

Plotting Idiograms

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April 30, 2018

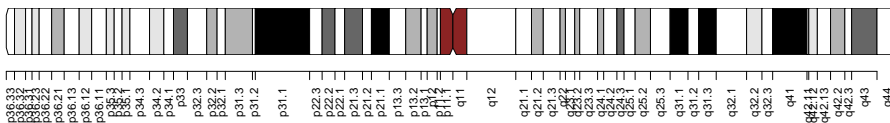
This package is no longer actively developed and maintained largely for historical reasons.

1 Simple Usage

```
> library(SNPchip)
```

Plot an idiogram for chromosome 1 with labels for the bands on the x-axis.

```
> plotIdiogram("1", build="hg19", cex=0.8)
```



Suppressing labels:

```
> plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE)
```



With user-defined y-axis limits and y-coordinates for the idiogram:

```
> plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE, ylim=c(0,1), cytoband.ycoords=c(0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0))
```



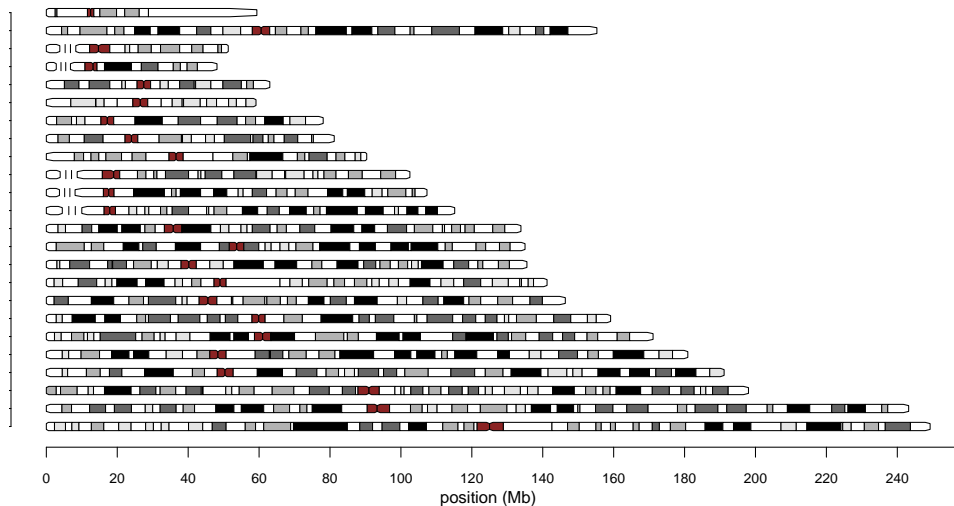
Plot an idiogram for all chromosomes.

```
> library(oligoClasses)
> sl <- getSequenceLengths("hg19")[c(paste("chr", 1:22, sep=""), "chrX", "chrY")]
> ybottom <- seq(0, 1, length.out=length(sl)) - 0.01
> ytop <- seq(0, 1, length.out=length(sl)) + 0.01
> for(i in seq_along(sl)){
+   chr <- names(sl)[i]
+   if(i == 1){
+     plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE, ylim=c(-0.05,1.05), cytoband.ycoords=c(0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0))
+   }
+ }
```

```

+             xlim=c(0, max(sl)))
+         }
+         if(i > 1){
+             plotIdiogram(names(sl)[i], build="hg19", cex=0.8, label.cytoband=FALSE, cytoband.ycoord=i)
+         }
+     }
> axis(1, at=pretty(c(0, max(sl)), n=10), labels=pretty(c(0, max(sl)), n=10)/1e6, cex.axis=0.8)
> mtext("position (Mb)", 1, line=2)
> par(las=1)
> axis(2, at=ybottom+0.01, names(sl), cex.axis=0.6)

```



2 Session Information

The version number of R and packages loaded for generating the vignette were:

- R version 3.5.0 (2018-04-23), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.4 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.7-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.7-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: SNPchip 2.26.0, oligoClasses 1.42.0
- Loaded via a namespace (and not attached): Biobase 2.40.0, BiocGenerics 0.26.0, BiocInstaller 1.30.0, BiocParallel 1.14.0, Biostrings 2.48.0, DBI 0.8, DelayedArray 0.6.0, GenomeInfoDb 1.16.0, GenomeInfoDbData 1.1.0, GenomicRanges 1.32.0, IRanges 2.14.0, Matrix 1.2-14, RCurl 1.95-4.10, S4Vectors 0.18.0, SummarizedExperiment 1.10.0, XVector 0.20.0, affyio 1.50.0, bit 1.1-12,

bitops 1.0-6, codetools 0.2-15, compiler 3.5.0, ff 2.2-13, foreach 1.4.4, grid 3.5.0, iterators 1.0.9,
lattice 0.20-35, matrixStats 0.53.1, parallel 3.5.0, stats4 3.5.0, tools 3.5.0, zlibbioc 1.26.0