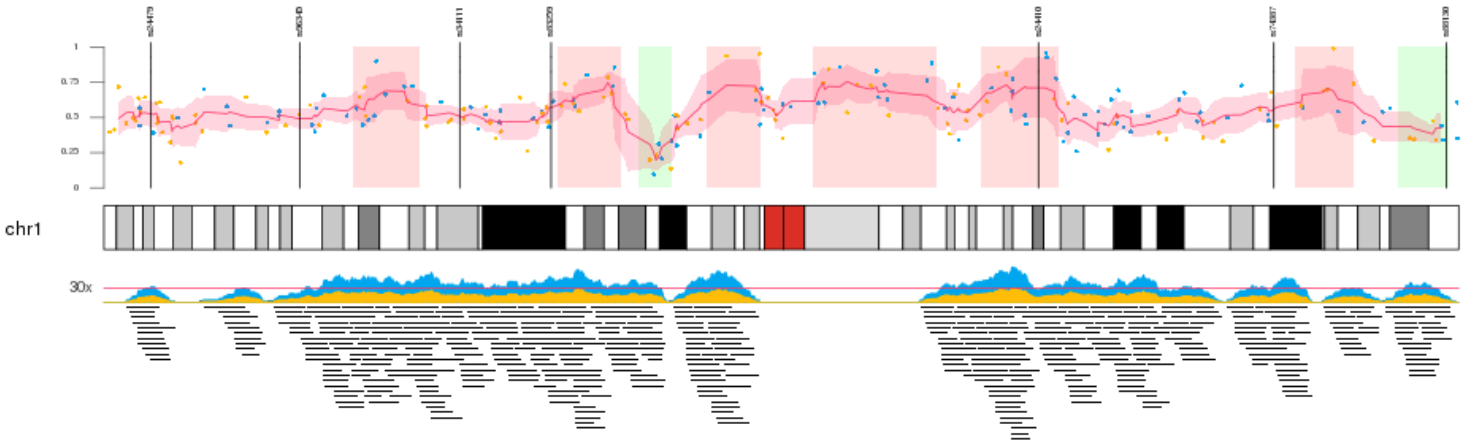
Visualizing genomic data with karyoploteR

Quick disclaimer

- R = several ways to get the same result
- Figures arent perfect
- Brief overview

Introduction

- karyoploteR allows you to easily *plot* data across the genome
- built upon base R (sorry Tidyverse people!)



Installing karyoploteR

Current version:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
  BiocManager::install("karyoploteR")
```

Developmental version can also be downloaded from github using `devtools::install_github()`

Getting started

```
library(karyoploteR)

kp <- plotKaryotype()
```

Layouts

- plot.type = 1
  - data panel above ideogram
- plot.type = 2
  - two data panels one above and one below ideogram
- plot.type = 3
  - plot type 2 but arranged in a row
- plot.type = 4
  - plot type 1 but arranged in a row
- plot.type = 5
  - ideograms in a row with a data panel below
- plot.type = 6
  - no ideogram
- plot.type = 7
  - ideograms only in a row (caution!)

Adding layers

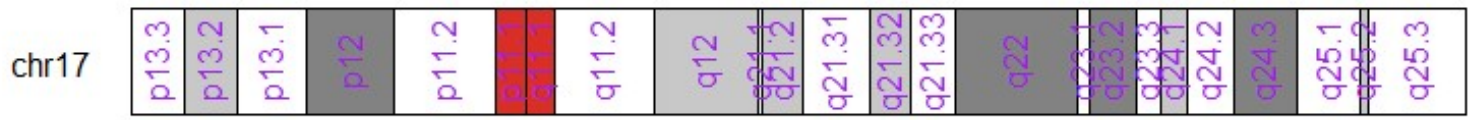
Base R

```
kp <- plotKaryotype(chromosomes="chr17")
kpAddCytobandLabels(kp, force.all=TRUE, srt=90, col="purple", cex=1)
```

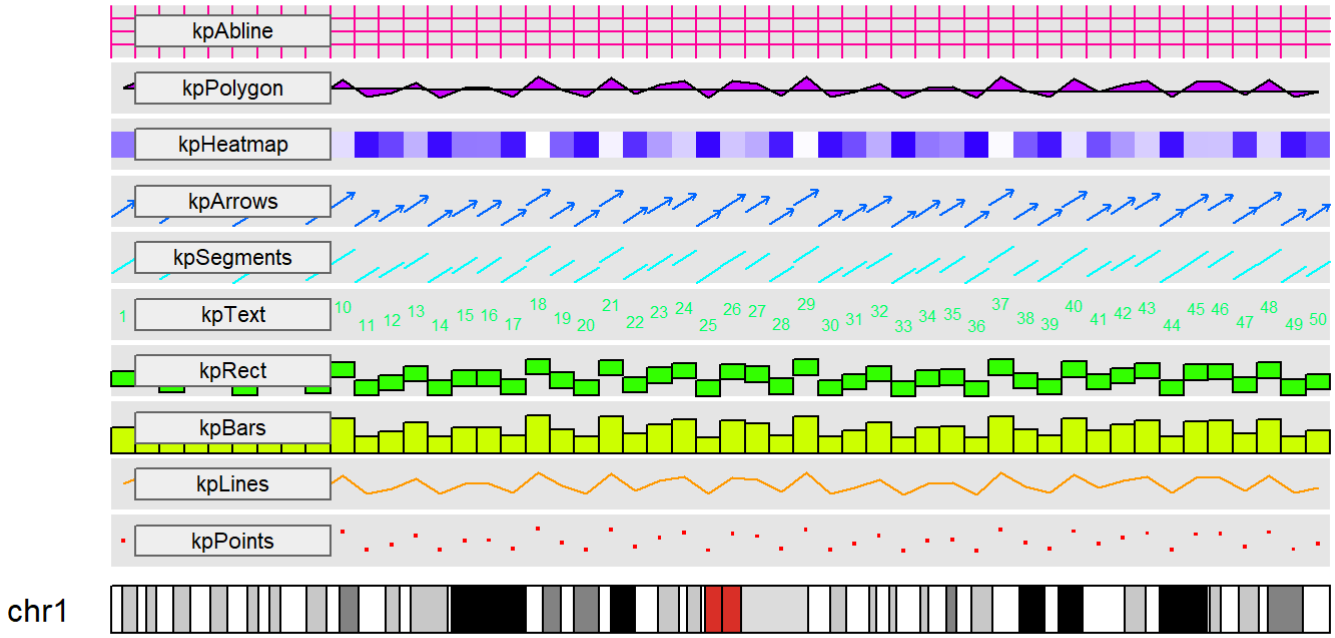
magrittr

```
library(magrittr)

kp <- plotKaryotype(chromosomes="chr17") %>%
  kpAddCytobandLabels(force.all=TRUE, srt=90, col="purple", cex=1)
```



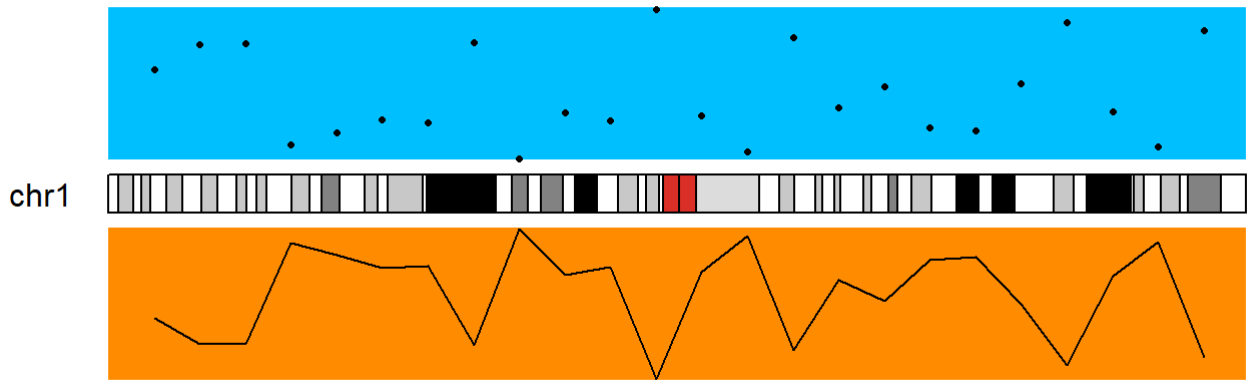
Basic data types



Adding data

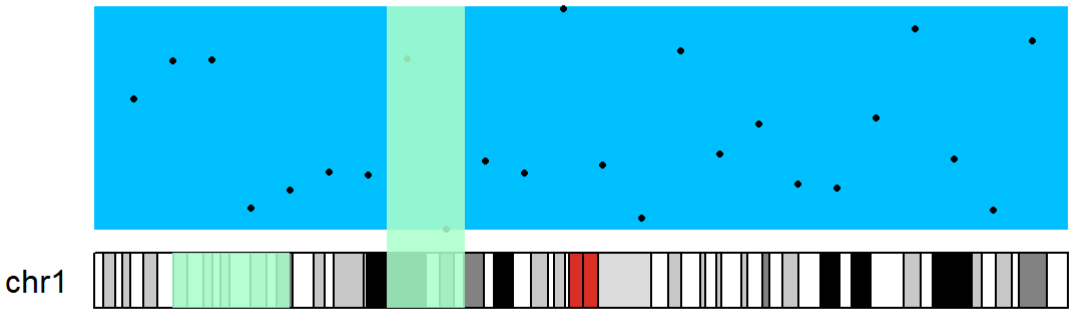
```
x <- 1:24*10e6 # genomic location
y <- runif(n = 24, min = 0, max = 1) #random values for plotting
```

```
plotKaryotype(plot.type=2, chromosomes = "chr1") %>%
  kpDataBackground(data.panel = 1, col="deepskyblue") %>%
  kpDataBackground(data.panel = 2, col="darkorange") %>%
  kpPoints(chr="chr1", x=x, y=y, data.panel = 1) %>%
  kpLines(chr="chr1", x=x, y=y, data.panel = 2)
```



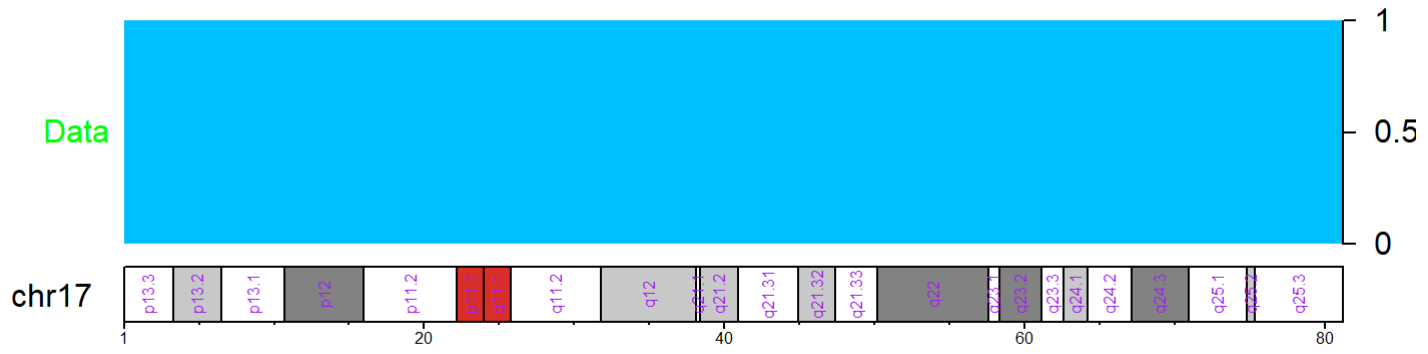
Data Panels

```
plotKaryotype(plot.type=1, chromosomes = "chr1") %>%
  kpDataBackground(data.panel = 1, col="deepskyblue") %>%
  kpPoints(chr="chr1", x=x, y=y, data.panel = 1) %>%
  kpRect(chr="chr1", x0=20e6, x1=50e6, y0=0, y1=1, col="#AAFFCBDD",
         data.panel="ideogram", border=NA) %>%
  kpRect(chr="chr1", x0=75e6, x1=95e6, y0=0, y1=1, col="#AAFFCBDD",
         data.panel="all", border=NA)
```



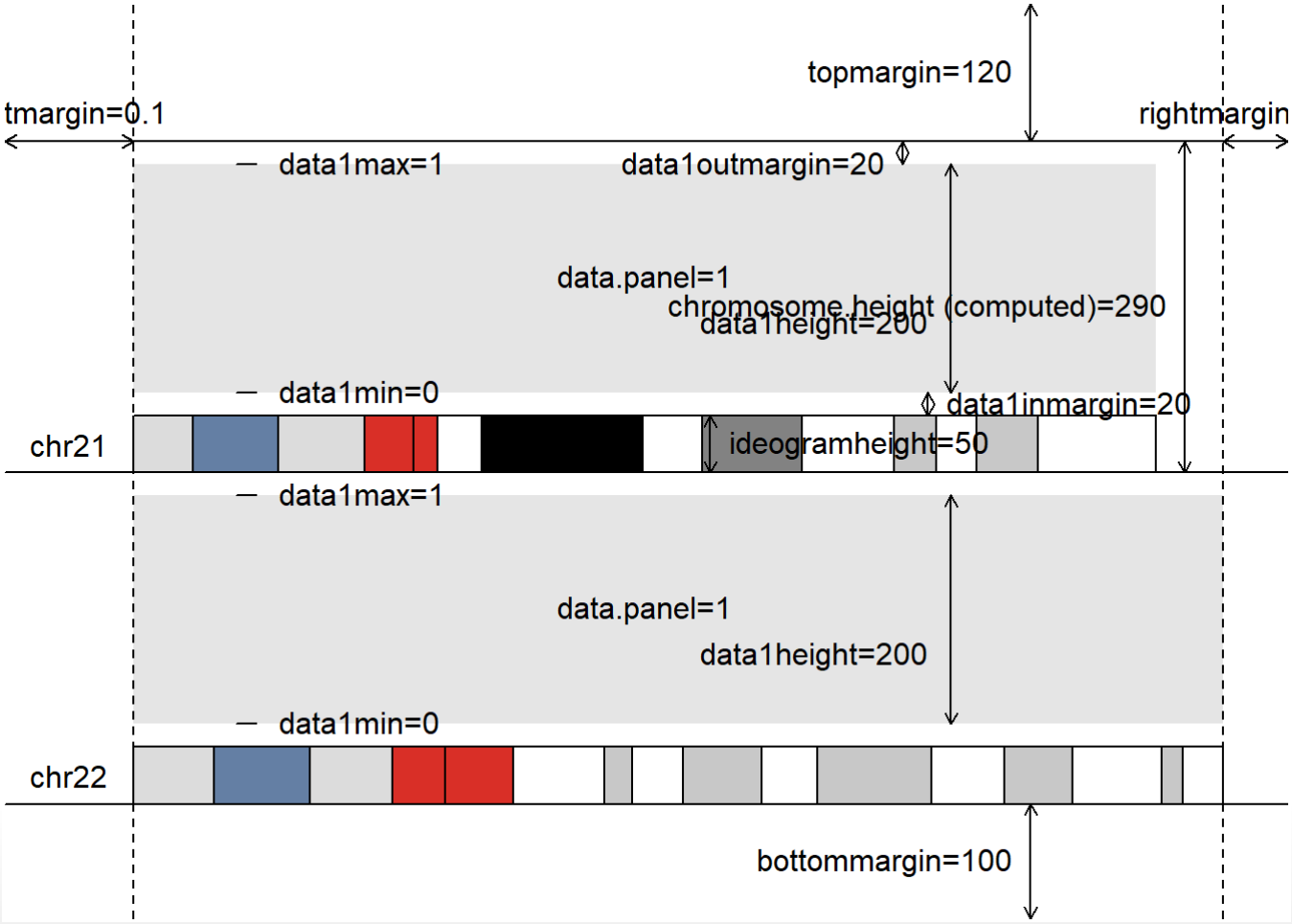
Adding plot features

```
plotKaryotype(chromosomes="chr17", plot.type = 1) %>%
  kpDataBackground(data.panel = 1, col="deepskyblue") %>%
  kpAddCytobandLabels(force.all=TRUE, srt=90, col="purple", cex=0.5) %>%
  kpAddBaseNumbers() %>%
  kpAddLabels(labels="Data", data.panel = 1, col="green") %>%
  kpAxis(data.panel=1, side=2)
```



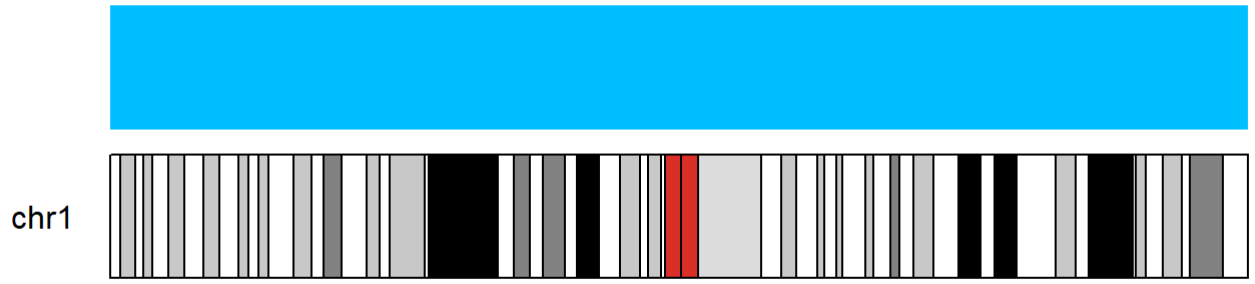
Viewing plotting parameters

```
plotDefaultPlotParams(plot.type=1)
```



Changing plotting parameters

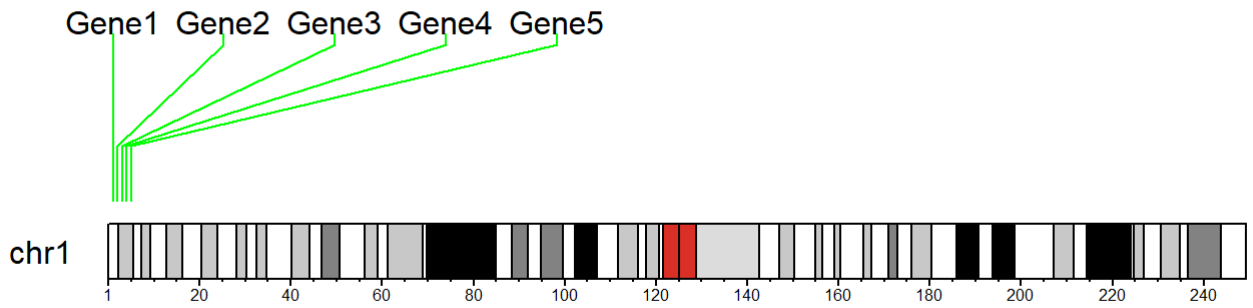
```
pp <- getDefaultPlotParams(plot.type=1)
pp$ideogramheight <- 100 ; pp$data1height <- 100
plotKaryotype(chromosomes="chr1", plot.type=2, plot.params = pp) %>%
  kpDataBackground(color = "deepskyblue")
```



karyoploteR specific commands

Gene markers

```
plotKaryotype(chromosomes="chr1") %>%
  kpAddBaseNumbers() %>%
  kpPlotMarkers(chr=markers$chr, x=markers$pos, labels=markers$labels,
                text.orientation = "horizontal",
                marker.parts = c(0.5, 0.9, 0.1),line.color = "green",
                label.color = "black",  label.dist = 0.01,
                max.iter = 1000)
```



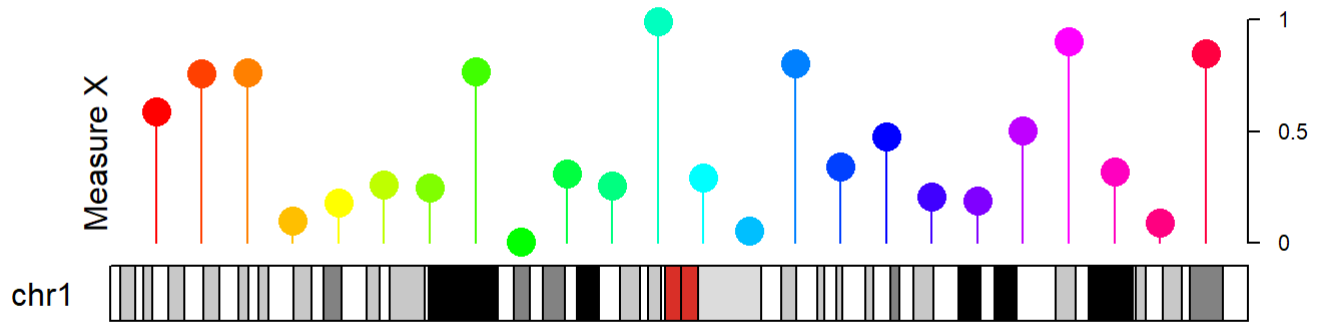
Linking regions

```
plotKaryotype() %>%
kpPlotLinks(data=start.regs, data2=end.regs, col="#fac7ffaa")
```

Examples

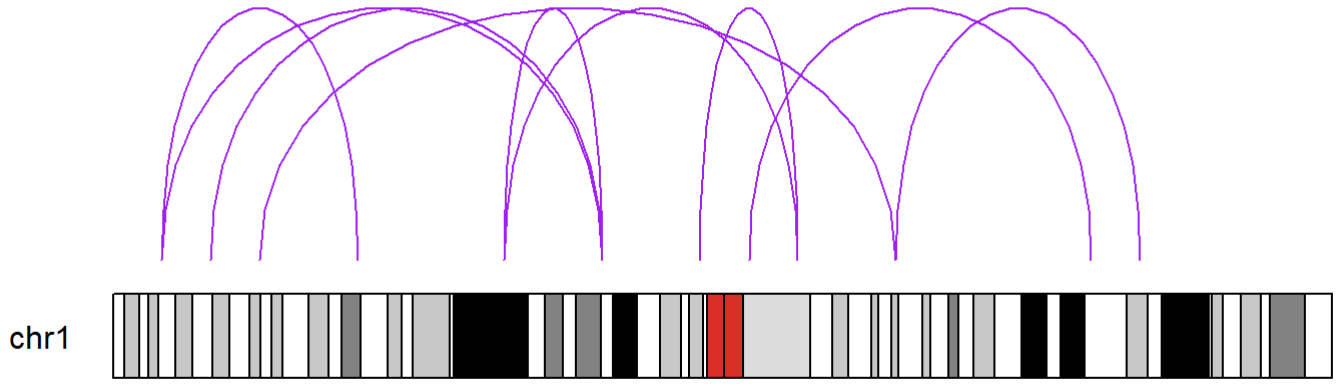
Lollipop Plot

```
plotKaryotype(plot.type=1, chromosomes = "chr1") %>%
  kpPoints(chr="chr1", x=x, y=y, col=rainbow(length(x)), cex=2) %>%
  kpSegments(chr="chr1", x0=x, x1=x, y0=0, y1=y,
             col=rainbow(length(x))) %>%
  kpAxis(side=2, cex=0.7) %>%
  kpAddLabels("Measure X", srt=90, r0=0.5)
```



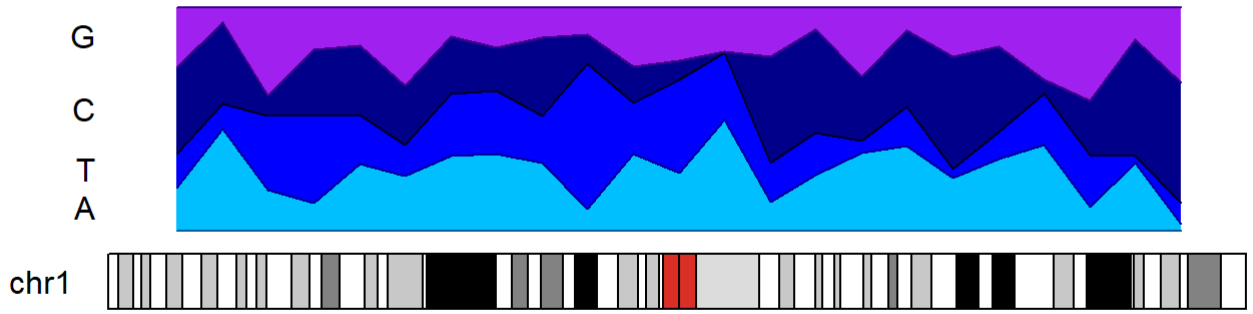
5C

```
plotKaryotype(chromosomes = "chr1") %>%
kpPlotLinks(data=start.regs, data2=end.regs, border="purple")
```



Nucleotide coverage

```
plotKaryotype(chromosomes = "chr1") %>%
  kpPlotRibbon(data=tmp, y0=0, y1=tmp$A, col="deepskyblue") %>%
  kpPlotRibbon(data=tmp, y0=tmp$A, y1=tmp$T, col="blue") %>%
  kpPlotRibbon(data=tmp, y0=tmp$T, y1=tmp$C, col="darkblue") %>%
  kpPlotRibbon(data=tmp, y0=tmp$C, y1=tmp$G, col="purple") %>%
  kpAddLabels(r0 = 0, r1=tmp$A[1], labels = "A") %>%
  kpAddLabels(r0 = tmp$A[1], r1=tmp$T[1], labels = "T") %>%
  kpAddLabels(r0 = tmp$T[1], r1=tmp$C[1], labels = "C") %>%
  kpAddLabels(r0 = tmp$C[1], r1=tmp$G[1], labels = "G")
```



Other ideogram options

ggbio

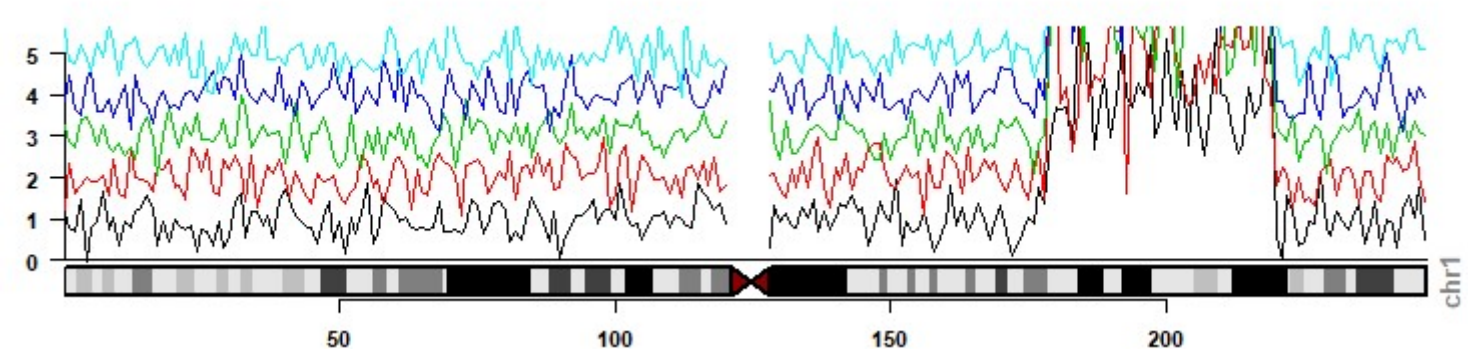
```
library(ggbio)
p.ideo <- Ideogram(genome = "hg19", subchr = "chr1")

track1 <- ggplot() + geom_blank()

tracks(CHR = p.ideo, TRACK = track1)
```

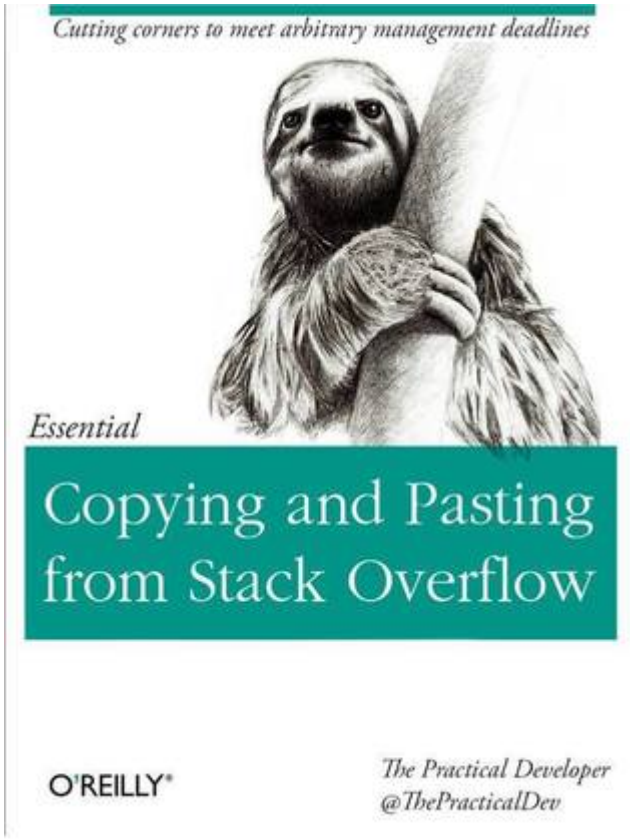
IdeoViz

```
library(IdeoViz)
data(binned_multiSeries)
data(hg18_ideo)
plotOnIdeo(chrom=seqlevels(binned_multiSeries),
           ideoTable=hg18_ideo,
           values_GR=binned_multiSeries,
           value_cols=colnames(mcols(binned_multiSeries)),
           col=1:5)
```



Additional resources

- bioconductor vignettes
- github tutorial

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