Lab 2: solutions

September 14, 2005

Exercise 0.1 : nothing to do

Exercise 0.2 :

Re-create the data frame to play with:

```
> loc = factor(rep(LETTERS[1:3], 2))
> day = factor(rep(1:2, each = 3))
> set.seed(1001)
> val = round(runif(6), 3)
> d = data.frame(loc, day, val)
> d

  loc day   val
1   A   1 0.986
2   B   1 0.413
3   C   1 0.430
4   A   2 0.419
5   B   2 0.427
6   C   2 0.888
```

Separate data with one row for each location and one column for each day:

```
> unstack(d, val ~ day)

     X1    X2
1 0.986 0.419
2 0.413 0.427
3 0.430 0.888
```

Because R doesn't allow numbers alone as column names, it puts an `X` in front of the values of `day` to get the column names `X1` and `X2`.

Separate data with one row for each day and one column for each location:

```
> unstack(d, val ~ loc)
```

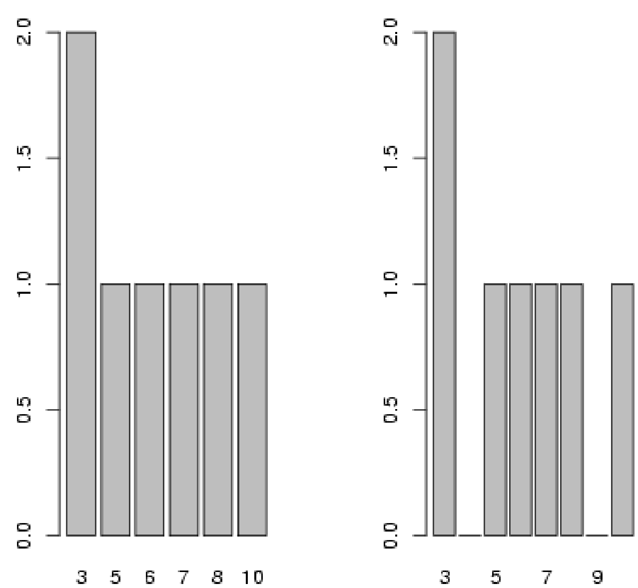
```
      A     B     C
1 0.986 0.413 0.430
2 0.419 0.427 0.888
```

While less complicated than `reshape()`, `stack()` and `unstack()` don't preserve information very well: for example, the row names in the first example are not set to `A`, `B`, `C`.

Exercise 0.3:

Use `levels=3:10` to make sure that all values between 3 and 10, even those not represented in the data set, are included in the factor definition and thus appear as zeros rather than being skipped when you plot the factor.

```
> f = factor(c(3, 3, 5, 6, 7, 8, 10))
> op = par(mfrow = c(1, 2))
> plot(f)
> f = factor(c(3, 3, 5, 6, 7, 8, 10), levels = 3:10)
> plot(f)
> par(op)
```



Exercise 0.4:

Read in and recreate the seed predation data and table:

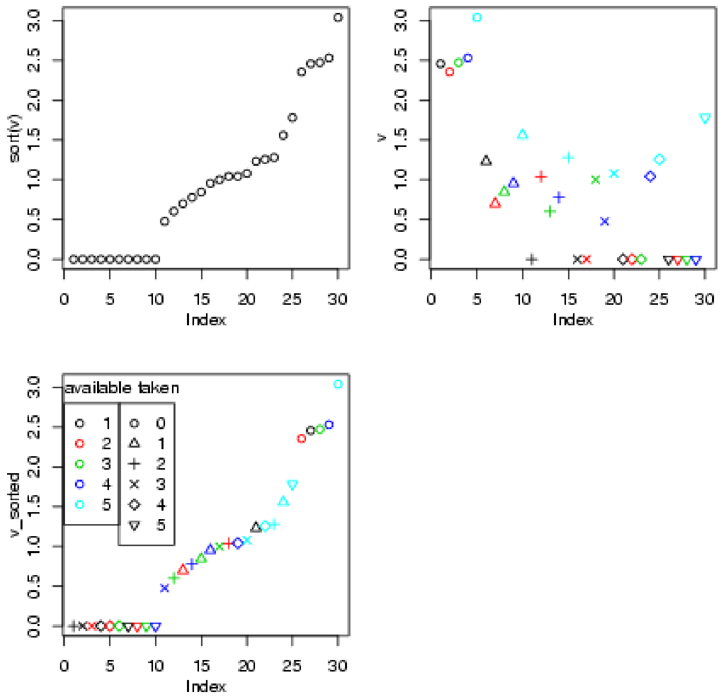
```
> data = read.table("seedpred.dat", header = TRUE)
> data$available = data$remaining + data$taken
> t1 = table(data$available, data$taken)
> v = as.numeric(log10(1 + t1))
> r = row(t1)
> c = col(t1)
```

Create versions of the variables that are sorted in order of increasing values of `v` (`v_sorted=sort(v)` would have the same effect as the first line):

```
> v_sorted = v[order(v)]
> r_sorted = r[order(v)]
> c_sorted = c[order(v)]
```

Draw the plots:

```
> op = par(mfrow = c(2, 2), mgp = c(2, 1, 0), mar = c(4.2, 3, 1,
+     1))
> plot(sort(v))
> plot(v, col = r, pch = c)
> plot(v_sorted, col = r_sorted, pch = c_sorted)
> legend(0, 2.8, pch = 1, col = 1:5, legend = 1:5)
> legend(6, 2.8, pch = 1:6, col = 1, legend = 0:5)
> text(0, 3, "available", adj = 0)
> text(8, 3, "taken", adj = 0)
> par(op)
```



The first plot shows the sorted data; the second plot shows the data coded by color, and the third shows the data sorted and coded (thanks to Ian and Jeff for the idea of the legends). I tweaked the margins and label spacing slightly with `mgp` and `mar` in the `par()` command.

In fact, this plot probably *doesn't* give a lot of insights that aren't better conveyed by the barplots or the bubble plot . . .

Exercise 0.5 :

Read in the data (again), take the subset with 5 seeds available, and generate the table of (number taken) × (Species):

```
> data = read.table("seedpred.dat", header = TRUE)
> data2 = data
> data2$available = data2$remaining + data2$taken
> data2 = data2[data2$available == 5, ]
> t1 = table(data2$taken, data2$Species)
```

Draw the plots:

```
> op = par(mfrow = c(2, 1), mgp = c(2.5, 1, 0), mar = c(4.1, 3.5,
+     1.1, 1.1))
> logt1 = log10(1 + t1)
> barplot(logt1, beside = TRUE, ylab = "log10(1+taken)")
> library(gplots)
```

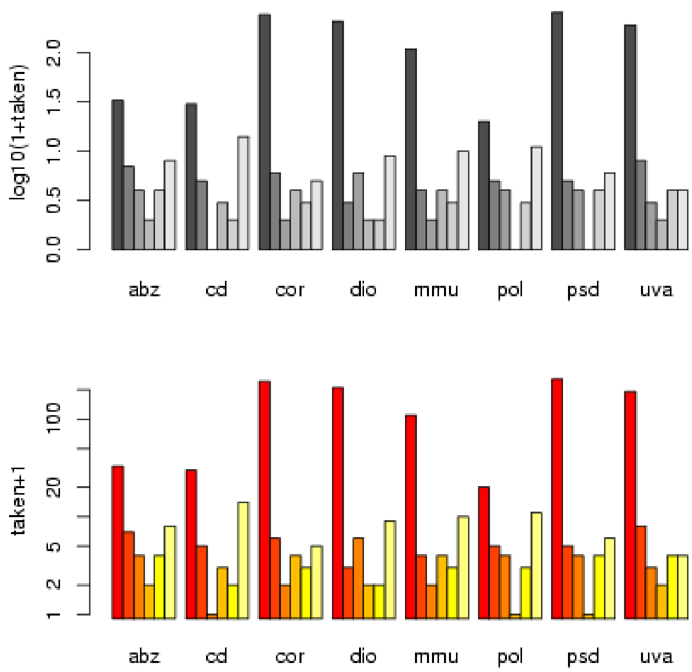
```
Loading required package: gdata
Loading required package: gtools

Attaching package: 'gplots'


        The following object(s) are masked from package:stats :

         lowess
```

```
> barplot2(t1 + 1, beside = TRUE, log = "y", ylab = "taken+1")
> par(op)
```



Once again, I'm using `par()` to tweak graphics options and squeeze the plots a little closer together. `barplot2()` has a `log` option that lets us plot the values on a logarithmic scale rather than converting to logs — but it hiccups if we have 0 values, so we still have to plot `t1+1`. (`barplot2()` also uses different default bar colors.)

Exercise 0.6 :

Read in the measles data again:

```
> data = read.table("ewcitmeas.dat", header = TRUE, na.strings = "*")
```

Separate out the incidence data (columns 4 through 10), find the minima and maxima by column, and compute the range:

```
> incidence = data[, 4:10]
> imin = apply(incidence, 2, min, na.rm = TRUE)
> imax = apply(incidence, 2, max, na.rm = TRUE)
> irange = imax - imin
```

Another way to get the range: apply the `range()` command, which will return a matrix where the first row is the minima and the second row — then subtract:

```
> iranges = apply(incidence, 2, range, na.rm = TRUE)
> iranges

     London Bristol Liverpool Manchester Newcastle Birmingham Sheffield
[1,]      1       0         0          0         0          0         0
[2,]   5464     835       813        894       616       2336       804
```

```
> irange = iranges[2, ] - iranges[1, ]
```

Or you could define a function that computes the difference:

```
> rangediff = function(x) {
+     diff(range(x, na.rm = TRUE))
+ }
> irange = apply(incidence, 2, rangediff)
```

Now use `scale()` to subtract the minimum and divide by the range:

```
> scaled_incidence = scale(incidence, center = imin, scale = irange)
```

Checking:

```
> summary(scaled_incidence)

     London            Bristol           Liverpool          Manchester
 Min.   :0.00000   Min.   :0.00000   Min.   :0.00000   Min.   :0.00000
 1st Qu.:0.01501   1st Qu.:0.00479   1st Qu.:0.01968   1st Qu.:0.01119
 Median :0.03496   Median :0.01557   Median :0.05904   Median :0.03244
 Mean   :0.07665   Mean   :0.05710   Mean   :0.11312   Mean   :0.08352
 3rd Qu.:0.08915   3rd Qu.:0.04551   3rd Qu.:0.16697   3rd Qu.:0.09172
 Max.   :1.00000   Max.   :1.00000   Max.   :1.00000   Max.   :1.00000
 NA's   :1.00000   NA's   :1.00000   NA's   :2.00000
   Newcastle          Birmingham          Sheffield
 Min.   :0.00000   Min.   :0.000000   Min.   :0.000000
 1st Qu.:0.00487   1st Qu.:0.006849   1st Qu.:0.007463
 Median :0.01299   Median :0.020120   Median :0.023632
 Mean   :0.05199   Mean   :0.054013   Mean   :0.078439
 3rd Qu.:0.04383   3rd Qu.:0.048587   3rd Qu.:0.085821
 Max.   :1.00000   Max.   :1.000000   Max.   :1.000000
                   NA's   :1.000000
```

```
> apply(scaled_incidence, 2, range, na.rm = TRUE)

     London Bristol Liverpool Manchester Newcastle Birmingham Sheffield
[1,]      0       0         0          0         0          0         0
[2,]      1       1         1          1         1          1         1
```

Exercise 0.7 :
You first need to calculate the column means so you can tell `sweep()` to subtract them (which is what `scale(x,center=TRUE,scale=FALSE)` does):

```
> imean = colMeans(incidence, na.rm = TRUE)
> scaled_incidence = sweep(incidence, 2, imean, "-")
```

Check:

```
> c1 = colMeans(scaled_incidence, na.rm = TRUE)
> c1

       London       Bristol     Liverpool    Manchester     Newcastle 
 4.789583e-12 -1.342629e-14  9.693277e-13 -9.520250e-13 -3.216842e-13 
   Birmingham     Sheffield 
 1.045927e-12 -2.389592e-13 
```

(these numbers are very close to zero . . . but not exactly equal, because of round-off error)

```
> all(abs(c1) < 1e-11)

[1] TRUE
```

Exercise 0.8 *: Resurrect long-format data:

```
> date = as.Date(paste(data$year + 1900, data$mon, data$day, sep = "/"))
> city_names = colnames(data)[4:10]
> data = cbind(data, date)
> data_long = reshape(data, direction = "long", varying = list(city_names),
+     v.name = "incidence", drop = c("day", "mon", "year"), times = factor(city_names),
+     timevar = "city")
```

Calculate min, max, and range difference:

```
> city_max = tapply(data_long$incidence, data_long$city, max, na.rm = TRUE)
> city_min = tapply(data_long$incidence, data_long$city, min, na.rm = TRUE)
> range1 = city_max - city_min

> scdat1 = data_long$incidence - city_min[data_long$city]
> scdat = scdat1/range1[data_long$city]
```

Check:

```
> tapply(scdat, data_long$city, range, na.rm = TRUE)

$Birmingham
[1] 0 1

$Bristol
[1] 0 1

$Liverpool
[1] 0 1

$London
[1] 0 1

$Manchester
[1] 0 1

$Newcastle
[1] 0 1

$Sheffield
[1] 0 1
```

Exercise 0.9 *: ???