

Package ‘rmimp’

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Type Package

Title Predicting the impact of mutations on kinase-substrate phosphorylation

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Description MIMP is a machine learning method that predicts the impact of missense single-nucleotide variants (SNVs) on kinase-substrate interactions. MIMP analyzes kinase sequence specificities and predicts whether SNVs disrupt existing phosphorylation sites or create new sites. This helps discover mutations that modify protein function by altering kinase networks and provides insight into disease biology and therapy development.

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computeBinding	<i>Score wt and mt sequences for a pwm</i>
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Description

Score wt and mt sequences for a pwm

Usage

```
computeBinding(obj, mut_ss, mut_location, prob.thresh = 0.5,
  log2.thresh = 1)
```

Arguments

obj	MIMP object containing PWM, GMM parameters, and etc.
mut_ss	snvs data frame containing wt and mt sequences computed from SNVs function
mut_location	list of mutation locations
prob.thresh	Probability threshold of gains and losses. This value should be between 0.5 and 1.
log2.thresh	Threshold for the absolute value of log ratio between wild type and mutant scores. Anything less than this value is discarded (default: 1).

dohtml	<i>Helper function for results2html</i>
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Description

Helper function for results2html

Usage

```
dohtml(x, LOGO_DIR, HL_DIR, logoExt = ".svg", .webserver = F)
```

Arguments

x	Data frame resulting from mimp call.
LOGO_DIR	Directory containing sequence logo images.
HL_DIR	Directory containing overlays
logoExt	Extension of logo files
.webserver	Request coming from webserver?

dohtmlSh3

*Helper function for results2html and sh3 binding***Description**

Helper function for results2html and sh3 binding

Usage

```
dohtmlSh3(x, LOGO_DIR, HL_DIR, logoExt = ".svg", .webserver = F)
```

Arguments

x	Data frame resulting from mimp call.
LOGO_DIR	Directory containing sequence logo images.
HL_DIR	Directory containing overlays
logoExt	Extension of logo files
.webserver	Request coming from webserver?

domain_mimp

*Predict the impact of single variants on domains.***Description**

This function takes in mutation, sequence and phosphorylation data to predict the impact the mutation has on domains.

Usage

```
domain_mimp(muts, seqs, domain = "sh2", species = "human",
  terminal.range = 5, prob.thresh = 0.5, log2.thresh = 1,
  display.results = T, include.cent = F, model.data = "hconf")
```

Arguments

muts	Mutation data file: a space delimited text file OR data frame containing two columns (1) gene and (1) mutation. Example:
------	--

```
TP53      R282W
CTNNB1    S33C
CTNNB1    S37F
```

seqs	Sequence data file containing protein sequences in FASTA format OR named list
------	---

	of sequences where each list element is the uppercase sequence and the name of each element is that of the protein. Example: <code>list(GENEA="ARNDGH", GENE="YVRRHS")</code>
<code>domain</code>	Which binding domain to run mimp for
<code>terminal.range</code>	The number of amino acids used for predicting terminal domain binding.
<code>prob.thresh</code>	Probability threshold of gains and losses. This value should be between 0.5 and 1.
<code>log2.thresh</code>	Threshold for the absolute value of log ratio between wild type and mutant scores. Anything less than this value is discarded (default: 1).
<code>display.results</code>	If TRUE results are visualised in an html document after analysis is complete
<code>include.cent</code>	If TRUE, gains and losses caused by mutation in the central STY residue are kept. Scores of peptides with a non-STY central residue is given a score of 0 (default: FALSE).
<code>model.data</code>	Name of specificity model data to use, can be "hconf" : individual experimental kinase specificity models used to scan for rewiring events. For experimental kinase specificity models, grouped by family, set to "hconf-fam". Both are considered high confidence. For lower confidence predicted specificity models, set to "lconf". NOTE: Predicted models are purely speculative and should be used with caution

Value

The data is returned in a `data.frame` with the following columns:

<code>gene</code>	Gene with the rewiring event
<code>mut</code>	Mutation causing the rewiring event
<code>wt</code>	Sequence of the wildtype phosphosite (before the mutation). Score is NA if the central residue is not S, T or Y
<code>mt</code>	Sequence of the mutated phosphosite (after the mutation). Score is NA if the central residue is not S, T or Y
<code>score_wt</code>	Matrix similarity score of the wildtype phosphosite
<code>score_mt</code>	Matrix similarity score of the mutated phosphosite
<code>log_ratio</code>	Log2 ratio between mutant and wildtype scores. A high positive log ratio represents a high confidence gain-of-phosphorylation event. A high negative log ratio represents a high confidence loss-of-phosphorylation event. This ratio is NA for mutations that affect the central phosphorylation sites
<code>pwm</code>	Name of the kinase being rewired
<code>prob</code>	Joint probability of wild type sequence belonging to the foreground distribution and mutated sequence belonging to the background distribution, for loss and vice versa for gain.
<code>effect</code>	Type of rewiring event, can be "loss" or "gain"

Examples

```
# Get the path to example mutation data
mut.file = system.file("extdata", "sample_muts.tab", package = "rmimp")

# Get the path to example FASTA sequence data
seq.file = system.file("extdata", "sample_seqs.fa", package = "rmimp")

# View the files in a text editor
browseURL(mut.file)
browseURL(seq.file)

# Run rewiring analysis
results = domain_mimp(mut.file, seq.file, display.results=TRUE)

# Show head of results
head(results)
```

get_domain_mut_sites *Helper function for domain mimp*

Description

Helper function for domain mimp

Usage

```
get_domain_mut_sites(md, seqdata, mdata, flank)
```

predictKinasePhosphosites

Compute posterior probability of wild type phosphosites for kinases

Description

Compute posterior probability of wild type phosphosites for kinases

Usage

```
predictKinasePhosphosites(psites, seqs, model.data = "hconf",
  posterior_thresh = 0.8, intermediate = F, kinases)
```

Arguments

<code>psites</code>	phosphorylation data, see ?mimp for details
<code>seqs</code>	sequence data, see ?mimp for details
<code>model.data</code>	MIMP model used, see ?mimp for details
<code>posterior_thresh</code>	posterior probability threshold that the score belongs to the foreground distribution of the kinase, probabilities below this value are discarded (default 0.8)
<code>intermediate</code>	if TRUE intermediate MSS scores and likelihoods are reported (default FALSE)
<code>kinases</code>	vector of kinases used for the scoring (e.g. <code>c("AURKB", "CDK2")</code>), if this isn't provided all kinases will be used .

Value

The data is returned in a `data.frame` with the following columns:

<code>gene</code>	Gene with the rewiring event
<code>pos</code>	Position of the phosphosite
<code>wt</code>	Sequence of the wildtype phosphosite
<code>score_wt</code>	(intermediate value) matrix similarity score of sequence
<code>l.wt.fg</code>	(intermediate value) likelihood of score given foreground distribution
<code>l.wt.bg</code>	(intermediate value) likelihood of score given background distribution
<code>post.wt.fg</code>	posterior probability of score in foreground distribution
<code>post.wt.bg</code>	posterior probability of score in background distribution
<code>pwm</code>	Name of the predicted kinase
<code>pwm_fam</code>	Family/subfamily of the predicted kinase. If a kinase subfamily is available the family and subfamily will be separated by an underscore e.g. "DMPK_ROCK". If no subfamily is available, only the family is shown e.g. "GSK"

If no predictions were made, function returns NULL

Examples

```
# Get the path to example phosphorylation data
psite.file = system.file("extdata", "sample_phosphosites.tab", package = "rmimp")

# Get the path to example FASTA sequence data
seq.file = system.file("extdata", "sample_seqs.fa", package = "rmimp")

# Run for all kinases
results_all = predictKinasePhosphosites(psite.file, seq.file)

# Run for select kinases
results_select = predictKinasePhosphosites(psite.file, seq.file, kinases=c("AURKB", "CDK2"))
```

results2html	<i>Display MIMP results interactively in browser</i>
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Description

Display MIMP results interactively in browser

Usage

```
results2html(x, domain = "phos", max.rows = 5000)
```

Arguments

x	Data frame resulting from mimp call.
domain	Which binding domain to run mimp for
max.rows	If data contains more rows than this value, results won't be displayed.

scoreArrayRolling	<i>Get weight/probability for each amino acid in a sequence</i>
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Description

Gets weight/probability for the amino acid at each position of the sequence as an array.

Usage

```
scoreArrayRolling(seqs, pwm)
```

Arguments

seqs	One or more sequences to be processed
pwm	Position weight matrix

Examples

```
# No Examples
```

scoreWTSequence	<i>Score wt sequence using PWMs in the model</i>
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Description

Score wt sequence using PWMs in the model

Usage

```
scoreWTSequence(wt_seqs, central = T, domain = "phos", species = "human",
  model.data = "hconf", cores = 2)
```

Arguments

wt_seqs	A list of sequences to be scored
central	Whether the mutation site is at the central residue of the sequence
cores	Number of cores the function could use

site_mimp	<i>Predict the impact of single variants on phosphorylation.</i>
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Description

This function takes in mutation, sequence and phosphorylation data to predict the impact the mutation has on phosphorylation.

Usage

```
site_mimp(muts, seqs, site_type = "phos", species = "human", sites = NULL,
  terminal.range = 5, prob.thresh = 0.5, log2.thresh = 1,
  display.results = T, include.cent = F, model.data = "hconf")
```

Arguments

muts	Mutation data file: a space delimited text file OR data frame containing two columns (1) gene and (1) mutation. Example:
------	--

```
TP53      R282W
CTNNB1    S33C
CTNNB1    S37F
```

seqs	Sequence data file containing protein sequences in FASTA format OR named list of sequences where each list element is the uppercase sequence and the name of each element is that of the protein. Example: list(GENEA="ARNDGH",
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	GENEB="YVRRHS")						
prob.thresh	Probability threshold of gains and losses. This value should be between 0.5 and 1.						
log2.thresh	Threshold for the absolute value of log ratio between wild type and mutant scores. Anything less than this value is discarded (default: 1).						
display.results	If TRUE results are visualised in an html document after analysis is complete						
include.cent	If TRUE, gains and losses caused by mutation in the central STY residue are kept. Scores of peptides with a non-STY central residue is given a score of 0 (default: FALSE).						
model.data	Name of specificity model data to use, can be "hconf" : individual experimental kinase specificity models used to scan for rewiring events. For experimental kinase specificity models, grouped by family, set to "hconf-fam". Both are considered high confidence. For lower confidence predicted specificity models, set to "lconf". NOTE: Predicted models are purely speculative and should be used with caution						
psites	Phosphorylation data file: a space delimited text file OR data frame containing two columns (1) gene and (1) positions of phosphorylation sites. Example: <table data-bbox="714 919 906 1010"> <tr><td>TP53</td><td>280</td></tr> <tr><td>CTNNB1</td><td>29</td></tr> <tr><td>CTNNB1</td><td>44</td></tr> </table>	TP53	280	CTNNB1	29	CTNNB1	44
TP53	280						
CTNNB1	29						
CTNNB1	44						

Value

The data is returned in a `data.frame` with the following columns:

gene	Gene with the rewiring event
mut	Mutation causing the rewiring event
psite_pos	Position of the phosphosite
mut_dist	Distance of the mutation relative to the central residue
wt	Sequence of the wildtype phosphosite (before the mutation). Score is NA if the central residue is not S, T or Y
mt	Sequence of the mutated phosphosite (after the mutation). Score is NA if the central residue is not S, T or Y
score_wt	Matrix similarity score of the wildtype phosphosite
score_mt	Matrix similarity score of the mutated phosphosite
log_ratio	Log2 ratio between mutant and wildtype scores. A high positive log ratio represents a high confidence gain-of-phosphorylation event. A high negative log ratio represents a high confidence loss-of-phosphorylation event. This ratio is NA for mutations that affect the central phosphorylation sites
pwm	Name of the kinase being rewired

pwm_fam	Family/subfamily of kinase being rewired. If a kinase subfamily is available the family and subfamily will be separated by an underscore e.g. "DMPK_ROCK". If no subfamily is available, only the family is shown e.g. "GSK"
nseqs	Number of sequences used to construct the PWM. PWMs constructed with a higher number of sequences are generally considered of better quality.
prob	Joint probability of wild type sequence belonging to the foreground distribution and mutated sequence belonging to the background distribution, for loss and vice versa for gain.
effect	Type of rewiring event, can be "loss" or "gain"

Examples

```
# Get the path to example mutation data
mut.file = system.file("extdata", "sample_muts.tab", package = "rmimp")

# Get the path to example FASTA sequence data
seq.file = system.file("extdata", "sample_seqs.fa", package = "rmimp")

# View the files in a text editor
browseURL(mut.file)
browseURL(seq.file)

# Run rewiring analysis
results = mimp(mut.file, seq.file, display.results=TRUE)

# Show head of results
head(results)
```

SNVs

Find non-central variants (SNVs)

Description

Given mutation data, find variants that exist in the flanking regions of the psite

Usage

```
SNVs(md, seqdata, flank)
```

Arguments

md	Mutation data as data frame of two columns (1) name of gene or protein (2) mutation in the format X123Y, where X is the reference amino acid and Y is the alternative amino acid.
seqdata	Phosphorylation data as a data frame of two columns (1) name of gene or protein (2) Position of the phosphorylated residue
flank	Number of amino acids flanking the site to be considered

Examples

```
# No examples
```

```
terminal_mut_sites_getter
```

Helper function for domain mimp

Description

Helper function for domain mimp

Usage

```
terminal_mut_sites_getter(terminal.range)
```

```
trainModel
```

Train GMM model and return as a list to be used later. If file is passed, the model will also be save to a .mimp file.

Description

Train GMM model and return as a list to be used later. If file is passed, the model will also be save to a .mimp file.

Usage

```
trainModel(pos.dir, neg.dir, kinase.domain = F, cores = 2, file = NULL,
  threshold = 10, min.auc = 0.65, priors, residues_groups = c("S|T", "Y"))
```

Arguments

pos.dir	the path to the directory contains positive entries
neg.dir	the path to the directory contains negative entries
kinase.domain	Whether the domain to be trained is a kinase domain.
cores	(optional) the number of CPU cores that can be used to train the model
file	(optional) the path to save the model
threshold	(optional) the minimum number of scores needed for each domain to train the model
min.auc	(optional) the minimum number of AUC needed for each domain to train the model
priors	Named character vector containing priors of amino acids.
residues_groups	a vector of regular expressions used to group kinases by central residue they target; if a sequence does not have a central residue matching a group chosen from modified.residues by the algorithm (based on PWM), the sequence will be discarded.

Value

a GMM model

Examples

No examples

tSNVs

Find terminal variants (tSNVs)

Description

Given mutation data, find variants that exist in the flanking regions of the psite

Usage

tSNVs(md, seqdata, terminal)

Arguments

md	Mutation data as data frame of two columns (1) name of gene or protein (2) mutation in the format X123Y, where X is the reference amino acid and Y is the alternative amino acid.
seqdata	Phosphorylation data as a data frame of two columns (1) name of gene or protein (2) Position of the phosphorylated residue
terminal	Number of amino acids flanking the site to be considered

Examples

No examples