Primer: CMAPCollections from Bioconductor annotation packages

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1 reactome

The `reactome.db` package offers access to pathway annotations from the reactome database `http://www.reactome.org/`. This primer demonstrates how to use this annotaiton to generate a species-specific `CMAPCollection` with Entrez gene identifiers.

First, we access the genes identifiers associated with each pathway. In a second step, we retrieve the names of the pathways and perform some basic filtering to remove duplicated or un-named sets.

```
> library(reactome.db)
> library(gCMAP)
> library(Matrix)
> ## use multiple cores if available
> options(mc.cores=2)
> ## retrieve entrez ids of pathway members
> pathways <- as.list(reactomePATHID2EXTID)
> ## retrieve names
> pathway.names <- unlist(mget(names(pathways), reactomePATHID2NAME))
> pathway.names <- pathway.names[ match(names( pathways),
+                                       names( pathway.names )) ]
> ## remove categories with duplicated or missing names
> filtered.names <- duplicated( names( pathway.names)) | is.na(pathway.names)
> pathways <- pathways[ ! filtered.names ]
> pathway.names <- pathway.names[ ! filtered.names]
```

Each pathway name contains the name of the respective species. We can use this information to generate species-specific reactome collections:

```
> head( pathway.names )
```

```
                                                    70326
                          "Homo sapiens: Glucose metabolism"
                                                    70221
          "Homo sapiens: Glycogen breakdown (glycogenolysis)"
                                                  1430728
                                "Homo sapiens: Metabolism"
                                                    71387
                 "Homo sapiens: Metabolism of carbohydrates"
                                                  2496304
              "Saccharomyces cerevisiae: Glucose metabolism"
                                                  2496314
"Saccharomyces cerevisiae: Glycogen breakdown (glycogenolysis)"
```

```
> human <- grepl( "^Homo sapiens", pathway.names)
```

Next, we create new CMAPCollection, providing pathway names in the phenoData slot.

```
> pheno.data <- as(
+     data.frame(name=pathway.names[ human ],
+                row.names=names(pathways[ human ])
+               ),
+               "AnnotatedDataFrame")
> i.matrix <- Matrix::t( incidence( pathways[ human ] ) )
> reactome.hs <- CMAPCollection( i.matrix,
+                               phenoData=pheno.data,
+                               annotation='org.Hs.eg',
+                               signed=rep( FALSE, ncol(i.matrix)) )
```

To simplify this process in the future, we can define a helper function.

```
> pathway2cmap <- function(pathways, pathway.names, selected, anno){
+   pheno.data <- as(
+                    data.frame(name=pathway.names[ selected ],
+                               row.names=names(pathways[ selected ])
+                               ),
+                    "AnnotatedDataFrame")
+   i.matrix <- Matrix::t( incidence(pathways[ selected ]) )
+   CMAPCollection(i.matrix,
+                  phenoData=pheno.data,
+                  annotation=anno,
+                  signed=rep(FALSE, ncol(i.matrix)))
+ }
```

Now, generating `CMAPCollections` for other species is straightforward:

```
> mouse <- grepl( "^Mus musculus", pathway.names)
> reactome.mm <- pathway2cmap( pathways, pathway.names,
+                              selected=mouse, "org.Mm.eg")
```

2 KEGG

Similarly, the `KEGG.db` package offers the last public release of the KEGG gene annotation database `http://www.genome.jp/kegg/`. Analogous to the `reactome.db` package, species are identified by specific prefixes in the pathway identfiers. For example, human gene sets start with 'hsa', mouse sets begin with 'mmu' instead.'

```
> library(KEGG.db)
> ## retrieve entrez ids of pathway members
> pathways <- as.list(KEGGPATHID2EXTID)
> ## retrieve names
> pathway.names <- unlist(mget(sub("^...", "",names(pathways)), KEGGPATHID2NAME))
> ## species-specific CMAPCollections
> human <- grepl( "^hsa", names( pathways ))
> KEGG.hs <- pathway2cmap( pathways, pathway.names, selected=human, "org.Hs.eg")
> mouse <-  grepl( "^mmu", names( pathways ))
> KEGG.mm <- pathway2cmap( pathways, pathway.names, selected=mouse, "org.Mm.eg")
```

```
>   sessionInfo()

R version 2.15.2 (2012-10-26)
Platform: i386-apple-darwin9.8.0/i386 (32-bit)

locale:
[1] C/en_US.US-ASCII/en_US.US-ASCII/C/en_US.US-ASCII/en_US.US-ASCII

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] KEGG.db_2.8.0        Matrix_1.0-10        reactome.db_1.42.0
 [4] RSQLite_0.11.2       DBI_0.2-5            reshape_0.8.4
 [7] plyr_1.8             gCMAP_1.1.7          DESeq_1.10.1
[10] lattice_0.20-13      locfit_1.5-8         GSEABase_1.20.2
[13] graph_1.36.2         annotate_1.36.0      AnnotationDbi_1.20.3
[16] Biobase_2.18.0       BiocGenerics_0.4.0

loaded via a namespace (and not attached):
 [1] GSEAlm_1.18.0          IRanges_1.16.4         RColorBrewer_1.0-5
 [4] XML_3.95-0.1           bigmemory_4.3.0        bigmemory.sri_0.1.2
 [7] bigmemoryExtras_1.0.0 genefilter_1.40.0      geneplotter_1.36.0
[10] grid_2.15.2           latticeExtra_0.6-24    limma_3.14.4
[13] parallel_2.15.2       splines_2.15.2         stats4_2.15.2
[16] survival_2.37-2       tools_2.15.2           xtable_1.7-0
```