

# CodelinkSet

Diego Diez

October 23, 2008

## 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` 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

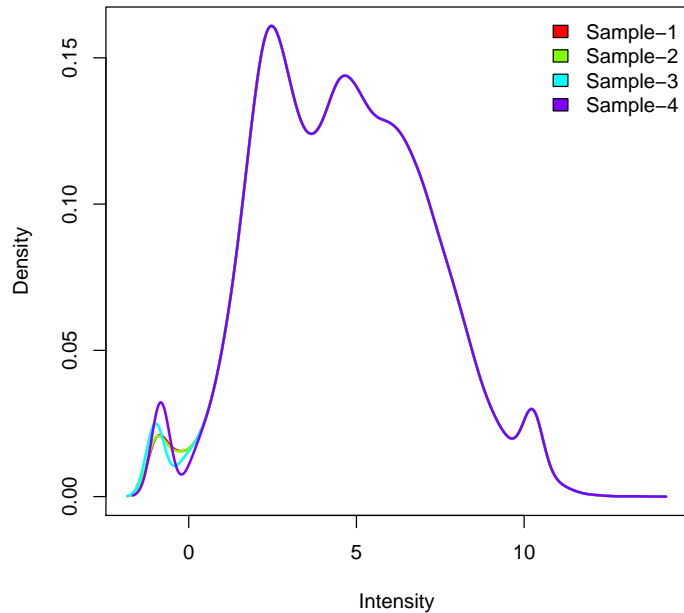
`codCorrect` is used for background correction and `codNormalize` for normalization. A convenience function called `codPreprocess` is also available to combine in one step background correction and normalization. The default values found in the older functions are preserved, i.e. *half* for `codCorrect` and *quantile* for `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 chosen 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 2.9.0 Under development (unstable) (2008-10-19 r46752)  
x86\_64-unknown-linux-gnu

locale:

LC\_CTYPE=en\_US.UTF-8;LC\_NUMERIC=C;LC\_TIME=en\_US.UTF-8;LC\_COLLATE=en\_US.UTF-8;LC\_MONETARY=C;LC\_PAPER=C;LC\_MESSAGES=en\_US.UTF-8

attached base packages:

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

other attached packages:

[1] codelink\_1.11.0 genefilter\_1.23.0 survival\_2.34-1  
[4] annotate\_1.21.0 xtable\_1.5-4 AnnotationDbi\_1.5.0  
[7] limma\_2.17.2 Biobase\_2.3.0

loaded via a namespace (and not attached):

[1] DBI\_0.2-4 RSQLite\_0.7-0