

CodelinkSet

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1 Introduction

The **CodelinkSet** is an extension of the **ExpressionSet** class, that improves the 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. Furthermore, 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 the **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 accommodate 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 accessing 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` suffix. 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

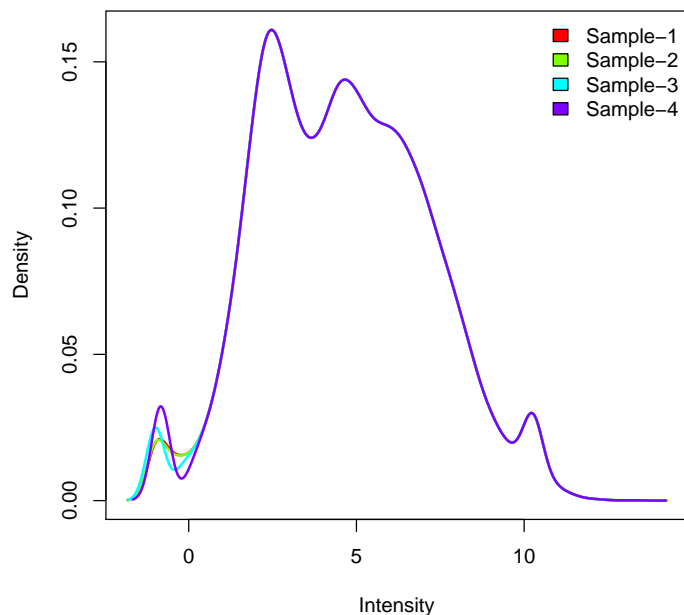
`codCorrect` is used for background correction and `codNormalize` for normalization. A convenience function called `codPreprocess` is also available to combine in one step background correction and normalization. The default values found in the older functions are preserved, i.e. *half* for `codCorrect`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

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

3.3 Plots

`codPlotMA`, `codPlotDensities`, `codPlotCorrelation` and `codPlotImage` are the corresponding new functions. A convenience function `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.

```
> 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 Session Info

```
> sessionInfo()
```

R version 2.8.1 Patched (2009-03-18 r48200)
i386-apple-darwin9.6.0

locale:
C

attached base packages:

[1]	splines	tools	stats	graphics	grDevices	utils	datasets
[8]	methods	base					

other attached packages:

[1]	codelink_1.10.0	genefilter_1.22.0	survival_2.35-4
[4]	annotate_1.20.1	xtable_1.5-5	AnnotationDbi_1.4.3
[7]	limma_2.16.5	Biobase_2.2.2	

loaded via a namespace (and not attached):

[1]	DBI_0.2-4	RSQLite_0.7-1
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