CodelinkSet

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October 1, 2012

1 Introduction

The CodelinkSet is an extension of the ExpressionSet class, that improves de user experience in terms of integration with other Bioconductor packages. Because this class is derived from ExpressionSet, most functions that work on ExpressionSet will work in CodelinkSet objects. Futhermore, extension of existing methods and functions is easier.

2 Loading of data

There is a new function called readCodelinkSet that will load the data in the old format and convert it into the CodelinkSet format. This function will replace in the future readCodelink. It is possible to include phenoData and featureData when calling readCodelinkSet. In addition, the correct annotation package is guessed from the first file and assigned to the annotation slot.

Instead of giving the list of files to read, it is possible to give it the location of a targets file. This will be preferred and the information in the targets file will be used to fill de phenoData slot.

```
> cset <- readCodelinkSet("targets.txt")
>
```

2.1 Feature data

The CodelinkSet stores intensity data in the exprs slot, much the same as Affymetrix derived data. It also contains a slot background, to accomodate background intensities. The featureData object will contain further information like ProbeName, ProbeType, meanSNR (computed when loading data), Row and Col locations in the chip, etc. The FeatureID is used to name rows, although the ProbeName is the useful information when accesing annotation data.

2.2 Annotations

The CodelinkSet class supports by default new style (*AnnotationDbi* based) annotation packages, i.e. all annotations will contain the .db subfix. To change to the old style you can assign the annotation package by hand:

```
> library(codelink)
> data(codelink.exprset)
> annotation(codelink.exprset)

[1] "rwgcod"

> annotation(codelink.exprset) <- "rwgcod"
> annotation(codelink.exprset)

[1] "rwgcod"

>
```

NOTE: Old style annotation packages will be deprecated for BioC 2.3

3 The User Interface

The user interface has changed to be more consistent and easier to use. All user method for CodelinkSet object have the prefix ”cod” followed by the corresponding method name.

3.1 Data accession

getInt getBkd getSNR
featureNames probeNames sampleNames

3.2 Preprocessing

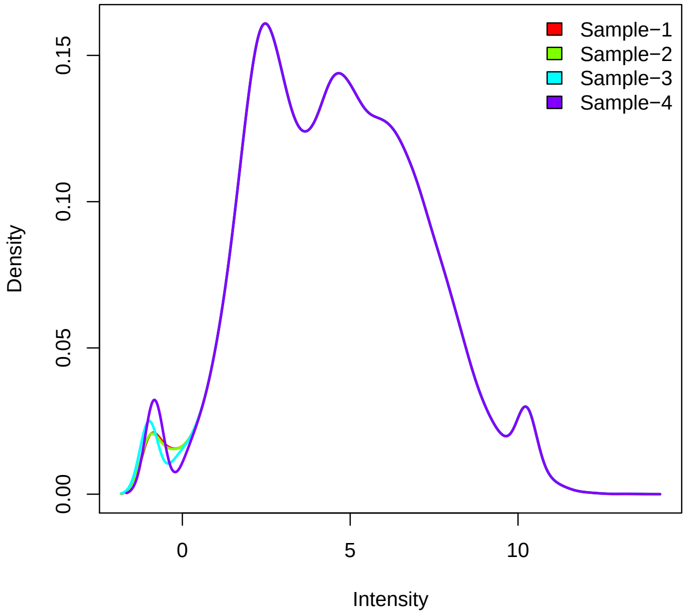
codCorrect is used for background correction and codNormalize for normalization. A convenience function called codPreprocess is also available to combine in one step background correction and normalization. The devault values found in the older functions are preserved, i.e. *half* for codCorrect and *quantile* codNormalize

```
> cset <- codPreprocess(codelink.exprset)
>
```

3.3 Plots

`codPlotMA`, `codPlotDensities`, `codPlotCorrelation` and `codPlotImage` are the corresponding new functions. A convinience funcion `codPlot` is provided and the type of plot is choose with the parameter *what*.

```
> codPlot(cset, what = "density")
> codPlot(cset, what = "ma")
> codPlot(cset, what = "image")
>
```



4 Analysis with limma

Analysis using *limma* is straightforward. The design matrix can be specified using the `phenoData` information. In the fit step, the `CodelinkSet` object can be passed directly to `lmFit`. Making life easier for users of the Codelink platform.

```
> # assign example experimental conditions:
> cset$Treatment = c("C", "C", "T", "T")
> # create and fit model:
> design <- model.matrix(~ -1 + factor(cset$Treatment))
> fit <- lmFit(cset, design)
>
```

5 Exporting data to a file

You may want to export your normalized data to use it with other analysis tools. The function writeCodelink allows to do that. By default the index, probe names, accession number, entrez gene identifiers, intensity and SNR values are output. If flag = TRUE, then the flags are also output.

```
> writeCodelink(codelink.exprset, file = "intensities.txt")
```

6 Creating CodelinkSetUnique objects

CodelinkSet objects use the feature id of each probe to obtain unique identifiers. This feature id is related to the physical location of the probe in the array. This means that when we use featureNames in a CodelinkSet object we get these feature ids. To get the probe ids we need to use probeNames instead. This can be inconvenient when we want to use our data with other packages that use featureNames to obtain the probe names and feed this ids to the annotation package. Because the annotation packages use probe names, the probes wouldn't be found. To solve this problem a CodelinkSet with unique probe names as featureNames is needed. To construct such an object we can use the function averageProbes, that takes a CodelinkSet object and computes the mean of the intensities for replicated probes. The results are stored in a CodelinkSetUnique object.

```
> foo.avg <- averageProbes(codelink.exprset)
```

This computation takes a lot of time. It is possible to use a parallelized version (using the package *multicore*) by making 'parallel=TRUE' in averageProbes. See the help for averageProbes for more details on this approach. The package *multicore* needs to be loaded in advance by typing library(multicore).

7 Session Info

```
> sessionInfo()
```

```
R version 2.15.1 (2012-06-22)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=C                 LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

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

other attached packages:
[1] codelink_1.26.0    limma_3.14.0       Biobase_2.18.0     BiocGenerics_0.4.0

loaded via a namespace (and not attached):
 [1] AnnotationDbi_1.20.0 DBI_0.2-5            IRanges_1.16.0
 [4] RSQLite_0.11.2       XML_3.95-0           annotate_1.36.0
 [7] parallel_2.15.1      stats4_2.15.1        tools_2.15.1
[10] xtable_1.7-0
```