

Classes *SNPExperiment* and *CNVExperiment*: Derivatives of
SummarizedExperiment for use with genotype and intensity data
in package *trioClasses*

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```
> library("trioClasses")
> library("vcf2R")
> data(targets)
> data("BMP4-european-all.sm")
> df <- DataFrame(dx = rep(1, 10), sex = rep(1, 10), row.names = paste0("sub",
  1:10))
> class(df)

[1] "DataFrame"
attr(,"package")
[1] "IRanges"

> class(sm)

[1] "SnpMatrix"
attr(,"package")
[1] "snpStats"

> logR <- matrix(runif(130), nrow = 13, ncol = 10)
> baf <- matrix(runif(130), nrow = 13, ncol = 10)

> snpEx <- new("SNPTrioExperiment", Pedigree = data.frame(1:10),
  assays = SimpleList(geno = sm[1:13, 1:10], logR = logR,
    baf = baf), colData = df, rowData = targets.gr)
> show(snpEx)

class: SNPTrioExperiment
dim: 13 10
exptData(0):
assays(3): geno logR baf
rownames(13): IRF6 MAFB ... FGFR2 PTCH1
rowData values names(0):
colnames(10): sub1 sub2 ... sub9 sub10
colData names(2): dx sex

> class(geno(snpEx))
```

```
[1] "SnpMatrix"  
attr("package")  
[1] "snpStats"  
  
> class(logR(snpEx))  
  
[1] "matrix"  
  
> class(baf(snpEx))  
  
[1] "matrix"
```