

# Package ‘MOMA’

September 25, 2024

**Title** Multi Omic Master Regulator Analysis

**Version** 1.17.0

**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>

**RoxygenNote** 7.1.0

**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

**Suggests** BiocStyle, knitr, rmarkdown, testthat, viper

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/MOMA>

**git\_branch** devel

**git\_last\_commit** f2d9ee4

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-09-24

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<i>areaEnrich</i>	<i>aREA.enrich Compute aREA enrichment between all pairwise combinations of VIPER proteins and gene-level events</i>
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**Description**

*aREA.enrich* Compute aREA enrichment between all pairwise combinations of VIPER proteins and gene-level events

**Usage**

```
areaEnrich(events.mat, viper.mat, event.type, verbose)
```

**Arguments**

<code>events.mat</code>	A Binary 0/1 matrix with columns as samples, and rows as proteins
<code>viper.mat</code>	A VIPER network of inferred activity scores with columns as samples, and rows as proteins
<code>event.type</code>	Name of the event type for printing purposes
<code>verbose</code>	whether to print extra progress statements

**Value**

A matrix of enrichment scores with rows as event/gene names and columns as VIPER protein names

<i>associateEvents</i>	<i>Use 'aREA' to calculate the enrichment between each genomic event - VIPER inferred protein pair.</i>
------------------------	---

**Description**

Requires pre-computed VIPER scores and a binary events matrix. Will use only samples in both event and VIPER matrices.

**Usage**

```
associateEvents(
  viper.mat,
  events.mat,
  min.events = NA,
  whitelist = NA,
  event.type = c("Amplifications", "Deletions", "Mutations", "Fusions", NA),
  verbose
)
```

**Arguments**

vipermat	Pre-computed VIPER scores with samples as columns and proteins as rows
events.mat	Binary 0/1 events matrix with samples as columns and genes or events as rows
min.events	Only compute enrichment if the number of samples with these events is GTE to this
whitelist	Only compute associations for events in this list
event.type	Name of the event type being analyzed
verbose	whether to print extra progress statements

**Value**

A matrix of aREA scores, dimensions are nrow(events.mat) x nrow(vipermat)

---

checkGeneMap	<i>Check Gene Map</i>
--------------	-----------------------

---

**Description**

Check Gene Map

**Usage**

```
checkGeneMap(gene.loc.mapping)
```

**Arguments**

gene.loc.mapping	dataframe with gene names, entrez ids and cytoband locations
------------------	--

**Value**

nothing

---

checkList	<i>Check List of Assays</i>
-----------	-----------------------------

---

**Description**

Check List of Assays

**Usage**

```
checkList(assaylist)
```

**Arguments**

assaylist	list of assays (viper, cnv, mut and fusion)
-----------	---

**Value**

updated/filter assaylist obj

---

checkMAE	<i>Check MultiAssayExperiment</i>
----------	-----------------------------------

---

**Description**

Check MultiAssayExperiment

**Usage**

```
checkMAE(mae)
```

**Arguments**

mae	MultiAssayExperiment object
-----	-----------------------------

**Value**

updated/filtered MAE

---

checkPathways	<i>Check Pathways</i>
---------------	-----------------------

---

**Description**

Check Pathways

**Usage**

```
checkPathways(pathways, x, type)
```

**Arguments**

pathways	A named list of lists. Each named list represents interactions between proteins (keys) and their associated partners
x	the MAE or Assaylist
type	whether x is MAE or Assaylist

**Value**

nothing

---

clusterRange	<i>Cluster Range</i>
--------------	----------------------

---

### Description

This function generate an cluster structure with 'k' groups and computes the cluster reliability score where 'k' is a range of values

### Usage

```
clusterRange(
  dis,
  range = c(2, 100),
  step = 1,
  cores = 1,
  method = c("pam", "kmeans"),
  data = NULL
)
```

### Arguments

dis	Distance object
range	vector with start and end 'k'
step	Integer indicating the incremental number of clusters to add in each iteration
cores	Maximum number of CPU cores to use
method	Either 'pam' k-medoids or kmeans. Must supply the original data matrix if using kmeans
data	Original data matrix

### Value

list of cluster reliability scores by 'k', 'clustering' (the vector solution) and 'reliability' as well as 'medoids' labels

---

clusterReliability	<i>Cluster membership reliability estimated by enrichment analysis</i>
--------------------	--

---

### Description

This function estimates the cluster membership reliability using aREA

### Usage

```
clusterReliability(
  cluster,
  similarity,
  xlim = NULL,
  method = c("element", "cluster", "global")
)
```

**Arguments**

cluster	Vector of cluster memberships or list of cluster memberships
similarity	Similarity matrix
xlim	Optional vector of 2 components indicating the limits for computing AUC
method	Character string indicating the method to compute reliability, either by element, by cluster or global

**Value**

Reliability score for each element

---

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

---

**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'

---

conditionalModel	<i>Implements the conditional Bayes model to combine VIPER scores with diggit and pathway scores</i>
------------------	--

---

### Description

Implements the conditional Bayes model to combine VIPER scores with diggit and pathway scores

### Usage

```
conditionalModel(viper.scores, diggit.scores, pathway.scores)
```

### Arguments

viper.scores	numeric Vector
diggit.scores	List indexed by type char, with numeric score vectors in [0,R+] for each
pathway.scores	List, double indexed by each pathway dataset, then with type char. Each points to a numeric score vectors in [0,R+] for each

### Value

a named vector of empirical p-values for each protein/candidate Master Regulator

---

conditionalP	<i>Get the conditional p-value of a gene</i>
--------------	--

---

### Description

Get the conditional p-value of a gene

### Usage

```
conditionalP(gene.name, condition.on, x)
```

### Arguments

gene.name	Character
condition.on	named Vector of scores for the distribution we are conditioning ON
x	named Vector of scores for the dependent distribution

### Value

a numeric p-value between 0 and 1



---

empiricalP                      *Get the empirical p-value from a distribution (vector)*

---

### Description

Get the empirical p-value from a distribution (vector)

### Usage

```
empiricalP(gene.name, x)
```

### Arguments

gene.name	Character
x	named Vector of scores for the distribution

### Value

a numeric p-value between 0 and 1

---

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

---

fitCurvePercent	<i>Fit based on fractional overall coverage of genomic events</i>
-----------------	---

---

**Description**

Fit based on fractional overall coverage of genomic events

**Usage**

```
fitCurvePercent(sweep, frac = 0.85)
```

**Arguments**

sweep	Numeric vector of genomic coverage values, named by -k- threshold
frac	Fraction of coverage to use as a threshold (default .85 = 85 percent)

**Value**

The -k- integer where coverage is achieved

---

gbm.pathways	<i>Glioblastoma (GBM) Pathways</i>
--------------	------------------------------------

---

**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/>

---

`genomicPlotSmall`*Make small genomic plot*

---

**Description**

Make small genomic plot

**Usage**

```
genomicPlotSmall(input.df, fraction = 0.85, tissue.cluster = NULL)
```

**Arguments**

`input.df` : tissue.coverage.df with mean, k, fraction and unique events.

`fraction` : what fraction coverage to use for genomic curve threshold

`tissue.cluster` : which cluster subsample to look at

**Value**

output .png

---

getCoverage	<i>Get coverage of interactions</i>
-------------	-------------------------------------

---

**Description**

Get coverage of interactions

**Usage**

```
getCoverage(
  MomaObject,
  cMR.ranking,
  viper.samples,
  topN = 100,
  mutation.filter = NULL,
  verbose = FALSE
)
```

**Arguments**

MomaObject	A numeric vector with cluster membership, names are samples
cMR.ranking	A vector entrez IDs, in order
viper.samples	Calculate the genomic coverage only for these sample
topN	Compute coverage for only the top -N- Master Regulators
mutation.filter	Retain only mutation events in this (positive) list

**Value**

A list of lists, indexed by sample name, with coverage statistics for each sample

---

getDataFrame	<i>Helper function to get data frame for bar plot plot.events function</i>
--------------	--

---

**Description**

Helper function to get data frame for bar plot plot.events function

**Usage**

```
getDataFrame(
  data,
  highlight.genes,
  genomeBand_2_gene,
  max.muts = 10,
  max.cnv = 5
)
```

**Arguments**

data	data.frame with \$type, \$id, \$Freq per event
highlight.genes	genes to look for in mutations/cnv lists (if looking for specific genes because of prior knowledge)
genomeBand_2_gene	mapping of genomic location IDs to gene name: vector of HUGO gene ids, named by genomic loci
max.muts	maximum number of mutations to get per sample, default is 10
max.cnv	maximum number of cnvs to per sample, default is 5

**Value**

ordered data frame with each genomic event and it's frequency

---

```
getDiggItEmpiricalQvalues
```

*Compute the empirical q-values of each genomic-event/VIPER gene pair*

---

**Description**

Use against the background distribution of associations with a given set of 'null' VIPER genes (i.e. low activity TFs)

**Usage**

```
getDiggItEmpiricalQvalues(vipermat, nes, null.TFs, alternative = "both")
```

**Arguments**

vipermat	viper inferences matrix, samples are columns, rows are TF entrez gene IDs
nes	scores for each mutation (rows) against each TF (columns)
null.TFs	low-importance TFs used to calculate null distributions
alternative	Alternative defaults to 'both' : significant p-values can come from both sides of the null distribution

**Value**

A named list of qvalues for each TF/cMR protein. Each entry contains a vector of q-values for all associated events; names are gene ids

---

getEmpiricalQvals      *Get empirical qvals*

---

**Description**

Get empirical qvals

**Usage**

```
getEmpiricalQvals(test.statistics, null.statistics, alternative = "both")
```

**Arguments**

test.statistics      P-values generated from the test comparisons  
null.statistics      P-values generated under the null (permutation) model  
alternative      Optional : 1 or 2 tails used to generate the p-value

**Value**

A list with both the qvalues and empirical p-values from the supplied test and null stats

---

getPvalsMatrix      *Utility function*

---

**Description**

Utility function

**Usage**

```
getPvalsMatrix(corrected.scores)
```

**Arguments**

corrected.scores  
- corrected p-values processed by 'qvals' package

**Value**

A matrix of p-values for scores between genes/events (rows) and TFs (columns)

---

getSubtypeEventTables *Helper function to get subtype specific events*

---

**Description**

Helper function to get subtype specific events

**Usage**

```
getSubtypeEventTables(saturation.data, sample.clustering, checkpoints)
```

**Arguments**

saturation.data : genomic saturation object from MOMA. List indexed by cluster then sample then regulator with the number of events associated with each additional regulator

sample.clustering : clustering vector with sample names and cluster designations

checkpoints : from momaObj

**Value**

a table that has counts of how many times a particular event happens in a cluster

---

integrateFunction *Numerical integration of functions*

---

**Description**

Integrates numerically a function over a range using the trapezoid method

**Usage**

```
integrateFunction(f, xmin, xmax, steps = 100, ...)
```

**Arguments**

f : Function of 1 variable (first argument)

xmin : Number indicating the min x value

xmax : Number indicating the max x value

steps : Integer indicating the number of steps to evaluate

... : Additional arguments for f

**Value**

Number

---

integrateTZ	<i>Integration with trapezoid method</i>
-------------	--

---

**Description**

This function integrate over a numerical range using the trapezoid method

**Usage**

```
integrateTZ(x, y)
```

**Arguments**

x	Numeric vector of x values
y	Numeric vector of y values

**Value**

Number

---

makeCoverageDf	<i>Helper function for making the coverage dataframe</i>
----------------	--

---

**Description**

Helper function for making the coverage dataframe

**Usage**

```
makeCoverageDf(coverage.list, cutoff)
```

**Arguments**

coverage.list	: List indexed by sample name, contains mut/fus/amp/del interactions
cutoff	: number of regulators to include

**Value**

dataframe with each sample and which events are captured by the checkpoint mrs



---

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                *Convert from entrez ids to hugo gene names*

---

### 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

*Convert from hugo gene names to entrez ids*

---

**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

---

mergeData	<i>Helper function for mergeDataBySubtype</i>
-----------	---

---

**Description**

Helper function for mergeDataBySubtype

**Usage**

```
mergeData(coverage.range, topN)
```

**Arguments**

coverage.range	: genomic saturation for a particular subtype
topN	: max number of top regulators to search through

**Value**

dataframe with coverage data for genomic events

---

mergeDataBySubtype	<i>Create data frame from coverage data, including number of total events 'covered' and unique events</i>
--------------------	---

---

**Description**

Create data frame from coverage data, including number of total events 'covered' and unique events

**Usage**

```
mergeDataBySubtype(genomic.saturation, sample.clustering, topN = 100)
```

**Arguments**

genomic.saturation  
: data from genomic saturation function

sample.clustering  
: clustering vector with sample names and cluster designations

topN  
: number of regulators to look through. default is 100

**Value**

dataframe with coverage data for genomic events

---

mergeGenomicSaturation	<i>mergeGenomicSaturation Create data frame from coverage data, including number of total events 'covered' and unique events</i>
------------------------	--

---

**Description**

mergeGenomicSaturation Create data frame from coverage data, including number of total events 'covered' and unique events

**Usage**

```
mergeGenomicSaturation(coverage.range, topN)
```

**Arguments**

coverage.range List indexed by sample, then sub-indexed by # of master regulators, then by event type (mut/amp/del/fus). Holds all events by sample

topN Maximum number of master regulators to compute coverage

**Value**

A data frame with summary statistics for genomic saturation at each k

---

mergeLists	<i>Helper function</i>
------------	------------------------

---

**Description**

Helper function

**Usage**

```
mergeLists(l1, l2)
```

**Arguments**

l1	list 1
l2	list 2

**Value**

single merged list

---

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

---

**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 = 1 )
  Rank MRs based on DIGGIT scores and number of associated events
runDIGGIT(fCNV = NULL, cnvthr = 0.5, min.events = 4, verbose = FALSE) Run DIGGIT association 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.)
<b>viper</b>	VIPER protein activity matrix with samples as columns and rows as protein IDs
<b>mut</b>	An indicator matrix (0/1) of mutation events with samples as columns and genes as rows
<b>cnv</b>	A matrix of CNV scores (typically SNP6 array scores from TCGA) with samples as columns and genes as rows
<b>fusion</b>	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>
--------	---------------------------------

---

**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>

---

oncoprintPlot	<i>Function to plot genomic events in the style of oncoPrint/cBioPortal</i>
---------------	---

---

### Description

Function to plot genomic events in the style of oncoPrint/cBioPortal

### Usage

```
oncoprintPlot(  
  summary.vec,  
  snpmat.thisClus,  
  amps.thisClus,  
  dels.thisClus,  
  fusions.thisClus,  
  important.genes,  
  band2gene,  
  max.events,  
  k  
)
```

### Arguments

`summary.vec` : named vector of the counts, named 'Event name': 'Type' where type is 'mut', 'amp', 'del', 'fus'. Mutations are in Entrez ID Amp/Deletion CNV events are in genomic band location

`snpmat.thisClus` : SNP matrix subset to samples in current cluster

`amps.thisClus` : CNV matrix subset to samples in current cluster (just amplifications)

`dels.thisClus` : CNV matrix subset to samples in current cluster (just deletions)

`fusions.thisClus` : Fusion matrix subset to samples in current cluster

`important.genes` : well known genes to highlight in the analysis

`band2gene` : mapping of genomic location IDs to gene name: vector of HUGO gene ids, named by genomic location

`max.events` : maximum number of events to plot for the oncoplots

`k` : current cluster number

### Value

oncoprint event plot



---

 pathwayDiggItIntersect

*Combine DIGGIT inferences with pathway knowledge*


---

**Description**

Combine DIGGIT inferences with pathway knowledge

**Usage**

```
pathwayDiggItIntersect(diggIt.int, pathway, pos.nes.only = TRUE, cores = 1)
```

**Arguments**

diggIt.int	List of interactions between MRs - Genomic events, inferred by DIGGIT
pathway	- a list indexed by TF/MR entrez ID, contains the named vector of p-values for interactions
pos.nes.only	Only use positive associations between MR activity and presence of events (default = True)
cores	Number of cores to use if parallel is selected

**Value**

numeric vector, zscores for each TF/MR

---

 plotEvents

*Plot barchart of genomic events*


---

**Description**

Plot barchart of genomic events

**Usage**

```
plotEvents(
  summary.vec,
  highlight.genes = NULL,
  genomeBand_2_gene = NULL,
  samples.total,
  max.muts = 10,
  max.cnv = 5
)
```

**Arguments**

summary.vec : named vector of the counts, named 'Event name': 'Type' where type is 'mut', 'amp', 'del', 'fus'. Mutations are in Entrez ID Amp/Deletion CNV events are in genomic band location

highlight.genes : well known genes to highlight in the analysis in

genomeBand\_2\_gene : mapping of genomic location IDs to gene name: vector of HUGO gene ids, named by genomic loci

samples.total : number of samples in the subtype, used to calculate percentages

max.muts : maximum number of mutations to get per sample, default is 10

max.cnv : maximum number of cnvs to per sample, default is 5

**Value**

plot object

---

rea	<i>This function calculates an Enrichment Score of Association based on how the features rank on the samples sorted by a specific gene</i>
-----	--

---

**Description**

This function calculates an Enrichment Score of Association based on how the features rank on the samples sorted by a specific gene

**Usage**

```
rea(eset, regulon, minsize = 1, maxsize = Inf, event.type = NA, verbose)
```

**Arguments**

eset Numerical matrix

regulon A list with genomic features as its names and samples as its entries, indicating presence of event

minsize The minimum number of events to use when calculating enrichment

maxsize The maximum number of events to use when calculating enrichment

event.type Type of event being analyzed

verbose whether to print extra progress statements

**Value**

A list containing two elements:

**groups** Regulon-specific NULL model containing the enrichment scores

**ss** Direction of the regulon-specific NULL model

---

reaNULL	<i>This function generates the NULL model function, which computes the normalized enrichment score and associated p-value</i>
---------	---

---

**Description**

This function generates the NULL model function, which computes the normalized enrichment score and associated p-value

**Usage**

```
reaNULL(regulon, minsize = 1, maxsize = Inf)
```

**Arguments**

regulon	A list with genomic features as its names and samples as its entries
minsize	Minimum number of event (or size of regulon)
maxsize	Maximum number of event (or size of regulon)

**Value**

A list of functions to compute NES and p-value

---

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)
```

---

sampleOverlap	<i>The core function to compute which sample-specific alterations overlap with genomic events that are explained via DIGGIT.</i>
---------------	--

---

### Description

The core function to compute which sample-specific alterations overlap with genomic events that are explained via DIGGIT.

### Usage

```
sampleOverlap(
  MomaObject,
  viper.samples,
  selected.tfs,
  interaction.map,
  cnv.threshold = 0.5,
  mutation.filter = NULL,
  idx.range = NULL,
  verbose = FALSE
)
```

### Arguments

MomaObject	Object reference of momaRunner class
viper.samples	Sample vector to restrict sample-specific analysis to
selected.tfs	Transcription factors being analyzed
interaction.map	List object of events 'covered' by the supplied interactions of type mut/amp/del/fus
cnv.threshold	Numeric absolute value to threshold SNP6 and/or GISTIC or other CNV scores. Above that absolute value is considered a positive event.
mutation.filter	A vector of whitelisted mutation events, in entrez gene IDs
idx.range	Number of tfs to check for genomic saturation calculation, default is 1253
verbose	Output status during the run (default=FALSE)

### Value

A list of lists, indexed by sample name, with coverage statistics/data for each sample

---

sigInteractorsDIGGIT *Filter interactions from NES (DIGGIT) scores and corresponding background-corrected scores.*

---

### Description

Use this version in the Bayes model to rank TFs

### Usage

```
sigInteractorsDIGGIT(
  corrected.scores,
  nes.scores,
  cindy,
  p.thresh = 0.05,
  cindy.only = TRUE
)
```

### Arguments

corrected.scores	A list indexed by the genomic event/gene with corresponding pvals and qvals for each TF
nes.scores	Matrix with tfs as columns, rows are genomic events
cindy	CINDy algorithm output matrix
p.thresh	P-value threshold (default=0.05)
cindy.only	Consider only CINDy validated interactions (default=TRUE)

### Value

a list (indexed by VIPER protein) of significant genomic interactions and associated pvals over the background (null TF) model, and NES scores

---

sREA *Simple one-tail rank based enrichment analysis sREA (for cluster analysis)*

---

### Description

This function performs simple 1-tail rank based enrichment analysis

### Usage

```
sREA(signatures, groups)
```

### Arguments

signatures	Numeric matrix of signatures
groups	List containing the groups as vectors of sample names

**Value**

Matrix of Normalized Enrichment Zcores

---

stoufferIntegrate      *dispatch method for either CNV location corrected or SNV*

---

**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**

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

**Value**

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

---

subsetListInteractions

*Helper function: subset a list to the set of keys supplied return the names of interactions with positive values, in a list structure*

---

### Description

Helper function: subset a list to the set of keys supplied return the names of interactions with positive values, in a list structure

### Usage

```
subsetListInteractions(int.l, keys)
```

### Arguments

int.l	List of interactions, at each index this is a numeric named vector
keys	Keys used to reduce interactions

### Value

Returns a filtered list of interactions in the same format as the input

---

validDiggItInteractions

*Return a set of events 'covered' by specified cMR-event interactions*

---

### Description

Return a set of events 'covered' by specified cMR-event interactions

### Usage

```
validDiggItInteractions(interactions, gene.loc.mapping, selected.tfs)
```

### Arguments

interactions	List indexed by amp/mut/del/fus from cMRs to interacting events
gene.loc.mapping	Data.frame mapping entrezIDs to cytoband locations
selected.tfs	For each event type list, search within only these cMRS

### Value

a list of events 'covered' by the supplied interactions of type mut/amp/del/fus

---

viperGetSigTFS	<i>Calculate p-values from pseudo zscores / VIPER aREA scores, threshold</i>
----------------	--

---

**Description**

Calculate p-values from pseudo zscores / VIPER aREA scores, threshold

**Usage**

```
viperGetSigTFS(zscores, fdr.thresh = 0.05)
```

**Arguments**

zscores	Vector of normally distributed z-scores representing protein activities.
fdr.thresh	Threshold for false discovery rate, default is 0.05

**Value**

Get the names of proteins with significant z-scores, after multi-hypothesis correction

---

viperGetTFScores	<i>Function to normalize TF scores</i>
------------------	--

---

**Description**

Function to normalize TF scores

**Usage**

```
viperGetTFScores(vipermat, fdr.thresh = 0.05)
```

**Arguments**

vipermat	- matrix of VIPER scores with columns as samples, rows as protein names
fdr.thresh	- BH-FDR threshold (default 0.05 FDR rate)

**Value**

A vector of normalized z-scores, named by TF id



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