(penicillin),
                 streptomycin=log10(streptomycin),
                 neomycin=log10(neomycin))
dat <- transform(dat, sgn = ifelse(dat$gramstain=="neg", "-", "+"))
dat <- transform(dat,
                 bacteria = paste(bacteria, sgn))
dat <- transform(dat, bacteria=reorder(bacteria, -penicillin))

dat <- melt(dat)

op <- tpg <- trellis.par.get()
tpg$superpose.symbol$pch <- toupper(substring(levels(dat$variable),1,1))
tpg$superpose.symbol$col <- c("darkgreen","purple","orange")
trellis.par.set(tpg)
dotplot(bacteria ~ value, data=dat, group=variable,
        cex=2,
        scales=list(x=list(at= -3:3,
                            labels=c('.001', '.01', '.1', '1', '10', '100', '1000'))),
        main="Bacterial response to Neomycin, Streptomycin, and Penicillin",
        xlab="Minimum Inhibitory Concentration (mg/L)")

trellis.par.set(op)

## End(Not run)

```

lucid

Lucid printing

Description

Format a column of numbers in a way to make it easy to understand.

Usage

```
lucid(x, dig = 3, na.value = NULL, ...)
```

```
## Default S3 method:
```

```
lucid(x, dig = 3, na.value = NULL, ...)
```

```
## S3 method for class 'numeric'
```

```
lucid(x, dig = 3, na.value = NULL, ...)
```

```
## S3 method for class 'data.frame'
```

```
lucid(x, dig = 3, na.value = NULL, ...)
```

```
## S3 method for class 'matrix'
lucid(x, dig = 3, na.value = NULL, ...)

## S3 method for class 'list'
lucid(x, dig = 3, na.value = NULL, ...)

## S3 method for class 'tbl_df'
lucid(x, dig = 3, na.value = NULL, ...)
```

Arguments

x	Object to format.
dig	Number of significant digits to use in printing.
na.value	Character string to use instead of 'NA' for numeric missing values. Default is NULL, which does nothing.
...	Additional arguments passed to the data.frame method.

Details

Output from R is often in scientific notation, which makes it difficult to quickly glance at numbers and gain an understanding of the relative values. This function formats the numbers in a way that makes interpretation of the numbers *_immediately_* apparent.

The sequence of steps in formatting the output is: (1) zap to zero (2) use significant digits (3) drop trailing zeros after decimal (4) align decimals.

Value

Text, formatted in a human-readable way. Standard R methods are used to print the value.

See Also

[signif](#)

Examples

```
x0 <- c(123, 12.3, 1.23, .123456) # From Finney, page 352
print(x0)
lucid(x0, dig=2)

x1 <- c(123, NA, 1.23, NA)
lucid(x1, na.value="--")

signif(mtcars[15:20,])
lucid(mtcars[15:20,])

x2 <- c(1/3, 5/3, 1, 1.5, 2, 11/6, 5/6, 8.43215652105343e-17)
print(x2)
lucid(x2)

# Which coef is 0 ? How large is the intercept?
```

```
df1 <- data.frame(effect=c(-13.5, 4.5, 24.5, 6.927792e-14, -1.75,
                          16.5, 113.5000))
rownames(df1) <- c("A","B","C","C1","C2","D","(Intercept)")
print(df1)
lucid(df1)

df2 <- data.frame(effect=c("hyb","region","region:loc","hyb:region",
                          "yr","hyb:yr","region:yr","R!variance"),
                  component=c(10.9,277,493,1.30E-04,126,22.3,481,268),
                  std.error=c(4.40,166,26.1,1.58E-06,119,4.50,108,3.25),
                  z.ratio=c(2.471,1.669,18.899,82.242,
                           1.060,4.951,4.442,82.242),
                  constraint=c("pos","pos","pos","bnd",
                               "pos","pos","pos","pos"))

print(df2)
lucid(df2)
```

vc

Extract variance components from mixed models

Description

Extract the variance components from a fitted model. Currently supports `asreml`, `lme4`, `mmer`, `nlme` and `mcmc.list` objects.

Usage

```
vc(object, ...)

## Default S3 method:
vc(object, ...)

## S3 method for class 'asreml'
vc(object, gamma = FALSE, ...)

## S3 method for class 'lme'
vc(object, ...)

## S3 method for class 'glmerMod'
vc(object, ...)

## S3 method for class 'lmerMod'
vc(object, ...)

## S3 method for class 'mcmc.list'
vc(object, quantiles = c(0.025, 0.5, 0.975), ...)

## S3 method for class 'mmer'
vc(object, ...)
```

Arguments

object	A fitted model object
...	Not used. Extra arguments.
gamma	If gamma=FALSE, then the 'gamma' column is omitted from the results from asreml
quantiles	The quantiles to use for printing mcmc.list objects

Details

The extracted variance components are stored in a data frame with an additional 'vc.xxx' class that has an associated print method.

Value

A data frame or other object.

Examples

```
## Not run:

require("nlme")
data(Rail)
m3 <- lme(travel~1, random=~1|Rail, data=Rail)
vc(m3)
##      effect variance stddev
## (Intercept)  615.3  24.81
##   Residual    16.17  4.021

require("lme4")
m4 <- lmer(travel~1 + (1|Rail), data=Rail)
vc(m4)
##      grp      var1 var2  vcov  sdcor
## Rail (Intercept) <NA> 615.3  24.81
## Residual        <NA> <NA>  16.17  4.021

require("asreml")
ma <- asreml(travel~1, random=~Rail, data=Rail)
vc(ma)
##      effect component std.error z.ratio constr
## Rail!Rail.var    615.3    392.6    1.6    pos
##   R!variance    16.17     6.6    2.4    pos

# See vignette for rjags example

# To change the number of digits, use the print function.
print(vc(m3), dig=5)

## End(Not run)
```

Index

* **datasets**

antibiotic, 2

antibiotic, 2

lucid, 3

signif, 4

vc, 5