

Package ‘Pirat’

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Type Package

Title Precursor or Peptide Imputation under Random Truncation

Description Pirat enables the imputation of missing values (either MNARs or MCARs) in bottom-up LC-MS/MS proteomics data using a penalized maximum likelihood strategy. It does not require any parameter tuning, it models the instrument censorship from the data available. It accounts for sibling peptides correlations and it can leverage complementary transcriptomics measurements.

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Contents

envPirat	2
estimate_gamma	3
estimate_psi_df	3
get_indexes_embedded_protos	4
impute_block_llk_reset	4
impute_block_llk_reset_PG	6
impute_from_blocks	8
pipeline_llkimpute	9
pirat2SE	10
plot2hists	11
plot_pep_correlations	12
rm_pg_from_idx_merge_pg	13
roppers	13
split_large_pg	14
split_large_pg_PG	14
subbouyssie	15
subropers	16
wrapper_pipeline_llkimpute	16
Index	18

envPirat	<i>Creates a BasiliskEnvironment class</i>
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Description

Please refer to the package ‘basilisk’.

Usage

```
envPirat
```

Format

An object of class BasiliskEnvironment of length 1.

Value

An instance of the class ‘BasiliskEnvironment’

estimate_gamma	<i>Estimate missingness parameters Gamma</i>
----------------	--

Description

Estimate missingness parameters Gamma

Usage

```
estimate_gamma(pep.ab.table, mcar = FALSE)
```

Arguments

pep.ab.table	The peptide or precursor abundance matrix, with molecules in columns and samples in row.
mcar	If TRUE, forces gamma_1 = 0.

Value

A list of the containing missingness parameters gamma_0 and gamma_1.

Examples

```
data(subbouyssie)
estimate_gamma(subbouyssie$peptides_ab)
```

estimate_psi_df	<i>Estimate psi and degrees of freedom</i>
-----------------	--

Description

Estimate the inverse-gamma parameters from the distribution of observed peptide variances in an abundance table.

Usage

```
estimate_psi_df(pep.ab.table)
```

Arguments

pep.ab.table	The peptide or precursor abundance matrix, with molecules in columns and samples in row (can contain missing values).
--------------	---

Value

List containing estimated fitted hyperparameters df (degrees of freedom) and psi (inverse scale).

Examples

```
data(subbouyssie)
obj <- subbouyssie
# Keep only fully observed peptides
obs2NApep <- obj$peptides_ab[ ,colSums(is.na(obj$peptides_ab)) <= 0]
estimate_psi_df(obs2NApep)
```

get_indexes_embedded_prots

Indexes of PGs embedded in each others

Description

Returns indexes of PGs that are embedded in others

Usage

```
get_indexes_embedded_prots(adj)
```

Arguments

adj An adjacency matrix between precursors/peptides and PGs

Value

A vector of indices

Examples

```
data(subbouyssie)
get_indexes_embedded_prots(subbouyssie$adj)
```

impute_block_llk_reset

Impute each PG.

Description

Imputes each PG separately and return the results for each PG.

Usage

```
impute_block_llk_reset(
  data.pep.rna.crop,
  psi,
  pep_ab_or = NULL,
  df = 1,
  nu_factor = 2,
  max_pg_size = NULL,
  min.pg.size2imp = 1,
  verbose = FALSE,
  ...
)
```

Arguments

data.pep.rna.crop	A list representing dataset
psi	Inverse scale parameter for IW prior of peptides abundances
pep_ab_or	In case we impute a dataset with pseudo-MVS, we can provide the ground truth abundance table, such that imputation will be done only for pseudo-MVs. This will accelerate imputation algorithm.
df	Estimate degree of freedom of the IG distribution fitted on observed variance.
nu_factor	Multiplication factor on degree of freedom. 2 by default.
max_pg_size	Maximum PGs size authorized for imputation. PG size is plitted if its size is above this threshold.
min.pg.size2imp	Minimum PG size to impute after splitting. PGs for which size is greater are not imputed. Should be lower than max_pg_size to have effect.
verbose	A boolean (FALSE as default) which indicates whether to display more details on the process
...	Additional arguments

Value

A list containing imputation results for each PG, the execution time, and adjacency matrix between peptides and PGs corresponding to the imputed PGs.

Examples

```
Py_impute_block_llk_reset <- function(data.pep.rna.mis, psi) {
  proc <- basilisk::basiliskStart(envPirat)

  func <- basilisk::basiliskRun(proc,
    fun = function(arg1, arg2) {

      imputed_pgs <- Pirat::impute_block_llk_reset(arg1, arg2)
      imputed_pgs
    }, arg1 = data.pep.rna.mis, arg2 = psi)

  basilisk::basiliskStop(proc)
  func
}
```

```

data(subbouyssie)
obs2NApep <- subbouyssie$peptides_ab[, colSums(is.na(subbouyssie$peptides_ab)) <= 0]
res_hyperparam <- estimate_psi_df(obs2NApep)
psi <- res_hyperparam$psi
Py_impute_block_llk_reset(subbouyssie, psi)

```

```
impute_block_llk_reset_PG
```

Impute each PG.

Description

Imputes each PG separately accounting for transcriptomic dataset and returns the results for each PG.

Usage

```

impute_block_llk_reset_PG(
  data.pep.rna.crop,
  psi,
  psi_rna,
  rna.cond.mask,
  pep.cond.mask,
  pep_ab_or = NULL,
  df = 2,
  nu_factor = 1,
  max_pg_size = NULL,
  max.pg.size2imp = 1,
  verbose = FALSE,
  ...
)

```

Arguments

<code>data.pep.rna.crop</code>	A list representing dataset, with mRNA normalized counts and mRNA/PGs adjacency table.
<code>psi</code>	Inverse scale parameter for IW prior of peptides abundances
<code>psi_rna</code>	Inverse scale parameter for IW prior of mRNA abundances
<code>rna.cond.mask</code>	Vector of size equal to the number of samples in mRNA abundance table, containing indices of conditions of each sample.
<code>pep.cond.mask</code>	Vector of size equal to the number of samples in peptide abundance table, containing indices of conditions of each sample.
<code>pep_ab_or</code>	In case we impute a dataset with pseudo-MVS, we can provide the ground truth abundance table, such that imputation will be done only for pseudo-MVs. This will accelerate imputation algorithm.
<code>df</code>	Estimate degree of freedom of the IG distribution fitted on observed variance.

<code>nu_factor</code>	Multiplication factor on degree of freedom. 2 by default.
<code>max_pg_size</code>	Maximum PGs size authorized for imputation. PG size is plitted if its size is above this threshold.
<code>max.pg.size2imp</code>	Maximum PG size to impute after splitting. PGs for which size is greater are not imputed. Should be lower than <code>max_pg_size</code> to have effect.
<code>verbose</code>	A boolean (FALSE as default) which indicates whether to display more details ont the process
<code>...</code>	Additional parameters

Value

A list containing imputation results for each PG, the execution time, and adjacency matrix between peptides and PGs corresponding to the imputed PGs.

Examples

```
Py_impute_block_llk_reset_PG <- function(data.pep.rna.crop, ...) {
  proc <- basilisk::basiliskStart(envPirat)

  func <- basilisk::basiliskRun(proc,
    fun = function(arg1, ...) {
      Pirat::impute_block_llk_reset_PG(arg1, ...)
    }, arg1 = data.pep.rna.crop, ...)
  basilisk::basiliskStop(proc)
  func
}

data(subroppers)
obj <- subroppers
# Keep only fully observed peptides
obs2NApep <- obj$peptides_ab[ ,colSums(is.na(obj$peptides_ab)) <= 0]
res_hyperparam_pep = estimate_psi_df(obs2NApep)
psi_pep <- res_hyperparam_pep$psi
obs2NArna <- obj$rnas_ab[ ,colSums(obj$rnas_ab == 0) <= 0]
res_hyperparam_rna = estimate_psi_df(obs2NArna)
psi_rna <- res_hyperparam_rna$psi
# paired proteomic transcriptomic setting
cond_mask <- seq(nrow(obj$peptides_ab))
imputed_pgs <- Py_impute_block_llk_reset_PG(
  data.pep.rna.crop = obj,
  psi = psi_pep,
  psi_rna = psi_rna,
  rna.cond.mask = cond_mask,
  pep.cond.mask = cond_mask)
```

impute_from_blocks	<i>Impute abundance table from PGs results</i>
--------------------	--

Description

From imputation results in each PG and the associate adjacency peptide/PG matrix, imputes the original abundance table. .

Usage

```
impute_from_blocks(logs.blocks, data.pep.rna, idx_blocks = NULL)
```

Arguments

logs.blocks	List of PGs imputation results, that also contains related peptide/PGs adjacency matrix.
data.pep.rna	List representing the dataset not yet imputed
idx_blocks	Indices of PGs for which imputation results should be integrated

Value

The original peptide abundance table with imputed values.

Examples

```
Py_impute_block_llk_reset <- function(data.pep.rna.mis, psi) {
  proc <- basilisk::basiliskStart(envPirat)

  func <- basilisk::basiliskRun(proc,
    fun = function(arg1, arg2) {

      imputed_pgs <- Pirat::impute_block_llk_reset(arg1, arg2)
      imputed_pgs
    }, arg1 = data.pep.rna.mis, arg2 = psi)

  basilisk::basiliskStop(proc)
  func
}

data(subbouyssie)
obj <- subbouyssie
# Keep only fully observed peptides
obs2NApep <- obj$peptides_ab[, colSums(is.na(obj$peptides_ab)) <= 0]
res_hyperparam <- estimate_psi_df(obs2NApep)
psi <- res_hyperparam$psi
imputed_pgs <- Py_impute_block_llk_reset(obj, psi)
impute_from_blocks(imputed_pgs, obj)
```

pipeline_llkimpute *Pirat imputation function*

Description

Imputation pipeline of Pirat. First, it creates PGs. Then, it estimates parameters of the penalty term (that amounts to an inverse-Wishart prior). Second, it estimates the missingness mechanism parameters. Finally, it imputes the peptide/precursor-level dataset with desired extension.

Usage

```
my_pipeline_llkimpute(data.pep.rna.mis, ...)
```

```
pipeline_llkimpute(
  data.pep.rna.mis,
  pep.ab.comp = NULL,
  alpha.factor = 2,
  rna.cond.mask = NULL,
  pep.cond.mask = NULL,
  extension = c("base", "2", "T", "S"),
  mcar = FALSE,
  degenerated = FALSE,
  max.pg.size.pirat.t = 1,
  verbose = FALSE
)
```

Arguments

data.pep.rna.mis	Parameter 'data.pep.rna.mis' of the function 'pipeline_llkimpute()'
...	Additional parameters for the function 'pipeline_llkimpute()'
pep.ab.comp	The pseudo-complete peptide or precursor abundance matrix, with samples in row and peptides or precursors in column. Useful only in mask-and-impute experiments, if one wants to impute solely peptides containing pseudo-MVs.
alpha.factor	Factor that multiplies the parameter alpha of the penalty described in the original paper.
rna.cond.mask	Vector of indexes representing conditions of samples of mRNA table, only mandatory if extension == "T". For paired proteomic and transcriptomic tables, should be c(1:n_samples).
pep.cond.mask	Vector of indexes representing conditions of samples of mRNA table, only mandatory if extension == "T". For paired proteomic and transcriptomic tables, should be c(1:n_samples).
extension	If NULL (default), classical Pirat is applied. If "2", only imputes PGs containing at least 2 peptides or precursors, and remaining peptides are left unchanged. If "S", Pirat-S is applied, considering sample-wise correlations only for singleton PGs. If "T", Pirat-T is applied, thus requiring rnas_ab and adj_rna_pg in list data.pep.rna.mis , as well as non-NULL rna.cond.mask and pep.cond.mask . Also, the maximum size of PGs for which transcriptomic data can be used is controlled with max.pg.size.pirat.t .

<code>mcar</code>	If TRUE, forces <code>gamma_1 = 0</code> , thus no MNAR mechanism is considered.
<code>degenerated</code>	If TRUE, applies Pirat-Degenerated (i.e. its univariate alternative) as described in original paper. Should not be TRUE unless for experimental purposes.
<code>max.pg.size.pirat.t</code>	When <code>extension == "T"</code> , the maximum PG size for which transcriptomic information is used for imputation.
<code>verbose</code>	A boolean (FALSE as default) which indicates whether to display more details on the process

Value

The imputed `**data.pep.rna.mis$peptides_ab**` table.

The imputed `**data.pep.rna.mis$peptides_ab**` table.

NA

See Also

`[pipeline_llkimpute()]`

Examples

```
# Pirat classical mode
data(subbouyssie)
myResult <- my_pipeline_llkimpute(subbouyssie)

# Pirat with transcriptomic integration for singleton PGs
data(subroppers)
nsamples = nrow(subroppers$peptides_ab)
myResult <- my_pipeline_llkimpute(subroppers,
  extension = "T",
  rna.cond.mask = seq(nsamples),
  pep.cond.mask = seq(nsamples),
  max.pg.size.pirat.t = 1)

## Not run:
myResult <- pipeline_llkimpute(subbouyssie)

## End(Not run)
```

pirat2SE

COnvert Pirat dataset to SummarizedExperiment

Description

This function converts the original dataset structure into a `SummarizedExperiment` .

Usage

```
pirat2SE(peptides_ab, adj, mask_prot_diff = NULL, mask_pep_diff = NULL)
```

Arguments

peptides_ab	the peptide or precursor abundance matrix to impute, with samples in row and peptides or precursors in column;
adj	a n_peptide x n_protein adjacency matrix between peptides and proteins containing 0 and 1, or TRUE and FALSE. Can contain: **rnas_ab** , the mRNA normalized count matrix, with samples in row and mRNAs in column; **adj_rna_pg** , a n_mrna x n_protein adjacency matrix n_mrna and proteins containing 0 and 1, or TRUE and FALSE;
mask_prot_diff	(Optional) boolean vector of size equal to the number of proteins, indicating whether proteins are ground truth differentially abundant (typically in spike-in benchmark datasets).
mask_pep_diff	(Optional) boolean vector of size equal to the number of peptides, indicating whether peptides are ground truth differentially abundant (typically in spike-in benchmark datasets).

Value

An instance of the class ‘SummarizedExperiment’

Examples

```
data(subbouyssie)
peptides_ab <- subbouyssie$peptides_ab
adj <- subbouyssie$adj
mask_prot_diff <- subbouyssie$mask_prot_diff
mask_pep_diff <- subbouyssie$mask_pep_diff
obj <- pirat2SE(peptides_ab, adj, mask_prot_diff, mask_pep_diff )
obj
```

plot2hists

Plot 2 histograms

Description

Plot 2 histograms on the same graph.

Usage

```
plot2hists(
  d1,
  d2,
  name1 = "name1",
  name2 = "name2",
  titlename = "myTitle",
  xlab = "",
  freq = TRUE
)
```

Arguments

d1	vector of values for the first histogram
d2	vector of values for the first histogram
name1	Label for first histogram
name2	Label for 2nd histogram
titlename	Title of figure
xlab	X-axis label
freq	If True, bins heights correspond to raw counts, otherwise bins are normalized.

Value

A plot

Examples

```
v1 <- 1:10
v2 <- 5:25
plot2hists(v1, v2)
```

plot_pep_correlations *Empirical density of peptide correlations*

Description

Plot empirical densities of correlations between peptides within PG and at random, estimated by gaussian kernel. Note that only correlations between fully observed peptides are considered here.

Usage

```
plot_pep_correlations(pep.data, titlename = NULL, xlabel = "Correlations")
```

Arguments

pep.data	List representing dataset
titlename	Title of the graph displayed
xlabel	Label of x-axis

Value

The ggplot2 graph

Examples

```
data(subbouyssie)
plot_pep_correlations(subbouyssie, 'test')
```

rm_pg_from_idx_merge_pg

Remove PGs by index and merge

Description

Remove PG by index and merge transcripts (if transcriptomic information is available) of PG included in one another (under condition that they have peptide). Then it removes transcripts without PG. Do not remove peptides that are left without PG.

Usage

```
rm_pg_from_idx_merge_pg(l_pep_rna, pg_idx)
```

Arguments

l_pep_rna	A list representing dataset, formatted as in pipeline_llkimpute function
pg_idx	Vector of indices

Value

A list representing dataset.

Examples

```
data(ropers)
idxs_emb_prot = get_indexes_embedded_prots(ropers$adj)
ropers_wo_emb_prot = rm_pg_from_idx_merge_pg(ropers, idxs_emb_prot)
```

ropers

Ropers dataset

Description

This dataset corresponds to ‘Ropers2021’ dataset, described in Pirat article.

Format

A list containing: - peptides_ab: numeric matrix of precursors log2 abundances. - adj: adjacency matrix between peptides and PGs - rnas_ab: numeric matrix of gene expression log2 counts from mRNA analysis. - adj_rna_pg: adjacency matrix between genes and PGs

Value

A dataset

References

Ropers, D., Couté, Y., Faure, L., Ferré, S., Labourdette, D., Shabani, A., Trouilh, L., Vasseur, P., Corre, G., Ferro, M., Teste, M. A., Geiselmann, J., & de Jong, H. (2021). Multiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. *ACS Synthetic Biology*, 10(11), 2910–2926. https://doi.org/10.1021/ACSSYNBIO.1C00115/SUPPL_FILE/SB1C00115_SI_010.ZIP

split_large_pg	<i>Split too large PGs</i>
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Description

Randomly splits PGs with too many peptides/precursors, while keeping other PGs untouched. The new PGs created all have size equal to size_max. Hence, some peptides can be duplicated in the new PGs created.

Usage

```
split_large_pg(adj, size_max)
```

Arguments

adj	Adjacency matrix between peptides and PGs.
size_max	Maximum PG size desired.

Value

New adjacency matrix between peptides and PGs.

Examples

```
data(subbouyssie)
split.obj <- split_large_pg(subbouyssie$adj, 5)
```

split_large_pg_PG	<i>Splits too large PGs in proteogenomics context</i>
-------------------	---

Description

Randomly splits PGs with too many peptides/precursors, while keeping other PGs untouched, and adapts adjacency matrix between mRNA and PGs accordingly. The new PGs created all have size equal to size_max (including peptides and mRNAs). Hence, some peptides and mRNA can be duplicated in the new PGs.

Usage

```
split_large_pg_PG(adj, size_max, adj_rna_pg)
```

Arguments

adj	Adjacency matrix between peptides and PGs.
size_max	Maximum PG size desired.
adj_rna_pg	Adjacency matrix between mRNA and PGs.

Value

List containing new adjacency matrix between peptides and PGs, and new adjacency matrix between mRNA and PGs.

Examples

```
data(subrovers)
split.obj <- split_large_pg_PG(subrovers$adj, 5, subrovers$adj_rna_pg)
```

subbouyssie	<i>Sub-Bouyssie dataset</i>
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Description

This dataset is extracted from the original ‘Bouyssie2020’ dataset mentioned in Pirat article, where only 5 PGs were randomly selected.

Format

A list containing: - peptides_ab: numeric matrix of peptide (or precursors) log2 abundances. - adj: adjacency matrix between peptides and PGs.

Value

A dataset

References

Bouyssié, D., Hesse, A. M., Mouton-Barbosa, E., Rompais, M., MacRon, C., Carapito, C., Gonzalez De Peredo, A., Couté, Y., Dupierris, V., Burel, A., Menetrey, J. P., Kalaitzakis, A., Poisat, J., Romdhani, A., Burlet-Schiltz, O., Cianférani, S., Garin, J., & Bruley, C. (2020). Proline: an efficient and user-friendly software suite for large-scale proteomics. *Bioinformatics*, 36(10), 3148–3155. <https://doi.org/10.1093/BIOINFORMATICS/BTAA118>

subropers

Sub-Ropers dataset

Description

This dataset is extracted from the original ‘Ropers2021’ dataset described in Pirat article, where only 10 PGs were randomly selected.

Format

A list containing: - peptides_ab: numeric matrix of peptide (or precursors) log2 abundances. - adj: adjacency matrix between peptides and PGs - rnas_ab: numeric matrix of gene expression log2 counts from mRNA analysis. - adj_rna_pg: adjacency matrix between genes and PGs

Value

A dataset

References

Ropers, D., Couté, Y., Faure, L., Ferré, S., Labourdette, D., Shabani, A., Trouilh, L., Vasseur, P., Corre, G., Ferro, M., Teste, M. A., Geiselmann, J., & de Jong, H. (2021). Multiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. ACS Synthetic Biology, 10(11), 2910–2926. https://doi.org/10.1021/ACSSYNBIO.1C00115/SUPPL_FILE/SB1C00115_SI_010.ZIP

wrapper_pipeline_llkimpute

Imputation method using SummarizedExperiment dataset

Description

This function imputes data from an instance of the SummarizedExperiment structure data. After a conversion step, it calls the function ‘my_pipeline_llkimpute’.

Usage

```
wrapper_pipeline_llkimpute(se, ...)
```

Arguments

se	An instance of the class SummarizedExperiment
...	Additional arguments to pass to ‘my_pipeline_llkimpute()’

Value

See my_pipeline_llkimpute() function

Examples

```
data(subbouyssie)
obj <- pirat2SE(subbouyssie$peptides_ab, subbouyssie$adj,
subbouyssie$mask_prot_diff, subbouyssie$mask_pep_diff )
res <- wrapper_pipeline_llkimpute(obj)
```

Index

- * **datasets**
 - envPirat, [2](#)
 - roppers, [13](#)
 - subbouyssie, [15](#)
 - subroppers, [16](#)
- * **data**
 - roppers, [13](#)
 - subbouyssie, [15](#)
 - subroppers, [16](#)
- envPirat, [2](#)
- estimate_gamma, [3](#)
- estimate_psi_df, [3](#)
- get_indexes_embedded_prots, [4](#)
- impute_block_llk_reset, [4](#)
- impute_block_llk_reset_PG, [6](#)
- impute_from_blocks, [8](#)
- my_pipeline_llkimpute
 - (pipeline_llkimpute), [9](#)
- pipeline_llkimpute, [9](#)
- pirat2SE, [10](#)
- plot2hists, [11](#)
- plot_pep_correlations, [12](#)
- rm_pg_from_idx_merge_pg, [13](#)
- roppers, [13](#)
- split_large_pg, [14](#)
- split_large_pg_PG, [14](#)
- subbouyssie, [15](#)
- subroppers, [16](#)
- wrapper_pipeline_llkimpute, [16](#)