

# 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  
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.ucstrack.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.ucstrack <- biovizBase::getIdeogram("hg18", cytoband = TRUE)

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

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