

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 [9, 5, 4, 6, 7, 4, 11, 8, 3, 7, 8, 1, 8, 12, 2, 10]. 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 [2, 13], this tool implements a number of improvements proposed in [14] 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 = 630

```
> 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 [14]. 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	21.5034630	128.32957	0.88183508	3.216737	0.014925373
path:hsa05110	22.8375919	87.30055	5.18483326	6.156575	0.004975124
path:hsa04142	0.2232419	90.73185	-0.02349932	4.959145	0.004975124
path:hsa04145	0.0000000	102.93799	NA	6.413285	0.004975124
path:hsa05152	140.0243475	237.47577	6.33138599	8.054898	0.004975124
path:hsa03015	0.0000000	54.07253	NA	3.399158	0.004975124
	pAcc	pORA	pComb	pPert.fdr	pAcc.fdr
path:hsa05010	0.263681592	8.544061e-06	2.151951e-06	0.02625427	0.40724157
path:hsa05110	0.004975124	1.085083e-04	8.330837e-06	0.01320669	0.03639696
path:hsa04142	0.950248756	2.047498e-04	1.507308e-05	0.01320669	0.98570580
path:hsa04145	NA	2.424942e-04	1.764759e-05	0.01320669	NA

```

path:hsa05152 0.004975124 5.666823e-04 3.884739e-05 0.01320669 0.03639696
path:hsa03015      NA 6.821488e-04 4.613351e-05 0.01320669      NA
      pORA.fdr    pComb.fdr
path:hsa05010 0.001264521 0.0003141849
path:hsa05110 0.008029611 0.0006081511
path:hsa04142 0.008972285 0.0006441370
path:hsa04145 0.008972285 0.0006441370
path:hsa05152 0.012677874 0.0009663181
path:hsa03015 0.012677874 0.0009663181

```

```

> 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	0.01320669
path:hsa03015	mRNA surveillance pathway	0.004975124	0.01320669
path:hsa03460	Fanconi anemia pathway	0.004975124	0.01320669
path:hsa04010	MAPK signaling pathway	0.004975124	0.01320669
path:hsa04020	Calcium signaling pathway	0.004975124	0.01320669
path:hsa04060	Cytokine-cytokine receptor interaction	0.004975124	0.01320669

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.

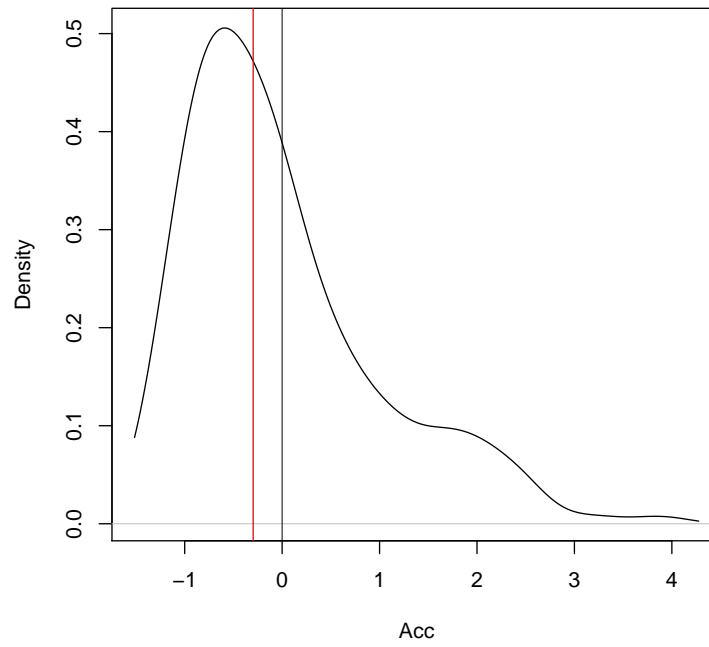
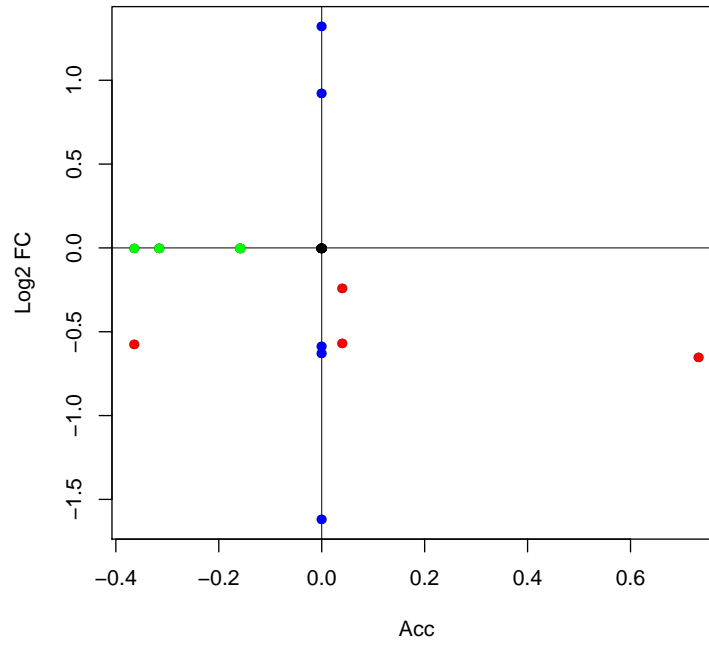


Figure 2: Pathway level statistics: perturbation accumulation versus the measured expression change (above) and the bootstrap simulations of the perturbation accumulation (below).

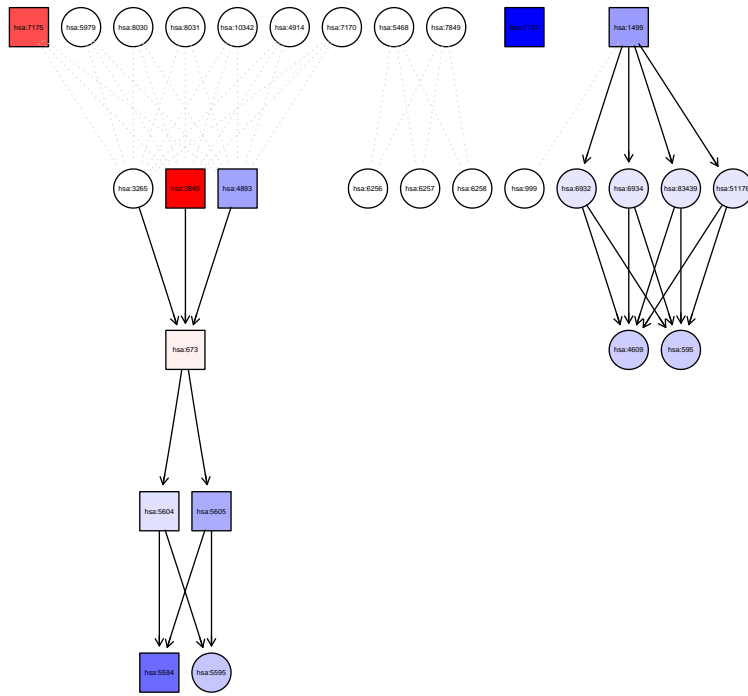


Figure 3: Perturbation propagation on the *Thyroid cancer signaling pathway*.

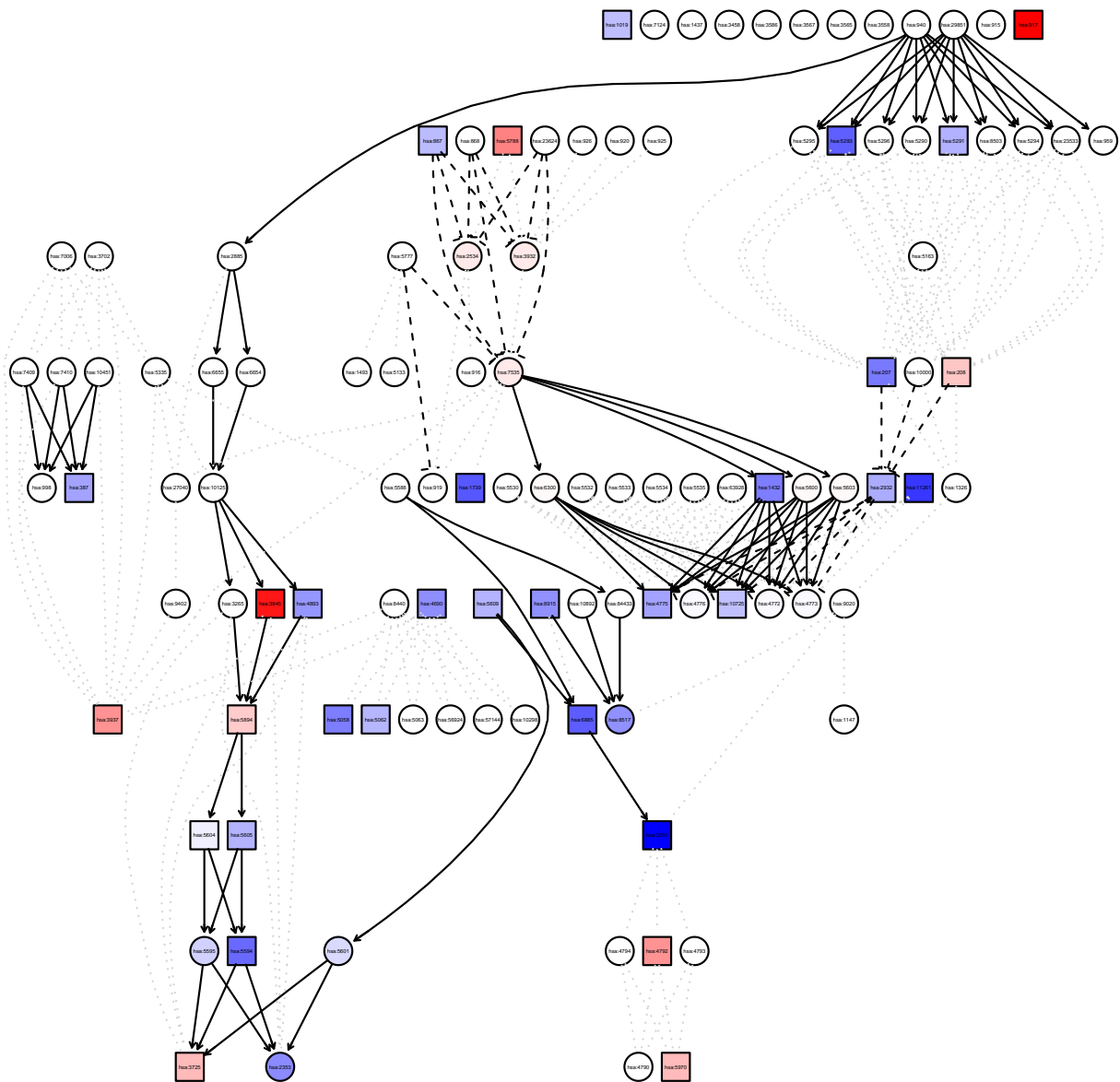


Figure 4: Perturbation propagation on the *T cell receptor signaling pathway*.

References

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