Lucid printing

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1 Abstract

The lucid package provides a method for pretty-printing vectors of floating point numbers, with special application to printing of variance components from mixed models.

2 Intro

Numerical output from R is often in scientific notation, which can make it difficult to quickly glance at numbers and understand the relative sizes of the numbers. This not a new phenomenon. Before R had been created, (Finney, 1988, 351-352) had this to say about numerical output:

> Certainly, in initiating analyses by standard software or in writing one's own software, the aim should be to have output that is easy to read and easily intelligible to others. ... Especially undesirable is the so-called 'scientific notation' for numbers in which every number is shown as a value between 0.0 and 1.0 with a power of 10 by which it must be multiplied. For example:
>
> ```
> 0.1234E00 is 0.1234
> 0.1234E02 is 12.34
> 0.1234E-1 is 0.01234
> ```
>
> This is an abomination which obscures the comparison of related quantities; tables of means or of analyses of variance become very difficult to read. It is acceptable as a default when a value is unexpectedly very much larger or smaller than its companions, but its appearance as standard output denotes either lazy programming or failure to use good software properly. Like avoidance of 'E', neat arrangement of output values in columns, with decimal points on a vertical line, requires extra effort by a programmer but should be almost mandatory for any software that is to be used often.

One recommendation for improving the display of tables of numbers is to round numbers a lot (Wainer, 1997). Humans cannot understand more than two digits very easily. It is rare that more than two digits of accuracy can be justified, and even if we could justify more than two digits, we seldom care about more than two digits. In R, using the round and signif functions can help improve numerical output, but can still print results in scientific notation and leave much to be desired. The lucid package provides functions to improve the presentation of floating point numbers in a way that makes interpretation of the numbers **immediately** apparent.

Consider the following vector of coefficients from a fitted model:

```
##                     effect
## A            -1.350000e+01
## B             4.500000e+00
## C             2.450000e+01
## C1            6.927792e-14
## C2           -1.750000e+00
## D             1.650000e+01
## (Intercept)  1.135000e+02
```

Which coeficient is basically zero? How large is the intercept?

Both questions can be answered using the output shown above, but it takes too much effort to answer the questions. Now examine the same vector of coefficients with prettier formatting:

```
require("lucid")
options(digits=7) # knitr defaults to 4, R console uses 7
lucid(df1)
```

```
##              effect
## A            -13.5
## B              4.5
## C             24.5
## C1             0
## C2            -1.75
## D             16.5
## (Intercept) 114
```

Which coeficient is basically zero? How large is the intercept?

Printing the numbers with the `lucid` function has made the questions much easier to answer.

The sequence of steps used by `lucid` to format and print the output is.

1. Zap to zero
2. Round using significant digits
3. Drop trailing zeros
4. Align numbers at the decimal point

The `lucid` package contains a generic function `lucid` with specific methods for numeric vectors, matrices, lists and data frames. The methods for matrices and data frames apply formatting to each numeric column and leave other columns unchanged.

3 Example: Antibiotic effectiveness

Wainer and Larsen (2009) present data published by Will Burtin in 1951 on the effectiveness of antibiotics against 16 types of bacteria. The data is included in the `lucid` package as a dataframe called `antibiotic`. The default view of this data is:

```
print(antibiotic)
```

```
##                             bacteria penicillin streptomycin neomycin gramstain
## 1              Aerobacter aerogenes    870.000         1.00    1.600       neg
## 2                  Brucella abortus      1.000         2.00    0.020       neg
## 3                 Brucella antracis      0.001         0.01    0.007       pos
## 4             Diplococcus pneumoniae     0.005        11.00   10.000       pos
## 5                  Escherichia coli    100.000         0.40    0.100       neg
## 6              Klebsiella pneumoniae   850.000         1.20    1.000       neg
## 7         Mycobacterium tuberculosis   800.000         5.00    2.000       neg
## 8                  Proteus vulgaris      3.000         0.10    0.100       neg
## 9             Pseudomonas aeruginosa   850.000         2.00    0.400       neg
## 10 Salmonella (Eberthella) typhosa       1.000         0.40    0.008       neg
## 11        Salmonella schottmuelleri     10.000         0.80    0.090       neg
## 12             Staphylococcus albus      0.007         0.10    0.001       pos
## 13            Staphylococcus aureus      0.030         0.03    0.001       pos
## 14            Streptococcus fecalis      1.000         1.00    0.100       pos
## 15        Streptococcus hemolyticus      0.001        14.00   10.000       pos
## 16           Streptococcus viridans      0.005        10.00   40.000       pos
```

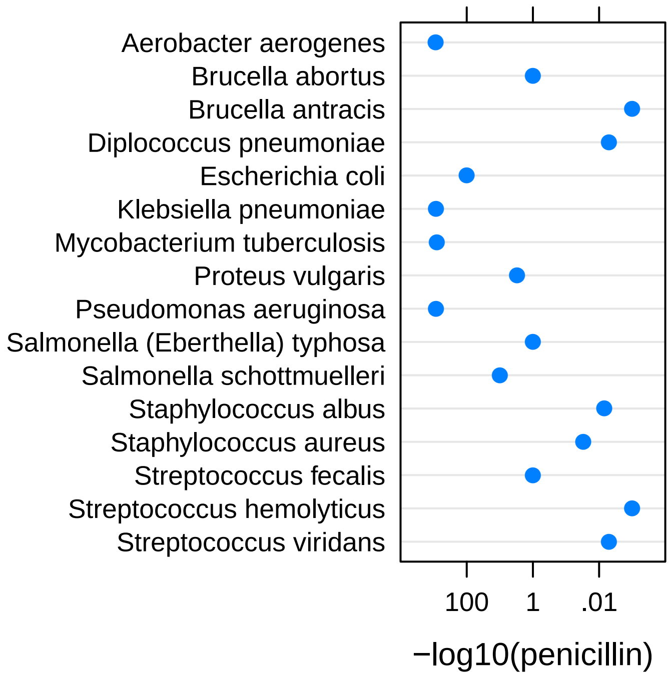
Due to the wide range in magnitude of the values, nearly half of the floating-point numbers in the default view contain trailing zeros after the decimal, which adds significant clutter and impedes interpretation. The `lucid` display of the data is:

```
lucid(antibiotic)
```

```
##                             bacteria penicillin streptomycin neomycin gramstain
## 1              Aerobacter aerogenes    870             1        1.6         neg
## 2                  Brucella abortus      1             2        0.02        neg
## 3                 Brucella antracis      0.001         0.01     0.007       pos
## 4             Diplococcus pneumoniae     0.005        11       10           pos
## 5                  Escherichia coli    100             0.4      0.1         neg
## 6              Klebsiella pneumoniae   850             1.2      1           neg
## 7         Mycobacterium tuberculosis   800             5        2           neg
## 8                  Proteus vulgaris      3             0.1      0.1         neg
## 9             Pseudomonas aeruginosa   850             2        0.4         neg
## 10 Salmonella (Eberthella) typhosa       1             0.4      0.008       neg
## 11        Salmonella schottmuelleri     10             0.8      0.09        neg
## 12             Staphylococcus albus      0.007         0.1      0.001       pos
## 13            Staphylococcus aureus      0.03          0.03     0.001       pos
## 14            Streptococcus fecalis      1             1        0.1         pos
## 15        Streptococcus hemolyticus      0.001        14       10           pos
## 16           Streptococcus viridans      0.005        10       40           pos
```

The `lucid` display is dramatically simplified, providing a much clearer picture of the effectiveness of the antibiotics against bacteria. This view of the data matches exactly the appearance of Table 1 in Wainer and Larsen (2009).

A stem-and-leaf plot is a semi-graphical display of data, in that the *positions* of the numbers create a display similar to a histogram. In a similar manner, the lucid output is a semi-graphical view of the data. The figure below shows a dotplot of the penicillin values on a reverse log10 scale. Note the similarity in the overall shape of the positions of the left-most significant digit in the penicillin column of the output and the dotplot. Also, as noted by Gelman (2011), the amount of ink in printing the significant digit has a surprisingly large correlation with the value of the digit, increasing the information in the semi-graphical view from lucid printing.



4 Application to mixed models

During the process of iterative fitting of mixed models, it is often useful to compare fits of different models to data, for example using loglikelihood or AIC values, or with the help of resiudal plots. It can also be very informative to inspect the variance components. The lucid package provides a function called vc that makes it easy to extract the estimated variances and correlations from fitted models and prints them in friendly format using the lucid function.

The vc function has methods that can be used with the nlme (Pinheiro et al., 2014), lme4 (Bates et al., 2014), and asreml (Butler, 2009) packages. The VarCorr function can be used to similar effect with the nlme and lme4 packages, but it shows variances for nlme models and standard deviations for lme4 models. The VarCorr function is not available for the asreml package. The vc function provides a unified interface for extracting the variance components from fitted models and prints the results using lucid. The following simple example illustrates use of the vc function.

```
require("nlme")
data(Rail)
mn <- lme(travel~1, random=~1|Rail, data=Rail)
vc(mn)
```

```
##       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
```

A second example is more complex. The example is no longer reproducible due to changes in the mixed-models software, so only the output is shown. A single model was fit to data using two different optimization methods. The goal was to compare the results from the two optimizers. In the output below, the first two columns identify terms in the model, the next two columns are the variance and standard deviation from one optimizer, while the final two columns are from the other optimizer.

The default printing is shown first.

```
cbind(d1,d2[,3:4])
```

```
##      Groups        Name  Variance Std.Dev. Variance   Std.Dev.
## 1   new.gen (Intercept)   2869.45   53.567 3.23e+03  56.818310
## 2       one       r1:c3   5531.60   74.375 7.69e+03  87.675211
## 3     one.1       r1:c2  58225.75  241.300 6.98e+04 264.123506
## 4     one.2       r1:c1 128003.60  357.776 1.07e+05 327.750047
## 5     one.3          c8   6455.77   80.348 6.79e+03  82.381314
## 6     one.4          c6   1399.73   37.413 1.64e+03  40.446339
## 7     one.5          c4   1791.65   42.328 1.23e+04 110.764195
## 8     one.6          c3   2548.89   50.486 2.69e+03  51.831045
## 9     one.7          c2   5941.80   77.083 7.64e+03  87.435345
## 10    one.8          c1      0.00    0.000 9.56e-04   0.030918
## 11    one.9         r10   1132.95   33.659 1.98e+03  44.446766
## 12   one.10          r8   1355.23   36.813 1.24e+03  35.234043
## 13   one.11          r4   2268.73   47.631 2.81e+03  53.020431
## 14   one.12          r2    241.79   15.550 9.28e+02  30.465617
## 15   one.13          r1   9199.94   95.916 1.04e+04 101.802960
## 16 Residual               4412.11   66.424 4.13e+03  64.240858
```

Do the two optimization methods give similar results? It is difficult to compare the results due to the clutter of extra digits, and even more importantly, because of a quirk in the way R formats the output. The variances in column 3 are shown in non-scientific format, while the variances in column 5 are shown in scientific format!

The lucid function is now used to show the results.

```
lucid(cbind(d1,d2[,3:4]))
```

```
##      Groups        Name Variance Std.Dev. Variance Std.Dev.
## 1   new.gen (Intercept)     2870     53.6     3230  56.8
## 2       one       r1:c3     5530     74.4     7690  87.7
## 3     one.1       r1:c2    58200    241      69800 264
## 4     one.2       r1:c1   128000    358     107000 328
## 5     one.3          c8     6460     80.3     6790  82.4
## 6     one.4          c6     1400     37.4     1640  40.4
## 7     one.5          c4     1790     42.3    12300 111
## 8     one.6          c3     2550     50.5     2690  51.8
## 9     one.7          c2     5940     77.1     7640  87.4
## 10    one.8          c1        0      0          0   0.0309
## 11    one.9         r10     1130     33.7     1980  44.4
## 12   one.10          r8     1360     36.8     1240  35.2
## 13   one.11          r4     2270     47.6     2810  53
## 14   one.12          r2      242     15.6      928  30.5
## 15   one.13          r1     9200     95.9    10400 102
## 16 Residual                 4410     66.4     4130  64.2
```

The formatting of the variance columns is now consistent and simplified with fewer digits shown. It is easy to compare the columns and see that the two optimizers are giving quite different answers.

5 Appendix

This document was prepared November 25, 2014 with the following configuration:

- R version 3.1.2 (2014-10-31), `x86_64-w64-mingw32`
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: Matrix 1.1-4, Rcpp 0.11.3, knitr 1.7, lattice 0.20-29, lme4 1.1-7, lucid 1.0, nlme 3.1-118
- Loaded via a namespace (and not attached): MASS 7.3-35, evaluate 0.5.5, formatR 1.0, grid 3.1.2, highr 0.4, minqa 1.2.4, nloptr 1.0.4, splines 3.1.2, stringr 0.6.2, tools 3.1.2

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