

How to obtain Cytoband and Stain Information

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

library(GenomicRanges)
library(rtracklayer)
library(biovizBase) #needed for stain information

## Warning: replacing previous import 'utils::findMatches' by
## 'S4Vectors::findMatches' when loading 'AnnotationDbi'

library(IRanges)
library(R.utils)
library(TxDb.Hsapiens.UCSC.hg18.knownGene)
```

Introduction

This document explains how to obtain the cytoband and stain information. The user must ensure that the input object is a GRanges object

Method 1 - Using rtracklayer package

```
# create a query against a UCSC Table browser
query <- rtracklayer::ucscTableQuery("hg18", "cytoBandIdeo")
table1 <- rtracklayer::getTable(query) # retrieve table
head(table1)

#Add an extra column with strand information
table1$Strand <- c("*")

## Convert object into GRanges object
table1.gr <- GRanges(table1$chrom,
                     IRanges(table1$chromStart, table1$chromEnd),
                     table1$Strand,
                     table1$name, table1$gieStain)

head(table1.gr, n = 3)

#Save this object for future use
```

```
save(table1.gr, file = "hg18.ucsctrack.RData")
```

#NOTE : For hg19, simply use "hg19" in query instead of "hg18"

Method 2 - directly from UCSC Genome Browser

This example shows how to download cytoband and stain information for hg18, and hg19 genomes from the UCSC Genome Browser

URL for hg18

```
url <- "http://hgdownload.soe.ucsc.edu/goldenPath/hg18/database/cytoBand.txt.gz"
```

#Download file and un-compress it

```
download.file(url, destfile = "cyto.txt.gz")
```

```
R.utils::gunzip("cyto.txt.gz")
```

#Read in the downloaded cytoband ideogram txt file

```
cyto1 <- read.table(file = "cyto.txt",  
                   header = FALSE, sep = "\t")
```

#Adding column names

```
colnames(cyto1) <- c("Chrom", "Start", "End", "CytobandName", "Stain")
```

#Add an extra column with strand information

```
cyto1$Strand <- c("*")
```

#The user must ensure that the input object is a GRanges object

Convert object into GRanges object

```
cyto1.gr <- GRanges(cyto1$Chrom,  
                   IRanges(cyto1$Start, cyto1$End),  
                   cyto1$Strand,  
                   cyto1$CytobandName, cyto1$Stain)
```

```
head(cyto1.gr, n = 3)
```

#The user must ensure that the input object is a GRanges object

#Save this object for future use

```
save(cyto1.gr, file = "hg18.ucsctrack.RData")
```

#NOTE : URL for hg19

```
#url <- "http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/cytoBand.txt.gz"
```

URL FOR hg38

```
#url <- "http://hgdownload.soe.ucsc.edu/goldenPath/hg38/database/cytoBand.txt.gz"
```

Method 3 - Using biovizBase package

```
hg18.ucsctrack <- biovizBase::getIdeogram("hg18", cytoband = TRUE)

head(hg18.ucsctrack, n=3)
#The user must ensure that the input object is a GRanges object

#Save this object for future use
save(hg18.ucsctrack, file = "hg18.ucsctrack.RData")
```