

Introduction to Siganature Analysis

Jubayer Hossain

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Mutational Patterns

```
# Load Packages
library(BSgenome) # for available ref-genome

## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##   dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##   grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##   order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##   rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##   union, unique, unsplit, which, which.max, which.min
## Loading required package: S4Vectors
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##
##   expand.grid
## Loading required package: IRanges
## Loading required package: GenomeInfoDb
## Loading required package: GenomicRanges
## Loading required package: Biostrings
```

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## Loading required package: XVector
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:base':
##
##     strsplit
## Loading required package: rtracklayer
library(MutationalPatterns) # for mutational signature analysis

## Loading required package: NMF
## Loading required package: pkgmaker
## Loading required package: registry
##
## Attaching package: 'pkgmaker'
## The following object is masked from 'package:S4Vectors':
##
##     new2
## Loading required package: rngtools
## Loading required package: cluster
## NMF - BioConductor layer [OK] | Shared memory capabilities [NO: bigmemory] | Cores 3/4
## To enable shared memory capabilities, try: install.extras('
## NMF
## ')
##
## Attaching package: 'NMF'
## The following object is masked from 'package:S4Vectors':
##
##     nrun
library(NMF) # for non-negative matrix factorization(NMF or NNMF)
library(gridExtra) # for managing plots and grid system

##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:Biobase':
##
##     combine
## The following object is masked from 'package:BiocGenerics':
##
##     combine

```

Including Plots