

# 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] "/tmp/Rtmp1ZJALR"
```

## Build an NChannelSet from the RGList

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

```

> sessionInfo()

R version 4.2.1 (2022-06-23)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.5 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.16-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.16-bioc/R/lib/libRlapack.so

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_GB            LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8     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] CCl4_1.36.0      limma_3.54.0      Biobase_2.58.0
[4] BiocGenerics_0.44.0

loaded via a namespace (and not attached):
[1] compiler_4.2.1 tools_4.2.1

```

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

```

> featureData = new("AnnotatedDataFrame", data = CCl4_RGList$genes)
> assayData = with(CCl4_RGList, assayDataNew(R=R, G=G, Rb=Rb, Gb=Gb))
> varMetadata(p)$channel=factor(c("G", "R", "G", "R"),
+                               levels=c(ls(assayData), "_ALL_"))
> CCl4 <- new("NChannelSet",
+           assayData = assayData,
+           featureData = featureData,
+           phenoData = p)
> save(CCl4, file = file.path(outdir, "CCl4.RData"))

```