

From the Genepix data files to RGList to NChannelSet

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Load the required packages

```
> library("Biobase")
> library("limma")
> library("CCl4")
```

Read the data and convert them into an RGList

The Genepix (`.gpr`) data files are in the `extdata` directory of the *CCl4* package. If you have the package installed, we can locate them on your filesystem with the function `system.file`. If the files are somewhere else, please adapt the below assignment to `datapath`.

```
> datapath = system.file("extdata", package="CCl4")

> p = read.AnnotatedDataFrame("samplesInfo.txt", path=datapath)
> CCl4_RGList = read.maimages(files=sampleNames(p),
+   path = datapath,
+   source = "genepix",
+   columns = list(R = "F635 Median", Rb = "B635 Median",
+     G = "F532 Median", Gb = "B532 Median"))
```

If this code is run in the `inst/doc` directory of the *CCl4* (source) package, the output data files will be written directly into the `data` directory of the package. Otherwise, just write into a temporary directory.

```
> outdir = file.path("../", "..", "data")
> if(!isTRUE(file.info(outdir)$isdir))
+   outdir = tempdir()
> save(CCl4_RGList, file = file.path(outdir, "CCl4_RGList.RData"))
```

The function `read.maimages` from the *limma* package reads the `.gpr` files and builds an *RGList* object from it.

The output is written to

```
> outdir

[1] "../../data"
```

Build an NChannelSet from the RGList

Once the *RGList* object has been created, we can build an *NChannelSet*.

```

> sessionInfo()

R version 3.0.0 (2013-04-03)
Platform: i386-w64-mingw32/i386 (32-bit)

locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252

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

other attached packages:
[1] CC14_1.0.14 limma_3.16.0 Biobase_2.20.0 BiocGenerics_0.6.0

loaded via a namespace (and not attached):
[1] tools_3.0.0

```

Table 1: The output of `sessionInfo` on the build system after running this vignette.

```

> featureData = new("AnnotatedDataFrame", data = CC14_RGList$genes)
> assayData = with(CC14_RGList, assayDataNew(R=R, G=G, Rb=Rb, Gb=Gb))
> varMetadata(p)$channel=factor(c("G", "R", "G", "R"),
+                               levels=c(ls(assayData), "_ALL_"))
> CC14 <- new("NChannelSet",
+            assayData = assayData,
+            featureData = featureData,
+            phenoData = p)
> save(CC14, file = file.path(outdir, "CC14.RData"))

```