

ROntoTools: The R Onto-Tools suite

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Abstract

This package is indented to be the R implementation of the web-based data mining and analysis suite of tools called Onto-Tools [10, 6, 5, 7, 8, 5, 12, 9, 4, 8, 9, 2, 9, 13, 3, 11]. Among these, Onto-Express (OE) was the first publicly available tool for the GO profiling of high throughput data and Pathway-Express (PE) the first tool to perform analysis of signaling pathways using important biological factors like all the interactions between the genes, the type of interaction between them and the position and magnitude of expression change for all the differentially expressed genes. We currently have over 10,000 registered users from 53 countries. Approximately, 5,000 of these are regular users (more than 10 data sets processed). This R package will provide these users with access to the direct functionalities of the online version, to new analysis methods and also expose the tools to a larger audience. As part of the first version, the pathway analysis tool Pathway-Express is made available.

1 Pathway-Express

Pathway-Express (**pe**) is a tool for the analysis of signaling pathways. Besides the original implementation [3, 14], this tool implements a number of improvements proposed in [15] that include the incorporation of gene significance and the elimination of the need to select differentially expressed genes. Pathway-Express uses two sources of data: one is the experiment data and the other is the database of pathways.

1.1 Pathway database

Pathway-Express is a general tool that accepts any set of signaling pathways defined using the standard implementation provided in the *graph* package. The only requirement is that each pathway, defined as an object of type *graph*, has a weight defined for each edge, representing the efficiency of the propagation between the two genes, and a weight for each node, that will capture the type of gene or the significance of the measured expression change. This package provides tools to access the KEGG database for signaling pathways and also tools to set these weights.

For example, to download and parse the signaling pathways available in KEGG use:

```
> require(graph)
> require(ROntoTools)
> kpg <- keggPathwayGraphs("hsa", verbose = FALSE)
```

The above code will load the available cached data for human (i.e., KEGG id *hsa*). To update the cache and download the latest KEGG pathways available use the `updateCache` parameter:

```
> kpg <- keggPathwayGraphs("hsa", updateCache = TRUE, verbose = TRUE)
```

This command is time consuming and depends on the available bandwidth.

The `kpg` is a list of *graph* objects:

```
> head(names(kpg))
```

```
[1] "path:hsa03008" "path:hsa03013" "path:hsa03015" "path:hsa03018"
[5] "path:hsa03320" "path:hsa03460"
```

To inspect one of the pathway graphs, only the ID is required. Here is an example for the Cell Cycle:

```
> kpg[["path:hsa04110"]]
```

A graphNEL graph with directed edges

Number of Nodes = 124

Number of Edges = 632

```
> head(nodes(kpg[["path:hsa04110"]]))
```

```
[1] "hsa:1029" "hsa:51343" "hsa:4171" "hsa:4172" "hsa:4173" "hsa:4174"
```

```
> head(edges(kpg[["path:hsa04110"]]))
```

```
$`hsa:1029`
```

```
[1] "hsa:4193" "hsa:1019" "hsa:1021" "hsa:595" "hsa:894" "hsa:896"
```

```
$`hsa:51343`
```

```
[1] "hsa:983" "hsa:85417" "hsa:891" "hsa:9133"
```

```
$`hsa:4171`
```

```
character(0)
```

```
$`hsa:4172`
```

```
character(0)
```

```
$`hsa:4173`
```

```
character(0)
```

```
$`hsa:4174`
```

```
character(0)
```

In addition the parser extracted the type of interaction for each gene-gene interaction in an attribute called `subtype`:

```
> head(edgeData(kpg[["path:hsa04110"]], attr = "subtype"))
```

```
$`hsa:1029|hsa:4193`
```

```
[1] "inhibition"
```

```
$`hsa:1029|hsa:1019`
```

```
[1] "inhibition"
```

```
$`hsa:1029|hsa:1021`  
[1] "inhibition"
```

```
$`hsa:1029|hsa:595`  
[1] "inhibition"
```

```
$`hsa:1029|hsa:894`  
[1] "inhibition"
```

```
$`hsa:1029|hsa:896`  
[1] "inhibition"
```

Using this attribute the function `setEdgeWeights` sets the same weight for all the interactions of the same type:

```
> kpg <- setEdgeWeights(kpg, edgeTypeAttr = "subtype",  
+   edgeWeightByType = list(activation = 1, inhibition = -1,  
+   expression = 1, repression = -1),  
+   defaultWeight = 0)
```

At this point, `kpg` contains a list of graphs with weighted edges:

```
> head(edgeData(kpg[["path:hsa04110"]], attr = "weight"))
```

```
$`hsa:1029|hsa:4193`  
[1] -1
```

```
$`hsa:1029|hsa:1019`  
[1] -1
```

```
$`hsa:1029|hsa:1021`  
[1] -1
```

```
$`hsa:1029|hsa:595`  
[1] -1
```

```
$`hsa:1029|hsa:894`  
[1] -1
```

```
$`hsa:1029|hsa:896`  
[1] -1
```

To retrieve the title of the pathways and not just their ids the function `keggPathwayNames` can be used:

```
> kpn <- keggPathwayNames("hsa")  
> head(kpn)
```

| | |
|-------------------------------------|--------------------------|
| path:hsa03008 | path:hsa03013 |
| "Ribosome biogenesis in eukaryotes" | "RNA transport" |
| path:hsa03015 | path:hsa03018 |
| "mRNA surveillance pathway" | "RNA degradation" |
| path:hsa03320 | path:hsa03460 |
| "PPAR signaling pathway" | "Fanconi anemia pathway" |

1.2 Experiment data

As an example, we provided a pre-processed data set from ArrayExpress (E-GEOD-21942) that studies the expression change in peripheral blood mononuclear cells (PBMC) between 12 MS patients and 15 controls. The data was preprocessed using the *limma* package. Only probe sets with a gene associated to them have been kept and for each gene only the most significant probe set has been selected (the table is already ordered by p-value):

```
> load(system.file("extdata/E-GEOD-21942.topTable.RData", package = "ROntoTools"))
> head(top)
```

| | logFC | P.Value | adj.P.Val | entrez |
|-------------|------------|--------------|--------------|------------|
| 200946_x_at | -1.0175141 | 5.833411e-13 | 4.172652e-09 | hsa:2746 |
| 228697_at | -3.6479368 | 7.985427e-13 | 4.172652e-09 | hsa:135114 |
| 210254_at | 3.2807123 | 3.086572e-12 | 9.677020e-09 | hsa:932 |
| 234726_s_at | -0.9792301 | 7.368175e-12 | 1.760593e-08 | hsa:64418 |
| 215905_s_at | -1.7733135 | 7.861797e-12 | 1.760593e-08 | hsa:9410 |
| 235542_at | -0.9447467 | 1.617944e-11 | 2.536288e-08 | hsa:200424 |

Select differentially expressed genes at 1% and save their fold change in a vector *fc* and their p-values in a vector *pv*:

```
> fc <- top$logFC[top$adj.P.Val <= .01]
> names(fc) <- top$entrez[top$adj.P.Val <= .01]
> pv <- top$P.Value[top$adj.P.Val <= .01]
> names(pv) <- top$entrez[top$adj.P.Val <= .01]
> head(fc)
```

| | | | | | |
|------------|------------|-----------|------------|------------|------------|
| hsa:2746 | hsa:135114 | hsa:932 | hsa:64418 | hsa:9410 | hsa:200424 |
| -1.0175141 | -3.6479368 | 3.2807123 | -0.9792301 | -1.7733135 | -0.9447467 |

```
> head(pv)
```

| | | | | | |
|--------------|--------------|--------------|--------------|--------------|--------------|
| hsa:2746 | hsa:135114 | hsa:932 | hsa:64418 | hsa:9410 | hsa:200424 |
| 5.833411e-13 | 7.985427e-13 | 3.086572e-12 | 7.368175e-12 | 7.861797e-12 | 1.617944e-11 |

Alternatively, an analysis with all genes can be performed:

```
> fcAll <- top$logFC
> names(fcAll) <- top$entrez
> pvAll <- top$P.Value
> names(pvAll) <- top$entrez
```

The reference contains all the genes measured in the analysis:

```
> ref <- top$entrez
> head(ref)

[1] "hsa:2746"    "hsa:135114" "hsa:932"     "hsa:64418"   "hsa:9410"
[6] "hsa:200424"
```

1.3 Setting the node weights

The node weights are used to encode for the significance of each gene, the term described as α in [15]. The two alternative formulas to incorporate the gene significance:

$$\alpha = 1 - p/p_{thr} \text{ and } \alpha = -\log(p/p_{thr}) \quad (1)$$

are implemented as two function `alpha1MR` and `alphaMLG`.

To set the node weights the function `setNodeWeights` is used:

```
> kpg <- setNodeWeights(kpg, weights = alphaMLG(pv), defaultWeight = 1)
> head(nodeWeights(kpg[["path:hsa04110"]]))

hsa:1029 hsa:51343 hsa:4171 hsa:4172 hsa:4173 hsa:4174
1.0000000 1.0000000 0.8120949 1.0000000 1.0000000 1.0000000
```

1.4 Pathway analysis and results summary

Up to this point all the pieces need for the analysis have been assembled:

- the pathway database with the experiment specific gene significance - `kpg`
- the experiment data - `fc` and `ref`

To perform the analysis the function `pe` is used (increase the parameter `nboot` to obtain more accurate results):

```
> peRes <- pe(x = fc, graphs = kpg, ref = ref, nboot = 200, verbose = FALSE)
```

The result object can be summarized in a table format with the desired columns using the function `Summary`:

```
> head(Summary(peRes))
```

| | totalAcc | totalPert | totalAccNorm | totalPertNorm | pPert |
|---------------|-------------|--------------|--------------|---------------|-------------|
| path:hsa05010 | 17.90716 | 121.13696 | 0.4899790 | 2.940115 | 0.014925373 |
| path:hsa05110 | 22.83759 | 87.30055 | 5.2775634 | 5.998538 | 0.004975124 |
| path:hsa04145 | 0.00000 | 102.93799 | NA | 5.849708 | 0.004975124 |
| path:hsa04722 | 56.17539 | 117.15557 | 1.7614006 | 3.286228 | 0.004975124 |
| path:hsa03015 | 0.00000 | 54.07253 | -0.8190048 | 3.786534 | 0.004975124 |
| path:hsa05152 | 140.10374 | 233.91461 | 6.2820731 | 7.218819 | 0.004975124 |
| | pAcc | pORA | pComb | pPert.fdr | pAcc.fdr |
| path:hsa05010 | 0.547263682 | 1.360242e-05 | 3.331570e-06 | 0.02546093 | 0.69788671 |
| path:hsa05110 | 0.004975124 | 1.085083e-04 | 8.330837e-06 | 0.01361119 | 0.03639696 |
| path:hsa04145 | NA | 2.424942e-04 | 1.764759e-05 | 0.01361119 | NA |
| path:hsa04722 | 0.064676617 | 4.644830e-04 | 3.230096e-05 | 0.01361119 | 0.14269920 |

```

path:hsa03015 0.159203980 6.821488e-04 4.613351e-05 0.01361119 0.26344468
path:hsa05152 0.004975124 8.354186e-04 5.565668e-05 0.01361119 0.03639696
      pORA.fdr    pComb.fdr
path:hsa05010 0.001999556 0.0004830776
path:hsa05110 0.007975357 0.0006039857
path:hsa04145 0.011882215 0.0008529668
path:hsa04722 0.016789618 0.0011709098
path:hsa03015 0.016789618 0.0013378718
path:hsa05152 0.017204791 0.0013450364

```

```

> head(Summary(peRes, pathNames = kpn, totalAcc = FALSE, totalPert = FALSE,
+             pAcc = FALSE, pORA = FALSE, comb.pv = NULL, order.by = "pPert"))

```

| | pathNames | pPert | pPert.fdr |
|---------------|--|-------------|------------|
| path:hsa03013 | RNA transport | 0.004975124 | 0.01361119 |
| path:hsa03015 | mRNA surveillance pathway | 0.004975124 | 0.01361119 |
| path:hsa04010 | MAPK signaling pathway | 0.004975124 | 0.01361119 |
| path:hsa04020 | Calcium signaling pathway | 0.004975124 | 0.01361119 |
| path:hsa04060 | Cytokine-cytokine receptor interaction | 0.004975124 | 0.01361119 |
| path:hsa04062 | Chemokine signaling pathway | 0.004975124 | 0.01361119 |

1.5 Graphical representation of results

To visualize the summary of the Pathway-Express results use the function `plot` (see Fig. 1):

```

> plot(peRes)

> plot(peRes, c("pAcc", "pORA"), comb.pv.func = compute.normalInv, threshold = .01)

```

Pathway level statistics can also be displayed one at a time using the function `plot` (see Fig. 2):

```

> plot(peRes@pathways[["path:hsa05216"]], type = "two.way")

> plot(peRes@pathways[["path:hsa05216"]], type = "boot")

```

To visualize the propagation across the pathway, two functions - `peNodeRenderInfo` and `peEdgeRenderInfo` - are provided to extract the required information from a `pePathway` object:

```

> p <- peRes@pathways[["path:hsa05216"]]
> g <- layoutGraph(p@map, layoutType = "dot")
> graphRenderInfo(g) <- list(fixedsize = FALSE)
> edgeRenderInfo(g) <- peEdgeRenderInfo(p)
> nodeRenderInfo(g) <- peNodeRenderInfo(p)
> renderGraph(g)

```

This is the *Thyroid cancer* signaling pathway and is shown in Fig. 3. Another example is the *T cell receptor signaling pathway* and is presented in Fig. 4.

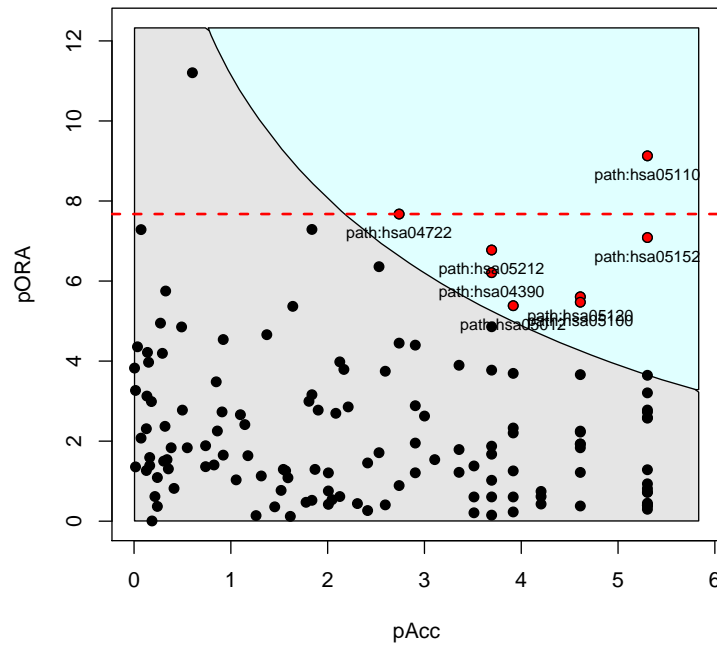
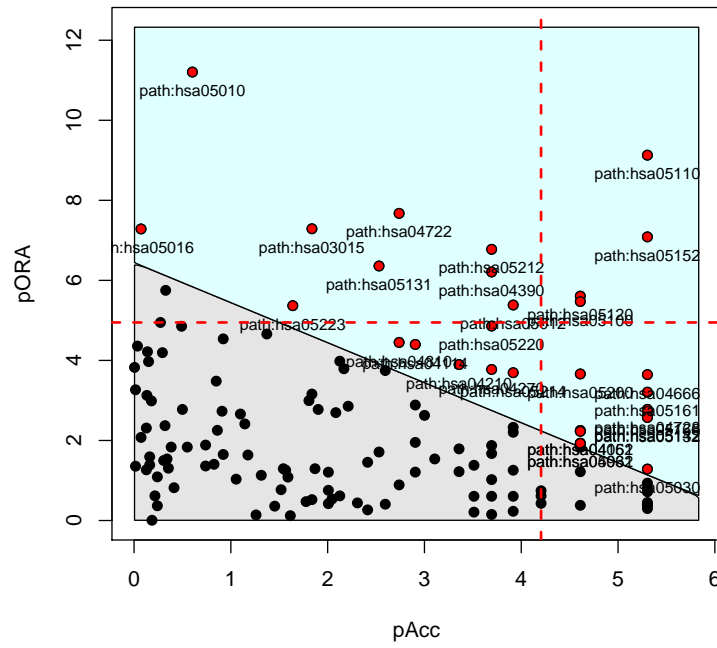


Figure 1: Two-way plot of Pathway-Express result

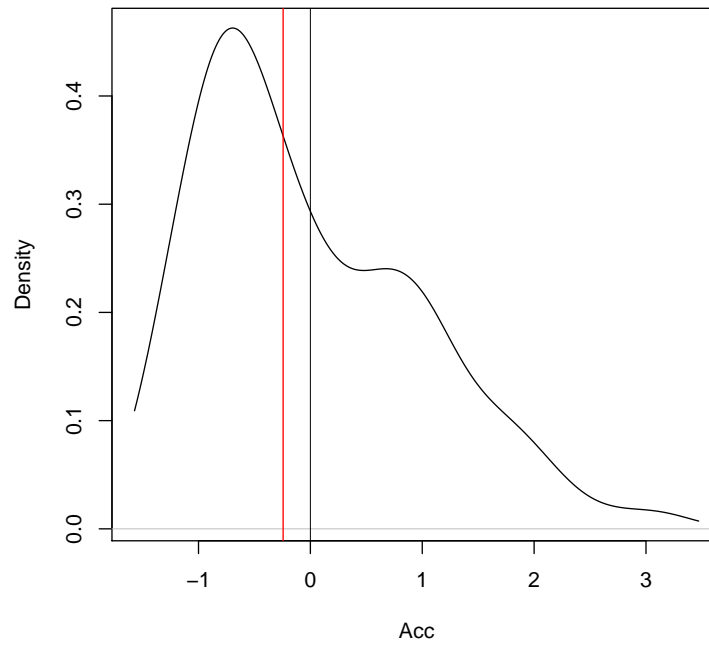
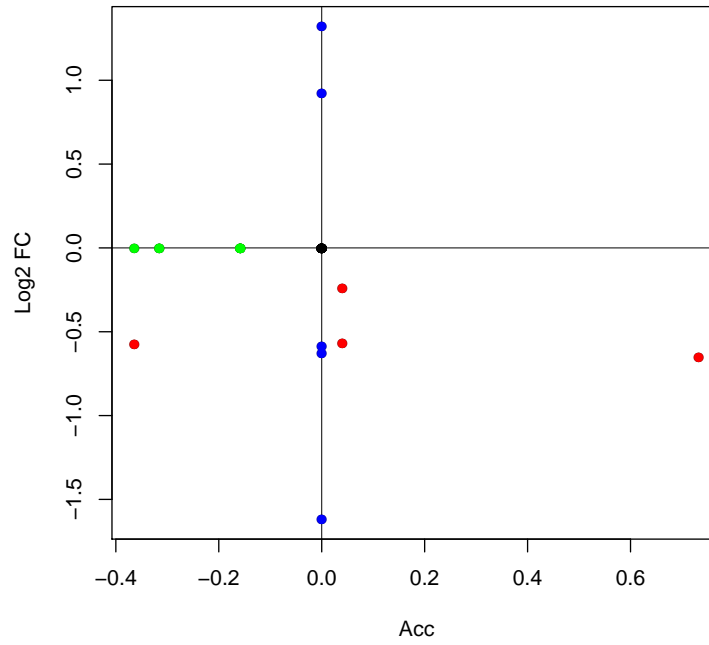


Figure 2: Pathway level statistics: perturbation accumulation versus the measured expression change (above) and the bootstrap simulations of the perturbation accumulation (below).

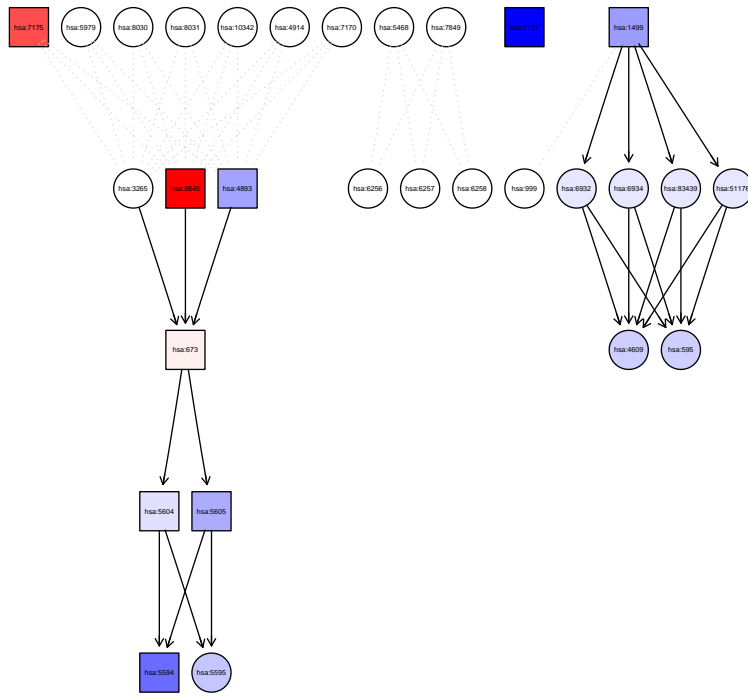


Figure 3: Perturbation propagation on the *Thyroid cancer signaling pathway*.

2 Primary dis-regulation

Primary dis-regulation analysis (pDis) is a tool for the analysis of signaling pathways. This is the original implementation of the algorithm introduced in [1]. This method takes into consideration the primary dis-regulation of a given gene itself and the effects of signaling coming from upstream. Similar to Pathway Express, primary dis-regulation uses two sources of data: one is the experiment data and the other is the database of pathways.

The pathway database can be obtained from KEGG as explained in section Pathway database.

For example, to download and parse the signaling pathways available in KEGG use:

```
> require(graph)
> require(ROntoTools)
> kpg <- keggPathwayGraphs("hsa", verbose = FALSE)
```

The above code will load the available cached data for human (i.e., KEGG id *hsa*). To update the cache and download the latest KEGG pathways available use the `updateCache` parameter:

```
> kpg <- keggPathwayGraphs("hsa", updateCache = TRUE, verbose = TRUE)
```

This command is time consuming and depends on the available bandwidth.

To retrieve the title of the pathways and not just their ids the function `keggPathwayNames` can be used:

```
> kpn <- keggPathwayNames("hsa")
> head(kpn)
```

| | |
|-------------------------------------|--------------------------|
| path:hsa03008 | path:hsa03013 |
| "Ribosome biogenesis in eukaryotes" | "RNA transport" |
| path:hsa03015 | path:hsa03018 |
| "mRNA surveillance pathway" | "RNA degradation" |
| path:hsa03320 | path:hsa03460 |
| "PPAR signaling pathway" | "Fanconi anemia pathway" |

As an example, a publicly available data is provided in the package. For more information please refer to Experimental data section.

```
> load(system.file("extdata/E-GEOD-21942.topTable.RData", package = "ROntoTools"))
> head(top)
```

| | logFC | P.Value | adj.P.Val | entrez |
|-------------|------------|--------------|--------------|------------|
| 200946_x_at | -1.0175141 | 5.833411e-13 | 4.172652e-09 | hsa:2746 |
| 228697_at | -3.6479368 | 7.985427e-13 | 4.172652e-09 | hsa:135114 |
| 210254_at | 3.2807123 | 3.086572e-12 | 9.677020e-09 | hsa:932 |
| 234726_s_at | -0.9792301 | 7.368175e-12 | 1.760593e-08 | hsa:64418 |
| 215905_s_at | -1.7733135 | 7.861797e-12 | 1.760593e-08 | hsa:9410 |
| 235542_at | -0.9447467 | 1.617944e-11 | 2.536288e-08 | hsa:200424 |

Select differentially expressed genes at 1% and save their fold change in a vector *fc* and their p-values in a vector *pv*:

```

> fc <- top$logFC[top$adj.P.Val <= .01]
> names(fc) <- top$entrez[top$adj.P.Val <= .01]
> pv <- top$P.Value[top$adj.P.Val <= .01]
> names(pv) <- top$entrez[top$adj.P.Val <= .01]
> head(fc)

    hsa:2746 hsa:135114    hsa:932 hsa:64418    hsa:9410 hsa:200424
-1.0175141 -3.6479368  3.2807123 -0.9792301 -1.7733135 -0.9447467

> head(pv)

    hsa:2746    hsa:135114    hsa:932    hsa:64418    hsa:9410    hsa:200424
5.833411e-13 7.985427e-13 3.086572e-12 7.368175e-12 7.861797e-12 1.617944e-11

```

Alternatively, an analysis with all genes can be performed:

```

> fcAll <- top$logFC
> names(fcAll) <- top$entrez
> pvAll <- top$P.Value
> names(pvAll) <- top$entrez

```

The reference contains all the genes measured in the analysis:

```

> ref <- top$entrez
> head(ref)

[1] "hsa:2746"    "hsa:135114" "hsa:932"     "hsa:64418"  "hsa:9410"
[6] "hsa:200424"

```

2.1 Pathway analysis and results summary

Here are the input needed to run a sample test:

- the pathway database with the experiment specific gene significance - `kpg`
- the experiment data - `fc` and `ref`

To perform the analysis the function `pDis` is used (increase the parameter `nboot` to obtain more accurate results):

```

> pDisRes <- pDis(x = fc, graphs = kpg, ref = ref, nboot = 200, verbose = FALSE)

```

The result object can be summarized in a table format with the desired columns using the function `Summary`:

```

> head(Summary(pDisRes))

```

| | totalpDis | totalpDisNorm | ppDis | pORA | pComb |
|---------------|-----------|---------------|------------|--------------|--------------|
| path:hsa05010 | 38.59681 | -1.4177281 | 0.13432836 | 1.360242e-05 | 2.596938e-05 |
| path:hsa05110 | 20.46240 | 1.7407242 | 0.08955224 | 1.085083e-04 | 1.218689e-04 |
| path:hsa04390 | 36.64334 | 2.2546657 | 0.02487562 | 2.008410e-03 | 5.447826e-04 |
| path:hsa03015 | 23.11144 | -1.3988863 | 0.13432836 | 6.821488e-04 | 9.436009e-04 |
| path:hsa04145 | 37.06796 | 0.7728713 | 0.40796020 | 2.424942e-04 | 1.011155e-03 |

```

path:hsa04722  32.98817      -0.8307954  0.36318408  4.644830e-04  1.634200e-03
                ppDis.fdr      pORA.fdr      pComb.fdr
path:hsa05010  0.5983718  0.001999556  0.003817499
path:hsa05110  0.5063146  0.007975357  0.008957362
path:hsa04390  0.3656716  0.026839656  0.026694346
path:hsa03015  0.5983718  0.016789618  0.029727943
path:hsa04145  0.7978290  0.011882215  0.029727943
path:hsa04722  0.7714169  0.016789618  0.040037906

> head(Summary(pDisRes, pathNames = kpn, totalpDis = FALSE,
+             pORA = FALSE, comb.pv = NULL, order.by = "ppDis"))

                pathNames      ppDis ppDis.fdr
path:hsa05142  Chagas disease (American trypanosomiasis) 0.009950249 0.3134328
path:hsa05144                Malaria 0.009950249 0.3134328
path:hsa05161                Hepatitis B 0.009950249 0.3134328
path:hsa04972                Pancreatic secretion 0.014925373 0.3134328
path:hsa05030                Cocaine addiction 0.014925373 0.3134328
path:hsa05143                African trypanosomiasis 0.014925373 0.3134328

```

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