

# Package: ATACCoGAPS (via r-universe)

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**Title** Analysis Tools for scATACseq Data with CoGAPS

**Version** 1.7.0

**Description** Provides tools for running the CoGAPS algorithm (Fertig et al, 2010) on single-cell ATAC sequencing data and analysis of the results. Can be used to perform analyses at the level of genes, motifs, TFs, or pathways. Additionally provides tools for transfer learning and data integration with single-cell RNA sequencing data.

**License** Artistic-2.0

**Depends** R (>= 4.2.0), CoGAPS (>= 3.5.13)

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---

applyGREAT

*Find Enrichment of GO Terms in PatternMarker Peaks using GREAT*

---

### Description

Use the rGREAT package to find enrichment of GO terms or genes for the peaks found to be most pattern differentiating using the PatternMarker statistic.

### Usage

```
applyGREAT(
  cogapsResult,
  granges,
  genome,
  scoreThreshold = NULL,
  GREATcategory = "GO"
)
```

**Arguments**

|                |   |
|----------------|---|
| cogapsResult   | result object from CoGAPS   |
| granges        | GRanges object corresponding to the peaks of the scATAC-seq data CoGAPS was applied to  |
| genome         | UCSC genome designation for input to the submitGreatJob function from the rGREAT package (e.g. "hg19")  |
| scoreThreshold | threshold of PatternMarker score to take peaks for analysis, higher values return more peaks. Defaults to use all PatternMarker genes with value NULL |
| GREATCategory  | input to the category argument of the rGREAT getEnrichmentTables function. Usually "GO" or "Genes"  |

**Value**

list containing enrichment results for each pattern

**Examples**

```
data("schepCogapsResult")
data(schepGranges)

GOenrichment <- applyGREAT(cogapsResult = schepCogapsResult,
  granges = schepGranges, genome = "hg19")
```

---

ATACTransferLearning *Transfer Learning between ATACseq data sets using projectR*

---

**Description**

Wrapper function for projectR which finds overlaps between the peaks of the atac data CoGAPS was run on and maps them to new data set the user wishes to project learned patterns into.

**Usage**

```
ATACTransferLearning(
  newData,
  CoGAPSResult,
  originalPeaks,
  originalGranges,
  newGranges
)
```

**Arguments**

|                 |   |
|-----------------|---|
| newData         | the ATAC data to project into                           |
| CoGAPSResult    | result from CoGAPS run on original ATAC data            |
| originalPeaks   | peaks from the ATAC data Cogaps was run on              |
| originalGranges | granges of the peaks for the data set Cogaps was run on |
| newGranges      | granges of the peaks for the new data set               |

**Value**

A matrix of the projected patterns in the input data as well as p-values for each element of that matrix.

---

|           |  |
|-----------|--|
| cgapsPlot | <i>Plot Individual CoGAPS Patterns</i> |
|-----------|--|

---

**Description**

Function to plot each pattern of the pattern matrix from a cogapsResult and color by cell classifier information to identify which patterns identify which cell classes.

**Usage**

```
cgapsPlot(
  cgaps_result,
  sample.classifier,
  cols = NULL,
  sort = TRUE,
  patterns = NULL,
  matrix = FALSE,
  ...
)
```

**Arguments**

|                   |  |
|-------------------|--|
| cgaps_result      | CoGAPSResult object from a CoGAPS run or the pattern matrix (matrix must be set equal to TRUE in the latter case)  |
| sample.classifier | factor of sample classifications for all cells for the data to be plotted by (e.g. celltypes)  |
| cols              | vector of colors to be used for the cell classes; should have the same number of colors as levels of the sample.classifier factor. If left null a list of colors is produced |
| sort              | TRUE if samples will be sorted according to sample.classifier prior to plotting  |
| patterns          | numerical vector of patterns to be plotted; if null all patterns are plotted   |

|        |   |
|--------|---|
| matrix | if false cgaps_result is interpreted as a CoGAPSRresult object, if true it is interpreted as the pattern matrix |
| ...    | addition arguments to plot function   |

**Value**

Series of plots of pattern matrix patterns colored by cell classifications

**Examples**

```
data("schepCogapsResult")
data(schepCellTypes)

cgapsPlot(schepCogapsResult, schepCellTypes)
```

---

dataSubsetBySparsity *Filter scATACseq by sparsity*

---

**Description**

Function to filter a set of scATACseq data by sparsity and return a subset of filtered data, as well as list of the remaining cells and peaks.

**Usage**

```
dataSubsetBySparsity(
  data,
  cell_list,
  peak_list,
  cell_cut = 0.99,
  peak_cut = 0.99
)
```

**Arguments**

|           |   |
|-----------|---|
| data      | matrix of read counts peaks x cells   |
| cell_list | list of cell names/identifiers for the data   |
| peak_list | list of peaks from the data   |
| cell_cut  | threshold of sparsity to filter at (eg. 0.99 filters all cells with more than 99 percent zero values) |
| peak_cut  | threshold of sparsity to filter at for peaks  |

**Value**

nested list containing the subset data, a list of peaks, and list of cells

**Examples**

```
data("subsetSchepData")
data("schepPeaks")
data("schepCellTypes")

outData = dataSubsetBySparsity(subsetSchepData, schepCellTypes, schepPeaks)
```

---

```
exampleMotifList      Example list of motifs for examples
```

---

**Description**

PWMMatrixList used for examples with functions based on DNA motifs. Each entry contains the motif ID and the probability of each nucleotide at each position, as a matrix.

**Usage**

```
exampleMotifList
```

**Format**

PWMMatrixList of length 100

---

```
foldAccessibility    Estimate fold Accessibility of a Gene Relative to Average
```

---

**Description**

Compares the accessibility of peaks overlapping with a gene, as returned by the geneAccessibility function to the average accessibility of peaks within a given cell population. Meant to provide a rough estimate of how accessible a gene is with values higher than 1 providing evidence of differential accessibility (and thus implying possible transcription), with values lower than 1 indicating the opposite.

**Usage**

```
foldAccessibility(peaksAccessibility, cellTypeList, cellType, binaryMatrix)
```

**Arguments**

```
peaksAccessibility    the binarized accessibility of a set of peaks; one value returned from the geneAccessibility function
cellTypeList          list of celltypes grouping cells in the data
cellType              the particular cell type of interest from within cellTypeList
binaryMatrix          binarized scATAC data matrix
```

**Value**

Fold accessibility value as compared to average peaks for a given cell type

**Examples**

```
data("subsetSchepData")
data(schepCellTypes)
library(Homo.sapiens)
geneList <- c("TAL1", "IRF1")
data(schepGranges)
binarizedData <- (subsetSchepData > 0) + 0
accessiblePeaks <- geneAccessibility(geneList = geneList, peakGranges = schepGranges,
  atacData = subsetSchepData, genome = Homo.sapiens)
foldAccessibility(peaksAccessibility = accessiblePeaks$TAL1, cellTypeList = schepCellTypes,
  cellType = "K562 Erythroleukemia", binaryMatrix = binarizedData)
```

---

|                   |   |
|-------------------|---|
| geneAccessibility | <i>Find the accessibility of the peaks overlapping a set of genes and their promoters</i> |
|-------------------|---|

---

**Description**

The accessibility of a particular set of interest genes is checked by testing overlap of peaks with the genes and gene promoters and then returning the binarized accesibility data for those peaks

**Usage**

```
geneAccessibility(geneList, peakGranges, atacData, genome)
```

**Arguments**

|             |  |
|-------------|--|
| geneList    | vector of HGNC gene symbols to find overlapping peaks for in the data  |
| peakGranges | a GRanges object corresponding to the peaks in the atacData matrix, in the same order as the rows of the atacData matrix |
| atacData    | a single-cell ATAC-seq count matrix peaks by cells   |
| genome      | TxDb object to produce gene GRanges from   |

**Value**

List of matrices corresponding to the accessible peaks overlapping with each gene across all cells in the data

**Examples**

```
library(Homo.sapiens)
geneList <- c("TAL1", "IRF1")
data(schepGranges)
data("subsetSchepData")
accessiblePeaks <- geneAccessibility(geneList = geneList, peakGranges = schepGranges,
  atacData = subsetSchepData, genome = Homo.sapiens)
```

---

genePatternMatch      *Match genes to pattern differentiating peaks*

---

**Description**

Function to take as input CoGAPS results for ATAC-seq data and find genes within the most "pattern-defining" regions (as identified by cut thresholded pattern Marker statistic from the CoGAPS package), as well as the nearest gene and the nearest gene following the region. Note: a TxDb object for the genome of interest must be loaded prior to running this function.

**Usage**

```
genePatternMatch(cogapsResult, generanges, genome, scoreThreshold = NULL)
```

**Arguments**

|                |  |
|----------------|--|
| cogapsResult   | the CogapsResult object produced by a CoGAPS run   |
| generanges     | GRanges object corresponding to the genomic regions identified as peaks for the ATAC-seq data that CoGAPS was run on   |
| genome         | A TxDb object for the genome of interest, it must be loaded prior to calling this function   |
| scoreThreshold | threshold for the most pattern defining peaks as per the PatternMarker statistic from the CoGAPS package. Default is NULL, returning all PatternMarker peaks. Useful to reduce computational time, as top results are reasonably robust to using more stringent thresholds |

**Value**

double nested list containing lists of the genes in, nearest, and following the peaks matched each pattern

**Examples**

```
data("schepCogapsResult")
data(schepGranges)

library(Homo.sapiens)

genes = genePatternMatch(cogapsResult = schepCogapsResult,
  generanges = schepGranges, genome = Homo.sapiens)
```



---

`heatmapGeneAccessibility`*Heatmap Gene Accessibility*

---

**Description**

Use the output from `geneAccessibility` function to plot a heatmap of the accessible peaks for a particular gene.

**Usage**

```
heatmapGeneAccessibility(  
  genePeaks,  
  celltypes,  
  colColors = NULL,  
  order = TRUE,  
  ...  
)
```

**Arguments**

|                        |  |
|------------------------|--|
| <code>genePeaks</code> | The peaks corresponding to a singular gene; one element of the list output by <code>geneAccessibility()</code> |
| <code>celltypes</code> | List or factor of celltypes corresponding to the cells in the scATAC-seq data set the peaks were found in      |
| <code>colColors</code> | A vector of colors to color the celltypes by, if NULL a random vector of colors is generated                   |
| <code>order</code>     | should the data be ordered by the celltype classifier? TRUE by default   |
| <code>...</code>       | additional arguments to the <code>heatmap.2</code> function from the <code>gplots</code> package               |

**Value**

A plot of the peaks overlapping with a particular gene of interest

**Examples**

```
library(Homo.sapiens)  
geneList <- c("TAL1", "EGR1")  
data(schepGranges)  
data("subsetSchepData")  
data(schepCellTypes)  
accessiblePeaks <- geneAccessibility(geneList = geneList,  
  peakGranges = schepGranges, atacData = subsetSchepData, genome = Homo.sapiens)  
heatmapGeneAccessibility(genePeaks = accessiblePeaks$EGR1, celltypes = schepCellTypes)
```

---

**heatmapPatternMarkers** *Create Heatmap of PatternMarker Peaks*

---

**Description**

Function to make a heatmap of the accessibility of the most differentially accessible regions as discovered by CoGAPS.

**Usage**

```
heatmapPatternMarkers(  
  cgaps_result,  
  atac_data,  
  celltypes,  
  numregions = 50,  
  colColors = NULL,  
  rowColors = NULL,  
  patterns = NULL,  
  order = TRUE,  
  ...  
)
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>cgaps_result</code> | CogapsResult object from CoGAPS run  |
| <code>atac_data</code>    | a numeric matrix of the ATAC data input to CoGAPS  |
| <code>celltypes</code>    | a list or factor of celltypes corresponding to the positions of those cells in the <code>atac_data</code> matrix   |
| <code>numregions</code>   | number of chromosomal regions/peaks to plot for each CoGAPS pattern. Default is 50. Plotting very large numbers of regions can cause significant slowdown in runtime |
| <code>colColors</code>    | column-wise colors for distinguishing celltypes. If NULL, will be generated randomly   |
| <code>rowColors</code>    | row-wise colors for distinguishing patterns. If NULL will be generated randomly  |
| <code>patterns</code>     | which patterns should be plotted, if NULL all will be plotted  |
| <code>order</code>        | option whether to sort the data by celltype before plotting, TRUE by default   |
| <code>...</code>          | additional arguments to the heatmap.2 function   |

**Value**

heatmap of the accessibility for numregions for each pattern

**Note**

If you get the error: "Error in plot.new() : figure margins too large" while using this function in RStudio just make the plotting pane in Rstudio larger and run the code again; this error only means the legend is being cut off in any case, the main plot will still appear correctly

**Examples**

```
data("schepCogapsResult")
data(schepCellTypes)
data("subsetSchepData")

heatmapPatternMarkers(schepCogapsResult, atac_data = subsetSchepData,
                      celltypes = schepCellTypes, numregions = 50)
```

---

heatmapPatternMatrix *Plot the patternMatrix as a heatmap*

---

**Description**

Selects the patternMatrix (patterns by cells) from the CoGAPSRresult and plots the data as a heatmap. Intended to visualize the celltypes distinguished by the patterns found by CoGAPS.

**Usage**

```
heatmapPatternMatrix(
  cgaps_result,
  sample.classifier,
  cellCols = NULL,
  sort = TRUE,
  patterns = NULL,
  matrix = FALSE,
  rowColors = NULL,
  ...
)
```

**Arguments**

|                   |  |
|-------------------|--|
| cgaps_result      | CoGAPSRresult object from a CoGAPS run or the pattern matrix (matrix must be set equal to TRUE in the latter case)   |
| sample.classifier | factor of sample classifications for all cells for the data to be plotted by (e.g. celltypes)  |
| cellCols          | vector of colors to be used for the cell classes; should have the same number of colors as levels of the sample.classifier factor. If left null a list of colors is produced |
| sort              | TRUE if samples will be sorted according to sample.classifier prior to plotting  |

|           |   |
|-----------|---|
| patterns  | numerical vector of patterns to be plotted; if null all patterns are plotted  |
| matrix    | if false cgaps_result is interpreted as a CoGAPSResult object, if true it is interpreted as the pattern matrix being input directly |
| rowColors | vector of colors to plot along patterns, if NULL generated automatically  |
| ...       | additional arguments to the heatmap.2 function  |

**Value**

Heatmap of patternMatrix with color labels for samples

**Examples**

```
data("schepCogapsResult")
data(schepCellTypes)

heatmapPatternMatrix(schepCogapsResult, sample.classifier = schepCellTypes)
```

---

motifPatternMatch      *Find Motifs and TFs from PatternMarker Peaks*

---

**Description**

Function that takes CoGAPS result and list of DNA motifs as input and returns motifs which match to the most pattern-defining peaks for each pattern.

**Usage**

```
motifPatternMatch(
  cogapsResult,
  generanges,
  motiflist,
  genome,
  scoreThreshold = NULL,
  motifsPerRegion = 1
)

getTFs(motifList, tfData)

findRegulatoryNetworks(TFs, networks)

getTFDescriptions(TFs)
```

**Arguments**

|                 |  |
|-----------------|--|
| cogapsResult    | the result object from a CoGAPS run  |
| generanges      | GRanges objects corresponding to the genomic regions which form the rows of the ATAC-seq data that CoGAPS was run on   |
| motiflist       | a PWMlist of motifs to search the regions for  |
| genome          | the ucsc genome version to use e.g. "hg19", "mm10"   |
| scoreThreshold  | threshold for the most pattern defining peaks as per the PatternMarker statistic from the CoGAPS package. By default is NULL, in which case all Pattern defining peaks will be used for motif matching. Used to reduce compute time, as results are quite robust across thresholds |
| motifsPerRegion | number of top motifs to return from each peak  |
| motifList       | list produced by the motifPatternMatch function  |
| tfData          | dataframe of motifs and TFs from cisBP database  |
| TFs             | object of TF info returned from the getTFs function  |
| networks        | a list of regulatory networks of genes corresponding to TFs; we include human-RegNets and mouseRegNets, downloaded from the TTrust database (Han et al Nucleic Acid Res. 2018)   |

**Value**

motifPatternMatch: nested list of the top motif for each region for x number of regions for each pattern

getTFs: list containing list of dataframes of tfData subset to matched TFs and list of how many times each TF was matched to a motif/peak

findRegulatoryNetworks: list of TFs for which we have annotations and the corresponding gene networks for each pattern

getTFDescriptions: list of functional annotations for all TFs in each pattern

**Functions**

- getTFs: Match motifs to TFs based on the list of motifs returned by motifPatternMatch
- findRegulatoryNetworks: function to match TFs identified by getTFs function to a list of regulatory networks of genes known for those TFs
- getTFDescriptions: function to match functional annotation to a list of TFs from the getTFs function

**Examples**

```
data(exampleMotifList)
data(schepGranges)
data(schepCogapsResult)
```

```
motifsByPattern = motifPatternMatch(schepCogapsResult, schepGranges,
  exampleMotifList, "hg19")
```

```

data(exampleMotifList)
data(schepGranges)
data(schepCogapsResult)
data(tfData)

motifsByPattern = motifPatternMatch(schepCogapsResult, schepGranges, exampleMotifList, "hg19")
motifTFs = getTFs(motifsByPattern, tfData)
data(exampleMotifList)
data(schepGranges)
data(schepCogapsResult)
data(tfData)

motifsByPattern = motifPatternMatch(schepCogapsResult, schepGranges, exampleMotifList, "hg19")
motifTFs = getTFs(motifsByPattern, tfData)

regNets = findRegulatoryNetworks(motifTFs, ATACCoGAPS:::humanRegNets)
data(exampleMotifList)
data(schepGranges)
data(schepCogapsResult)
data(tfData)

motifsByPattern = motifPatternMatch(schepCogapsResult, schepGranges, exampleMotifList, "hg19")
motifTFs = getTFs(motifsByPattern, tfData)

tfDesc = getTFDescriptions(motifTFs)

```

---

motifSummarization      *Map Peaks to DNA motifs in scATAC-seq Data*

---

## Description

Provides functionality to summarize scATAC-seq data by motifs from peak summary. Uses motifmatchr to prepare data for CoGAPS run using motif summarization

## Usage

```

motifSummarization(
  motifList,
  scATACData,
  granges,
  genome,
  cellNames,
  pCutoff = 5e-09
)

```

## Arguments

|            |   |
|------------|---|
| motifList  | PWMatrixList object of motifs (from the TFBS tools package) |
| scATACData | matrix of scATACseq data, peaks (rows) by cells (columns)   |

|           |  |
|-----------|--|
| granges   | GenomicRanges object corresponding to all peaks used to summarize scATAC-Data                  |
| genome    | The UCSC Genome to use for input to motifmatchr (e.g "hg19")                                   |
| cellNames | List of cellnames corresponding to the cells in scATACData                                     |
| pCutoff   | p-value cutoff for motifmatchr, 5e-09 by default to identify only matches with high confidence |

**Value**

matrix for input to CoGAPS with summary to motifs; motifs by cells

**Examples**

```
## Not run:
motifSummTest = motifSummarization(motifList = motifs, scATACData = scatac,
  granges = peakGranges, genome = "hg19", cellNames = cells, pCutoff = 5e-09)

## End(Not run)
```

---

pathwayMatch                      *Matches list of genes to pathways*

---

**Description**

Takes the result of the genePatternMatch function and finds significantly enriched pathways for each pattern.

**Usage**

```
pathwayMatch(gene_list, pathways, p_threshold = 0.05, pAdjustMethod = "BH")
```

**Arguments**

|               |   |
|---------------|---|
| gene_list     | Result from the genePatternMatch function, a list of genes for each pattern                         |
| pathways      | List of pathways to perform gene enrichment on. Recommended to download using msigdb (see examples) |
| p_threshold   | significance level to use in enrichment analysis  |
| pAdjustMethod | multiple testing correction method to apply using the p.adjust options (e.g. "BH")                  |

**Value**

List of gene overlap objects, pathways with significant overlap and pathway names for each pattern

## Examples

```
data(schepCogapsResult)
data(schepGranges)
library(Homo.sapiens)

genes <- genePatternMatch(cogapsResult = schepCogapsResult,
  generanges = schepGranges, genome = Homo.sapiens)

library(dplyr)
pathways = msigdb::msigdb(species = "Homo sapiens", category = "H") %>%
dplyr::select(gs_name, gene_symbol) %>% as.data.frame()

matchedPathways = pathwayMatch(genes, pathways, p_threshold = 0.001)
```

---

patternMarkerCellClassifier  
*Match cells to patterns*

---

## Description

Use the patternMarker statistic to determine which cells belong to each pattern in the data

## Usage

```
patternMarkerCellClassifier(cgapsResult)
```

## Arguments

cgapsResult     a CoGAPSRresult object

## Value

list containing a prediction matrix and vector classifying cells to patterns

## Examples

```
data("schepCogapsResult")
pClass <- patternMarkerCellClassifier(schepCogapsResult)
```



---

|                |                                 |
|----------------|---------------------------------|
| peaksToGRanges | <i>List of peaks to GRanges</i> |
|----------------|---------------------------------|

---

**Description**

Wrapper function for `makeGrangesFromDataFrame()` from the `GenomicRanges` package to build `GRanges` objects from character list of chromosomal regions because this is a common format to receive peak information.

**Usage**

```
peaksToGRanges(region_list, sep)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>region_list</code> | character list or vector of chromosomal regions/peaks in form chromosomenumber(sep)start(sep)end eg. Chr1-345678-398744 |
| <code>sep</code>         | separator between information pieces of string (conventionally "-" or ".")  |

**Value**

`GRanges` corresponding to input list of region information

**Note**

If `region_list` is a dataframe you should use the `GenomicRanges` function `makeGRangesFromDataFrame` which this function applies

**Examples**

```
data(schepPeaks)

schepGranges = peaksToGRanges(schepPeaks, sep = "-")
```

---

|                    |   |
|--------------------|---|
| RNAseqTFValidation | <i>Validate TF Findings with RNA-seq CoGAPS</i> |
|--------------------|---|

---

**Description**

Use results from CoGAPS run on matched RNA-seq data to verify TF activity suggested by motif matching analysis of ATAC CoGAPS output. Uses the `fgsea` package to find enrichment of Pattern-Marker genes among genes regulated by identified candidate TFs

**Usage**

```

RNaseqTFValidation(
  TFGenes,
  RNACoGAPSResult,
  ATACPatternSet,
  RNAPatternSet,
  matrix = FALSE
)

```

**Arguments**

|                 |  |
|-----------------|--|
| TFGenes         | genes regulated by the TFs as returned by simpleMotifTFMatch() or findRegulatoryNetworks()   |
| RNACoGAPSResult | CoGAPSResult object from matched RNA-seq data, or, if matrix = TRUE, a matrix containing patternMarker gene ranks. Must contain gene names |
| ATACPatternSet  | vector of patterns found by CoGAPS in the ATAC data to match against patterns found in RNA   |
| RNAPatternSet   | vector of patterns found by CoGAPS in RNA to match against those found in ATAC   |
| matrix          | TRUE if inputting matrix of PatternMarker genes, FALSE if inputting CoGAPS result object. FALSE by default                                 |

**Value**

Result matrices from the fgsea function for each pattern comparison

**Examples**

```

## Not run:
gseaList = RNaseqTFValidation(TFMatchResult$RegulatoryNetworks, RNACoGAPS,
  c(1,3), c(2,7), matrix = FALSE)

## End(Not run)

```

---

schepCellTypes

*Cell types corresponding to subsetSchepData*

---

**Description**

Factor of cell types in the order of the subsetSchepData object from the Schep et al, 2017, Nature Methods paper.

**Usage**

```
schepCellTypes
```

**Format**

Factor of length 600 with 12 levels

**Source**

[10.1038/nmeth.4401](https://doi.org/10.1038/nmeth.4401)

---

*schepCogapsResult*      *CogapsResult from the subsetSchepData object*

---

**Description**

Output from applying the CoGAPS algorithm to the *subsetSchepData* object.

**Usage**

*schepCogapsResult*

**Format**

Large *CogapsResult*

---

*schepGranges*      *GRanges corresponding to subsetSchepData*

---

**Description**

*GRanges* in the order of the peaks of the *subsetSchepData* object from the Schep et al, 2017, Nature Methods paper.

**Usage**

*schepGranges*

**Format**

*GRanges* of length 5036

**Source**

[10.1038/nmeth.4401](https://doi.org/10.1038/nmeth.4401)

---

`schepPeaks`*Peaks corresponding to subsetSchepData*

---

**Description**

Character vector of peaks in the order of the peaks of the `subsetSchepData` object from the Schep et al, 2017, Nature Methods paper.

**Usage**

```
schepPeaks
```

**Format**

Character vector of length 5036

**Source**

[10.1038/nmeth.4401](https://doi.org/10.1038/nmeth.4401)

---

`simpleMotifTFMatch`*Motif/TF Matching in a Single Function*

---

**Description**

If the user does not have a specific set of motifs, transcription factors, or regulatory networks that they want to match against, simply uses the core motifs from the JASPAR database to find motifs and TFs in the most Pattern differentiating peaks, as well as regulatory networks from TTrust database corresponding to the identified TFs. This is used to provide transcription factors with functional annotation which may suggest plausible unknown regulatory mechanisms operating in the cell types of interest within the data.

**Usage**

```
simpleMotifTFMatch(  
  cogapsResult,  
  generanges,  
  organism,  
  genome,  
  scoreThreshold = NULL,  
  motifsPerRegion = 1  
)
```

**Arguments**

cogapsResult    result object from CoGAPS run  
 generanges     GRanges object corresponding to peaks in ATACseq data CoGAPS was run on  
 organism        organism name (e.g. "Homo sapiens")  
 genome          genome version to use (e.g. hg19, mm10)  
 scoreThreshold threshold for the most pattern defining peaks as per the PatternMarker statistic from the CoGAPS package. By default is NULL, in which case all Pattern defining peaks will be used for motif matching. Used to reduce compute time, as results are quite robust across thresholds  
 motifsPerRegion number of motifs to attempt to find within each peak

**Value**

list containing list of matched motifs, list of transcription factors, regulatory gene networks known for those TFs, functional annotations, summary showing how many times each TF was matched to a peak, and the downloaded set of motifs for the user to save for reproducibility

**Examples**

```

data("schepCogapsResult")
data(schepGranges)

motifResults = simpleMotifTFMatch(cogapsResult = schepCogapsResult,
  generanges = schepGranges, organism = "Homo sapiens",
  genome = "hg19", motifsPerRegion = 1)

```

---

subsetSchepData            *Small subset of the scATAC-seq data from Schep et al, 2017, Nature Methods paper.*

---

**Description**

Subset from the Schep et al data, used for examples in this package.

**Usage**

```
subsetSchepData
```

**Format**

A matrix with 5036 peaks and 600 cells in the order of the schepPeaks, schepCellTypes, and schepGranges data objects.

**Source**

[10.1038/nmeth.4401](https://doi.org/10.1038/nmeth.4401)

---

tfData

*List of human TFs and motifs from cisBP database*

---

**Description**

Information on human TFs and their corresponding DNA motifs

**Usage**

tfData

**Format**

Data frame with 95413 rows and 28 columns.

**Source**

<http://cisbp.cabr.utoronto.ca/>

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