

# Package ‘HERON’

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**Title** Hierarchical Epitope pROtein biNDing

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**Description** HERON is a software package for analyzing peptide binding array data. In addition to identifying significant binding probes, HERON also provides functions for finding epitopes (string of consecutive peptides within a protein). HERON also calculates significance on the probe, epitope, and protein level by employing meta p-value methods. HERON is designed for obtaining calls on the sample level and calculates fractions of hits for different conditions.

**License** GPL (>= 3)

**URL** <https://github.com/Ong-Research/HERON>

**BugReports** <https://github.com/Ong-Research/HERON/issues>

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HERON-package	<i>HERON: Hierarchical Epitope pROtein biNDing</i>
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## Description

HERON is a software package for analyzing peptide binding array data. In addition to identifying significant binding probes, HERON also provides functions for finding epitopes (string of consecutive peptides within a protein). HERON also calculates significance on the probe, epitope, and protein level by employing meta p-value methods. HERON is designed for obtaining calls on the sample level and calculates fractions of hits for different conditions.

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## See Also

Useful links:

- <https://github.com/Ong-Research/HERON>
- Report bugs at <https://github.com/Ong-Research/HERON/issues>

---

addSequenceAnnotations	<i>Add Sequence Annotations for Epitopes</i>
------------------------	----------------------------------------------

---

## Description

Add Sequence Annotations for Epitopes

## Usage

```
addSequenceAnnotations(eds)
```

## Arguments

eds	HERONEpitopeDataSet with probe_meta in metadata()
-----	---------------------------------------------------

**Value**

HERONEpitopeDataSet with the rowData() set with sequence annotations

**Examples**

```
data(heffron2021_wuhan)
pval_seq_res <- calcCombPValues(heffron2021_wuhan)
pval_pr_res <- convertSequenceDSToProbeDS(pval_seq_res)
calls_res <- makeProbeCalls(pval_pr_res)
segments_res <- findEpitopeSegments(calls_res, "unique")
epval_res <- calcEpitopePValues(calls_res, segments_res)
epval_res <- addSequenceAnnotations(epval_res)
```

---

calcCombPValues	<i>Calculate p-values using the "exprs" assay</i>
-----------------	---------------------------------------------------

---

**Description**

Calculate p-values using the "exprs" assay

**Usage**

```
calcCombPValues(
  obj,
  colData_in = NULL,
  t_sd_shift = NA,
  t_abs_shift = NA,
  t_paired = FALSE,
  z_sd_shift = 0,
  use = "both",
  p_adjust_method = "BH"
)
```

**Arguments**

obj	HERONSequenceDataSet or HERONProbeDataSet
colData_in	optional column DataFrame (default: NULL => colData(obj))
t_sd_shift	standard deviation shift for differential test
t_abs_shift	absolute shift for differential test
t_paired	run paired analysis
z_sd_shift	standard deviation shift for global test
use	use global-test ("z"), differential-test ("t"), or both ("both")
p_adjust_method	method for adjusting p-values

**Value**

HERONSequenceDataSet/HERONProbeDataSet with the pvalue assay added

**Examples**

```
data(heffron2021_wuhan)
seq_pval_res <- calcCombPValues(heffron2021_wuhan)
```

---

calcEpitopePValues      *Calculate epitope-level p-values*

---

**Description**

Calculate epitope-level p-values

**Usage**

```
calcEpitopePValues(
  probe_pds,
  epitope_ids,
  metap_method = "wmax1",
  p_adjust_method = "BH"
)
```

**Arguments**

probe\_pds      HERONProbeDataSet with the "pvalue" assay  
epitope\_ids    vector of epitope ids  
metap\_method   meta p-value method to use (see below)  
p\_adjust\_method      what p.adjust method to use.

**Details**

The meta p-value methods supported by calcEpitopePValues are: min\_bonf\*, min\*, max\*, fisher/sumlog, hmp/harmonicmeanp, wilkinsons\_min1/tippets, wilkinsons\_min2/wmin2, wilkinsons\_min3, wilkinsons\_min4, wilkinsons\_min5, wilkinsons\_max1/wmax1, wilkinsons\_max2/wmax2, and cct.

When choosing a p-value method, keep in mind that the epitope p-value should be one that requires most of the probe p-values to be small (e.g. \*wmax1\*) Other p-value methods such as the\*cct\* and the \*hmp\* have been shown to be more accurate with p-value that have dependencies.

**Value**

HERONEpitopeDataSet with "pvalue" and "padj" assays

**See Also**

[stats::p.adjust()] for p\_adjust\_parameter.

**Examples**

```
data(heffron2021_wuhan)
pval_seq_res <- calcCombPValues(heffron2021_wuhan)
pval_pr_res <- convertSequenceDSToProbeDS(pval_seq_res)
calls_res <- makeProbeCalls(pval_pr_res)
segments_res <- findEpitopeSegments(calls_res, "unique")
epval_res <- calcEpitopePValues(calls_res, segments_res)
```

---

calcProbePValuesTPaired

*Calculate Probe p-values using a differential paired t-test*

---

**Description**

Calculate Probe p-values using a differential paired t-test

**Usage**

```
calcProbePValuesTPaired(
  probe_mat,
  colData_in,
  sd_shift = NA,
  abs_shift = NA,
  debug = FALSE
)
```

**Arguments**

probe_mat	numeric matrix or data.frame of values
colData_in	design data.frame
sd_shift	standard deviation shift to use when calculating p-values. Either sd_shift or abs_shift should be set
abs_shift	absolute shift to use when calculating p-values.
debug	print debugging information

**Value**

matrix of p-values on the post columns defined in the colData matrix. Attributes of the matrix are:

pars - data.frame parameters used in the paired t-test for each row (e.g. df, sd)

mapping - data.frame of mapping used for pre-post column calculation  
diff\_mat - data.frame containing the post-pre differences for each sample (column) and probe (row)

**Examples**

```

data(heffron2021_wuhan)
colData_wu <- colData(heffron2021_wuhan)
pre_idx = which(colData_wu$visit == "pre")
## Make some samples paired
colData_post = colData_wu[colData_wu$visit == "post",]
new_ids = rownames(colData_post)[seq_len(5)]
colData_wu$ptid[pre_idx[seq_len(5)]] = new_ids
exprs <- assay(heffron2021_wuhan, "exprs")
pval_res <- calcProbePValuesTPaired(exprs, colData_wu)

```

---

calcProbePValuesTUnpaired

*Calculate Probe p-values using a differential unpaired t-test*

---

**Description**

Calculate Probe p-values using a differential unpaired t-test

**Usage**

```
calcProbePValuesTUnpaired(probe_mat, colData_in, sd_shift = NA, abs_shift = NA)
```

**Arguments**

probe_mat	numeric matrix or data.frame of values
colData_in	design data.frame
sd_shift	standard deviation shift to use when calculating p-values Either sd_shift or abs_shift should be set
abs_shift	absolute shift to use when calculating p-values

**Value**

matrix of p-values on the post columns defined in the colData matrix

**Examples**

```

data(heffron2021_wuhan)
colData_wu <- colData(heffron2021_wuhan)
pval_res <- calcProbePValuesTUnpaired(assay(heffron2021_wuhan), colData_wu)

```

---

calcProteinPValues     *Calculate protein-level p-values*

---

**Description**

Calculate protein-level p-values

**Usage**

```
calcProteinPValues(epitope_ds, metap_method = "wmin1", p_adjust_method = "BH")
```

**Arguments**

epitope_ds	HERONEpitopeDataSet with the "pvalue" assay
metap_method	meta p-value method to use
p_adjust_method	p.adjust method to use

**Details**

see calcEpitopePValues for a list of meta p-value methods supported by HERON. the protein should be one that requires at least one of the epitope p-values to be small (e.g. wmax1).

**Value**

HERONProteinDataSet with the "pvalue" and "p adj" assays

**See Also**

[stats::p.adjust()] for p\_adjust\_parameter.

[calcEpitopePValues()] for meta p-value methods

**Examples**

```
data(heffron2021_wuhan)
pval_seq_res <- calcCombPValues(heffron2021_wuhan)
pval_pr_res <- convertSequenceDSToProbeDS(pval_seq_res)
calls_res <- makeProbeCalls(pval_pr_res)
segments_res <- findEpitopeSegments(calls_res, "unique")
epval_res <- calcEpitopePValues(calls_res, segments_res)
ppval_res <- calcProteinPValues(epval_res)
```



---

catSequences	<i>Concatenate sequences together based upon their start positions. Assumes the probe sequences have an overlap.</i>
--------------	----------------------------------------------------------------------------------------------------------------------

---

**Description**

Concatenate sequences together based upon their start positions. Assumes the probe sequences have an overlap.

**Usage**

```
catSequences(positions, sequences)
```

**Arguments**

positions	start positions of probes in protein
sequences	probe sequences of probes

**Value**

concatenated sequence (character)

**Examples**

```
positions <- c(1,2)
sequences <- c("MSGASFEFGVFPYL", "SGSASFEFGVFPYL")
catSequences(positions, sequences)
```

---

```
convertSequenceDSToProbeDS
```

*Convert HERONSequenceDataSet to HERONProbeDataSet*

---

**Description**

Convert HERONSequenceDataSet to HERONProbeDataSet

**Usage**

```
convertSequenceDSToProbeDS(seq_ds, probe_meta)
```

**Arguments**

seq_ds	a HERONSequenceDataSet object
probe_meta	optional data.frame with the PROBE_SEQUENCE, PROBE_ID columns the probe meta data frame can be provided within the metadata()\$probe_meta or as a argument to the function. The argument supersedes the metadata list.

**Value**

HERONProbeDataSet

**Examples**

```
data(heffron2021_wuhan)
probe_ds <- convertSequenceDSToProbeDS(heffron2021_wuhan)
probe_meta <- metadata(heffron2021_wuhan)$probe_meta
probe_ds <- convertSequenceDSToProbeDS(heffron2021_wuhan, probe_meta)
```

---

findBlocksProbeT      *Find Blocks of consecutive probes*

---

**Description**

This function will find blocks of consecutive probes within the passed probe parameter

**Usage**

```
findBlocksProbeT(
  probes,
  protein_tiling,
  proteins = getProteinLabel(probes),
  starts = getProteinStart(probes)
)
```

**Arguments**

probes                vector of probe identifiers of the format c(Prot1;1, ... Prot1;10)  
protein\_tiling        tiling of the associated proteins  
proteins              associated proteins to probes (cache speed up)  
starts                associated starts from probes (cache speed up)

**Value**

data.frame with the Protein, Start, Stop, and Number.Of.Probes columns

**Examples**

```
findBlocksProbeT(c("A;1", "A;2", "A;3", "B;2", "B;3", "C;10", "A;5", "A;6"))
```

---

findBlocksT	<i>Find consecutive probes</i>
-------------	--------------------------------

---

**Description**

Find consecutive probes

**Usage**

```
findBlocksT(prot_df, protein_tiling)
```

**Arguments**

prot\_df            data.frame with the Protein and Starting position of the probe  
protein\_tiling    tiling for information for each protein

**Value**

data.frame with the Protein, Start, Stop, and Number.Of.Probes columns

**Examples**

```
probes = c("A;1", "A;2", "A;3", "A;5", "A;6", "A;8")  
prot_df = data.frame(  
  Protein = getProteinLabel(probes),  
  Pos = getProteinStart(probes)  
)  
findBlocksT(prot_df)
```

---

findEpitopeSegments	<i>Find Epitopes from probe stats and calls.</i>
---------------------	--------------------------------------------------

---

**Description**

Find Epitopes from probe stats and calls.

**Usage**

```
findEpitopeSegments(  
  PDS_obj,  
  segment_method = "unique",  
  segment_score_type = "binary",  
  segment_dist_method = "hamming",  
  segment_cutoff = "silhouette"  
)
```

**Arguments**

**PDS\_obj**           HERONProbeDataSet with pvalues and calls in the assay  
**segment\_method**   which epitope finding method to use (binary or zscore, applies for hclust or skater)  
**segment\_score\_type**           which type of scoring to use for probes  
**segment\_dist\_method**           what kind of distance score method to use  
**segment\_cutoff**   for clustering methods, what cutoff to use (either numeric value or 'silhouette')

**Value**

a vector of epitope identifiers or segments found

**Examples**

```

data(heffron2021_wuhan)
seq_pval_res <- calcCombPValues(heffron2021_wuhan)
pr_pval_res <- convertSequenceDSToProbeDS(seq_pval_res)
pr_calls_res <- makeProbeCalls(pr_pval_res)
segments_res <- findEpitopeSegments(pr_calls_res)
  
```

---

getEpitopeID

*Create EpitopeID from protein, first and last probes*

---

**Description**

Create EpitopeID from protein, first and last probes

**Usage**

```
getEpitopeID(protein, start, stop)
```

**Arguments**

**protein**           vector of proteins  
**start**             vector of first probe protein start positions  
**stop**              vector of last probe protein start positions

**Value**

vector of epitope ids

**Examples**

```
getEpitopeID("A", 1, 2)
```

---

`getEpitopeIDsToProbeIDs`*Get probe ids from a vector of epitope ids*

---

**Description**

Get probe ids from a vector of epitope ids

**Usage**

```
getEpitopeIDsToProbeIDs(epitope_ids, tiling = 1)
```

**Arguments**

`epitope_ids`     vector of epitope identifiers  
`tiling`            tiling of probes across proteins

**Value**

data.frame of epitope\_to\_probe mappings

**Examples**

```
getEpitopeIDsToProbeIDs(c("A_1_5", "C_8_12"))
```

---

`getEpitopeProbeIDs`*Get the vector of probes from an epitope id*

---

**Description**

Get the vector of probes from an epitope id

**Usage**

```
getEpitopeProbeIDs(epitope_id, tiling = 1)
```

**Arguments**

`epitope_id`     EpitopeID to obtain probes from  
`tiling`            Tiling of the probes across the protein (default 1)

**Value**

vector of probe\_ids that are contained within the epitope

**Examples**

```
getEpitopeProbeIDs("A_1_5")
```

---

getEpitopeProtein      *Obtain Protein Id from Epitope ID*

---

**Description**

Format of EpitopeID is A\_B\_C, where A is the protein label B is the protein start position of the first probe in the epitope and C is the protein start position of the last probe in the epitope.

**Usage**

```
getEpitopeProtein(epitope_ids)
```

**Arguments**

epitope\_ids      vector of epitope identifier character strings

**Value**

vector of protein labels

**Examples**

```
getEpitopeProtein("Prot1_1_5")
```

---

getEpitopeStart      *Obtain first probe's protein start position from Epitope ID*

---

**Description**

Obtain first probe's protein start position from Epitope ID

**Usage**

```
getEpitopeStart(epitope_ids)
```

**Arguments**

epitope\_ids      vector of epitope ids

**Value**

vector of integers indicating first probe start positions in the epitope(s)

**Examples**

```
getEpitopeStart("Prot1_1_5")
```

---

getEpitopeStop	<i>Obtain last probe's protein start position from EpitopeID</i>
----------------	------------------------------------------------------------------

---

**Description**

Obtain last probe's protein start position from EpitopeID

**Usage**

```
getEpitopeStop(epitope_ids)
```

**Arguments**

epitope\_ids      vector of epitope ids

**Value**

vector of integers indicating the last probe protein start position

**Examples**

```
getEpitopeStop("Prot1_1_5")
```

---

getKofN	<i>Get K of N statistics from an experiment with padj and calls</i>
---------	---------------------------------------------------------------------

---

**Description**

Calculates the number of samples (K), the frequency of samples (F), and the percentage of samples (P) called. If the colData DataFrame contains a condition column with at least two conditions, then a K, F, and P is calculated for each condition and the results are reported as separate columns.

**Usage**

```
getKofN(obj)
```

**Arguments**

obj                      HERON Dataset with a "calls" assay

**Value**

DataFrame with K (#calls), F (fraction calls), P (

**Examples**

```
data(heffron2021_wuhan)
seq_pval_res <- calcCombPValues(heffron2021_wuhan)
pr_pval_res <- convertSequenceDSToProbeDS(seq_pval_res)
pr_calls_res <- makeProbeCalls(pr_pval_res)
getKofN(pr_calls_res)
```

---

getProteinLabel      *Get Protein Label from Probe*

---

**Description**

Get Protein Label from Probe

**Usage**

```
getProteinLabel(probes)
```

**Arguments**

probes              vector of probes (i.e. c("A;1", "A;2"))

**Value**

vector of strings indicating the protein associated with the respective probes

**Examples**

```
getProteinLabel("A;1")
getProteinLabel("B;2")
getProteinLabel(c("A;1", "B;2"))
```

---

getProteinStart      *Get the amino-acid starting position of the probe within the protein.*

---

**Description**

Get the amino-acid starting position of the probe within the protein.

**Usage**

```
getProteinStart(probes)
```

**Arguments**

probes              vector of probes (i.e. c("A;1", "A;2"))



**Value**

starting locations of the probes with their associated proteins

**Examples**

```
getProteinStart("A;1")
getProteinStart("B;2")
getProteinStart(c("A;1", "B;2"))
```

---

getProteinTiling	<i>Get Protein Tiling</i>
------------------	---------------------------

---

**Description**

Given a set of probes, estimate the tiling of the probes across the protein. Usually, you will want to calculate this on all the probes available in the dataset.

**Usage**

```
getProteinTiling(probes, return.vector = TRUE)
```

**Arguments**

probes            vector of probes (i.e. A;1, A;2)  
return.vector    Return result as vector or return as data.frame

**Value**

For each protein, the estimating tiling (spacing) of the probes across the amino acid sequence.

**Examples**

```
getProteinTiling(c("A;1", "A;2", "A;3", "B;2", "B;3", "C;1", "C;3"))
```

---

heffron2021_wuhan	<i>SARS CoV-2 Wuhan Peptide Binding Array Data</i>
-------------------	----------------------------------------------------

---

**Description**

A subset of data from the paper <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8245122/> publication.

**Usage**

```
data(heffron2021_wuhan)
```

**Format**

## 'heffron2021\_wuhan' A HERONSequenceDataSet with and "exprs" assay DataFrame with 1945 rows and 60 columns. Each column is a pre-processed binding signal from a serum sample peptide array set for the SARS-CoV-2. The matrix is a subset of the full matrix and contains sequences from the membrane, envelope, surface (spike), and nucleocapsid proteins.

The metadata()\$probe\_meta is a data frame with 1945 rows and 6 columns. The columns are POSITION - starting position of probe within protein, PROBE\_SEQUENCE - amino acid sequence of probe, SEQ\_ID - protein identifier SEQ\_NAME - name of protein, PROBE\_ID - combination of protein identifier and starting position, e.g. prot1;5.

The colData() is a DataFrame with 60 rows and 2 columns. The columns are SampleName - name of the sample, visit - either pre or post, ptid - subject id, and condition - all COVID

**Value**

HERONSequenceDataSet

**Source**

<[https://github.com/Ong-Research/UW\\_Adult\\_Covid-19](https://github.com/Ong-Research/UW_Adult_Covid-19)>

---

HERONEpitopeDataSet-class

*HERONEpitopeDataSet object and constructors*

---

**Description**

HERONEpitopeDataSet is a subclass of SummarizedExperiment used to hold assay information on the epitope-level

**Usage**

```
HERONEpitopeDataSet(pvalue, ...)
```

**Arguments**

pvalue	calculate epitope p-value matrix
...	arguments provided to SummarizedExperiment, including metadata

**Value**

HERONEpitopeDataSet object

**Examples**

```
pval <- matrix(runif(100), ncol=4)
HERONEpitopeDataSet(pvalue = pval)
```

---

HERONProbeDataSet-class

*HERONProbeDataSet object and constructors*

---

**Description**

HERONProbeDataSet is a subclass of RangedSummarizedExperiment used to hold assay information on the probe level

**Usage**

```
HERONProbeDataSet(...)
```

**Arguments**

... arguments provided to SummarizedExperiment, including metadata.

**Value**

HERONProbeDataSet object

**Examples**

```
pds <- HERONProbeDataSet()
```

---

HERONProteinDataSet-class

*HERONProteinDataSet object and constructors*

---

**Description**

HERONProteinDataSet is a subclass of SummarizedExperiment used to hold assay information on the protein-level

**Usage**

```
HERONProteinDataSet(pvalue, ...)
```

**Arguments**

pvalue calculated protein p-value matrix  
... arguments provided to SummarizedExperiment, including metadata

**Value**

HERONProteinDataSet object

**Examples**

```
pval <- matrix(runif(100), ncol=4)
HERONProteinDataSet(pvalue = pval)
```

---

HERONSequenceDataSet-class

*HERONSequenceDataSet object and constructors*

---

**Description**

HERONSequenceDataSet is a subclass of SummarizedExperiment, used to store the expression values, intermediate calculations, and results of a differential binding code on the sequence-level.

**Usage**

```
HERONSequenceDataSet(exprs, ...)
```

**Arguments**

exprs	binding values with rows as sequences and columns as samples
...	arguments provided to SummarizedExperiment, including metadata metadata can contain a probe DataFrame, that maps sequences (column PROBE_SEQUENCE) to probe identifiers ( column PROBE_ID)

**Value**

HERONSequenceDataSet object

**Examples**

```
exprs <- matrix(seq_len(100), ncol=4)
colnames(exprs) <- c("C1", "C2", "C3", "C4")
sds <- HERONSequenceDataSet(exprs = exprs)
```

---

log2Transform	<i>log2 transform the "exprs" assay</i>
---------------	-----------------------------------------

---

**Description**

log2 transform the "exprs" assay

**Usage**

```
log2Transform(se)
```

**Arguments**

se SummarizedExperiment with "exprs" assay

**Value**

SummarizedExperiment with "exprs" assay log2 transformed

**Examples**

```
data(heffron2021_wuhan)
assay(heffron2021_wuhan, "exprs") <- 2^assay(heffron2021_wuhan, "exprs")
res <- log2Transform(heffron2021_wuhan)
```

---

makeEpitopeCalls	<i>Make Epitope Calls</i>
------------------	---------------------------

---

**Description**

Make Epitope Calls

**Usage**

```
makeEpitopeCalls(epi_ds, padj_cutoff = 0.05, one_hit_filter = TRUE)
```

**Arguments**

epi\_ds HERONEpitopeDataSet with pvalue assay  
 padj\_cutoff p-value cutoff to use  
 one\_hit\_filter filter one hit epitopes?

**Value**

HERONEpitopeDataSet with calls assay added

**Examples**

```
data(heffron2021_wuhan)
seq_pval_res <- calcCombPValues(heffron2021_wuhan)
pr_pval_res <- convertSequenceDSToProbeDS(seq_pval_res)
pr_calls_res <- makeProbeCalls(pr_pval_res)
epi_segments_uniq_res <- findEpitopeSegments(
  PDS_obj = pr_calls_res,
  segment_method = "unique"
)
epi_padj_uniq <- calcEpitopePValues(
  probe_pds = pr_calls_res,
  epitope_ids = epi_segments_uniq_res,
  metap_method = "wilkinsons_max1"
)
makeEpitopeCalls(epi_padj_uniq)
```

---

makeProbeCalls	<i>Making Probe-level Calls</i>
----------------	---------------------------------

---

**Description**

makeProbeCalls returns call information on a HERONProbeDataSet using the "padj" assay

**Usage**

```
makeProbeCalls(pds, padj_cutoff = 0.05, one_hit_filter = TRUE)
```

**Arguments**

pds	HERONProbeDataSet with the "padj" assay
padj_cutoff	cutoff to use
one_hit_filter	filter out one-hit probes?

**Value**

HERONProbeDataSet with the "calls" assay added

**Examples**

```
data(heffron2021_wuhan)
pval_seq_res <- calcCombPValues(heffron2021_wuhan)
pval_probe_res <- convertSequenceDSToProbeDS(pval_seq_res)
calls_res <- makeProbeCalls(pval_probe_res)
```

---

makeProteinCalls	<i>Make Protein-level Calls</i>
------------------	---------------------------------

---

**Description**

Make Protein-level Calls

**Usage**

```
makeProteinCalls(prot_ds, padj_cutoff = 0.05, one_hit_filter = FALSE)
```

**Arguments**

prot_ds	HERONProteinDataSet with the "padj" assay
padj_cutoff	cutoff to use
one_hit_filter	use the one-hit filter?

**Value**

HERONProteinDataSet with the "calls" assay added

**Examples**

```
data(heffron2021_wuhan)
seq_pval_res <- calcCombPValues(heffron2021_wuhan)
pr_pval_res <- convertSequenceDSToProbeDS(seq_pval_res)
pr_calls_res <- makeProbeCalls(pr_pval_res)
epi_segments_uniq_res <- findEpitopeSegments(
  PDS_obj = pr_calls_res,
  segment_method = "unique"
)
epi_padj_uniq <- calcEpitopePValues(
  probe_pds = pr_calls_res,
  epitope_ids = epi_segments_uniq_res,
  metap_method = "wilkinsons_max1"
)
prot_padj_uniq <- calcProteinPValues(
  epitope_ds = epi_padj_uniq,
  metap_method = "tippetts"
)
prot_calls <- makeProteinCalls(prot_padj_uniq)
```

---

min\_max

*Cap vector at minimum/maximum values*


---

**Description**

Cap vector at minimum/maximum values

**Usage**

```
min_max(val, min.value, max.value)
```

**Arguments**

val	vector of values to cap
min.value	minimum value
max.value	maximum value

**Value**

vector of capped values

**Examples**

```
min_max(10, 1, 5)
```

---

oneHitEpitopes      *Find One-hit epitopes*

---

**Description**

Find One-hit epitopes

**Usage**

```
oneHitEpitopes(sample_epitopes)
```

**Arguments**

sample\_epitopes      logical epitope matrix from makeCalls

**Value**

vector of one-hit, one-probe epitopes

**Examples**

```
hit_mat = data.frame(  
  row.names = c("A_1_1", "A_2_2", "A_3_3", "A_4_4"),  
  sample1 = c(TRUE, FALSE, FALSE, TRUE),  
  sample2 = c(TRUE, TRUE, FALSE, FALSE),  
  sample3 = c(TRUE, TRUE, FALSE, FALSE)  
)  
oneHitEpitopes(hit_mat)
```

---

oneHitProbes      *Find one hit probes*

---

**Description**

Find one hit probes

**Usage**

```
oneHitProbes(sample_probes)
```

**Arguments**

sample\_probes      logical probe matrix from makeCalls

**Value**

vector of probes that are one-hits



**Examples**

```
hit_mat <- data.frame(
  row.names = c("A;1", "A;2", "A;3", "A;4"),
  sample1 = c(TRUE, FALSE, FALSE, TRUE),
  sample2 = c(TRUE, TRUE, FALSE, FALSE),
  sample3 = c(TRUE, TRUE, FALSE, FALSE)
)
oneHitProbes(hit_mat)
```

---

oneProbeEpitopes      *Indicate which epitopes are just one probe.*

---

**Description**

Indicate which epitopes are just one probe.

**Usage**

```
oneProbeEpitopes(epitope_ids)
```

**Arguments**

epitope\_ids      vector of epitope ids

**Value**

vector of logical indicating epitopes that are one probe

**Examples**

```
oneProbeEpitopes(c("A_1_1", "B_1_1", "C_1_2"))
```

---

probeHitSupported      *Find probe hits with a consecutive probe or another sample*

---

**Description**

Find probe hits with a consecutive probe or another sample

**Usage**

```
probeHitSupported(hit_mat)
```

**Arguments**

hit\_mat              matrix of logical values that indicate a hit with a TRUE value

**Value**

matrix of logical values indicate that the TRUE hit is supported by a consecutive probe hit in the sample sample or the within another sample

---

pvalue\_to\_zscore      *Convert p-value matrix to a z-score matrix*

---

**Description**

Convert p-value matrix to a z-score matrix

**Usage**

```
pvalue_to_zscore(mat.in, one.sided = TRUE, log.p = FALSE, inf.zscore = 16)
```

**Arguments**

mat.in	matrix of p-values
one.sided	p-values one-sided
log.p	are p-values log transformed?
inf.zscore	infinite z-scores are capped to this value

**Value**

matrix of z-scores

**Examples**

```
mat <- matrix(runif(100), nrow=10)
rownames(mat) <- paste0("A;", seq_len(nrow(mat)))
pvalue_to_zscore(mat)
```

---

quantileNormalize      *Normalize the exprs assay using quantile normalization*

---

**Description**

Normalize the exprs assay using quantile normalization

**Usage**

```
quantileNormalize(se)
```

**Arguments**

se	SummarizedExperiment with exprs assay
----	---------------------------------------

**Value**

SummarizedExperiment with exprs assay normalized

**Examples**

```
data(heffron2021_wuhan)
seq_ds_qn <- quantileNormalize(heffron2021_wuhan)
```

---

smoothProbeDS	<i>Smooth probes across protein tiling</i>
---------------	--------------------------------------------

---

**Description**

Smooth probes across protein tiling

**Usage**

```
smoothProbeDS(probe_ds, w = 2, eps = 1e-06)
```

**Arguments**

probe_ds	HERONProbeDataSet to smooth
w	smoothing width, probes +/- w/2 before and after are used
eps	error tolerance

**Value**

HERONProbeDataSet with smoothed data in exprs object

**Examples**

```
data(heffron2021_wuhan)
probe_ds <- convertSequenceDSToProbeDS(heffron2021_wuhan)
smoothed_ds <- smoothProbeDS(probe_ds)
```

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