

Package: MOMA (via r-universe)

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Title Multi Omic Master Regulator Analysis

Version 1.24.0

Description This package implements the inference of candidate master regulator proteins from multi-omics' data (MOMA) algorithm, as well as ancillary analysis and visualization functions.

Depends R (>= 4.0)

License GPL-3

Encoding UTF-8

LazyData true

BugReports <https://github.com/califano-lab/MOMA/issues>

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biocViews Software, NetworkEnrichment, NetworkInference, Network, FeatureExtraction, Clustering, FunctionalGenomics, Transcriptomics, SystemsBiology

Imports circlize, cluster, ComplexHeatmap, dplyr, ggplot2, graphics, grid, grDevices, magrittr, methods, MKmisc, MultiAssayExperiment, parallel, qvalue, RColorBrewer, readr, reshape2, rlang, stats, stringr, tibble, tidyr, utils

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Contents

cnvScoreStouffer	2
example.gbm.mae	3
gbm.pathways	3
gene.map	4
makeSaturationPlots	4
mapEntrez	5
mapHugo	6
mapScoresCnvBand	6
Moma-class	7
MomaConstructor	8
mutSig	9
sampleNameFilter	10
stoufferIntegrate	10
stoufferIntegrateDiggitt	11
Index	12

cnvScoreStouffer	<i>Integrate CNV scores</i>
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Description

Integrate CNV scores

Usage

```
cnvScoreStouffer(  
  mapping,  
  diggit.interactions,  
  cytoband = TRUE,  
  from.p = FALSE,  
  pos.nes.only = TRUE  
)
```

Arguments

mapping	a named vector of genomic locations/cytoband IDs. names are the gene names for each–i.e. a many to one mapping from HUGO or entrez IDs to cytoband location
diggit.interactions	list indexed by MR/TF name in Entrez Space each points to a named vector of NES / z-scores associated with entrez IDs for each interacting event.
cytoband	Boolean to use cytoband locations for computing final integrated score
from.p	Boolean, set TRUE if diggit.interaction values are p-values instead of z-scores
pos.nes.only	Boolean, only consider positive DIGGIT association scores when ranking candidate MRs (default=TRUE)

Value

A vector of z-scores, named by the Master Regulators in 'diggit.interactions'

example.gbm.mae

Glioblastoma (GBM) Example Dataset

Description

MultiAssayExperiment Object containing all the genomic assays needed to run the example code for MOMA

Usage

example.gbm.mae

Format

An MultiAssayExperiment object with 4 different sets of GBM assays

viper matrix of viper scores with samples in columns and regulators across the rows

mut matrix of samples and genes with potential mutations. 0 for no mutation, 1 for presence of some non-silent mutation

cnv matrix of samples and genes with copy number variant scores

gbm.pathways

Glioblastoma (GBM) Pathways

Description

Object containing information about the biological pathways that will be used in the analysis

Usage

gbm.pathways

Format

A list of lists named "cindy" and "preppi" respectively

cindy list of regulators, each with a set of modulators and p values representing their CINDY inferred association

preppi list of regulators, each with a set of potential binding partners and PREPPi inferred p values for probability of binding

gene.map

Gene Location Mapping

Description

Table used for converting between different forms of gene information. Downloaded from HGNC's custom download portal using the "Approved Symbol", "NCBI Gene ID", "Chromosome" and "Ensembl Gene ID" curated data options and only those with "Approved" status. Updated December 2019.

Usage

gene.map

Format

A Data frame with 4 columns

Gene.Symbol Approved Symbol gene name

Entrez.IDs NCBI Gene ID

Cytoband Chromosome location

Ensembl Ensembl gene ID

@source <https://www.genenames.org/download/custom/>

makeSaturationPlots

Main function to generate the summary plots of the analysis

Description

Main function to generate the summary plots of the analysis

Usage

```
makeSaturationPlots(
  momaObj,
  clustering.solution = NULL,
  important.genes = NULL,
  fCNV = NULL,
  max.events = 30
)
```

Arguments

`momaObj` : momaObj that has already run the saturationCalculation function
`clustering.solution` : clustering vector with sample names and cluster designations
`important.genes` : vector of gene names to prioritize when plotting. Can be general genes of interest, oncogenes, tumor suppressors etc
`fCNV` : vector of confirmed functional CNVs if calculated. Will filter for only those CNVs
`max.events` : maximum number of events to plot for the oncoplots

Value

object with both types of summary plot for each subtype

Examples

```
## Not run:
makeSaturationPlots(momaObj, max.events = 20)

## End(Not run)
```

mapEntrez	<i>Convert from entrez ids to hugo gene names</i>
-----------	---

Description

Convert from entrez ids to hugo gene names

Usage

```
mapEntrez(entrez.ids)
```

Arguments

`entrez.ids` : vector of entrez ids requires hugo2entrez to be loaded

Value

: vector of hugo gene names

See Also

[mapHugo](#)

Examples

```
mapEntrez(c("29974", "5728"))
```

mapHugo	<i>Convert from hugo gene names to entrez ids</i>
---------	---

Description

Convert from hugo gene names to entrez ids

Usage

```
mapHugo(hugo.ids)
```

Arguments

hugo.ids : vector of hugo gene names, requires hugo2entrez to be loaded

Value

: vector of entrez ids

See Also

[mapEntrez](#)

Examples

```
mapHugo(c("A1CF", "PTEN"))
```

mapScoresCnvBand	<i>Map scores to cytoband location</i>
------------------	--

Description

Map scores to cytoband location

Usage

```
mapScoresCnvBand(  
  mapping,  
  diggit.interactions,  
  from.p = FALSE,  
  pos.nes.only = TRUE  
)
```

Arguments

mapping	a named vector of genomic locations/cytoband IDs. names are the gene names for each–i.e. a many to one mapping from HUGO or entrez IDs to cytoband location
diggIt.interactions	list indexed by MR/TF name in Entrez Space
from.p	DIGGIT interactions are in p-value format instead of z-score (default=FALSE)
pos.nes.only	Only consider positive associations with NES scores (default=TRUE) each points to a named vector of NES / z-scores associated with entrez IDs for each interacting event.

Value

A list of input scores, now named by cytoband location

Moma-class	<i>MOMA Object</i>
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Description

Main class encapsulating the input data and logic of the MOMA algorithm

Fields

viper matrix of inferred activity score inferred by viper

mut binary mutation matrix 1 for presence of mutation, 0 for not, NA if not determined

cnv matrix of cnv values. Can be binary or a range.

fusions binary matrix of fusion events if applicable

pathways list of pathways/connections to consider as extra evidence in the analysis

gene.blacklist character vector of genes to not include because of high mutation frequency

output.folder character vector of location to save files if desired

gene.loc.mapping data frame of gene names, entrez ids and cytoband locations

nes field for saving Normalized Enrichment Matrices from the associate events step

interactions field for saving the MR-interactions list

clustering.results results from clustering are saved here

ranks results field for ranking of MRs based on event association analysis

hypotheses results field for saving events that have enough occurrences to be considered

genomic.saturation results field for genomic saturation analysis

coverage.summaryStats results field for genomic saturation analysis

checkpoints results field with the MRs determined to be the checkpoint for each cluster

sample.clustering field to save sample clustering vector. Numbers are cluster assignments, names are sample ids

Methods

```
Cluster(clus.eval = c("reliability", "silhouette"), use.parallel = FALSE, cores = 1)
  Cluster the samples after applying the MOMA weights to the VIPER scores

makeInteractions( genomic.event.types = c("amp", "del", "mut", "fus"), cindy.only = FALSE )
  Make interaction web for significant MRs based on their associated events

Rank( use.cindy = TRUE, genomic.event.types = c("amp", "del", "mut", "fus"), use.parallel = FALSE, cores = )
  Rank MRs based on DIGGIT scores and number of associated events

runDIGGIT(fCNV = NULL, cnvthr = 0.5, min.events = 4, verbose = FALSE) Run DIGGIT asso-
  ciation function to get associations for driver genomic events

saturationCalculation( clustering.solution = NULL, cov.fraction = 0.85, topN = 100, verbose = FALSE )
  Calculate the number of MRs it takes to represent the desired coverage fraction of events
```

MomaConstructor	<i>MOMA Constructor Function</i>
-----------------	----------------------------------

Description

Create MOMA Object from either a MultiAssayExperiment object or a list of assays. See vignette for more information on how to set up and run the MOMA object

Usage

```
MomaConstructor(
  x,
  pathways,
  gene.blacklist = NA_character_,
  output.folder = NA_character_,
  gene.loc.mapping = gene.map,
  viperAssay = "viper",
  mutMat = "mut",
  cnvMat = "cnv",
  fusionMat = "fusion"
)
```

Arguments

x	A MultiAssayExperiment object or list object with the following assays: (note: by default assays must have these exact names. Otherwise they can be changed using the viperAssay, mutMat, cnvMat and fusionMat parameters.)
viper	VIPER protein activity matrix with samples as columns and rows as protein IDs
mut	An indicator matrix (0/1) of mutation events with samples as columns and genes as rows
cnv	A matrix of CNV scores (typically SNP6 array scores from TCGA) with samples as columns and genes as rows

	fusion	An indicator matrix (0/1) of fusion events with samples as columns and genes as rows
pathways		A named list of lists. Each named list represents interactions between proteins (keys) and their associated partners
gene.blacklist		A vector of genes to exclude from the analysis
output.folder		Location to store output and intermediate results
gene.loc.mapping		A data.frame of band locations and Entrez IDs
viperAssay		name associated with the viper assay in the assay object
mutMat		name associated with the mutation matrix in the assay object
cnvMat		name associated with the cnv matrix in the assay object
fusionMat		name associated with the fusion matrix in the assay object

Value

an instance of class Moma

Examples

```
momaObj <- MomaConstructor(example.gbm.mae, gbm.pathways)
```

mutSig	<i>MutSig Blacklisted genes</i>
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Description

List of genes to not include in the DIGGIT mutation inference because they have been found to be mutated more often than expected by chance given background mutation processes.

Usage

```
mutSig
```

Format

A character vector of Entrez Gene IDs

Source

<https://software.broadinstitute.org/cancer/cga/mutsig>

sampleNameFilter	<i>Retain TCGA sample ids without the final letter designation ('A/B/C')</i>
------------------	--

Description

Retain TCGA sample ids without the final letter designation ('A/B/C')

Usage

```
sampleNameFilter(input, desired.len = 15)
```

Arguments

input	Matrix of expression or protein activity scores. Columns are sample names, rows are genes. Input can also just be an input vector of sample names.
desired.len	length to reduce strings to. Default is 15 because of TCGA naming conventions

Value

An identical matrix with new (shorter) column names, or a vector with the shortened names.

Examples

```
sample.names <- c("TCGA-14-1825-01A", "TCGA-76-4931-01B", "TCGA-06-5418-01A")
sampleNameFilter(sample.names)
```

stoufferIntegrate	<i>dispatch method for either CNV location corrected or SNV</i>
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Description

dispatch method for either CNV location corrected or SNV

Usage

```
stoufferIntegrate(interactions, cytoband.map = NULL)
```

Arguments

interactions	List of MR - Genomic Event interactions, inferred by DIGGIT
cytoband.map	Data.frame mapping Entrez.IDs to cytoband locations

Value

Z-scores for each MR

`stoufferIntegrateDiggit`*Use Stouffer's method to combine z-scores of DIGGIT interactions for each cMR protein.*

Description

This function combines only positively associated DIGGIT scores by default to create a cumulative DIGGIT score for each cMR.

Usage

```
stoufferIntegrateDiggit(interactions, from.p = FALSE, pos.nes.only = TRUE)
```

Arguments

<code>interactions</code>	A list indexed by TF, includes z-scores or p-values for each interacting event
<code>from.p</code>	Integrate p-values or z-scores (default z-scores; <code>from.p = FALSE</code>)
<code>pos.nes.only</code>	Use only positive NES scores to rank proteins (default <code>TRUE</code>)

Value

A list indexed by TF, a stouffer integrated z-score

Index

* datasets

- [example.gbm.mae](#), [3](#)
 - [gbm.pathways](#), [3](#)
 - [gene.map](#), [4](#)
 - [mutSig](#), [9](#)
- [cnvScoreStouffer](#), [2](#)
- [example.gbm.mae](#), [3](#)
- [gbm.pathways](#), [3](#)
- [gene.map](#), [4](#)
- [makeSaturationPlots](#), [4](#)
- [mapEntrez](#), [5](#), [6](#)
- [mapHugo](#), [5](#), [6](#)
- [mapScoresCnvBand](#), [6](#)
- [Moma \(Moma-class\)](#), [7](#)
- [Moma-class](#), [7](#)
- [MomaConstructor](#), [8](#)
- [mutSig](#), [9](#)
- [sampleNameFilter](#), [10](#)
- [stoufferIntegrate](#), [10](#)
- [stoufferIntegrateDiggit](#), [11](#)