Package ‘lucid’
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Title Printing Floating Point Numbers in a Human-Friendly Format

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**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**


**References**


**Examples**

```r
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
```
\begin{verbatim}
lucid <- 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("Var.001", "Var.01", "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)
\end{verbatim}

\begin{itemize}
\item \textbf{lucid} \hspace{1cm} \textit{Lucid printing}
\end{itemize}

\section*{Description}
Format a column of numbers in a way to make it easy to understand.

\section*{Usage}

\begin{verbatim}
lucid(x, dig = 3, na.value = NULL, ...)
\end{verbatim}

\section*{Usage}

\begin{verbatim}
# 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, ...)
\end{verbatim}
## 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

```r
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?

```r
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)
```

```r
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**

```r
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

```r
## Not run:
require("nlme")
data(Rail)
m3 <- lme(travel~1, random=~1|Rail, data=Rail)
vc(m3)
## (Intercept) 615.3 24.81
## Residual 16.17 4.021

require("lme4")
m4 <- lmer(travel~1 + (1|Rail), data=Rail)
vc(m4)
## 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)
## 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.
```
vc

print(vc(m3), dig=5)

## End(Not run)
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