# Package: PepSetTest (via r-universe)

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**Title** Peptide Set Test

**Version** 1.7.0

**Description** Peptide Set Test (PepSetTest) is a peptide-centric strategy to infer differentially expressed proteins in LC-MS/MS proteomics data. This test detects coordinated changes in the expression of peptides originating from the same protein and compares these changes against the rest of the peptidome. Compared to traditional aggregation-based approaches, the peptide set test demonstrates improved statistical power, yet controlling the Type I error rate correctly in most cases. This test can be valuable for discovering novel biomarkers and prioritizing drug targets, especially when the direct application of statistical analysis to protein data fails to provide substantial insights.

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`AggLimmaWorkflow` *Aggregation-based LIMMA workflow*

---

## Description

Given peptide abundance and assignment of peptide sequences to proteins, execute the aggregation-based LIMMA workflow to compute the log2 fold change, p-value, and adjusted p-value of all proteins identified.

## Usage

```
AggLimmaWorkflow(
  dat,
  contrasts.par,
  group,
  pep_mapping_tbl,
  covar = NULL,
  method = c("sum", "robreg"),
  logged = c(TRUE, FALSE),
  npep.trend = FALSE,
  eb = TRUE
)
```

## Arguments

| | |
|---|---|
| `dat` | a dataframe or matrix of peptide abundance, or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| `contrasts.par` | group levels to be compared separated by dash (e.g., "B-A" if group B is to be compared against group A) |

| | |
|---|---|
| group | a vector of group levels corresponding to each sample. Alternatively, it can be the column name of the group in colData if dat is a SummarizedExperiment object. |
| pep_mapping_tbl | a table mapping peptides to proteins. Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| covar | covariate matrix. Alternatively, it can be the column names of the covariates in colData if dat is a SummarizedExperiment object. |
| method | method of aggregation. Options including "sum" (summed peptide intensity) and "robreg" (robust regression with M-Estimation). |
| logged | Boolean variable indicating whether abundance data have been log-transformed |
| npep.trend | logical, should a number-of-peptide-trend be allowed for the prior variance? Default is constant prior variance. |
| eb | logical, whether to output the result from the empirical Bayes or ordinary approach. |

## Value

AggLimmaWorkflow returns a dataframe containing the following columns

| | |
|---|---|
| feature | unique protein identifier |
| logFC | log2 fold change |
| t | t-statistic |
| P.Value | raw p-value |
| adj.P.Val | p-value adjusted via the Benjamini-Hochberg method |
| B | B-statistic (empirical Bayes only) |

## Author(s)

Junmin Wang

## References

Ritchie, ME, Phipson, B, Wu, D, Hu, Y, Law, CW, Shi, W, and Smyth, GK (2015). limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research* 43, e47.

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:500),
protein = paste0("Protein", rep(1:100, each = 5)))
```

```
# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

AggLimmaWorkflow(dat, contrasts.par = contrasts.par,
group = group,
pep_mapping_tbl = pep_mapping_tbl,
method = "sum",
logged = FALSE)

# Store data as a SummarizedExperiment object; add covariates
library(tibble)
library(SummarizedExperiment)
colData <- data.frame(sample = LETTERS[seq_along(group)], group = group,
sex = c("M", "F", "M", "F", "F", "M"), age = 1:6) |>
column_to_rownames(var = "sample")
rowData <- pep_mapping_tbl |> column_to_rownames(var = "peptide")
dat.nn <- dat
rownames(dat.nn) <- NULL
colnames(dat.nn) <- NULL
dat.se <- SummarizedExperiment(assays = list(int = dat.nn), colData = colData, rowData = rowData)

AggLimmaWorkflow(dat.se, contrasts.par = contrasts.par,
group = "group",
covar = c("sex", "age"),
pep_mapping_tbl = "protein",
method = "sum",
logged = FALSE)
```

---

AggPeps *Aggregate peptide abundance values*

---

## Description

Given peptide abundance and assignment of peptide sequences to proteins, aggregate peptide abundance values into protein abundance values.

## Usage

```
AggPeps(
  dat,
  pep_mapping_tbl,
  method = c("sum", "robreg"),
  logged = c(TRUE, FALSE)
)
```

## Arguments

| | |
|---|---|
| dat | a dataframe or matrix of peptide abundance, or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| pep_mapping_tbl | a table mapping peptides to proteins. Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| method | method of aggregation. Options including "sum" (summed peptide intensity) and "robreg" (robust regression with M-Estimation). |
| logged | Boolean variable indicating whether abundance data have been log-transformed |

## Value

AggPeps returns a list containing a matrix of protein abundance values and a vector of number of peptides

## Author(s)

Junmin Wang

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:500),
protein = paste0("Protein", rep(1:100, each = 5)))

AggPeps(dat, pep_mapping_tbl, method = "sum",
logged = FALSE)

# Store data as a SummarizedExperiment object
library(tibble)
library(SummarizedExperiment)
rowData <- pep_mapping_tbl |> column_to_rownames(var = "peptide")
dat.nn <- dat
rownames(dat.nn) <- NULL
colnames(dat.nn) <- NULL
dat.se <- SummarizedExperiment(assays = list(int = dat.nn), rowData = rowData)

AggPeps(dat.se, pep_mapping_tbl = "protein", method = "sum",
logged = FALSE)
```

`CompPepSetTest` *Competitive peptide set test*

## Description

Given peptide-wise t-statistics and assignment of peptides to proteins, conduct peptide set tests to assess differential protein expression.

## Usage

```
CompPepSetTest(
  result,
  pep_mapping_tbl,
  stat = c("t", "logFC"),
  cor_coef = 0,
  pepC.estim = c("sd", "mad")
)
```

## Arguments

| | |
|---|---|
| `result` | output from `EnframeContrastsRes` |
| `pep_mapping_tbl` | a table mapping peptides to proteins. Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| `stat` | statistics to be used in the peptide set test. Options include "t" (t-statistic) and "logFC" (log2 fold change). |
| `cor_coef` | inter-peptide correlation coefficient(s) |
| `pepC.estim` | estimator of the variance of peptide-wise t-statistics not belonging to the protein of interest, i.e., test set. Options include "sd" and "mad". "sd" represents sample standard deviation. "mad" represents sample median absolute deviation. |

## Value

`CompPepSetTest` returns a dataframe containing the following columns

| | |
|---|---|
| `protein` | unique protein identifier |
| `NPeps` | number of peptides |
| `Correlation` | inter-peptide correlation coefficient |
| `Direction` | direction of change |
| `PValue` | raw p-value |
| `adj.P.Val` | p-value adjusted via the Benjamini-Hochberg method |
| `logFC` | average log2 fold change of peptides |
| `Up` | number of upregulated peptides |
| `Down` | number of downregulated peptides |

## Author(s)

Junmin Wang

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:500),
protein = paste0("Protein", rep(1:100, each = 5)))

# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

fit.cont <- FitContrasts(dat, contrasts.par, group)
cont.res <- EnframeContrastsRes(fit.cont)

# Run peptide set test based on t-statistics and standard deviation
CompPepSetTest(cont.res, pep_mapping_tbl, stat = "t",
cor_coef = 0, pepC.estim = "sd")

# Run peptide set test based on log2 fold change and median absolute deviation
CompPepSetTest(cont.res, pep_mapping_tbl, stat = "logFC",
cor_coef = 0, pepC.estim = "mad")
```

---

# CompPepSetTestWorkflow

*Competitive Peptide Set Test Workflow*

---

## Description

Given peptide abundance and assignment of peptide sequences to proteins, execute the competitive peptide set test workflow to compute the log2 fold change, p-value, and adjusted p-value of all proteins identified.

## Usage

```
CompPepSetTestWorkflow(
  dat,
  contrasts.par,
  group,
  pep_mapping_tbl,
  covar = NULL,
  stat = c("t", "logFC"),
```

```
  correlated = FALSE,
  equal.correlation = FALSE,
  pepC.estim = c("sd", "mad"),
  logged = FALSE
)
```

## Arguments

| | |
|---|---|
| dat | a dataframe or matrix of peptide abundance (row names should be peptide sequences or peptide IDs), or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| contrasts.par | group levels to be compared separated by dash (e.g., "B-A" if group B is to be compared against group A) |
| group | a vector of group levels corresponding to each sample. Alternatively, it can be the column name of the group in colData if dat is a SummarizedExperiment object. |
| pep_mapping_tbl | a table mapping peptides to proteins (it should include two columns named "peptide" and "protein"). Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| covar | covariate matrix. Alternatively, it can be the column names of the covariates in colData if dat is a SummarizedExperiment object. |
| stat | statistics to be used in the peptide set test. Options include "t" (t-statistic) and "logFC" (log2 fold change). |
| correlated | Boolean variable indicating whether peptides are assumed to be correlated. If correlated, inter-peptide correlation will be estimated. |
| equal.correlation | Boolean variable indicating whether all pairwise inter-peptide correlation coefficients are assumed to be equal within a protein. If true, the mixed model approach will be applied; otherwise, the approach described in Wu and Smyth (2012), *Nucleic Acids Research* will be applied. Note that this parameter matters only if "correlated" is set to true. |
| pepC.estim | estimator of the variance of peptide-wise t-statistics not belonging to the protein of interest, i.e., test set. Options include "sd" and "mad". "sd" represents sample standard deviation. "mad" represents sample median absolute deviation. |
| logged | Boolean variable indicating whether abundance data have been log-transformed |

## Value

`CompPepSetTestWorkflow` returns a dataframe containing the following columns

| | |
|---|---|
| protein | unique protein identifier |
| NPeps | number of peptides |
| Correlation | inter-peptide correlation coefficient |
| Direction | direction of change |
| PValue | raw p-value |

| | |
|---|---|
| adj.P.Val | p-value adjusted via the Benjamini-Hochberg method |
| logFC | average log2 fold change of peptides |
| Up | number of upregulated peptides |
| Down | number of downregulated peptides |

## Author(s)

Junmin Wang

## References

Wu, D, and Smyth, GK (2012). Camera: a competitive gene set test accounting for inter-gene correlation. *Nucleic Acids Research* 40, e133

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:500),
protein = paste0("Protein", rep(1:100, each = 5)))

# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

CompPepSetTestWorkflow(dat, contrasts.par = contrasts.par,
group = group,
pep_mapping_tbl = pep_mapping_tbl,
stat = "t",
correlated = TRUE,
equal.correlation = TRUE,
pepC.estim = "mad",
logged = FALSE)

# Store data as a SummarizedExperiment object; add covariates
library(tibble)
library(SummarizedExperiment)
colData <- data.frame(sample = LETTERS[seq_along(group)], group = group,
sex = c("M", "F", "M", "F", "F", "M"), age = 1:6) |>
column_to_rownames(var = "sample")
rowData <- pep_mapping_tbl |> column_to_rownames(var = "peptide")
dat.nn <- dat
rownames(dat.nn) <- NULL
colnames(dat.nn) <- NULL
dat.se <- SummarizedExperiment(assays = list(int = dat.nn), colData = colData, rowData = rowData)

CompPepSetTestWorkflow(dat.se, contrasts.par = contrasts.par,
```

```
group = "group",
pep_mapping_tbl = "protein",
covar = c("sex", "age"),
stat = "t",
correlated = TRUE,
equal.correlation = TRUE,
pepC.estim = "mad",
logged = FALSE)
```

---

`EnframeContrastsRes` *Enframe result of LIMMA analysis*

---

## Description

Convert result of LIMMA analysis into a dataframe.

## Usage

```
EnframeContrastsRes(eBayes.fit, eb = TRUE)
```

## Arguments

| | |
|---|---|
| `eBayes.fit` | output from `FitContrasts`. See ?`limma::eBayes` for details. |
| `eb` | logical, whether to output the result from the empirical Bayes or ordinary approach. |

## Value

`EnframeContrastsRes` returns a dataframe containing the following columns

| | |
|---|---|
| `feature` | unique feature identifier |
| `logFC` | log2 fold change |
| `t` | t-statistic |
| `P.Value` | raw p-value |
| `adj.P.Val` | p-value adjusted via the Benjamini-Hochberg method |
| `B` | B-statistic (empirical Bayes only) |

## Author(s)

Junmin Wang

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

fit.cont <- FitContrasts(dat, contrasts.par, group)
EnframeContrastsRes(fit.cont)
```

---

`EstimInterPepCor` *Estimation of inter-peptide correlation*

---

## Description

Given peptide abundance and assignment of peptide sequences to proteins, estimate inter-peptide correlation coefficient for each protein via the mixed model approach or approach described in Wu and Smyth (2012), *Nucleic Acids Research*.

## Usage

```
EstimInterPepCor(
  dat,
  design,
  pep_mapping_tbl,
  equal.correlation = FALSE,
  logged = FALSE
)
```

## Arguments

| | |
|---|---|
| `dat` | a dataframe or matrix of peptide abundance, or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| `design` | design matrix |
| `pep_mapping_tbl` | a table mapping peptides to proteins. Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| `equal.correlation` | Boolean variable indicating whether all pairwise inter-peptide correlation coefficients are assumed to be equal within a protein. If true, the mixed model approach will be applied; otherwise, the approach described in Wu and Smyth (2012), *Nucleic Acids Research* will be applied. In either case, only non-negative mean correlations are allowed. |

`logged` Boolean variable indicating whether abundance data have been log-transformed

## Value

`EstimInterPepCor` returns a numeric vector of inter-peptide correlation coefficients (one value for each protein).

## Author(s)

Junmin Wang and Steven Novick

## References

Wu, D, and Smyth, GK (2012). Camera: a competitive gene set test accounting for inter-gene correlation. *Nucleic Acids Research* 40, e133

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(540), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:90)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:90),
protein = paste0("Protein", rep(1:30, each = 3)))

# Generate design matrix
group <- c(rep("A", 3), rep("B", 3))
group <- factor(group)
design <- stats::model.matrix(~ 0 + group)

EstimInterPepCor(dat, design, pep_mapping_tbl,
equal.correlation = TRUE, logged = FALSE)
```

---

# `FitContrasts` *Empirical Bayes moderated t-test*

---

## Description

Fit a linear model to feature abundance and compute moderated t-statistics via the empirical Bayes method.

## Usage

```
FitContrasts(
  dat,
  contrasts.par,
  group,
  covar = NULL,
  logged = FALSE,
  NPeptide = NULL
)
```

## Arguments

| | |
|---|---|
| dat | a dataframe or matrix of feature (e.g., peptide, protein) abundance |
| contrasts.par | group levels to be compared separated by dash (e.g., "B-A" if group B is to be compared against group A) |
| group | list of group levels corresponding to each sample. The order of group levels needs to match that of samples in the feature abundance table. |
| covar | covariate matrix |
| logged | Boolean variable indicating whether data have been log-transformed |
| NPeptide | numeric vector indicating number of peptides aggregated for each protein. logNPeptide will be passed to limma-trend. Constant prior variance if null. |

## Value

`FitContrasts` returns an object of class `MArrayLM`. See `?limma::eBayes` for details.

## Author(s)

Junmin Wang

## References

Ritchie, ME, Phipson, B, Wu, D, Hu, Y, Law, CW, Shi, W, and Smyth, GK (2015). limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research* 43, e47.

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

# Run moderated t-test without covariates
```

```
FitContrasts(dat, contrasts.par, group)

# Run moderated t-test with covariates
covar <- matrix(c(1:6, 0, 1, 0, 1, 1, 0), nrow = 6, ncol = 2, byrow = FALSE)
FitContrasts(dat, contrasts.par, group, covar = covar)
```

---

`FitLmerBySample` *Fit a linear mixed model*

---

## Description

Fit a linear mixed model to the abundance of peptides belonging to one protein and compute the correlation coefficient based on variance components. Sample is treated as a random effect in the mixed model.

## Usage

```
FitLmerBySample(y, design)
```

## Arguments

| | |
|---|---|
| `y` | a matrix of log2-transformed peptide abundance for one protein |
| `design` | design matrix |

## Value

`FitLmerBySample` returns the estimated inter-peptide correlation coefficient.

## Author(s)

Junmin Wang and Steven Novick

## Examples

```
y <- matrix(rnorm(1000*6), 1000, 6)
design <- cbind(Intercept = 1, Group = c(0, 0, 0, 1, 1, 1))

FitLmerBySample(y, design)
```

RobustReg *Robust Regression*

## Description

Estimate protein abundance by fitting a linear model to peptide abundance via robust regression.

## Usage

```
RobustReg(dat, logged = FALSE)
```

## Arguments

| | |
|---|---|
| dat | a dataframe or matrix of peptide abundance, or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| logged | Boolean variable indicating whether abundance data have been log-transformed |

## Value

RobustReg returns a numeric vector of estimated protein abundance.

## Author(s)

Junmin Wang

## References

Sticker, A, Goeminne, L, Martens, L, and Clement, L (2020). Robust Summarization and Inference in Proteome-wide Label-free Quantification. *Molecular & Cellular Proteomics* 19, 1209-19.

Gatto, L, Rainer, J, and Gibb, S (2021). MsCoreUtils: Core Utils for Mass Spectrometry Data. R packageversion 1.4.0. https://github.com/RforMassSpectrometry/MsCoreUtils

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(600), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:100)

RobustReg(dat, logged = FALSE)
```

`SelfContPepSetTestWorkflow` *Self-contained Peptide Set Test Workflow*

## Description

Given peptide abundance and assignment of peptide sequences to proteins, execute the self-contained peptide set test workflow to compute the log2 fold change, p-value, and adjusted p-value of all proteins identified.

## Usage

```
SelfContPepSetTestWorkflow(
  dat,
  contrasts.par,
  group,
  pep_mapping_tbl,
  covar = NULL,
  logged = FALSE
)
```

## Arguments

| | |
|---|---|
| `dat` | a dataframe or matrix of peptide abundance (row names should be peptide sequences or peptide IDs), or a SummarizedExperiment object where grouping and peptide-protein mapping are provided in colData and rowData, respectively. |
| `contrasts.par` | group levels to be compared separated by dash (e.g., "B-A" if group B is to be compared against group A) |
| `group` | a vector of group levels corresponding to each sample. Alternatively, it can be the column name of the group in colData if dat is a SummarizedExperiment object. |
| `pep_mapping_tbl` | a table mapping peptides to proteins (it should include two columns named "peptide" and "protein"). Alternatively, it can be the column name of the protein in rowData if dat is a SummarizedExperiment object. |
| `covar` | covariate matrix. Alternatively, it can be the column names of the covariates in colData if dat is a SummarizedExperiment object. |
| `logged` | Boolean variable indicating whether abundance data have been log-transformed |

## Value

`SelfContPepSetTestWorkflow` returns a dataframe containing the following columns

| | |
|---|---|
| `protein` | unique protein identifier |
| `NPeps` | number of peptides |

| | |
|---|---|
| Direction | direction of change |
| PValue | raw p-value |
| adj.P.Val | adjusted p-value |
| logFC | average log2 fold change of peptides |
| Up | number of upregulated peptides |
| Down | number of downregulated peptides |

## Author(s)

Junmin Wang

## References

Wu, D, Lim, E, Francois Vaillant, F, Asselin-Labat, M-L, Visvader, JE, and Smyth, GK (2010). ROAST: rotation gene set tests for complex microarray experiments. *Bioinformatics* 26, 2176-2182

## Examples

```
# Generate random peptide data
dat <- 2^matrix(rnorm(3000), ncol = 6)
colnames(dat) <- paste0("Sample", 1:6)
rownames(dat) <- paste0("Peptide", 1:500)

# Generate peptide mapping table
pep_mapping_tbl <- data.frame(peptide = paste0("Peptide", 1:500),
protein = paste0("Protein", rep(1:100, each = 5)))

# Generate groups and contrasts
group <- c(rep("A", 3), rep("B", 3))
contrasts.par <- "B-A"

SelfContPepSetTestWorkflow(dat, contrasts.par = contrasts.par,
group = group,
pep_mapping_tbl = pep_mapping_tbl,
logged = FALSE)

# Store data as a SummarizedExperiment object; add covariates
library(tibble)
library(SummarizedExperiment)
colData <- data.frame(sample = LETTERS[seq_along(group)], group = group,
sex = c("M", "F", "M", "F", "F", "M"), age = 1:6) |>
column_to_rownames(var = "sample")
rowData <- pep_mapping_tbl |> column_to_rownames(var = "peptide")
dat.nn <- dat
rownames(dat.nn) <- NULL
colnames(dat.nn) <- NULL
dat.se <- SummarizedExperiment(assays = list(int = dat.nn), colData = colData, rowData = rowData)

SelfContPepSetTestWorkflow(dat.se, contrasts.par = contrasts.par,
group = "group",
```

```
pep_mapping_tbl = "protein",
covar = c("sex", "age"),
logged = FALSE)
```

---

`TTestwCor` *Two-sample t-test accounting for inter-peptide correlation*

---

## Description

Test whether peptides belonging to the same protein are differentially expressed relative to the rest of the peptidome, accounting for inter-peptide correlation. This function is adapted from `cameraPR()` in LIMMA R package (Wu and Smyth (2012), *Nucleic Acids Research*).

## Usage

```
TTestwCor(statistic, index, inter.pep.cor, pepC.estim = c("sd", "mad"))
```

## Arguments

| | |
|---|---|
| `statistic` | a numeric vector of peptide-wise t-statistics. |
| `index` | an index vector or a list of index vectors. `statistic[index]` selects corresponding rows in the protein of interest, i.e., test set(s). |
| `inter.pep.cor` | a numeric vector of inter-peptide correlation coefficients within the protein of interest, i.e., test set(s). |
| `pepC.estim` | estimator of the variance of peptide-wise t-statistics not belonging to the protein of interest, i.e., test set. Options include "sd" and "mad". "sd" represents sample standard deviation. "mad" represents sample median absolute deviation. |

## Value

`TTestwCor` returns a dataframe in which each row represents a protein of interest, i.e., test set. Columns include

| | |
|---|---|
| `NPeps` | number of peptides |
| `Correlation` | inter-peptide correlation coefficient |
| `Direction` | direction of change |
| `PValue` | raw p-value |
| `adj.P.Val` | p-value adjusted via the Benjamini-Hochberg method |

## Author(s)

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## References

Wu, D, and Smyth, GK (2012). Camera: a competitive gene set test accounting for inter-gene correlation. *Nucleic Acids Research* 40, e133

## Examples

```
y <- matrix(rnorm(1000 * 6), 1000, 6)
design <- cbind(Intercept = 1, Group = c(0, 0, 0, 1, 1, 1))

# First set of 20 genes are genuinely differentially expressed
index1 <- 1:20
y[index1, 4:6] <- y[index1, 4:6]+1

fit <- limma::eBayes(limma::lmFit(y, design))
TTestwCor(fit$t[, 2], index = index1,
inter.pep.cor = 0,
pepC.estim = "sd")
```

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