# Package 'MSstatsQC'

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**License** Artistic License 2.0

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**Author** Eralp Dogu [aut, cre] (ORCID: <https://orcid.org/0000-0002-8256-7304>), Sara Taheri [aut] (ORCID: <https://orcid.org/0000-0002-6554-9083>), Olga Vitek [aut] (ORCID: <https://orcid.org/0000-0003-1728-1104>)

**Maintainer** Eralp Dogu <eralp.dogu@gmail.com>

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---

`ChangePointEstimator` *A function to identify the time of a change in the mean or variability of a metric*

---

## Description

A function to identify the time of a change in the mean or variability of a metric

## Usage

```
ChangePointEstimator(
  data = NULL,
  peptide,
  L = 1,
  U = 5,
  metric,
  normalization = TRUE,
  ytitle = "Change Point Plot - mean",
  type = "mean",
  selectMean = NULL,
  selectSD = NULL
)
```

## Arguments

| | |
|---|---|
| data | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each observation. |
| peptide | the name of precursor of interest. |
| L | Lower bound of the guide set. |
| U | Upper bound of the guide set. |
| metric | the name of metric of interest. |
| normalization | TRUE metric is standardized and FALSE if not standardized. |
| ytitle | the y-axis title of the plot. Defaults to "Change Point Plot - mean". The x-axis title is by default "QCno-name of peptide" |
| type | the type of the control chart. Two values can be assigned, "mean" or "variability". Default is "mean". |
| selectMean | the mean of a metric. It is used when mean is known. It is NULL when mean is not known. The default is NULL. |
| selectSD | the standard deviation of a metric. It is used when standard deviation is known. It is NULL when mean is not known. The default is NULL. |

## Value

A plot of likelihood statistics versus time per peptide and metric generated from `CP.data.prepare` data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Find the name of the peptides
levels(sampleData$Precursor)
# Calculate change point statistics
ChangePointEstimator(data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime")
ChangePointEstimator(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    ytitle = "Change Point Plot - variability", type = "variability"
)
ChangePointEstimator(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    selectMean = 27.78, selectSD = 8.19
)
ChangePointEstimator(data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea")
ChangePointEstimator(
    data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea",
    selectMean = 35097129, selectSD = 34132861
)
ChangePointEstimator(data = sampleData, peptide = "TAAYVNAIEK", metric = "MaxFWHM")
```

CUSUMChart *A function to create cumulative sum charts for mean (CUSUMm) and cumulative sum charts for variability (CUSUMv) control charts*

## Description

A function to create cumulative sum charts for mean (CUSUMm) and cumulative sum charts for variability (CUSUMv) control charts

## Usage

```
CUSUMChart(
  data = NULL,
  peptide,
  L = 1,
  U = 5,
  metric,
  normalization = TRUE,
  ytitle = "CUSUMm",
  type = "mean",
  selectMean = NULL,
  selectSD = NULL,
  referenceValue = 0.5,
  decisionInterval = 5
)
```

## Arguments

| | |
|---|---|
| data | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each observation. |
| peptide | the name of precursor of interest. |
| L | Lower bound of the guide set. |
| U | Upper bound of the guide set. |
| metric | the name of metric of interest. |
| normalization | TRUE if metric is standardized and FALSE if not standardized. |
| ytitle | the y-axis title of the plot. Defaults to "CUSUMm". The x-axis title is by default "Time : name of peptide" |
| type | the type of the control chart. Two values can be assigned, "mean" or "variability". Default is "mean" |
| selectMean | the mean of a metric. It is used when mean is known. It is NULL when mean is not known. The default is NULL. |
| selectSD | the standard deviation of a metric. It is used when standard deviation is known. It is NULL when mean is not known. The default is NULL. |
| referenceValue | the value that is used to tune the control chart for a proper shift size |
| decisionInterval | the threshold to detect an out-of-control observation |

## Value

A plot of pozitive and negative CUSUM statistics versus time per peptide and metric generated from `CUSUM.data.prepare` data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Find the name of the peptides
levels(sampleData$Precursor)
# Calculate CUSUM statistics
CUSUMChart(data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime")
CUSUMChart(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    ytitle = "CUSUMv", type = "variability"
)
CUSUMChart(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    selectMean = 27.78, selectSD = 8.19
)
CUSUMChart(data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea")
CUSUMChart(
    data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea",
    selectMean = 35097129, selectSD = 34132861
)
CUSUMChart(data = sampleData, peptide = "TAAYVNAIEK", metric = "MaxFWHM")
```

---

`DataProcess` *A data processing function*

---

## Description

A data processing function

## Usage

```
DataProcess(data = NULL)
```

## Arguments

| | |
|---|---|
| `data` | Comma-separated (*.csv), QC file format. It should contain a Precursor column and the metrics columns. |

## Value

A data frame that processes using `input.sanity.check` function.

## Examples

```
# The data is "S9Site54" which is defined in the package.
data <- DataProcess(S9Site54)
```

---

`DecisionMap` *A function to create heatmaps to compare performance with user defined performance criteria*

---

## Description

A function to create heatmaps to compare performance with user defined performance criteria

## Usage

```
DecisionMap(
  data = NULL,
  method = "XmR",
  peptideThresholdRed = 0.7,
  peptideThresholdYellow = 0.5,
  L = 1,
  U = 5,
  type = "mean",
  title = "heatmap plot",
  listMean = NULL,
  listSD = NULL
)
```

## Arguments

| | |
|---|---|
| `data` | Comma-separated (*.csv), QC file format. It should contain a Precursor column and the metrics columns. |
| `method` | It is either "CUSUM" or "XmR" |
| `peptideThresholdRed` | Is a threshold that marks percentage of peptides above it red on the heatmap. Defaults to 0.7 |
| `peptideThresholdYellow` | Is a threshold that marks percentage of peptides above it and below the peptideThresholdRed, yellow on the heatmap. Defaults to 0.5 |
| `L` | Lower bound of the giude set. Defaults to 1 |
| `U` | Upper bound of the guide set. Defaults to 5 |
| `type` | can take two values, "mean" or "dispersion". Defaults to "mean" |
| `title` | the title of the plot. Defaults to "heatmap plot" |
| `listMean` | List of the means for the metrics. If you don't know the means leave it as NULL and they will be calculated automatically by using L and U. The default is NULL. |

| | |
|---|---|
| listSD | List of the standard deviations for the metrics. If you don't know the standard deviations leave it as NULL and they will be calculated automatically by using L and U. The default is NULL. |

## Value

A heatmap to aggregate results per metric generated from heatmap.DataFrame data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Draw Decision maker plot
DecisionMap(data = sampleData, method = "CUSUM")
DecisionMap(data = sampleData, method = "CUSUM", type = "variability")
DecisionMap(data = sampleData, method = "XmR")
DecisionMap(data = sampleData, method = "XmR", type = "variability")
```

---

# MissingDataMap *A function to summarize missing values*

---

## Description

A function to summarize missing values

## Usage

```
MissingDataMap(data)
```

## Arguments

| | |
|---|---|
| data | Processed data |

## Value

A plot of missing values.

## Examples

```
# The data is "S9Site54" which is defined in the package.
data <- DataProcess(S9Site54)
MissingDataMap(data)
```

## MSnbaseToMSstatsQC *A function to convert MSnbase files to MSstatsQC format*

### Description

A function to convert MSnbase files to MSstatsQC format

### Usage

```
MSnbaseToMSstatsQC(msfile)
```

### Arguments

| | |
|---|---|
| msfile | data file to be converted |

### Value

A data frame that can be used with MSstatsQC

A csv file that is converted from raw files

### Examples

```
library(RforProteomics)

msfile <- getPXD000001mzXML()

MSnbaseToMSstatsQC(msfile)
```

## MSstatsQC.ML.deployR *A function to test random forest classifiers for QC data*

### Description

A function to test random forest classifiers for QC data

### Usage

```
MSstatsQC.ML.deployR(Test.set, guide.set, rf_model)
```

### Arguments

| | |
|---|---|
| Test.set | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each run. |
| guide.set | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each run. |
| rf_model | the model that was trained previosly by MSstatsQC-ML training process |

### Value

Probability of failure predictions based on a trained model

### Examples

```
S9Site54.dataML <- DataProcess(MSstatsQC::S9Site54[, ])
colnames(S9Site54.dataML)[1] <- c("idfile")
colnames(S9Site54.dataML)[2] <- c("peptide")
S9Site54.dataML$peptide <- as.factor(S9Site54.dataML$peptide)
S9Site54.dataML$idfile <- as.numeric(S9Site54.dataML$idfile)
S9Site54.dataML <- within(S9Site54.dataML, rm(Annotations, missing))
guide.set <- dplyr::filter(S9Site54.dataML, idfile <= 20)

rf_model <- MSstatsQC.ML.trainR(guide.set, sim.size = 10)

Test.set <- dplyr::filter(S9Site54.dataML, idfile > 20)

MSstatsQC.ML.deployR(Test.set, guide.set, rf_model = rf_model)

Test.set <- S9Site54.dataML

MSstatsQC.ML.deployR(Test.set, guide.set, rf_model = rf_model)
```

---

## MSstatsQC.ML.sim.size.detectR

*A function to train random forest classifiers for QC data*

---

### Description

A function to train random forest classifiers for QC data

### Usage

```
MSstatsQC.ML.sim.size.detectR(guide.set, sim.start, sim.end)
```

### Arguments

| | |
|---|---|
| guide.set | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each run. |
| sim.start | enter min simulation size. |
| sim.end | enter max simulation size. |

### Value

a plot for sim.size vs performance

### Examples

```
# First process the data to make sure it's ready to use
S9Site54.dataML <- DataProcess(MSstatsQC::S9Site54[, ])
colnames(S9Site54.dataML)[1] <- c("idfile")
colnames(S9Site54.dataML)[2] <- c("peptide")
S9Site54.dataML$peptide <- as.factor(S9Site54.dataML$peptide)
S9Site54.dataML$idfile <- as.numeric(S9Site54.dataML$idfile)
S9Site54.dataML <- within(S9Site54.dataML, rm(Annotations, missing))
guide.set <- dplyr::filter(S9Site54.dataML, idfile <= 20)

MSstatsQC.ML.sim.size.detectR(guide.set, sim.start = 10, sim.end = 2500)
```

---

## MSstatsQC.ML.trainR *A function to train random forest classifiers for QC data*

---

### Description

A function to train random forest classifiers for QC data

### Usage

```
MSstatsQC.ML.trainR(
  guide.set,
  sim.size,
  guide.set.annotations = NULL,
  nfolds = NULL,
  a = 1.5,
  b = 2
)
```

### Arguments

| | |
|---|---|
| guide.set | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each run. |
| sim.size | enter simulation size. |
| guide.set.annotations | comma-separated (.csv), metric file with annotations such as pass and fail. |
| nfolds | fold for cross validation |
| a | lower threshold to define shift size |
| b | upper threshold to define shift size |

### Value

A trained model and performance indicators from train/validation/test splits

### Examples

```
S9Site54.dataML <- DataProcess(MSstatsQC::S9Site54[, ])
colnames(S9Site54.dataML)[1] <- c("idfile")
colnames(S9Site54.dataML)[2] <- c("peptide")
S9Site54.dataML$peptide <- as.factor(S9Site54.dataML$peptide)
S9Site54.dataML$idfile <- as.numeric(S9Site54.dataML$idfile)
S9Site54.dataML <- within(S9Site54.dataML, rm(Annotations, missing))
guide.set <- dplyr::filter(S9Site54.dataML, idfile <= 20)

MSstatsQC.ML.trainR(guide.set, sim.size = 10)
```

---

## mzQCToMSstatsQC *A function to convert mzQC files to MSstatsQC format*

---

### Description

A function to convert mzQC files to MSstatsQC format

### Usage

```
mzQCToMSstatsQC(mzQCfile)
```

### Arguments

| | |
|---|---|
| mzQCfile | data file to be converted |

### Value

A data frame that can be used with MSstatsQC

A csv file that is converted from raw files

## Examples

```
library(RforProteomics)

msfile <- getPXD000001mzXML()

mzQCToMSstatsQC(msfile)
```

---

QCloudDDA *DDA QC data from QCloud System*

---

## Description

QC results generated from QCloud system

## Usage

```
data(QCloudDDA)
```

## Format

csv

## Details

DDA QC data from QCloud System

## Value

An example dataset generated from QCloud system

## Examples

```
head(QCloudDDA)
```

## QCloudSRM *SRM QC data from QCloud System*

### Description

QC results generated from QCloud system

### Usage

```
data(QCloudSRM)
```

### Format

csv

### Details

SRM QC data from QCloud System

### Value

An example dataset generated from QCloud system

### Examples

```
head(QCloudSRM)
```

## QuiCDIA *DIA iRT data from QuiC System*

### Description

QC results generated from QuiC system

### Usage

```
data(QuiCDIA)
```

### Format

csv

### Details

DIA iRT data from QuiC System

## Value

An example dataset generated from QuiC system

## Examples

```
head(QuiCDIA)
```

---

`RadarPlot` *A function to create radar plot to aggregate results from X and mR charts or CUSUMm and CUSUMv charts.*

---

## Description

A function to create radar plot to aggregate results from X and mR charts or CUSUMm and CUSUMv charts.

## Usage

```
RadarPlot(
  data = NULL,
  L = 1,
  U = 5,
  method = "XmR",
  listMean = NULL,
  listSD = NULL
)
```

## Arguments

| | |
|---|---|
| `data` | omma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each observation. |
| `L` | lower bound of the guide set. |
| `U` | upper bound of the guide set. |
| `method` | defines the method selected to construct control charts. |
| `listMean` | list of the means for each metric. It is used when mean is known. It is NULL when mean is not known. The default is NULL. |
| `listSD` | list of the standard deviations for each metric. It is used when standard deviation is known. It is NULL when mean is not known. The default is NULL. automatically by using L and U. The default is NULL. |

## Value

A radar plot to aggregate results per metric generated from `XmR.Radar.Plot.DataFrame` data frame or `CUSUM.Radar.Plot.DataFrame` data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Draw XmR radar plot
RadarPlot(data = sampleData)
RadarPlot(data = sampleData, method = "CUSUM")
RadarPlot(
    data = sampleData,
    listMean = list(
        "BestRetentionTime" = 27.78,
        "TotalArea" = 35097129,
        "MaxFWHM" = 0.28,
        "MinStartTime" = 24
    ),
    listSD = list(
        "BestRetentionTime" = 8.19,
        "TotalArea" = 34132861,
        "MaxFWHM" = 0.054,
        "MinStartTime" = 24
    )
)
```

---

# RemoveMissing *A data processing function for removing missing values*

---

## Description

A data processing function for removing missing values

## Usage

```
RemoveMissing(data = NULL)
```

## Arguments

| | |
|---|---|
| data | Comma-separated (*.csv), QC file format. It should contain a Precursor column and the metrics columns. |

## Value

A data frame that processes using `input.sanity.check` function.

## Examples

```
# The data is "S9Site54" which is defined in the package.
data <- RemoveMissing(S9Site54)
```

RiverPlot *A function to create river plot to aggregate results from X and mR charts or CUSUMm and CUSUMv charts.*

## Description

A function to create river plot to aggregate results from X and mR charts or CUSUMm and CUSUMv charts.

## Usage

```
RiverPlot(
  data = NULL,
  L = 1,
  U = 5,
  method = "XmR",
  listMean = NULL,
  listSD = NULL
)
```

## Arguments

| | |
|---|---|
| data | omma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each observation. |
| L | lower bound of the guide set. |
| U | upper bound of the guide set. |
| method | defines the method selected to construct control charts. |
| listMean | list of the means for each metric. It is used when mean is known. It is NULL when mean is not known. The default is NULL. |
| listSD | list of the standard deviations for each metric. It is used when standard deviation is known. It is NULL when mean is not known. The default is NULL. |

## Value

A river plot to aggregate results per metric generated from `XmR.Summary.DataFrame` data frame or `CUSUM.Summary.DataFrame` data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Draw XmR summary plot
RiverPlot(data = sampleData)
RiverPlot(
    data = sampleData, L = 1, U = 20, method = "XmR",
    listMean = list(
```

```
        "BestRetentionTime" = 27.78,
        "TotalArea" = 35097129,
        "MaxFWHM" = 0.28,
        "MinStartTime" = 24
    ),
    listSD = list(
        "BestRetentionTime" = 8.19,
        "TotalArea" = 34132861,
        "MaxFWHM" = 0.054,
        "MinStartTime" = 24
    )
)
```

---

S9Site54 *CPTAC study 9.1 site 54 dataset*

---

## Description

system suitabilty testing results generated during CPTAC Study 9.1 for Site 54

## Usage

```
data(S9Site54)
```

## Format

csv

## Details

CPTAC system suitability testing data for Site 54 from Study 9.1

## Value

An example dataset generated from CPTAC study 9.1

## References

http://www.mcponline.org/content/early/2015/02/18/mcp.M114.047050

## Examples

```
head(S9Site54)
```

XmRChart *A function to construct individual (X) and moving range (mR) control charts*

## Description

A function to construct individual (X) and moving range (mR) control charts

## Usage

```
XmRChart(
  data = NULL,
  peptide,
  L = 1,
  U = 5,
  metric,
  normalization = FALSE,
  ytitle = "Individual observations",
  type = "mean",
  selectMean = NULL,
  selectSD = NULL
)
```

## Arguments

| | |
|---|---|
| data | comma-separated (.csv), metric file. It should contain a "Precursor" column and the metrics columns. It should also include "Annotations" for each observation. |
| peptide | the name of precursor of interest. |
| L | Lower bound of the guide set. |
| U | Upper bound of the guide set. |
| metric | the name of metric of interest. |
| normalization | TRUE if metric is standardized and FALSE if not standardized. |
| ytitle | the y-axis title of the plot. Defaults to "Individual observations". The x-axis title is by default "Time : name of peptide" |
| type | the type of the control chart. Two values can be assigned, "mean" or "variability". Default is "mean". |
| selectMean | the mean of a metric. It is used when mean is known. It is NULL when mean is not known. The default is NULL. |
| selectSD | the standard deviation of a metric. It is used when standard deviation is known. It is NULL when mean is not known. The default is NULL. |

## Value

A plot of individual values or moving ranges versus time per peptide and metric generated from `XmR.data.prepare` data frame.

## Examples

```
# First process the data to make sure it's ready to use
sampleData <- DataProcess(S9Site54)
head(sampleData)
# Find the name of the peptides
levels(sampleData$Precursor)
# Calculate X and mR statistics
XmRChart(data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime")
XmRChart(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    ytitle = "moving ranges", type = "variability"
)
XmRChart(
    data = sampleData, peptide = "VLVLDTDYK", metric = "BestRetentionTime",
    selectMean = 27.78, selectSD = 8.19
)
XmRChart(data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea")
XmRChart(
    data = sampleData, peptide = "DDGSWEVIEGYR", metric = "TotalArea",
    selectMean = 35097129, selectSD = 34132861
)
XmRChart(data = sampleData, peptide = "TAAYVNAIEK", metric = "MaxFWHM")
XmRChart(data = sampleData, peptide = "LVNELTEFAK", metric = "MinStartTime")
```

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