

Primer: Preparing NChannelSet objects with differential expression scores

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This document exemplifies the processing of differential expression data using small, simulated datasets shipped with the gCMAP package. To see real-life examples with data from available from public databases, please refer to the documentation of the gCMAPWeb companion package.

1 Differential expression analysis

The gCMAP package offers a the `generate_gCMAP_NChannelSet` function to process multiple instances differential expression experiments with two classes (e.g. cases vs controls). For microarray data, the `limma` package is used to calculate a moderated t-statistic (default). Optionally, a standard t-test can be computed instead. For RNAseq data, the `DESeq` package is used instead.

Data preprocessing differs considerably between different technologies and array platforms and needs to be performed beforehand. Normalized microarray data and accompanying annotation is passed to `generate_gCMAP_NChannelSet` as a list of `ExpressionSet` objects, RNAseq data can be passed as a list of `CountDataSet` objects instead.

To generate a set of 3 example `CountDataSets` , we use the `makeExampleCountDataSet` function from the `DESeq` package.

```
> library(gCMAP)
> library(DESeq)
> set.seed( 123 )
> cds.list <- lapply( 1:3, function(n) {
+   cds <- makeExampleCountDataSet()
+   featureNames(cds) <- paste("gene",1:10000, sep="_")
+   cds
+ })
> names(cds.list) <- paste("Instance", 1:3, sep="")
> sapply(cds.list, dim)
```

	Instance1	Instance2	Instance3
Features	10000	10000	10000
Samples	5	5	5

```
> sapply(cds.list, function(n) pData(n)$condition )
```

	Instance1	Instance2	Instance3
[1,]	"A"	"A"	"A"
[2,]	"A"	"A"	"A"
[3,]	"B"	"B"	"B"
[4,]	"B"	"B"	"B"
[5,]	"B"	"B"	"B"

By default, each `CountDataSet` object contains counts for 10000 genes from five samples. Each sample is assigned to one of two conditions, A or B, in the `phenoData` slot of the `CountDataSet`. The `pData` column containing group membership information (e.g. "condition") is provided as the `control_perturb_col` parameter. The levels associated with control and treatment groups are specified as "control" and "perturb" character strings.

Each of the three `CountDataSet` instances is analyzed individually by `generate_gCMAP_NChannelSet`. To assemble the results into a single `NChannelSet`, the input `ExpressionSet` or `CountDataSet` objects must contain measurements for the same features (e.g. the vectors returned by "featureNames" must be identical across all instances).

To include information about the instances in the `NChannelSet`, a 'sample.annotation' data.frame can be provided, containing exactly one row for each element of the input list of `ExpressionSet` / `CountDataSet` objects.

```
> ## this step takes a little time
> cde <- generate_gCMAP_NChannelSet(cds.list,
+                               uids=1:3,
+                               sample.annotation=NULL,
+                               platform.annotation="Entrez",
+                               control_perturb_col="condition",
+                               control="A",
+                               perturb="B")
> channelNames(cde)

[1] "exprs" "log_fc" "mod_fc" "p" "z"
```

For array data, a `NChannelSet` with slots "exprs", "z", "p", and "log_fc" is returned, containing the average intensity across all samples within the instance, z-scores, (raw) p-values and log2 fold changes, respectively. If count data is processed, an additional "mod_fc" channel is returned, providing the moderated fold change, calculated after performing variance-stabilising transformation across all input instances. (Please consult the `DESeq` vignette for details.)

1.1 Storing assayData as BigMatrix objects on disk

When large numbers of instances are processed, the resulting `NChannelSet` objects can require large amounts of memory. The `bigmemory` and `bigmemoryExtras` packages can be used to create `BigMatrix` objects, allowing methods to subset large datasets without having to load them fully into memory first.

Note: at the time of writing, the `bigmemory` package was only available for Unix and Mac OS X operating systems but not for Windows. Windows users can take advantage of `gCMAP`'s functionality but datasets must be fully loaded into memory first.

If the `bigmemory` and `bigmemoryExtras` packages are available and a file name is provided via the "big.matrix" parameter, `generate_gCMAP_NChannelSet` uses the `BigMatrix` package to store data from each channel on disk. In the future, individual channels and / or subsets of the datasets can then be loaded without requiring the full object to be read into memory again.

To highlight this functionality, we derive three (arbitrary) instances from the `sample.ExpressionSet` object available from the `Biobase` package, process them and store the results in a temporary directory. Note: this section will only create the expected `big.matrix` files on disk if the `bigmemory` and `bigmemoryExtras` packages can be loaded. Otherwise, a standard Rdata object is created and a warning is issued.

```
> ## list of ExpressionSets
> data("sample.ExpressionSet") ## from Biobase
> es.list <- list( sample.ExpressionSet[,1:4],
+                 sample.ExpressionSet[,5:8],
```

```

+           sample.ExpressionSet[,9:12])
> ## three instances
> names(es.list) <- paste( "Instance", 1:3, sep=".")
> storage.file <- tempfile()
> storage.file ## filename prefix for BigMatrices

[1] "/tmp/RtmpGPzDvn/filef5e05a564a07"

> de <- generate_gCMAP_NChannelSet(
+   es.list,
+   1:3,
+   platform.annotation = annotation(es.list[[1]]),
+   control_perturb_col="type",
+   control="Control",
+   perturb="Case",
+   big.matrix=storage.file)
> channelNames(de)

[1] "exprs"  "log_fc" "p"      "z"

> head( assayDataElement(de, "z") )

              1          2          3
AFFX-MurIL2_at -1.36808562  0.04333555 -0.7255849
AFFX-MurIL10_at  1.56254427 -0.69203457  0.1589525
AFFX-MurIL4_at  -0.65915229 -0.85080055  0.1804448
AFFX-MurFAS_at  -0.31745996  0.43936805  0.2813885
AFFX-BioB-5_at  -0.08767134  0.15619365 -0.2836740
AFFX-BioB-M_at  -0.32253278  0.82819990 -0.5521458

> dir(dirname( storage.file ))

[1] "filef5e05a564a07_exprs"      "filef5e05a564a07_exprs.desc"
[3] "filef5e05a564a07_log_fc"    "filef5e05a564a07_log_fc.desc"
[5] "filef5e05a564a07_p"        "filef5e05a564a07_p.desc"
[7] "filef5e05a564a07_z"        "filef5e05a564a07_z.desc"
[9] "filef5e05a564a07.rdata"

```

If the `bigmemoryExtras` package is available, it generated a `BigMatrix` objects containing pointers to three files in the temporary directory, one for each channel (identified by their suffices). If the package is unavailable, a standard `eSet` is saved to disk, which will be read fully into memory upon reload.

To demonstrate the use of disk-based `NChannelSet` objects, we will first delete the object from the current R workspace and reload it from disk.

Accessing the complete matrix in the `assayData` slots, e.g. for the "z" channel, returns another `BigMatrix` object with `assayData` slot pointing to the associated file on disk. Upon subsetting, only the requested part of the dataset is loaded into memory.

```

> ## remove de object from R session and reload
> rm( de )
> de <-get( load( paste( storage.file, "rdata", sep=".") ) )
> class( assayDataElement(de, "z") )

[1] "BigMatrix"
attr(,"package")
[1] "bigmemoryExtras"

```

```
> assayDataElement(de, "z")[1:10,] ## load subset
```

```

              1          2          3
AFFX-MurIL2_at -1.36808562  0.04333555 -0.7255849
AFFX-MurIL10_at  1.56254427 -0.69203457  0.1589525
AFFX-MurIL4_at  -0.65915229 -0.85080055  0.1804448
AFFX-MurFAS_at  -0.31745996  0.43936805  0.2813885
AFFX-BioB-5_at  -0.08767134  0.15619365 -0.2836740
AFFX-BioB-M_at  -0.32253278  0.82819990 -0.5521458
AFFX-BioB-3_at  -0.30488232  1.79473755  0.4374636
AFFX-BioC-5_at  -0.29368831  0.34488031  0.0982909
AFFX-BioC-3_at   0.05507180 -1.89130218  0.2943413
AFFX-BioDn-5_at  0.78669240  0.74946863  1.0688364
```

The `memorize` function reads the complete `NChannelSet` into memory. In addition, one or more selected channels can be specified with the `'name'` parameter.

```
> ## read z-score channel into memory
> dem <- memorize( de, name="z" )
> channelNames(dem)
```

```
[1] "z"
```

```
> class( assayDataElement(dem, "z") ) ## matrix
```

```
[1] "matrix"
```

```
> sessionInfo()
```

```
R version 3.1.0 RC (2014-04-02 r65358)
Platform: x86_64-apple-darwin10.8.0 (64-bit)
```

```
locale:
```

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

```
[1] parallel stats      graphics grDevices utils      datasets methods
[8] base
```

```
other attached packages:
```

```

[1] bigmemoryExtras_1.8.0 bigmemory_4.4.6      BH_1.54.0-1
[4] bigmemory.sri_0.1.2   DESeq_1.16.0      lattice_0.20-29
[7] locfit_1.5-9.1        gCMAP_1.8.0       limma_3.20.0
[10] GSEABase_1.26.0       graph_1.42.0      annotate_1.42.0
[13] AnnotationDbi_1.26.0  GenomeInfoDb_1.0.0 Biobase_2.24.0
[16] BiocGenerics_0.10.0
```

```
loaded via a namespace (and not attached):
```

```

[1] biganalytics_1.1.1 DBI_0.2-7      genefilter_1.46.0 geneplotter_1.42.0
[5] grid_3.1.0         GSEAlm_1.24.0      IRanges_1.21.45   Matrix_1.1-3
[9] RColorBrewer_1.0-5 RSQLite_0.11.4     splines_3.1.0     stats4_3.1.0
[13] survival_2.37-7    tools_3.1.0        XML_3.98-1.1      xtable_1.7-3
```