PCOT2: Principal Coordinates and Hotelling's T^2 for the analysis of microarray data

Sarah Song and Mik Black

October 3, 2006

1 Overview

`pcot2` is an R-package for the analysis of groups of genes in microarray experiments. It utilizes inter-gene correlation information to detect significant alterations in the activities of gene sets. Incorporating additional (usually functional) information into the data analysis process allows gene interactions to be investigated in a statistical framework. One of the reasons that gene set analysis is becoming important is that it is suitable for detecting small coordinated changes in expression of groups of genes which are functionally related, which may not be considered significant in a single gene analysis. This vignette gives a tutorial-style introduction to the functions in the `pcot2` package. These functions are used for testing and visualizing changes in expression activity for groups of genes.

2 Example: ALL/AML data

In this example the ALL/AML leukemia data set of Golub *et al.*(1999) is used to illustrate the functionality of the `pcot2` package. This data set contains 38 bone marrow samples obtained from adult leukemia patients, 11 relating to acute myeloid leukemia (AML, class 1) and 27 relating to acute lymphoblastic leukemia (ALL, class 0). Gene expression levels were measured using Affymetrix high density oligonucleotide arrays containing 6817 human genes, of which 3051 genes were considered suitable for analysis by Golub et al.(1999) after preprocessing. This data set is available as part of the `multtest` package and gene sets are defined as KEGG pathways using the `hu6800` annotation package. Both packages can be downloaded from www.bioconductor.org.

```
> library(pcot2)
> library(multtest)
> library(hu6800)
> set.seed(1234567)
```

3 The `pcot2` function

The `pcot2` function implements the PCOT2 testing method, which is a two-stage permutation-based approach for testing changes in activity in pre-specified

gene sets. The function requires at least three inputs: gene expression data, sample class labels, and a gene category indicator matrix. The gene expression data should be in the form of a matrix with no missing values. Data pre-processing (e.g. normalization) must therefore take place before running the PCOT2 analysis.

```
> data(golub)
> rownames(golub) <- golub.gnames[, 3]
> colnames(golub) <- golub.cl
```

The class labels represent two distinct experimental conditions (e.g., AML and ALL).

```
> golub.cl
```

```
 [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1
```

The gene category indicator matrix is designed to indicate presence or absence of genes in the pre-defined gene categories (e.g., gene pathways). The indicator matrix contains rows representing gene identifiers for genes present in the expression data, and columns representing pre-defined group names. The values 1 or 0 indicate the presence or absence of a gene in a particular group.

In this example, the `hu6800` annotation package is used to define the KEGG (http://www.genome.jp/kegg/pathway.html) pathways for all of 3051 genes in the data. The `getImat` function is used to generate an indicator matrix which includes 65 KEGG pathways containing at least 10 of the total 3051 genes.

```
> KEGG.list <- as.list(hu6800PATH)
> imat <- getImat(golub, KEGG.list, ms = 10)
> colnames(imat) <- paste("KEGG", colnames(imat), sep = "")
> dim(imat)
```

```
[1] 3051   99
```

Permutations are used to produce p-values based on the null distribution of the T^2 statistic. By default `pcot2` will automatically run 1000 permutations. In order to minimize the time taken to build this vignette, only 10 permutations have been performed.

```
> results <- pcot2(golub, golub.cl, imat, iter = 10)
```

```
Comparison: 0-1
```

The output from the `pcot2` function can contain information on either all pathways or just significantly differentially expressed pathways, based on the value of α used in the function, where α determines the significance threshold for the permutation p-values. For each KEGG pathway, the number of genes in the pathway is listed, along with Hotelling's T^2 statistic. These are followed by parametric p-values for the test statistic, both raw and adjusted. The last two columns provide raw and adjusted permutation-based p-values. The default adjustment method is the false discovery rate controlling method of Benjamini and Yekutieli (2001).

```
> results$res.sig

[1] Num         T2          P.nor       P.adj       P.permu     P.permu.adj
<0 rows> (or 0-length row.names)

> results$res.all

          Num         T2        P.nor        P.adj P.permu P.permu.adj
KEGG01032  11  16.083606 1.559644e-03 1.229864e-02     0.1   0.5632532
KEGG04010 107  37.799126 3.502656e-06 4.852223e-05     0.1   0.5632532
KEGG04060  86  50.940814 1.990119e-07 5.666977e-06     0.1   0.5632532
KEGG04350  26  23.712919 1.425931e-04 1.379011e-03     0.1   0.5632532
KEGG04520  37  23.992055 1.314175e-04 1.320773e-03     0.1   0.5632532
KEGG00190  43  14.212036 2.959080e-03 2.166725e-02     0.1   0.5632532
KEGG00193  18  47.397496 4.122077e-07 9.186144e-06     0.1   0.5632532
KEGG04810  89  54.942820 9.054124e-08 3.569835e-06     0.1   0.5632532
KEGG04514  72  25.591713 8.291894e-05 8.673666e-04     0.1   0.5632532
KEGG04670  64 102.797497 5.541345e-11 1.420137e-08     0.1   0.5632532
KEGG00564  13  52.401665 1.486743e-07 4.762786e-06     0.1   0.5632532
KEGG00590  19  47.576677 3.970128e-07 9.186144e-06     0.1   0.5632532
KEGG04370  35  18.656730 6.707025e-04 5.729592e-03     0.1   0.5632532
KEGG04664  38  61.379812 2.735820e-08 1.558081e-06     0.1   0.5632532
KEGG04730  33  47.690379 3.876787e-07 9.186144e-06     0.1   0.5632532
KEGG04912  38  15.919109 1.648417e-03 1.261065e-02     0.1   0.5632532
KEGG04510  88  45.140440 6.662542e-07 1.219627e-05     0.1   0.5632532
KEGG00280  22  45.846527 5.725182e-07 1.086852e-05     0.1   0.5632532
KEGG00240  32  58.978644 4.234863e-08 2.170623e-06     0.1   0.5632532
KEGG04360  32  39.327865 2.446638e-06 3.800151e-05     0.1   0.5632532
KEGG03022  13  23.820339 1.381779e-04 1.362010e-03     0.1   0.5632532
KEGG00220  12   7.580525 3.529195e-02 2.032501e-01     0.1   0.5632532
KEGG00260  12   9.014209 2.002974e-02 1.222197e-01     0.1   0.5632532
KEGG00330  22  67.699684 9.103087e-09 5.832352e-07     0.1   0.5632532
KEGG03320  20  53.201493 1.269935e-07 4.339457e-06     0.1   0.5632532
KEGG04310  42  37.040273 4.197126e-06 5.661264e-05     0.1   0.5632532
KEGG04330  15  14.413820 2.758517e-03 2.049140e-02     0.1   0.5632532
KEGG05120  39  72.098995 4.399616e-09 3.758448e-07     0.1   0.5632532
KEGG00230  54  18.234794 7.681197e-04 6.454225e-03     0.1   0.5632532
KEGG04612  56  41.303014 1.555451e-06 2.559465e-05     0.1   0.5632532
KEGG00561  17  58.313748 4.788850e-08 2.231432e-06     0.1   0.5632532
KEGG04512  33  49.878215 2.467977e-07 6.657828e-06     0.1   0.5632532
KEGG04340  11   6.073128 6.534459e-02 3.640549e-01     0.1   0.5632532
KEGG04640  70 115.400542 1.210776e-11 6.205958e-09     0.1   0.5632532
KEGG04650  65  46.542476 4.936711e-07 9.732163e-06     0.1   0.5632532
KEGG04662  39  46.757474 4.717016e-07 9.732163e-06     0.1   0.5632532
KEGG04610  15  73.363867 3.589230e-09 3.758448e-07     0.1   0.5632532
KEGG04070  31  25.776064 7.869364e-05 8.403176e-04     0.1   0.5632532
KEGG00980  13  69.188212 7.093654e-09 5.194180e-07     0.1   0.5632532
KEGG00350  15   4.806800 1.115512e-01 6.082631e-01     0.1   0.5632532
KEGG04660  43  33.338131 1.042993e-05 1.243249e-04     0.1   0.5632532
KEGG00380  22  74.739625 2.883968e-09 3.758448e-07     0.1   0.5632532
KEGG04110  49  51.495005 1.780683e-07 5.368869e-06     0.1   0.5632532
```

KEGG01510	25	9.919144	1.413848e-02	9.058529e-02	0.1	0.5632532
KEGG00360	11	38.952479	2.670169e-06	4.025361e-05	0.1	0.5632532
KEGG04940	34	7.779280	3.259065e-02	1.920078e-01	0.1	0.5632532
KEGG04020	62	42.299762	1.243043e-06	2.197015e-05	0.1	0.5632532
KEGG04540	43	10.907225	9.740883e-03	6.401014e-02	0.1	0.5632532
KEGG03050	16	41.184124	1.597917e-06	2.559465e-05	0.1	0.5632532
KEGG00120	10	8.026618	2.953082e-02	1.760038e-01	0.1	0.5632532
KEGG04080	68	35.854072	5.589777e-06	7.162746e-05	0.1	0.5632532
KEGG05040	21	13.809328	3.406880e-03	2.459481e-02	0.1	0.5632532
KEGG04210	44	27.299352	5.138148e-05	5.603428e-04	0.1	0.5632532
KEGG04620	48	41.219369	1.585201e-06	2.559465e-05	0.1	0.5632532
KEGG04920	30	57.385632	5.693675e-08	2.431960e-06	0.1	0.5632532
KEGG05110	15	13.112465	4.359517e-03	3.060980e-02	0.1	0.5632532
KEGG00500	17	17.798230	8.848180e-04	7.314881e-03	0.1	0.5632532
KEGG00010	36	8.520856	2.429027e-02	1.464733e-01	0.1	0.5632532
KEGG00030	15	13.506746	3.790243e-03	2.698234e-02	0.1	0.5632532
KEGG00051	18	18.678736	6.659944e-04	5.729592e-03	0.1	0.5632532
KEGG00710	12	6.022369	6.673974e-02	3.678295e-01	0.1	0.5632532
KEGG04910	56	27.699624	4.601491e-05	5.241205e-04	0.1	0.5632532
KEGG04630	56	38.326364	3.092383e-06	4.402869e-05	0.1	0.5632532
KEGG00860	12	38.451145	3.002926e-06	4.397660e-05	0.1	0.5632532
KEGG05210	38	27.327734	5.097998e-05	5.603428e-04	0.1	0.5632532
KEGG00071	18	36.921968	4.317896e-06	5.674826e-05	0.1	0.5632532
KEGG04720	35	16.143909	1.528379e-03	1.224041e-02	0.1	0.5632532
KEGG04930	18	17.466958	9.858206e-04	8.020517e-03	0.1	0.5632532
KEGG00310	15	33.903265	9.048742e-06	1.131226e-04	0.1	0.5632532
KEGG04150	18	11.009560	9.376387e-03	6.241513e-02	0.1	0.5632532
KEGG04742	10	9.165107	1.889037e-02	1.166561e-01	0.1	0.5632532
KEGG04530	41	33.404722	1.025619e-05	1.243249e-04	0.1	0.5632532
KEGG05130	27	9.739467	1.514257e-02	9.465221e-02	0.1	0.5632532
KEGG05131	27	9.739467	1.514257e-02	9.465221e-02	0.1	0.5632532
KEGG00150	10	11.673533	7.335679e-03	4.947340e-02	0.1	0.5632532
KEGG05050	11	7.680916	3.389911e-02	1.974471e-01	0.1	0.5632532
KEGG00252	15	20.668382	3.563113e-04	3.261269e-03	0.1	0.5632532
KEGG00760	11	53.597908	1.175117e-07	4.302274e-06	0.1	0.5632532
KEGG00562	14	19.021299	5.970409e-04	5.276198e-03	0.1	0.5632532
KEGG00480	11	72.739759	3.967321e-09	3.758448e-07	0.1	0.5632532
KEGG04740	10	14.887889	2.341753e-03	1.765132e-02	0.1	0.5632532
KEGG00052	15	19.849740	4.596460e-04	4.133269e-03	0.1	0.5632532
KEGG00650	16	15.980992	1.614410e-03	1.253762e-02	0.1	0.5632532
KEGG00410	13	46.661226	4.814060e-07	9.732163e-06	0.1	0.5632532
KEGG00340	10	29.388643	2.910738e-05	3.390748e-04	0.1	0.5632532
KEGG00620	16	21.669123	2.622921e-04	2.444374e-03	0.1	0.5632532
KEGG00640	17	48.892360	3.020600e-07	7.741198e-06	0.1	0.5632532
KEGG00510	14	10.796492	1.015222e-02	6.586868e-02	0.1	0.5632532
KEGG01030	18	12.723491	5.010394e-03	3.470445e-02	0.1	0.5632532
KEGG00970	16	23.403392	1.561698e-04	1.482342e-03	0.1	0.5632532
KEGG05030	13	25.111697	9.508626e-05	9.747490e-04	0.1	0.5632532
KEGG00020	12	12.207513	6.036512e-03	4.125436e-02	0.2	1.0000000
KEGG05010	13	3.332612	2.123831e-01	1.000000e+00	0.2	1.0000000

```
KEGG04120  12   6.182388 6.244511e-02 3.517240e-01     0.2   1.0000000
KEGG00251  13   6.428522 5.640018e-02 3.212055e-01     0.2   1.0000000
KEGG01031  10   1.390378 5.152243e-01 1.000000e+00     0.4   1.0000000
KEGG00530  11   1.535339 4.814905e-01 1.000000e+00     0.4   1.0000000
KEGG01430  35   2.677797 2.849138e-01 1.000000e+00     0.5   1.0000000
KEGG04320  10   1.201290 5.630263e-01 1.000000e+00     0.7   1.0000000
```

In the `pcot2` function, the T^2 statistic can be calculated in two ways, using either a pooled estimate of correlation for the two classes (default) or an unpooled estimate. And users can set *var.equal=F* if the correlation structure is assumed to differ across the two classes.

In the first step of the PCOT2 analysis, the dimensionality of the gene expression data is reduced via principle coordinates. The default dimensionality in the `pcot2` function is set as *ncomp=2*. In the second step of the PCOT2 analysis, the distances between the transformed groups are calculated via euclidean distances by default. Other distances (e.g., correlation or Spearman distances) can also be used by defining *dist.method* in the function. A permutation p-value for each category is calculated by re-arranging the sample labels. The permutations can also be performed by permuting rows (genes), using `permu='ByRow'`.

Table 1 lists computation times (in minutes) required to run 1000 permutations of the `pcot2` function on the AML/ALL data under various parameter configurations. The two machines used were a 3.2GHz Pentium 4 with 1Gb RAM running Microsoft Windows XP and R 2.1.0 (PC), and a 1.70GHz Pentium M with 256Mb of RAM running Fedora Core 3 and R 2.2.0 (Unix).

Table 1: *Computation times (minutes, 1000 permutations)*

Changes	PC machine	UNIX machine
default setting	5.6	6.8
var.equal=F	5.5	6.8
comp=8	6	7.6
dist.method="euclidean"	4.8	6
permu="ByRow"	5.6	6.8

4 The `corplot` and `corplot2` functions

The `corplot` and `corplot2` functions enable visualization of both correlation and gene expression information for a particular gene category, in particular the groups identified as being differentially expressed. The plot produced by the `corplot` function displays the pooled correlation calculated from the two classes, while the `corplot2` function produces a plot based on unpooled correlation. Gene names can be added to the plot using *add.name=T* (default). The font size can be changed by setting the *font.size* argument. The *main* option specifies the title of the plot.

```
> sel <- c("04620", "04120")
> pvalue <- c(0.001, 0.72)
> library(KEGG)
> pname <- unlist(mget(sel, env = KEGGPATHID2NAME))
```

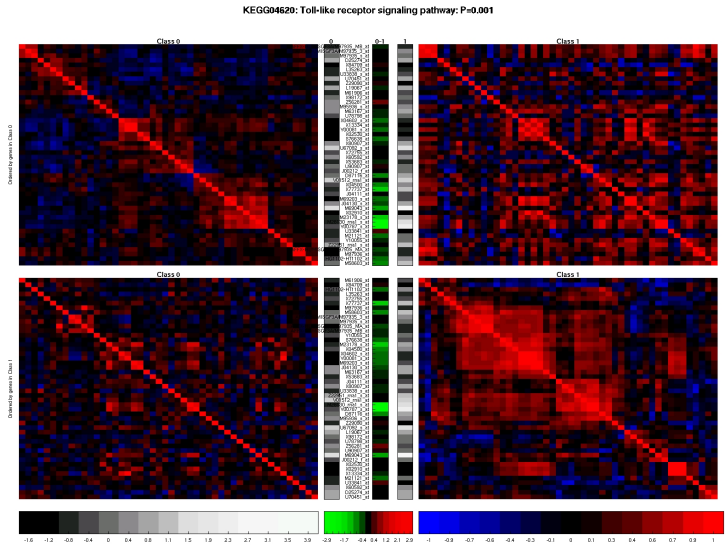

Figure 1: KEGG04620

```
> main <- paste("KEGG", sel, ": ", pname, ": ", "P=", pvalue, sep = "")
> for (i in 1:length(sel)) {
+     fname <- paste("corplot2-KEGG", sel[i], ".jpg", sep = "")
+     jpeg(fname, width = 1600, height = 1200, quality = 100)
+     selgene <- rownames(imat)[imat[, match(paste("KEGG", sel,
+         sep = "")[i], colnames(imat))] == 1]
+     corplot2(golub, selgene, golub.cl, main = main[i])
+     dev.off()
+ }
```

The argument *inputP* allows users to input the p-values of individual genes calculated using other approaches, such as the limma package (Smyth *et al.*, 2004), allowing the results from both per-gene and per-pathway analysis to be printed on a single plot. To allow users to identify genes from in correlation image plots, the argument *gene.locator=T* allows the selection of interesting (e.g., highly correlated and differential expressed between two classes) genes by clicking beginning and end points on the main diagonal of the image plots. This prints the identifiers for the selected genes. Further details of this functionality are provided in the HowToUseGeneLocator.pdf document. The usage of `corplot2` is similar to that for the `corplot` function.

5 The `aveProbes` function

In Affymetrix gene expression data, a unique gene can often link to multiple probe sets, with such genes then having a greater influence on the pathway analysis (particularly if the gene is differentially expressed). In order to solve this problem, the `aveProbe` function is provided to change the multiple probe data to the unique gene data by taking the median of the probe values. This

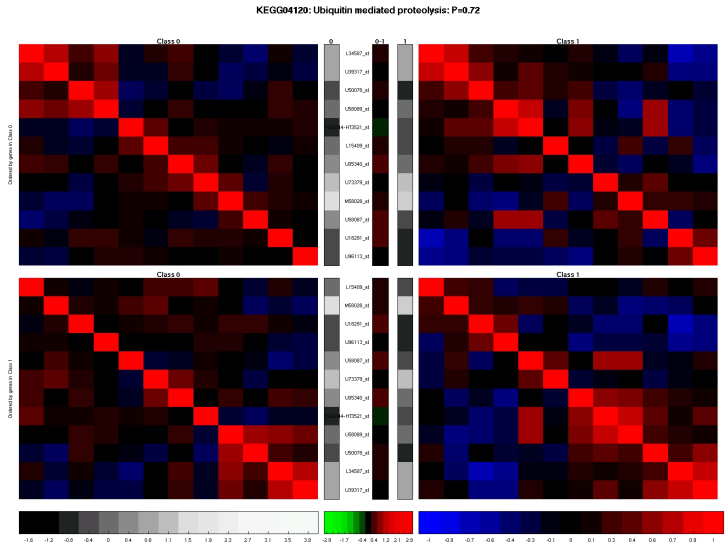

Figure 2: KEGG04120

function can be used to transform both expression data and the indicator matrix by providing a vector of unique gene identifiers.

```
> pathlist <- as.list(hu6800PATH)
> pathlist <- pathlist[match(rownames(golub), names(pathlist))]
> ids <- unlist(mget(names(pathlist), env = hu6800SYMBOL))
> newdata <- aveProbe(x = golub, ids = ids)$newx
> output <- aveProbe(x = golub, imat = imat, ids = ids)
> newdata <- output$newx
> newimat <- output$newimat
> newimat <- newimat[, apply(newimat, 2, sum) >= 10]
> dim(newdata)

[1] 2764   38

> dim(newimat)

[1] 2764   90
```

After the multiple probe data set has been changed to the unique gene symbol data, further analysis such as testing and visualizing pathways can be done on the new data set.

References

[1] Benjamini,B.Y. and Yekutieli,D. (2001) The control of the false discovery rate in multiple testing under dependency. *The Annals of Statistics*, **29**, 1165-1188.

[2] Gentleman,R.C., Carey,V.J., Bates,D.M., Bolstad,B., Dettling,M., Dudoit,S., Ellis,B., Gautier,L., Ge,Y., Gentry,J. *et al.* (2004) Bioconductor: open software development for computational biology and bioinformatics. *Genome Biology*, **5**, R80.

[3] Golub,T.R., Slonim,D.K., Tamayo,P., Huard,C., Gaasenbeek,M., Mesirov,J.P., Coller,H., Loh,M.L., Downing,J.R., Caligiuri,M.A. *et al.* (1999) Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring, *Science*, **286**, 531-537.

[4] Smyth,G.K. (2004) Linear models and empirical Bayes methods for assessing differential expression in microarray experiments. *Statistical Applications in Genetics and Molecular Biology*, **3**, No.1, Article 3.