

# Package ‘lucid’

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**Version** 1.4

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**Title** Printing Floating Point Numbers in a Human-Friendly Format

**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.

**LazyData** yes

**License** GPL-2

**URL** <https://github.com/kwstat/lucid>

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

**VignetteBuilder** knitr

**Imports** nlme

**Suggests** broom, dplyr, knitr, lattice, lme4, rjags, testthat

**RoxygenNote** 5.0.1

**NeedsCompilation** no

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**Repository** CRAN

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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. <http://chance.amstat.org/2009/02/visrev221/>

Wainer, H. (2009). Visual Revelations: Pictures at an Exhibition. *Chance*, 22(2), 46–54. <http://chance.amstat.org/2009/04/visrev222/>

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, ...)
```

### Arguments

<code>x</code>	Object to format.
<code>dig</code>	Number of significant digits to use in printing.
<code>na.value</code>	Character string to use instead of 'NA' for numeric missing values. Default is NULL, which does nothing.
<code>...</code>	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)

# Which are smallest/largest/significant variance components
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`, `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), ...)

```

## 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)
```

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