

# Testing association of a pathway with a clinical variable

Jelle Goeman      Jan Oosting

Package *globaltest*

## Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
<b>2</b>	<b>Preparation</b>	<b>4</b>
2.1	Leukemia Data . . . . .	4
2.2	Breast Cancer Data . . . . .	4
2.3	Annotation . . . . .	5
<b>3</b>	<b>The Global Test</b>	<b>5</b>
3.1	Testing a single pathway . . . . .	5
3.2	Multiple Global Testing . . . . .	7
3.3	Different types of response variable . . . . .	9
3.4	Different methods for calculating the p-value . . . . .	11
3.5	Adjusting for the presence of covariates . . . . .	13
<b>4</b>	<b>The Comparative P</b>	<b>15</b>
<b>5</b>	<b>Diagnostic plots</b>	<b>16</b>
5.1	Permutations histogram . . . . .	16
5.2	Gene Plot . . . . .	17
5.3	Sample Plot . . . . .	19
5.4	Other plots . . . . .	20
<b>6</b>	<b>Session Information</b>	<b>22</b>
	<b>References</b>	<b>23</b>

## Deprecated version

This vignette describes version 4 of the *globaltest* package. As the package has been completely rewritten, as of version 4.99.0 of *globaltest* this vignette and the functions described in it have been deprecated. Please switch to the new implementation based on the `gt` function. The functions described in this vignette will be removed from the package in a later version.

Use of the deprecated `globaltest` will result in a warning. To suppress this warning, use

```
> gt.options(warn.deprecated=FALSE)
```

## Important Note

As of version 4.0.0 the method for calculating the asymptotic p-value has much improved. To use gamma approximation results of earlier versions (and of the Bioinformatics paper add the option `method = "gamma"` to the `globaltest` function (not recommended). See section 3.4 for more details.

## 1 Introduction

This document shows the functionality of the R-package *globaltest*. The main function tests whether a given group of genes is significantly associated with a response. The explanation here focuses on practical use of the test. To understand the idea and the mathematics behind the test, and for more details on how to interpret a test result, we refer to the following papers (see page 23 for full references).

- Goeman et al. (2004) introduces the principle of global testing in microarray data analysis.
- Goeman et al. (2005) extends the approach to a survival time response and explains how to deal with covariates.
- Goeman et al. (2006) derives the mathematical properties of the test and proves its optimality under some conditions.

In recent years there has been a shift in focus from studying the effects of single genes to studying effects of multiple functionally related genes. Most of the current methods for studying pathways involve looking at increased proportions of differentially expressed genes in pathways of interest. These methods do not identify pathways where many genes have altered their expression in a small way. The *globaltest* was designed to address this issue.

The *globaltest* method is based on a prediction model for predicting a response variable from the gene expression measurements of a set of genes. The null hypothesis to be tested is that expression profile of the genes in the gene set is not associated with the response variable. A significant test result has three equivalent interpretations (see Goeman et al., 2004, 2005, for more details).

- If the test is significant, part of the variance of the response variable can be predicted from the gene expression measurements of the gene set.
- If the test is significant, the genes in the gene set are, on average, more associated with the response variable than would be expected under the null hypothesis. These associations may be both positive (upregulation) and negative (downregulation). Typically, a significant pathway is a mix of positively and negatively associated genes.
- If the test is significant, samples with similar values of the response variable tend to have relatively similar expression profiles over the genes in the gene set. Therefore, in an unsupervised cluster analysis, samples with the same value of the response variable have a tendency to turn up in the same clusters.

By grouping together genes before testing usually the number of tests will decrease and the severity of the correction for multiple testing will decrease. Genes can be grouped together into genesets in any meaningful way, for example based in function (KEGG, GO) or location (chromosome, cytoband). However, the choice of the gene sets may not be based in any way on the response variable that is used for testing.

## 2 Preparation

In the examples that follow we use two data sets. Both use the dataformat use BioConductor *ExpressionSet* input, which is the standard format for storing gene expression data in BioConductor. The *ExpressionSet* is the preferred input format for data in *globaltest*, but simple vector/matrix input is also possible. See `help(globaltest)`.

### 2.1 Leukemia Data

The first data set is the famous Leukemia data set by Golub et al. (1999), that is available from the *golubEsets* package on BioConductor. We load the data and normalize them using *vsn*. We reduce the data set in size in order to speed up the computations in this Vignette.

```
> library(golubEsets)
> library(vsn)
> data(Golub_Merge)
> Golub<-Golub_Merge[,1:34]
> exprs(Golub)<-exprs(vsn2(Golub_Merge[,1:34]))
```

This gives us a data set `Golub`, which is of the format *ExpressionSet*. It has 7,129 genes for 34 samples on Affymetrix hu6800 chips. We use *vsn* to normalize the data here, but any other normalization method may be used instead. Several phenotype variables are available with `Golub`, among them “ALL.AML”, the clinical variable that interests us, which separates the samples into Acute Lymphoblastic Leukemia and Acute Myelogenous Leukemia samples.

### 2.2 Breast Cancer Data

The second data set is a breast cancer data set from the Dutch Cancer Institute (Van de Vijver et al., 2002), which we have have included (by kind permission from the authors) in the *globaltest* package. To keep the package small we have reduced the data set to only 230 probes (those probes annotated to 64 pathways (all related to cell cycle) contained in our example annotation `annotation.vandeVijver`) and only 100 random patients.

```
> library(globaltest)
> data(vandeVijver)
```

This loads another *ExpressionSet*, called `vandeVijver`, which contains the data. The chip was done with Rosetta technology and the data are already normalized by Rosetta. The response of primary interest is the survival time, coded in variables “TIMEsurvival” (the survival time) and “EVENTdeath” (which indicates whether the observed time indicates a death or a censoring).

## 2.3 Annotation

To be able to use *globaltest* one must provide annotation to link the gene sets to be tested to the genes in the data.

The easiest way to do this is to use the metadata packages provided in BioConductor. These are provided for most commercially available chips and for many organisms. For example, to get GO and KEGG annotation for the Leukemia data set, we use the *hu6800.db* package.

```
> library(hu6800.db)
> kegg <- as.list(hu6800PATH2PROBE)
> go <- as.list(hu6800GO2ALLPROBES)
```

This creates a list `kegg` of 229 pathways and a list `go` of 15942 pathways. Each pathway in these lists is a vector of gene names.

In GO, it is sometimes wise to only consider annotations which were curated by experts and to exclude those inferred by electronic annotation (IEA). Excluding the electronic and unspecified GO-annotations can be done with

```
> go <- lapply(go, function(x) x[!is.na(names(x)) & (names(x) != "IEA")])
```

We can now retrieve the Cell Cycle genes according to these two annotations.

```
> GO.cellcycle <- go[["GO:0007049"]]
> KEGG.cellcycle <- kegg[["04110"]]
```

The vectors `KEGG.cellcycle` (109 probes) and `GO.cellcycle` (721 probes) contain the probes on the hu6800 chip that are annotated to the Cell Cycle pathway.

There is no `metaData` package for the Rosetta chips used in the Breast Cancer Data. Some annotation has been included in the *globaltest* package (see `help(annotation.vandevijver)`), but we will not use it in this vignette. See the help files.

## 3 The Global Test

This section explains the options of the `globaltest` function, which is the main function of the package.

### 3.1 Testing a single pathway

Suppose we are interested in testing whether AML and ALL patients have different overall gene expression profiles. We can test this by saying

```
> gt.all <- globaltest(Golub, "ALL.AML")
```

The first input  $X$  should be the object with the expression data (here the *ExpressionSet* object), the second input  $Y$  should give the response variable. Because the call above provides an *ExpressionSet* for  $X$ , we only need to specify the name of the response variable in  $Y$ . Alternatively, the user can provide the whole vector in  $Y$ . In that case  $X$  only needs to provide the matrix of gene expression measurements (but it may still be an *ExpressionSet*).

The third function argument should be the gene set(s) to be tested. The default is to test the gene set of all genes on the chip.

The test result is stored in a *gt.result* object, which also contains all the information needed to draw the diagnostic plots. Many methods offer access to the information contained in the *gt.result*. Type `help(gt.result)` for an overview.

```
> gt.all
```

```
Global Test result:
```

```
Data: 34 samples with 7129 genes; 1 gene set
```

```
Model: logistic
```

```
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	7129	7129	33.682	10	3.1364 2.754e-05

This gives a summary of the test and its result. The model was “logistic” because the response `ALL.AML` is two-valued. The p-value was calculated using the asymptotic distribution (see section 3.4 for details). The bottom part is the test result. The gene set of all genes has 7,129 genes, which were all included in the test. Then it gives the test statistic  $Q$ , its expectation and standard deviation under the null hypothesis, and finally the p-value.

From this we conclude that there is ample evidence that the overall gene expression profile for all 7,129 genes is associated with the response. This means that samples with the same AML/ALL status tend to have similar expression profiles. It also means that the expression profile of a non-negligible proportion of the 7,129 genes is differentially expressed between AML and ALL patients. And it also means that there is potential for prediction of ALL/AML status from the gene expression profile over all 7,129 genes.

In cases such as this one, in which the overall expression pattern is (highly) associated with the response variable, we can expect many pathways (especially the larger ones) also to be associated with the response variable. See section 4 for a way to deal with this situation.

To test a specific pathway, provide it as the third argument *genesets* to `globaltest`.

```
> globaltest(Golub, "ALL.AML", GO.cellcycle)
```

```
Global Test result:
```

```
Data: 34 samples with 7129 genes; 1 gene set
```

```
Model: logistic
```

```
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
[1,]	721	554	37.033	10.417	3.8094 0.0001808

Just as with the gene set of all genes, we conclude from the test result that the expression profile of the cell cycle pathway (as defined by GO) is notably different between AML and ALL samples. Patients with AML tend to be more similar to other AML patients than to ALL patients, with respect to their cell cycle expression profile (and vice versa).

Note that in the test result for the cell cycle pathway there is a difference between the values of “Genes” and “Tested”. “Genes” just gives the length of the input vector that defined the gene set, while “Tested” gives the number of unique probe ids that can be matched to probe ids in the gene expression matrix. The vector `GO.cellcycle` is of length 721, but only contains 554 unique probe ids. Duplicate probe ids are automatically found and left out by `globaltest`.

### 3.2 Multiple Global Testing

It is possible to test many pathways at once by providing a *list* of pathways. For example:

```
> cellcycle <- list(go = GO.cellcycle, kegg = KEGG.cellcycle)
> globaltest(Golub, "ALL.AML", cellcycle)
```

Global Test result:

Data: 34 samples with 7129 genes; 2 gene sets

Model: logistic

Method: Asymptotic distribution

	Genes	Tested	Statistic Q	Expected Q	sd of Q	P-value
go	721	554	37.033	10.417	3.8094	0.00018080
kegg	109	109	35.695	10.135	4.0625	0.00045098

We have already made lists of all KEGG and GO pathways in the Section 2.3, and stored them as `kegg` and `go`. To test all KEGG pathways we say:

```
> gt.kegg <- globaltest(Golub, "ALL.AML", kegg)
```

We will not display the whole result `gt.kegg`, but we can display part of it. To get the cell cycle result (KEGG 04110), or to get the first ten results, we can say

```
> gt.kegg["04110"]
> gt.kegg[1:10]
```

We might also want to sort the pathways by their p-value, and show only the top five. This can be done as follows

```
> sorted <- sort(gt.kegg)
> top5 <- sorted[1:5]
> top5
```

Global Test result:

Data: 34 samples with 7129 genes; 5 gene sets

Model: logistic

Method: Asymptotic distribution

	Genes	Tested	Statistic Q	Expected Q	sd of Q	P-value
03450	9	9	341.670	19.9610	19.5370	5.3258e-07
04662	68	68	124.150	14.1220	7.5052	6.6299e-07
00480	31	31	65.380	9.7337	4.5838	7.5537e-07
05150	56	56	148.590	16.7010	9.4461	9.1758e-07
00980	43	43	44.913	6.9181	3.1715	9.8892e-07

To make this list more readable, the pathway numbers can be replaced by the pathway names. For this we need the *KEGG.db* package, which contains the necessary information.

```
> library(KEGG.db)
> names(top5) <- as.list(KEGGPATHID2NAME)[names(top5)]
> top5
```

Global Test result:

Data: 34 samples with 7129 genes; 5 gene sets

Model: logistic

Method: Asymptotic distribution

	Genes Tested	Statistic	Q
Non-homologous end-joining	9	9	341.670
B cell receptor signaling pathway	68	68	124.150
Glutathione metabolism	31	31	65.380
Staphylococcus aureus infection	56	56	148.590
Metabolism of xenobiotics by cytochrome P450	43	43	44.913
	Expected Q	sd of Q	P-value
Non-homologous end-joining	19.9610	19.5370	5.3258e-07
B cell receptor signaling pathway	14.1220	7.5052	6.6299e-07
Glutathione metabolism	9.7337	4.5838	7.5537e-07
Staphylococcus aureus infection	16.7010	9.4461	9.1758e-07
Metabolism of xenobiotics by cytochrome P450	6.9181	3.1715	9.8892e-07

There are some other functions to extract useful information from a *gt.result* object. See also `help(gt.result)`. The most important are:

```
> p.value(top5)
```

```

Non-homologous end-joining
5.325841e-07
B cell receptor signaling pathway
6.629865e-07
Glutathione metabolism
7.553706e-07
Staphylococcus aureus infection
9.175798e-07
Metabolism of xenobiotics by cytochrome P450
9.889245e-07
```

```
> names(top5)
```

```
[1] "Non-homologous end-joining"
[2] "B cell receptor signaling pathway"
[3] "Glutathione metabolism"
[4] "Staphylococcus aureus infection"
[5] "Metabolism of xenobiotics by cytochrome P450"
```

```
> result(top5)
```



```

                                Genes Tested Statistic Q
Non-homologous end-joining      9      9    341.67097
B cell receptor signaling pathway 68     68    124.15037
Glutathione metabolism          31     31     65.38022
Staphylococcus aureus infection 56     56    148.58918
Metabolism of xenobiotics by cytochrome P450 43    43    44.91323
                                Expected Q    sd of Q    P-value
Non-homologous end-joining      19.960975 19.537470 5.325841e-07
B cell receptor signaling pathway 14.121682  7.505184 6.629865e-07
Glutathione metabolism          9.733666  4.583797 7.553706e-07
Staphylococcus aureus infection 16.701178  9.446071 9.175798e-07
Metabolism of xenobiotics by cytochrome P450 6.918054  3.171485 9.889245e-07
> length(top5)
[1] 5

```

When testing more than one pathway, it is important to correct for multiple testing. The function `multtest` calculates multiplicity-adjusted p-values.

```

> sorted <- gt.multtest(sorted, "FWER")
> sorted[1:5]

```

Global Test result:

Data: 34 samples with 7129 genes; 5 gene sets

Model: logistic

Method: Asymptotic distribution

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	FWER.adjusted	
03450	9	9	341.670	19.9610	19.5370	5.3258e-07	0.00012196
04662	68	68	124.150	14.1220	7.5052	6.6299e-07	0.00015116
00480	31	31	65.380	9.7337	4.5838	7.5537e-07	0.00017147
05150	56	56	148.590	16.7010	9.4461	9.1758e-07	0.00020737
00980	43	43	44.913	6.9181	3.1715	9.8892e-07	0.00022251

The second option *proc* takes values *FWER* for the family-wise error rate (Holm's method), and *FDR* for the false discovery rate (Benjamini and Hochberg). Be careful not to apply the `gt.multtest` function on a collection of pathways selected on their p-values. For more sophisticated multiple testing adjustments, see the *multtest* package, and Section ??.

### 3.3 Different types of response variable

The Global Test allows four different types of response variables to be tested. We give examples of each below. The statistical model that `globaltest` uses is usually determined from the input of the response variable, but the automatic choice can be overridden using the function argument *model*.

**Two-valued response** This is the most common type of response variable in microarray data analysis. If the response variable takes only two values, `globaltest` automatically chooses the logistic regression model. See the examples in the previous two sections.

A multi-valued response can be transformed to a two-valued response with the option *levels*. See Multi-valued Response, below.

**Multi-valued response** If the response is a *factor* which takes more than two values, `globaltest` automatically chooses a multinomial logistic regression model. For example, in the Leukemia data, we might want to know whether the overall expression profile depends on the center the samples came from (coded as *Source*) in Golub. We can test this with

```
> globaltest(Golub, "Source")
```

```
Global Test result:
```

```
Data: 34 samples with 7129 genes; 1 gene set
```

```
Model: multinomial
```

```
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	7129	7129	23.299	10 1.9695	2.3623e-05

It might have been expected that the expression profiles are different for different centers, as many centers provided only ALL or only AML samples. We can compare the samples from only the centers CALGB and CCG (which both provided only AML samples) using the option *levels*:

```
> globaltest(Golub, "Source", levels = c("CALGB", "CCG"))
```

```
Global Test result:
```

```
Data: 9 samples with 7129 genes; 1 gene set
```

```
Model: logistic
```

```
Method: All 126 permutations
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	7129	7129	12.751	11.25 1.8411	0.19048

For a more sophisticated way of correcting for confounders (such as ALL.AML in this case), see Section 3.5.

If only one level is given in *levels*, that outcome category is tested against the other categories combined.

```
> globaltest(Golub, "Source", levels = "St-Jude")
```

```
Global Test result:
```

```
Data: 34 samples with 7129 genes; 1 gene set
```

```
Model: logistic
```

```
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	7129	7129	20.142	10 3.1364	0.0076095

Note that if a multi-valued response is not explicitly coded as *factor*, `globaltest` will see it as continuous. The easiest way to let `globaltest` know that the response should not be treated as continuous is to make it a factor. This can be done with

```
> globaltest(Golub, "factor(Source)")
```

This is especially relevant for time series, as the time points in a time series should usually be tested with a multinomial model, but they are not usually coded as *factor*.

**Continuous response** If the response is continuous, `globaltest` uses a linear model. For example, in the Leukemia data, the percentage of blast cells was measured for the 15 AML samples from CALGB. To test whether this percentage is reflected in the overall expression profile, we can say:

```
> calgb <- pData(Golub)["Source"] == "CALGB"
> globaltest(Golub[,calgb], "pctBlasts")
```

Global Test result:

Data: 4 samples with 7129 genes; 1 gene set  
Model: linear  
Method: All 24 permutations

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	
all	7129	7129	8.428	10	2.5307	0.625

**Survival as response** The primary response in the Breast Cancer Data set is survival of patients. Survival time should be coded as a time for each patient (which is the last observation time for that patient) plus an *event indicator*, a dummy that indicates whether the patient died (had an event) at that point or was still alive (censored) at the last observation time.

```
> library(survival)
> globaltest(vandevijver, "Surv(TIMEsurvival, EVENTdeath)")
```

Global Test result:

Data: 100 samples with 230 genes; 1 gene set  
Model: survival  
Method: Asymptotic distribution

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	
all	230	230	3.039	0	1	0.0011867

By convention, the event indicator takes a 1 if the patient died, and zero otherwise. If the event indicator is coded differently, the value that indicates an event should be explicitly given. The following alternative calls give the same output as the above:

```
> globaltest(vandevijver, "Surv(TIMEsurvival, EVENTdeath == 1)")
> globaltest(vandevijver, "TIMEsurvival", d = "EVENTdeath")
> globaltest(vandevijver, "TIMEsurvival", d = "EVENTdeath", event = 1)
```

### 3.4 Different methods for calculating the p-value

The global test can calculate the p-value using different methods. The most important ones being permutations and the asymptotic distribution. The method to be used can be specified using the option *method*.

**Asymptotic method** This method calculates the p-value based on the asymptotic distribution. This is the recommended method for large sample sizes. It can be slightly conservative for small samples. This new asymptotic method supersedes the Gamma approximation described in Goeman et al. (2004).

For survival as response this uses the normal distribution as described in Goeman et al. (2005).

For continuous, two-valued and multi-valued response the asymptotic method uses numerical methods of Box (1954) and Kotz et al. (1967) for calculating the distribution of non-chi-squared distributed quadratic forms. The calculation of the p-values involves a step that smoothes away very small eigenvalues. An extra function argument *accuracy* can be given when calling `globaltest` to control the degree of smoothing. Low values of *accuracy* speed up the calculations but may result in somewhat conservative p-values. High values of *accuracy* result in slow calculations but accurate p-values. At the default value *accuracy* = 50 the conservativeness of the p-value is less than 0.1%. P-values below  $10^{-12}$  are numerically inaccurate for the asymptotic method and are reported as zero.

**Exact permutation method** If the number of possible permutations of the response values of the samples is small, it is possible to list all permutations and calculate an exact permutation based p-value.

**Random permutation method** If the number of possible permutations of the response values of the samples is large, one can take a random sample from all possible permutations. This gives an approximate permutation based p-value. This permutation p-value is not so accurate in the lower range as it is always a multiple of one over the number of permutations used. It also has some sampling variation, so that two calls to `globaltest` using this method will usually not give exactly the same p-values.

**Gamma method** This method uses the gamma distribution (also referred to as *scaled chi-squared*) as an approximation to the asymptotic distribution. This has the advantage that it is slightly quicker to calculate and that it is less conservative for small sample sizes. A drawback is that it can be anti-conservative, especially for large gene sets. This is the distribution that was used in Goeman et al. (2004). We recommend using the new asymptotic method instead. See above. There is no gamma approximation if the response variable is a survival time.

The user chooses the method by specifying the arguments *method* and *nperm*. The default `method = "auto"` is to use the exact permutation method if the number of possible permutations is less than the option *nperm* (default 10,000) and to use the asymptotic method otherwise. The threshold of 10,000 permutations is reached around 17 samples for a two-valued response and at 8 samples for a continuous or survival response. A second option is `method = "permutation"`, which also chooses the exact permutation method if the number of possible permutations is less than *nperm* (or 10,000), but uses *nperm* random permutations otherwise. Alternatively, `method = "asymptotic"` and `method = "gamma"` always use the asymptotic and gamma methods, respectively. Prior to version 4.0.0 the default method was `method = "gamma"`.

An example using the permutations method:

```
> globaltest(Golub, "ALL.AML", GO.cellcycle, method = "p", nperm = 1000)
```

Global Test result:

Data: 34 samples with 7129 genes; 1 gene set

Model: logistic

Method: 1000 random permutations

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	
[1,]	721	554	37.033	10.73	2.8131	0

Note that the different methods also have different ways of calculating the mean and standard deviation of the test statistic  $Q$ .

There is also a function called `permutations`, which recalculates the p-value using the permutation method, and which can also be used to later increase the number of permutations.

```
> gt <- globaltest(Golub, "ALL.AML", GO.cellcycle)
```

```
> permutations(gt, nperm = 2000)
```

Global Test result:

Data: 34 samples with 7129 genes; 1 gene set

Model: logistic

Method: 2000 random permutations

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	
[1,]	721	554	37.033	10.69	2.8168	0

All permutation test statistics are stored in the `gt.result` object for later use (for example in the function `hist`, see below). Using the permutation method on many pathways may therefore lead to memory problems.

### 3.5 Adjusting for the presence of covariates

It is also possible to adjust the `globaltest` for confounders or for known risk factors. For example in the Leukemia Data we may be concerned about a possible disturbance due to that the fact that some samples were taken from peripheral blood while others were taken from bone marrow. We can correct for this by incorporating the covariate `BM.PB`, which codes for bone marrow or peripheral blood, into the null hypothesis.

If covariates are incorporated into the null hypothesis of the Global Test, it tests whether the gene expression profile has an independent association with the response that cannot be explained away by the presence of the confounding covariates. For the statistical details of the model, see Goeman et al. (2005).

The three interpretations of the resulting test are now as follows

- If the test is significant, part of the *residual* variance of the response variable, *that could not be predicted from the included covariates*, can be predicted from the gene expression measurements of the gene set.

- If the test is significant, the genes in the gene set are, on average, more associated with the *residual* response variable than expected under the null hypothesis. These associations may be both positive (upregulation) and negative (downregulation). Typically, a significant pathway is a mix of positively and negatively associated genes. *The associations between the genes and the response are therefore genuine and cannot be explained by confounding with the included covariates.*
- If the test is significant, samples with similar values of the *residual* response variable tend to have relatively similar expression profiles over the genes in the gene set.

The Global Test will generally lose power if the covariate that is adjusted for is highly associated with the response variable. The test may also gain power if the confounding covariate is not associated with the response, but is a source of variation in the gene expression data.

The easiest way to adjust for confounders is to use a *formula* object. For example, in the Leukemia Data we can adjust for the confounder BM.PB with (note the absence of quotes!)

```
> globaltest(Golub, ALL.AML ~ BM.PB, GO.cellcycle)
```

Global Test result:

```
Data: 34 samples with 7129 genes; 1 gene set
Model: logistic, ALL.AML ~ BM.PB
Adjusted: 100 % of variance of Y remains after adjustment
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
[1,]	721	554	38.961	10.298	3.7926 0.00010569

There is still proof of a large difference in the cell cycle gene expression profile between AML and ALL patients if we correct for the difference in the way the samples were obtained.

In the linear, logistic and multinomial models `globaltest` will also give a percentage of the variance of the response variable that is lost in the adjustment. This gives an indication of the amount of variation in the response variable that the confounder explains and of the power lost in the adjustment process.

To adjust for more than one covariate or for interaction effects, one can use all possibilities offered by the *formula* object. See `help(formula)` for more details. In the Breast Cancer Data we can test to see if the gene expression profiles have anything to add to the prediction of survival from the known risk indicators included in the data: NIH and ESR1 (oestrogen receptor status), and Posnodes (lymph node status):

```
> globaltest(vandeVijver, Surv(TIMEsurvival, EVENTdeath) ~ NIH + ESR1 + Posnodes)
```

Global Test result:

```
Data: 100 samples with 230 genes; 1 gene set
Model: survival, Surv(TIMEsurvival, EVENTdeath) ~ NIH + ESR1 + Posnodes
Method: Asymptotic distribution
```

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	230	230	1.2906	0	1 0.098423

From the result we see that the microarray data do not seem to have any additional predictive value in this reduced data set. The p-value rose substantially relative to the unadjusted test, so at least one of these known risk factors is expected to be a confounder: it is strongly associated with survival and also with the gene expression data. This latter statement can be checked by using the covariate as the response

```
> globaltest(vandeVijver, "ESR1")
```

Global Test result:

Data: 100 samples with 230 genes; 1 gene set

Model: logistic

Method: Asymptotic distribution

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value
all	230	230	126.5	10 3.9274	0

This shows that ESR1 is clearly associated with gene expression.

The model that was fitted under the null hypothesis of the test can be retrieved and displayed with the command `fit`.

```
> gt <- globaltest(vandeVijver, Surv(TIMEsurvival, EVENTdeath) ~ ESR1)
> fit(gt)
```

Call:

```
coxph(formula = ff, data = pData, na.action = "na.fail", x = TRUE,
      y = TRUE)
```

	coef	exp(coef)	se(coef)	z	p
ESR1	-1.15	0.316	0.398	-2.9	0.0038

Likelihood ratio test=7.56 on 1 df, p=0.00597 n= 100, number of events= 26

This shows that oestrogen receptor status is also clearly associated with survival. Try `summary(fit(gt))` for a more detailed output.

## 4 The Comparative P

In some data sets, such as the two example data sets studied in this vignette, the Global Test for all genes is very significant. In this situation we can expect a substantial number of genes to be associated with the response variable. As a consequence, we can also expect many gene sets, especially the larger ones, also to be associated with the response.

A useful diagnostic to see whether a gene set is exceptionally significant is the “comparative p”, which can be calculated using the function `sampling`.

```
> gt <- globaltest(Golub, "ALL.AML", KEGG.cellcycle)
> sampled.gt <- sampling(gt)
> sampled.gt
```

Global Test result:

Data: 34 samples with 7129 genes; 1 gene set

Model: logistic

Method: Asymptotic distribution

	Genes Tested	Statistic Q	Expected Q	sd of Q	P-value	Comparative p
[1,]	109	109	35.695	10.135	4.0625	0.00045098
						0.386

This gives an extra output column “Comparative p”, which is the fraction of random genesets of the same size as the cell cycle pathway (109 genes) which have a larger standardized test statistic than the cell cycle pathway itself. Pathways of the same size with a larger standardized test statistic will almost invariably also have a lower p-value. In this case around 39 % of 1,000 random ‘pathways’ of size 109 have a larger standardized test statistic than the cell cycle pathway. This indicates that, although the cell cycle pathway is clearly differentially expressed between AML and ALL samples (low p-value), it is not exceptionally significant for a pathway of its size in this dataset.

Just like the p-value based on random permutations, the comparative p is a random quantity that has some sampling variation. It is always a multiple of one over the number of random pathways drawn; the accuracy can be increased by increasing that number. By default 1,000 random sets are sampled; this number can be changed with the option *ndraws*.

The Comparative P is a very useful diagnostic. However, it is not a p-value in the classical statistical sense, because it is based on permuting genes, not biological samples. It should always be interpreted together with the regular p-value.

## 5 Diagnostic plots

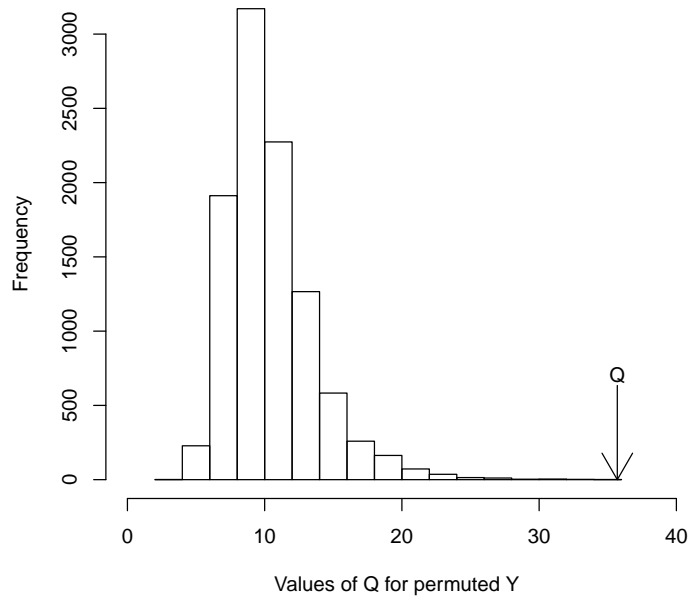
There are various types of diagnostic plots available to help the user interpret the `globaltest` result. The plot `permutations` can serve as a check whether the sample size was large enough not to use the permutation version of `globaltest`. The `genepoint` visualizes the influence of individual genes on the test result. The three plots `sampleplot`, `checkerboard` and `regressionplot` all visualize the influence of individual samples.

### 5.1 Permutations histogram

The permutations histogram plots the values of the test statistic  $Q$  calculated for permutations of the response in a histogram. The observed value of  $Q$  for the true values of the response is marked with an arrow.

```
> gt <- globaltest(Golub, "ALL.AML", KEGG.cellcycle, method = "p")
> hist(gt)
```





The output can be interpreted as a plot of the distribution of the test statistic under the null hypothesis that the pathway is not associated with the clinical variable.

## 5.2 Gene Plot

The second diagnostic plot is the Gene Plot, which can be used to assess the influence of each gene on the outcome of the test. The Gene Plot gives a bar and a reference line for each gene tested. The bar indicates the influence of each gene on the test statistic.

A reference line for each bar gives the expected height of the bar under the null hypothesis that the gene is not associated with the response (except in a survival model, where the expected height is zero). Marks indicate with how many standard deviations (under the null hypothesis) the bar exceeds the reference line. Finally the bars are colored to indicate a positive or a negative association of the gene with the response.

The geneplot influence bars have two interpretations. In the first place, each bar is the Global Test statistic for the single gene pathway containing only that gene. A positive bar that is many standard deviations above the reference line therefore indicates a gene that is significantly associated with the clinical variable in  $Y$ . Secondly, the bars indicate the influence of the gene on the test result of the whole pathway (the test statistic for the group is the average of the bars for the genes). Removing a gene with a low influence (relative to the reference line) or a negative influence from the pathway will generally result in a lower p-value for the pathway, removing a gene with a large positive influence will have the opposite effect.

```
> gt <- globaltest(Golub, "ALL.AML", kegg)
> geneplot(gt, "00561")
```

The second argument of `geneplot` is the name of the gene set to be plotted. This can be left out if `gt` contains only one gene set. For a large number of genes the plot might become overcrowded. Use the option `genesubset` to plot only a subset of the genes, `labelsize` to resize the gene labels or `drawlabels = FALSE` to remove them. Similarly, the legend can be suppressed with `addlegend = FALSE`. Alternatively, one can store the geneplot as a `gt.barplot` object to retrieve the numbers or to plot (part of) the plot later, optionally with the option `plot = FALSE` to suppress plotting at this point.

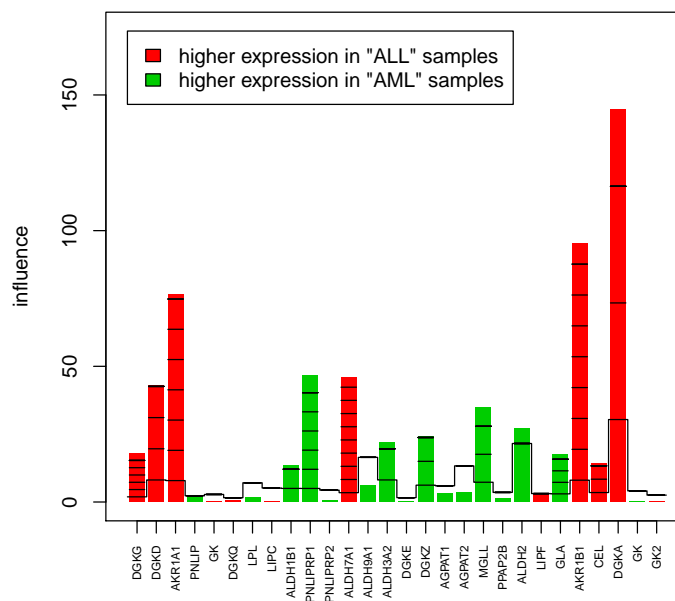
```
> myplot <- geneplot(gt, "00561", plot = FALSE)
```

The return of the `geneplot` is an object of type `gt.barplot` containing the numbers and names appearing in the plot. This allows the user to customize the plot to his or her liking. For example, to increase interpretability, the probe identifiers appearing in the plot can be replaced by the gene symbols in this object and plotted again:

```
> names(myplot) <- as.list(hu6800SYMBOL)[names(myplot)]
> plot(myplot)
```

It is possible to supply new values for `genesubset`, `labelsize`, `drawlabels` or `addlegend` when plotting a `gt.barplot` object.

Figure 1: Example geneplot



The *gt.barplot* object also allows one to look at subsets of a large pathway more closely. The gene plot can for example be sorted with the largest z-scores first. For example

```
> mysorted <- sort(myplot)
> top5 <- mysorted[1:5]
```

The numbers can be retrieved with the following functions. `z.score` counts the number of standard deviations of the influence above the reference line. See `help(gt.barplot)` for more details.

```
> z.score(top5)

ALDH7A1 AKR1B1 AKR1A1 DGKG PNLIPRP1
8.715279 7.674036 6.139146 5.897742 5.886430

> names(top5)

[1] "ALDH7A1" "AKR1B1" "AKR1A1" "DGKG" "PNLIPRP1"

> result(top5)

      name Influence Expected      SD z.score colouring
1 ALDH7A1  45.78616 3.436041  4.859296 8.715279 high in "ALL"
2 AKR1B1   95.32331 8.042311 11.373545 7.674036 high in "ALL"
3 AKR1A1   76.35321 7.886047 11.152555 6.139146 high in "ALL"
4 DGKG     17.73692 1.898893  2.685440 5.897742 high in "ALL"
5 PNLIPRP1 46.54614 4.991721  7.059359 5.886430 high in "AML"

> length(top5)

[1] 5
```

The option *scale* of `genepLOT` can be used to rescale the bars to have unit standard deviation (so that the z-scores are displayed). Alternatively, this can be done later with the command `scale`.

### 5.3 Sample Plot

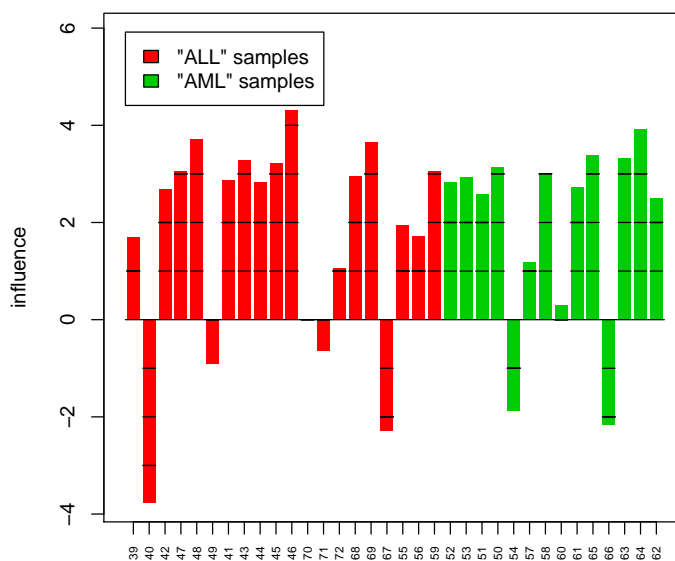
The Sample Plot looks very similar to the Gene Plot. It visualizes the influence of the individual samples on the test result. It has a bar and a reference line for each sample tested. The bar indicates the influence of each sample on the test statistic, similar to the `genepLOT`. The direction of the bar (upward or downward) indicates evidence against or in favour of the null hypothesis. If a sample has a positive bar, its expression profile is relatively similar to that of samples which have the same value of the clinical variable and relatively unlike the profile of the samples which have a different value of the clinical variable. If the bar is negative, it is the other way around: the sample is more similar in expression profile to samples with a different clinical variable. A small p-value will therefore generally coincide with many positive bars. If there are still tall negative bars, these indicate deviating samples: removing a sample with a negative bar would result in a lower p-value.

If the null hypothesis is true the expected influence is zero. Marks on the bars indicate the standard deviation of the influence of the sample under the null hypothesis. Finally the bars are coloured to distinguish the samples. In a logistic model the colours differentiate between the original groups, in an unadjusted linear model they differentiate the values above the mean from the values below the mean of  $Y$ . In an adjusted linear or the survival model they distinguish positive from negative residuals after fitting the null model.

```
> gt <- globaltest(Golub, "ALL.AML", KEGG.cellcycle)
> sampleplot(gt)
```

The `sampleplot` result can be stored in a `gt.barplot` object just as with `geneplot`. The function arguments and the handling of the `gt.barplot` object are the same as for “geneplot” above. One important difference is that the option `scale` defaults to `TRUE` in `sampleplot`.

Figure 2: Example sampleplot



## 5.4 Other plots

The checkerboard and regression plots are two alternative plots to assess the influence of each of the samples on the test result.

**Checkerboard plot** The checkerboard plot visualizes the similarity between samples. It makes a square figure with the samples both on the X and on the Y-axis, so that it has all comparisons between the samples. Samples which are

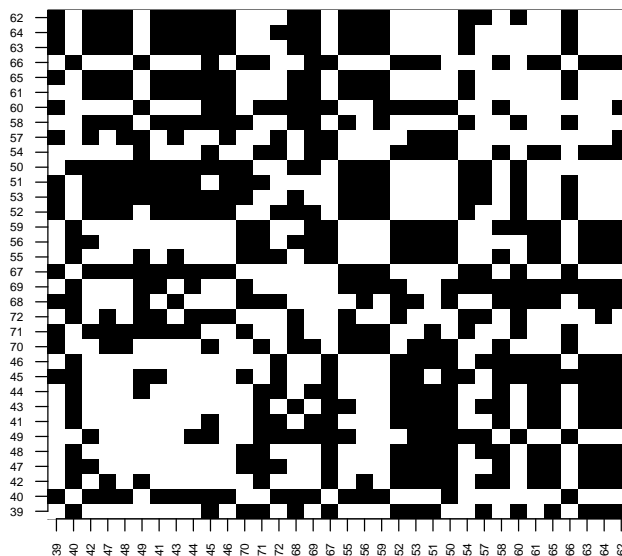
relatively similar are coded white and samples which are relatively dissimilar are coded black.

For easier interpretation the samples are sorted by their response value. If the test was (very) significant and the response has two values, a typical block-like structure will appear. If the response was continuous and the test is significant, the black squares will tend to stick together around the corners. By looking at these patterns some things can be learned about the structure of the data. For example, by looking at samples which deviate from the main pattern, outlying samples can be detected.

```
> gt <- globaltest(Golub, "ALL.AML", kegg)
> checkerboard(gt.kegg, "04110")
```

The function `checkerboard` also has options `labelsize` and `drawlabels`. It returns a legend to link the numbers appearing in the plot if `drawlabels = FALSE` to the sample names.

Figure 3: Example checkerboard plot



**Regression Plot** The regression plot plots all pairs of samples, just like the checkerboard plot, but now showing the covariance between their response values on the X-axis and the covariance between their gene expression patterns on the Y-axis. The comparisons of each sample with itself have been excluded.

The test statistic of the Global Test can be seen as a regression-coefficient for this plot, so it is visualized by drawing a least squares regression line. If

this regression line is steep, the test statistic has a large value (and is possibly significant).

The influence of specific samples can be assessed by drawing a second regression line through only those points in the plot, which are comparisons involving the sample of interest. For example if we are interested the sample with sample name "1", we take the points corresponding to the pairs (1,2) up to (1,34). If the regression line drawn through only these points deviates much from the general line, the sample deviates from the general pattern. This is especially the case if this line has a negative slope, which means that the sample is more similar (in its gene expression pattern) to the samples with a different response than to samples with a similar response.

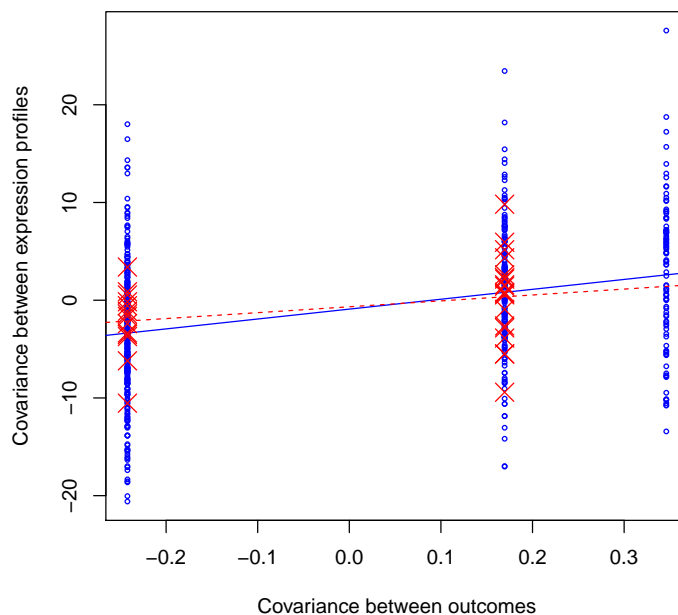
If we want to test sample "1", we say:

```
> gt <- globaltest(Golub, "ALL.AML", kegg)
> regressionplot(gt, "04110", sampleid = "39")
```

We can also use this plot for a group of samples, saying for example:

```
> regressionplot(gt, "04110", sampleid = c("39","40"))
```

Figure 4: Example regressionplot



## 6 Session Information

The version number of R and packages loaded for generating the vignette were:

- R version 2.15.0 (2012-03-30), x86\_64-unknown-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=C, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=en\_US.UTF-8, LC\_PAPER=C, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, grid, methods, splines, stats, utils
- Other packages: AnnotationDbi 1.18.0, Biobase 2.16.0, BiocGenerics 0.2.0, DBI 0.2-5, GO.db 2.7.1, KEGG.db 2.7.1, MASS 7.3-17, RSQLite 0.11.1, Rgraphviz 1.34.0, annotate 1.34.0, boot 1.3-4, globaltest 5.10.0, golubEsets 1.4.10, graph 1.34.0, gss 2.0-9, hu6800.db 2.7.1, lungExpression 0.0.12, org.Hs.eg.db 2.7.1, penalized 0.9-38, rpart 3.1-52, survival 2.36-12, vsn 3.24.0
- Loaded via a namespace (and not attached): BiocInstaller 1.4.0, IRanges 1.14.0, affy 1.34.0, affyio 1.24.0, lattice 0.20-6, limma 3.12.0, multtest 2.12.0, preprocessCore 1.18.0, stats4 2.15.0, tools 2.15.0, xtable 1.7-0, zlibbioc 1.2.0

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Van de Vijver, M. J., He, Y. D., van 't Veer, L. J., Dai, H., Hart, A. A. M., Voskuil, D. W., Schreiber, G. J., Peterse, J. L., Roberts, C., Marton, M. J., Parrish, M., Atsma, D., Witteveen, A., Glas, A., Delahaye, L., van der Velde, T., Bartelink, H., Rodenhuis, S., Rutgers, E. T., Friend, S. H., and Bernards, R. (2002). A gene-expression signature as a predictor of survival in breast cancer. *New England Journal of Medicine*, 347(25):1999–2009.