Package ‘ggQC’

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## Description

function to report listing of quality performance parameters

- **Proc. Tolerance (sigma)**: Describes the number of your process sigma (from QC charting) that can fit in your customer’s specification window (the larger the better).
- **DNS (sigma)**: Distance to Nearest Specification (DNS) limit. Measure of how centered your process is and how close you are to the nearest process limit in sigma units.
- **Cp**: Describes how many times your 6 sigma process window (from QC charting) can fit in your customer’s specification window (the larger the better).
- **Cpk**: Describes how centered your process is relative to customer specifications. How many times can you fit a 3 sigma window (from QC charting) between your process center and the nearest customer specification limit.
- **Pp**: Describes how many times your 6 sigma process window (overall standard deviation) can fit in your customer’s specification window (the larger the better).
- **Ppk**: Describes how centered your process is relative to customer specifications. How many times can you fit a 3 sigma window (overall standard deviation) between your process center and the nearest customer specification limit.

## Usage

```r
capability.summary(LSL, USL, QC.Center, QC.Sigma, s.Sigma, digits = 2)
```

## Arguments

- **LSL**
  number, customer’s lower specification limit.
- **USL**
  number, customer’s upper specification limit.
- **QC.Center**
  number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.
- **QC.Sigma**
  number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.
- **s.Sigma**
  number, the sigma value determined from overall standard deviation (i.e., sd()).
- **digits**
  integer, how many digits to report.

## Value

data frame, listing of metric labels and value
**cBar_LCL**

*Lower Control Limit: Count Data (c-chart)*

**Description**

Calculates lower control limit (LCL) for count data acquired over the same-sized area of opportunity. Negative values are reported as 0.

**Usage**

```r
cBar_LCL(y, na.rm = FALSE, ...)
```

**Arguments**

- `y` Vector of count data. Each observation having the same-area of opportunity.
- `na.rm` a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...` further arguments passed to or from other methods.

**Value**

A number; 3-sigma lower control limit (LCL). Function returns 0 for negative values.

**Examples**

```r
set.seed(5555)
y <- rpois(30, 9)
cBar_LCL(y)
```

---

**cBar_UCL**

*Upper Control Limit: Count Data (c-chart)*

**Description**

Calculates upper control limit (UCL) for count data acquired over the same-sized area of opportunity.

**Usage**

```r
cBar_UCL(y, na.rm = FALSE, ...)
```
Arguments

- **y** Vector of count data. Each observation having the same-area of opportunity.
- **na.rm** a logical value indicating whether NA values should be stripped before the computation proceeds.
- **...** further arguments passed to or from other methods.

Value

A number; 3-sigma upper control limit (UCL)

Examples

```r
set.seed(5555)
y <- rpois(30, 9)
cBar_UCL(y)
```

---

**Cp**

*Calculate Cp*

Description

function to calculate Cp - "The elbowroom or margin your process"

Usage

```
Cp(LSL, USL, QC.Sigma)
```

Arguments

- **LSL** number, customer's lower specification limit.
- **USL** number, customer's upper specification limit.
- **QC.Sigma** number, the sigma value determined from an Xmr plot or a Studentized (e.g., xBar) analysis.

Value

numeric, Cp value (unitless)
Cpk  

*Calculate Cpk*

**Description**

function to calculate Cpk - "measure of process centering"

**Usage**

Cpk(LSL, USL, QC.Center, QC.Sigma)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LSL</td>
<td>number, customer’s lower specification limit.</td>
</tr>
<tr>
<td>USL</td>
<td>number, customer’s upper specification limit.</td>
</tr>
<tr>
<td>QC.Center</td>
<td>number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.</td>
</tr>
<tr>
<td>QC.Sigma</td>
<td>number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.</td>
</tr>
</tbody>
</table>

**Value**

numeric, Cpk value (unitless)

DNS  

*Calculate Distance to Nearest Specification Limit*

**Description**

function to calculate a standardized distance to the nearest specification limit (sigma units)

**Usage**

DNS(LSL, USL, QC.Center, QC.Sigma)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LSL</td>
<td>number, customer’s lower specification limit.</td>
</tr>
<tr>
<td>USL</td>
<td>number, customer’s upper specification limit.</td>
</tr>
<tr>
<td>QC.Center</td>
<td>number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.</td>
</tr>
<tr>
<td>QC.Sigma</td>
<td>number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.</td>
</tr>
</tbody>
</table>

**Value**

numeric, standardized distance to the nearest specification limit (sigma units)
Calculate Distance to Lower Specification Limit

**Description**

function to calculate a standardized distance to the Lower specification limit (sigma units)

**Usage**

LD(LSL, USL, QC.Center, QC.Sigma)

**Arguments**

- **LSL** number, customer’s lower specification limit.
- **USL** number, customer’s upper specification limit.
- **QC.Center** number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.
- **QC.Sigma** number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.

**Value**

umeric, standardized distance to the lower specification limit (sigma units)

---

Mean One-Point Moving Range

**Description**

Calculates the mean one-point moving range used when constructing a moving-range chart.

**Usage**

mR(y, na.rm = TRUE, ...)

**Arguments**

- **y** Vector of values
- **na.rm** a logical value indicating whether NA values should be stripped before the computation proceeds.
- **...** further arguments passed to or from other methods.

**Value**

A number; mean one-point moving range.
Examples

```r
set.seed(5555)
values <- rnorm(n = 100, mean = 25, sd = 1)
mR(values)
```

**mR_points**

*One Point Moving Range of Vector*

**Description**

Calculates a one-point moving range vector given an input vector of values. Output often used to produce mR-chart.

**Usage**

```r
mR_points(y)
```

**Arguments**

- `y`: vector of values

**Value**

Vector of one-point moving range.

**Examples**

```r
y <- seq(-5:5)
mR_points(y)
```

**mR_UCL**

*Mean One-Point Moving Range Upper Control Limit (UCL)*

**Description**

Calculates the mean one-point moving range UCL used when constructing a moving-range chart.

**Usage**

```r
mR_UCL(y, na.rm = FALSE, ...)
```

**Arguments**

- `y`: Vector of values
- `na.rm`: a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...`: further arguments passed to or from other methods.
npBar

Value

A number; mean one-point moving range UCL.

Examples

set.seed(5555)
values <- rnorm(n = 100, mean = 25, sd = 1)
mR_UCL(values)

npBar

Mean Value: Binomial Data (np-chart)

Description

Calculates the mean value for binomial count data acquired over the same-sized area of opportunity.

Usage

npBar(y, n, na.rm = FALSE, ...)

Arguments

y Vector of binomial count data (not proportions). Each observation having the same-area of opportunity.

n A number representing the area of opportunity.

na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

... further arguments passed to or from other methods.

Value

A number; mean value

Examples

set.seed(5555)
p <- rbinom(n = 100, size = 30, prob = .2)
npBar(y = p, n = 30)
npBar_LCL  
*Lower Control Limit: Binomial Data (np-chart)*

**Description**

Calculates lower control limit (LCL) for binomial count data acquired over the same-sized area of opportunity.

**Usage**

\[
\text{npBar}_\text{LCL}(y, n, \text{na.rm = FALSE}, \ldots)
\]

**Arguments**

- \(y\)  
  Vector of binomial count data (not proportions). Each observation having the same-area of opportunity.
- \(n\)  
  A number representing the area of opportunity.
- \(\text{na.rm}\)  
  A logical value indicating whether NA values should be stripped before the computation proceeds.
- \(\ldots\)  
  Further arguments passed to or from other methods.

**Value**

A number; 3-sigma upper control limit (LCL)

**Examples**

```r
set.seed(5555)
p <- rbinom(n = 100, size = 30, prob = .2)
npBar_LCL(y = p, n = 30)
```

---

npBar_UCL  
*Upper Control Limit: Binomial Data (np-chart)*

**Description**

Calculates upper control limit (UCL) for binomial count data acquired over the same-sized area of opportunity.

**Usage**

\[
\text{npBar}_\text{UCL}(y, n, \text{na.rm = FALSE}, \ldots)
\]
### pBar

**Mean Proportion: Binomial Data (p-chart)**

#### Description
Calculates overall mean proportion for binomial proportion data acquired over a variable area of opportunity.

#### Usage
```r
pBar(y, n, na.rm = FALSE, ...)
```

#### Arguments
- **y**: Vector of binomial proportion data (not counts). Observations may have a different area of opportunity, n.
- **n**: A vector representing the area of opportunity.
- **na.rm**: a logical value indicating whether NA values should be stripped before the computation proceeds.
- **...**: further arguments passed to or from other methods.

#### Value
A vector of mean proportion, length equal to length of parameter y.
Examples

```r
set.seed(5555)
p <- rbinom(n = 100, size = 30, prob = .2)
n <- rpois(100, 100)
pBar(y = p/n, n = n)
```

Description

Calculates point-wise lower control limit (LCL) for binomial proportion data acquired over a variable area of opportunity.

Usage

```r
pBar_LCL(y, n, na.rm = FALSE, ...)
```

Arguments

- `y` Vector of binomial proportion data (not counts). Observations may have a different area of opportunity, `n`.
- `n` A vector representing the area of opportunity.
- `na.rm` a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...` further arguments passed to or from other methods.

Value

A vector; point-wise 3-sigma lower control limit (LCL)

Examples

```r
set.seed(5555)
p <- rbinom(n = 100, size = 30, prob = .2)
n <- rpois(100, 100)
pBar_LCL(y = p/n, n = n)
```
### pBar_UCL

**Upper Control Limit: Binomial Data (p-chart)**

**Description**

Calculates point-wise upper control limit (UCL) for binomial proportion data acquired over a variable area of opportunity.

**Usage**

```r
pBar_UCL(y, n, na.rm = FALSE, ...)
```

**Arguments**

- `y`: Vector of binomial proportion data (not counts). Observations may have a different area of opportunity, `n`.
- `n`: A vector representing the area of opportunity.
- `na.rm`: a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...`: further arguments passed to or from other methods.

**Value**

A vector; point-wise 3-sigma upper control limit (UCL)

**Examples**

```r
set.seed(5555)
p <- rbinom(n = 100, size = 30, prob = .2)
n <- rpois(100, 100)
pBar_UCL(y = p/n, n = n)
```

---

### Pp

**Calculate Pp**

**Description**

function to calculate Pp - "The elbowroom or margin your process" uses overall sigma value not the QC chart sigma values.

**Usage**

```r
Pp(LSL, USL, s.Sigma)
```
**process_tolerance**

**Arguments**

- **LSL** number, customer’s lower specification limit.
- **USL** number, customer’s upper specification limit.
- **s.Sigma** number, the sigma value determined from overall standard deviation (i.e., sd()).

**Value**

numeric, Pp value (unitless)

---

**Ppk**  
**Calculate Cpk**

**Description**

function to calculate Cpk - "measure of process centering"

**Usage**

`Ppk(LSL, USL, QC.Center, s.Sigma)`

**Arguments**

- **LSL** number, customer’s lower specification limit.
- **USL** number, customer’s upper specification limit.
- **QC.Center** number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.
- **s.Sigma** number, the sigma value determined from overall standard deviation (i.e., sd()).

**Value**

numeric, Ppk value (unitless)

---

**process_tolerance**  
**Calculate QC Process Tolerance**

**Description**

function to calculate a standardized process tolerance with sigma unit

**Usage**

`process_tolerance(LSL, USL, QC.Sigma)`
**Arguments**

- **LSL**: number, customer’s lower specification limit.
- **USL**: number, customer’s upper specification limit.
- **QC.Sigma**: number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.

**Value**

numeric, standardized process tolerance value in sigma units

---

<table>
<thead>
<tr>
<th>QCrane</th>
<th>Range: Max Min Difference</th>
</tr>
</thead>
</table>

**Description**

Given a set of numbers, function calculates the difference between the maximum and minimum value.

**Usage**

QCrane(y)

**Arguments**

- **y**: vector of values

**Value**

a number.

**Examples**

```r
y <- seq(-5:5)
QCrane(y)
```
**QC_Capability**  
*Calculate Summary of Quality Performance Parameters*

**Description**

function to report listing of quality performance parameters

**Usage**

```
QC_Capability(data = NULL, value = NULL, grouping = NULL,
              formula = NULL, method = "xBar.rBar", na.rm = FALSE, LSL = NULL,
              USL = NULL, digits = 2)
```

**Arguments**

- **data**: vector or dataframe, as indicated below for each chart type
  - **Individuals (XmR)**: vector of values;
  - **Studentized**: dataframe

- **value**: string, **Studentized Charts**, name of numeric vector in dataframe with values of interest.

- **grouping**: string, **Studentized Charts**, name of single factor/variable to split the dataframe "values" by

- **formula**: **Studentized Charts**: a formula, such as `y ~ x1 + x2`, where the `y` variable is numeric data to be split into groups according to the grouping `x` factors/variables

- **method**: string, calling one of the following methods:
  - **Individuals Charts**: XmR,
  - **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar

- **na.rm**: a logical value indicating whether NA values should be stripped before the computation proceeds.

- **LSL**: numeric, Customer’s lower specification limit

- **USL**: numeric, Customer’s Upper specification limit

  - **Proc. Tolerance (sigma)**: Describes the number of your process sigma (from QC charting) that can fit in your customer’s specification window (the larger the better).

  - **DNS (sigma)**: Distance to Nearest Specification (DNS) limit. Measure of how centered your process is and how close you are to the nearest process limit in sigma units.

  - **Cp**: Describes how many times your 6 sigma process window (from QC charting) can fit in your customer’s specification window (the larger the better)

  - **Cpk**: Describes how centered your process is relative to customer specifications. How many times can you fit a 3 sigma window (from QC charting) between your process center and the nearest customer specification limit.
• **Pp**: Describes how many times your 6 sigma process window (overall standard deviation) can fit in your customer’s specification window (the larger the better)

• **Ppk**: Describes how centered your process is relative to customer specifications. How many times can you fit a 3 sigma window (overall standard deviation) between your process center and the nearest customer specification limit.

digits integer, how many digits to report.

**Value**

data frame, listing of metric labels and value

---

**QC_Lines**

*Calculate QC Limits*

**Description**

Calculates QC chart lines for the following chart types and reports in a dataframe:

- **Individuals Charts**: mR, XmR,
- **Attribute Charts**: c, np, p, u,
- **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian,
- **Dispersion Charts**: rBar, rMedian, sBar.

**Usage**

QC_Lines(data = NULL, value = NULL, grouping = NULL, formula = NULL, n = NULL, method = "xBar.rBar", na.rm = FALSE)

**Arguments**

data vector or dataframe, as indicated below for each chart type

- **Individuals & Attribute Charts**: vector of values;
- **Studentized & Dispersion Charts**: dataframe

value string, **Studentized Charts** and **Dispersion Charts**, numeric vector in dataframe with values of interest

grouping string, **Studentized Charts** and **Dispersion Charts**: single factor/variable to split the dataframe "values" by

formula **Studentized Charts** and **Dispersion Charts**: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

n number or vector as indicated below for each chart type.

- **Individuals Charts**: No effect
• **Attribute Charts**: (p and u) vector, indicating sample area of opportunity.
• **Attribute Charts**: (np) number, indicating constant sampling area of opportunity.
• **Studentized Charts**: number, user specified subgroup size.
• **Dispersion Charts**: No effect

method string, calling the following methods:
• **Individuals Charts**: mR, XmR,
• **Attribute Charts**: c, np, p, u,
• **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar,
  xMedian.rMedian
• **Dispersion Charts**: rBar, rMedian, sBar.

na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

Value

a dataframe,

• **Attribute Data**: (p and u) Center Line, Upper Control Limit and Lower Control limit for each point.
• **Other Data**: single line dataframe, with relevant control limits noted in column headings.

Note

If using the formula argument do not use value and group arguments.

References


Examples

```
# Example 1: Charts other than "p" or "u" #

# Load Libraries
require(ggQC)
require(plyr)
require(ggplot2)

# Setup Data
set.seed(5555)
Process1 <- data.frame(processID = as.factor(rep(1,100)),
  metric_value = rnorm(100,0,1),
  subgroup_sample=rep(1:20, each=5),
  Process_run_id = 1:100)

set.seed(5555)
```
```r
Process2 <- data.frame(processID = as.factor(rep(2,100)),
                      metric_value = rnorm(100,5, 1),
                      subgroup_sample=rep(1:10, each=10),
                      Process_run_id = 101:200)

Both_Processes <- rbind(Process1, Process2)

# QC Values For Individuals -----------------------------------------------
# All Together
QC_Lines(data = Both_Processes$metric_value, method = "XmR")

# For Each Process
ddply(Both_Processes, .variables = "processID",
    .fun =function(df){
        QC_Lines(data = df$metric_value, method = "XmR")
    })

# QC Values For Studentized Runs-------------------------------------------
# All Together
QC_Lines(data = Both_Processes,
    formula = metric_value ~ subgroup_sample)

# For Each Process
ddply(Both_Processes, .variables = "processID",
    .fun =function(df){
        QC_Lines(data = df, formula = metric_value ~ subgroup_sample)
    })

########################
# Example 2 "p" data #
########################

# Setup p Data --------------------------------------------------------------
set.seed(5555)
bin_data <- data.frame(
    trial = 1:30,
    Num_Incomplete_Items = rpois(n = 30, lambda = 30),
    Num_Items_in_Set = runif(n = 30, min = 50, max = 100))

bin_data$Proportion_Incomplete <- bin_data$Num_Incomplete_Items/bin_data$Num_Items_in_Set

# QC_Lines for "p" data ------------------------------------------------------
QC_Lines(data = bin_data$Proportion_Incomplete,
    n = bin_data$Num_Items_in_Set, method="p")

########################
# Example 3 "u" data #
########################
```
### QC_Violations

#### Description

function that calculates QC violations on sequentially ordered data based on the following 4 rules:

- **Violation Same Side**: 8 or more consecutive, same-side points
- **Violation 1 Sigma**: 4 or more consecutive, same-side points exceeding 1 sigma
- **Violation 2 Sigma**: 2 or more consecutive, same-side points exceeding 2 sigma
- **Violation 3 Sigma**: any points exceeding 3 sigma

#### Usage

```r
QC_Violations(data, value = NULL, grouping = NULL, formula = NULL, method = NULL, ...)
```

#### Arguments

- **data**: vector or dataframe, as indicated below for each chart type
  - **Individuals**: vector of values;
  - **Studentized Charts**: dataframe
- **value**
  - **Studentized Charts**: numeric vector in dataframe with values of interest
- **grouping**
  - **Studentized Charts**: single factor/variable to split the dataframe "values" by
- **formula**
  - **Studentized Charts**: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
- **method**
  - string, calling the following methods:
    - **Individuals Charts**: XmR,
    - **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian

... further arguments passed to or from other methods.
Value

a dataframe, with the following columns

- **data**: The input data if XmR, mean or median by group for Studentized methods
- **z_score**: z-score for the data point
- **Index**: number, indicating the order of the input data
- **Violation_Result**: description of the type of test being run.
  - Violation Same Side: 8 or more consecutive, same-side points
  - Violation 1 Sigma: 4 or more consecutive, same-side points exceeding 1 sigma
  - Violation 2 Sigma: 2 or more consecutive, same-side points exceeding 2 sigma
  - Violation 3 Sigma: any points exceeding 3 sigma
- **Index**: boolean, does the data point violate the rule?

Note

If using the `formula` argument do not use `value` and `group` arguments.

References


Examples

```r
# Example 1: XmR Check Violations

# Load Libraries
require(ggQC)
# Setup Data
set.seed(5555)
QC_XmR <- data.frame(
  data = c(c(-1, 2.3, 2.4, 2.5), #Outlier Data
           sample(c(rnorm(60),5,-5), 62, replace = FALSE), #Normal Data
           c(1,-.3, -2.4,-2.6,-2.5,-2.7, .3)), #Outlier Data
  Run_Order = 1:73 #Run Order
)
QC_Vs <- QC_Violations(data = QC_XmR$data, method = "XmR")
```

```r
# Example 2: Xbar Check Violations

# Setup Some Data
QC_xBar.rBar <- do.call(rbind, lapply(1:3, function(X{
  set.seed(5555+X)
  }
```

```r
# Loop over 3 seeds
```
data.frame(
    sub_group = rep(1:42), #Define Subgroups
    sub_class = letters[X],
    c(
        c(runif(n = 5, min = 2.0,3.2)), #Outlier Data
        sample(c(rnorm(30),5,-4), 32, replace = FALSE), #Normal Data
        c(runif(n = 5, min = -3.2, max = -2.0)) #Outlier Data
    )
)
)
)
)
)
)
)

colnames(QC_xBar.rBar) <- c("sub_group","sub_class", "value")
QC_Vs <- QC_Violations(data = QC_xBar.rBar,
    formula = value~sub_group,
    method = "xBar.rBar")

---

**rBar**

**Mean Subgroup Range**

**Description**

Calculates the mean subgroup range used when constructing a XbarR chart.

**Usage**

```
rBar(data, value, grouping, formula = NULL, ...)
```

**Arguments**

- `data` : data frame to be processed
- `value` : numeric vector in a data frame with values of interest.
- `grouping` : single factor/variable to split the data frame "values" by.
- `formula` : a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
- `...` : further arguments passed to or from other methods.

**Value**

A number; mean subgroup range.

**Examples**

```
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
rBar(data = df, formula = v~g)
```
Description

Calculates the mean subgroup range Lower control limit (UCL) used when constructing a XbarR chart.

Usage

\[ rBar_LCL(data = data, value = value, grouping = grouping, formula = NULL, ...) \]

Arguments

data | data frame to be processed
value | numeric vector in a data frame with values of interest.
grouping | single factor/variable to split the data frame "values" by.
formula | a formula, such as \( y \sim x1 + x2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
... | further arguments passed to or from other methods.

Value

A number; mean subgroup range lower control limit (LCL).

Examples

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
rBar_LCL(data = df, formula = v~g)
```

---

---

Description

Calculates the mean subgroup range upper control limit (UCL) used when constructing a XbarR chart.

Usage

\[ rBar_UCL(data = data, value = value, grouping = grouping, formula = NULL, ...) \]

Arguments

data | data frame to be processed
value | numeric vector in a data frame with values of interest.
grouping | single factor/variable to split the data frame "values" by.
formula | a formula, such as \( y \sim x1 + x2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
... | further arguments passed to or from other methods.
**Arguments**

- **data**
  data frame to be processed
- **value**
  numeric vector in a data frame with values of interest.
- **grouping**
  single factor/variable to split the data frame "values" by.
- **formula**
  a formula, such as \( y \sim x1 + x2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
- ... further arguments passed to or from other methods.

**Value**

A number; mean subgroup range upper control limit (UCL).

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
rBar_UCL(data = df, formula = v~g)
```

---

**rMedian**

**Median of Subgroup Ranges**

**Description**

Calculates the median of subgroup ranges, used when constructing xBar_rMedian charts.

**Usage**

```r
rMedian(data, value, grouping, formula = NULL, ...)
```

**Arguments**

- **data**
  data frame to be processed
- **value**
  numeric vector in a data frame with values of interest.
- **grouping**
  single factor/variable to split the data frame "values" by.
- **formula**
  a formula, such as \( y \sim x1 + x2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
- ... further arguments passed to or from other methods.

**Value**

A number; median subgroup range.

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
rMedian(data = df, formula = v~g)
```
**rMedian_LCL**  
*Median of Subgroup Ranges Lower Control Limit (LCL)*

**Description**
Calculates the median of subgroup range Lower control limit (LCL) used when constructing a xBar_rMedian chart.

**Usage**
```r
rMedian_LCL(data = data, value = value, grouping = grouping, formula = NULL, ...)```

**Arguments**
- `data` data frame to be processed
- `value` numeric vector in a data frame with values of interest.
- `grouping` single factor/variable to split the data frame "values" by.
- `formula` a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
- `...` further arguments passed to or from other methods.

**Value**
A number; median of subgroup range lower control limit (LCL).

**Examples**
```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
rMedian_LCL(data = df, formula = v~g)
```

---

**rMedian_UCL**  
*Median of Subgroup Ranges Upper Control Limit (UCL)*

**Description**
Calculates the median of subgroup range upper control limit (UCL) used when constructing a xBar_rMedian chart.

**Usage**
```r
rMedian_UCL(data = data, value = value, grouping = grouping, formula = NULL, ...)```

**Arguments**
- `data` data frame to be processed
- `value` numeric vector in a data frame with values of interest.
- `grouping` single factor/variable to split the data frame "values" by.
- `formula` a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
- `...` further arguments passed to or from other methods.
sBar

Mean Subgroup Standard Deviation

Description

Calculates the mean subgroup standard deviation used when constructing a XbarS chart.

Usage

sBar(data, value, grouping, formula = NULL, ...)

Arguments

data data frame to be processed
value numeric vector in a data frame with values of interest.
grouping single factor/variable to split the data frame "values" by.
formula a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
... further arguments passed to or from other methods.

Value

A number; mean subgroup standard deviation.

Examples

set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
sBar(data = df, formula = v~g)
**sBar_LCL**

*Mean Subgroup Standard Deviation Lower Control Limit (LCL)*

**Description**

Calculates the mean subgroup standard deviation Lower control limit (LCL) used when constructing a XbarS chart.

**Usage**

`sBar_LCL(data = data, value = value, grouping = grouping, formula = NULL, ...)`

**Arguments**

- `data`: data frame to be processed
- `value`: numeric vector in a data frame with values of interest.
- `grouping`: single factor/variable to split the data frame "values" by.
- `formula`: a formula, such as `y ~ x1 + x2`, where the `y` variable is numeric data to be split into groups according to the grouping `x` factors/variables
- `...`: further arguments passed to or from other methods.

**Value**

A number; mean subgroup standard deviation lower control limit (LCL).

**Examples**

```
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
sBar_LCL(data = df, formula = v~g)
```

---

**sBar_UCL**

*Mean Subgroup Standard Deviation Upper Control Limit (UCL)*

**Description**

Calculates the mean subgroup standard deviation upper control limit (UCL) used when constructing a XbarS chart.

**Usage**

`sBar_UCL(data = data, value = value, grouping = grouping, formula = NULL, ...)`

**Value**

A number; mean subgroup standard deviation upper control limit (UCL).
stat_mR

Arguments

- **data**: data frame to be processed
- **value**: numeric vector in a data frame with values of interest.
- **grouping**: single factor/variable to split the data frame "values" by.
- **formula**: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables
- ... further arguments passed to or from other methods.

Value

A number; mean subgroup standard deviation upper control limit (UCL).

Examples

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
sBar_UCL(data = df, formula = v~g)
```

stat_mR

Generate mR chart in ggplot

Description

ggplot stat used to create a mR chart in ggplot

Usage

```r
stat_mR(mapping = NULL, data = NULL, geom = "point", position = "identity", show.legend = NA, inherit.aes = TRUE, na.rm = FALSE, color.mr_point = "black", color.mr_line = "black", color.qc_limits = "red", color.qc_center = "blue", ...)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()` or `aes_()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.
stat_mR

geometry object to use display the data

position
Position adjustment, either as a string, or the result of a call to a position adjustment function.

show.legend
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

na.rm
a logical value indicating whether NA values should be stripped before the computation proceeds.

color.mr_point
color, to be used for the mR points.

color.mr_line
color, to be used for line connecting points.

color.qc_limits
color, used to colorize the plot’s upper and lower mR control limits.

color.qc_center
color, used to colorize the plot’s center line.

...
Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = “red” or size = 3. They may also be parameters to the paired geom/stat.

Value
data need to produce the mR plot in ggplot.

Examples

# Example 1: mR Chart #

# Load Libraries ----------------------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data ----------------------------------------------------------------
set.seed(5555)
Process1 <- data.frame(processID = as.factor(rep(1,100)),
    metric_value = rnorm(100,0,1),
    subgroup_sample=rep(1:20, each=5),
    Process_run_id = 1:100)

set.seed(5556)
Process2 <- data.frame(processID = as.factor(rep(2,100)),
    metric_value = rnorm(100,5, 1),
    subgroup_sample=rep(1:10, each=10),
    Process_run_id = 101:200)

Both_Processes <- rbind(Process1, Process2)
# One Plot Both Processes ----------------------------------------------

```r
ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
  stat_mR() + ylab("Moving Range")
```

# Facet Plot - Both Processes ---------------------------------------------

```r
ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
  stat_mR() + ylab("Moving Range") +
  facet_grid(.~processID, scales = "free_x")
```

---

**stat_pareto**  
*Generate a Pareto Plot with ggplot*

- **Description**
  - stat function to create ggplot Pareto chart

- **Usage**
  ```r
  stat_pareto(mapping = NULL, data = NULL, geom = "point",
  position = "identity", show.legend = NA, inherit.aes = TRUE,
  group = 1, na.rm = FALSE, point.color = "black", point.size = 2,
  line.color = "black", line.size = 0.5, bars.fill = c("red",
  "white"), ...)`
  ```

- **Arguments**
  - **mapping**: Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes` = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
  - **data**: The data to be displayed in this layer. There are three options: If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`. A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.
  - **geom**: The geometric object to use display the data
  - **position**: Position adjustment, either as a string, or the result of a call to a position adjustment function.
  - **show.legend**: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
  - **inherit.aes**: If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.
### stat_pareto

defines grouping for variable for pareto plot, default and suggested is 1.

**na.rm**
a logical value indicating whether NA values should be stripped before the computation proceeds.

**point.color**
color, used to define point color of cumulative percentage line

**point.size**
number, used to define point size of cumulative percentage line

**line.color**
color, used to define line color of cumulative percentage line

**line.size**
color, used to define line weight of cumulative percentage line

**bars.fill**
character vector length 2, start and end colors for pareto bars.

... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `color = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

### Value

Pareto plot.

### Examples

```
# Example 1: Pareto Plot

# Load Libraries ----------------------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data --------------------------------------------------------------
df <- data.frame(
  x = letters[1:10],
  y = as.integer(runif(n = 10, min = 0, max=100))
)

# Render Pareto Plot ------------------------------------------------------

ggplot(df, aes(x=x, y=y)) +
  stat_pareto(point.color = "red",
              point.size = 3,
              line.color = "black",
              #size.line = 1,
              bars.fill = c("blue", "orange"),
  )
```
Produce QC Charts with ggplot Framework.

Description

Produce QC charts with ggplot framework. Support for faceting and layering of multiple QC chart lines on a single plot. Charts supported (see method argument for call):

- **Individuals Charts**: mR, XmR,
- **Attribute Charts**: c, np, p, u,
- **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian,
- **Dispersion Charts**: rBar, rMedian, sBar.

To label chart lines see `stat_QC_labels`

Usage

```r
stat_QC(mapping = NULL, data = NULL, geom = "hline", position = "identity", na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, n = NULL, method = "xBar.rBar", color.qc_limits = "red", color.qc_center = "blue", color.point = "black", color.line = "black", physical.limits = c(NA, NA), auto.label = FALSE, limit.txt.label = c("LCL", "UCL"), label.digits = 1, show.1n2.sigma = FALSE, ...)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.

- **geom**: The geometric object to use display the data

- **position**: Position adjustment, either as a string, or the result of a call to a position adjustment function.

- **na.rm**: a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

n number, for

- **Studentized Charts**, used for custom or hypothetical subgroup size.
- **np Charts**, used to specify a fixed area of opportunity.

method string, calling the following methods:

- **Individuals Charts**: mR, XmR,
- **Attribute Charts**: c, np, p, u,
- **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian
- **Dispersion Charts**: rBar, rMedian, sBar.

color.qc_limits color, used to colorize the plot's upper and lower control limits.

color.qc_center color, used to colorize the plot's center line.

color.point color, used to colorize points in studentized plots. You will need geom_point() for C, P, U, NP, and XmR charts.

color.line color, used to colorize lines connecting points in studentized plots. You will need geom_line() for C, P, U, NP, and XmR charts.

physical.limits vector, specify lower physical boundary and upper physical boundary

auto.label boolean setting, if T labels graph with control limits.

limit.txt.label vector, provides option for naming or not showing the limit text labels (e.g., UCL, LCL)

- **limit.txt.label = c("LCL", "UCL")**: default
- **limit.txt.label = c("Low", "High")**: changes the label text to low and high
- **limit.txt.label = NA**: does not show label text.

label.digits integer, number of decimal places to display.

show.1n2.sigma boolean setting, if T labels graph 1 and 2 sigma lines. Line color is set by color.qc_limits

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

Value

**ggplot control charts.**
Examples

```r
# Load Libraries ---------------------------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data ------------------------------------------------------------------
set.seed(5555)
Process1 <- data.frame(processID = as.factor(rep(1,100)),
metric_value = rnorm(100,0,1),
subgroup_sample = rep(1:20, each=5),
Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(processID = as.factor(rep(2,100)),
metric_value = rnorm(100,5, 1),
subgroup_sample = rep(1:10, each=10),
Process_run_id = 101:200)
Both_Processes <- rbind(Process1, Process2)

# Example 1: XmR Chart #
EX1.1 <- ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
  geom_point() + geom_line() + stat_QC(method="XmR") +
  stat_QC_labels(method="XmR", digits = 2) +
  facet_grid(.~processID, scales = "free_x")
#EX1.1
EX1.2 <- ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
  stat_mR() + ylab("Moving Range") +
  stat_QC_labels(method="mR", digits = 2) +
  facet_grid(.~processID, scales = "free_x")
#EX1.2

# Example 2: XbarR Chart #
EX2.1 <- ggplot(Both_Processes, aes(x = subgroup_sample,
y = metric_value,
group = processID)) +
  stat_summary(fun.y = "mean", color = "blue", geom = c("point")) +
  stat_summary(fun.y = "mean", color = "blue", geom = c("line")) +
  stat_QC(method = "xBar.rBar") + facet_grid(.~processID, scales = "free_x")
#EX2.1
EX2.2 <- ggplot(Both_Processes, aes(x = subgroup_sample,
y = metric_value,
group = processID)) +
  stat_summary(fun.y = "QCrange", color = "blue", geom = "point") +
  ```
```r
stat_summary(fun.y = "QCrange", color = "blue", geom = "line") +
stat_QC(method = "rBar") +
ylab("Range") +
facet_grid(~processID, scales = "free_x")
#EX2.2

# Example 3: p Chart

# p chart Setup -----------------------------------------------------------
set.seed(5556)
bin_data <- data.frame(
  trial=1:30,
  Num_Incomplete_Items = rpois(30, lambda = 30),
  Num_Items_in_Set = runif(n = 30, min = 50, max = 100))
bin_data$Proportion_Incomplete <- bin_data$Num_Incomplete_Items/bin_data$Num_Items_in_Set

# P Chart ------------------------------------------------------------
EX3.1 <- ggplot(data = bin_data, aes(x=trial,
  y=Proportion_Incomplete,
  n=Num_Items_in_Set)) +
  geom_point() + geom_line() +
  stat_QC(method = "p")
#EX3.1

# Example 4: u Chart

# u chart Setup -----------------------------------------------------------
set.seed(5555)
bin_data <- data.frame(
  trial=1:30,
  Num_of_Blemishes = rpois(30, lambda = 30),
  Num_Items_Inspected = runif(n = 30, min = 50, max = 100))

bin_data$Blemish_Rate <- bin_data$Num_of_Blemishes/bin_data$Num_Items_Inspected

# U Chart ------------------------------------------------------------
EX4.1 <- ggplot(data = bin_data, aes(x=trial,
  y=Blemish_Rate,
  n=Num_Items_Inspected)) +
  geom_point() + geom_line() +
  stat_QC(method = "u")
#EX4.1

# Example 5: np Chart

# np chart Setup -----------------------------------------------------------
set.seed(5555)
bin_data <- data.frame(
  trial=1:30,
  NumNonConforming = rbinom(30, 30, prob = .50))
```
Units_Tested_Per_Batch <- 60

# Plot np chart ----------------------------------------------------------
EX5.1 <- ggplot(data = bin_data, aes(trial, NumNonConforming)) +
    geom_point() +
    stat_QC(method = "np", n = Units_Tested_Per_Batch)
#EX5.1

#################################################
# Example 6: c Chart  #
#################################################

# c chart Setup ----------------------------------------------------------
set.seed(5555)
Process1 <- data.frame(Process_run_id = 1:30,
    Counts=rpois(n = 30, lambda = 25),
    Group = "A")
Process2 <- data.frame(Process_run_id = 1:30,
    Counts = rpois(n = 30, lambda = 5),
    Group = "B")

all_processes <- rbind(Process1, Process2)

# Plot C Chart -----------------------------------------------------------
EX6.1 <- ggplot(all_processes, aes(x=Process_run_id, y = Counts)) +
    geom_point() + geom_line() +
    stat_QC(method = "c", auto.label = TRUE, label.digits = 2) +
    scale_x_continuous(expand = expand_scale(mult = .25)) +
    facet_grid(.~Group)
# EX6.1

---

**stat_QC_CAPA**

*Generic Function for drawing QC capability information on plots*

**Description**

Generic Function for drawing QC capability information on plots

**Usage**

```r
stat_QC_CAPA(LSL, USL, method = "xBar.rBar", digits = 1,
    mapping = NULL, data = NULL, geom = "vline",
    position = "identity", na.rm = FALSE, show.legend = NA,
    inherit.aes = TRUE, show = c("LSL", "USL"), direction = "v",
    type = NA, ...)
```

**Arguments**

- **LSL** numeric, Customer’s lower specification limit
- **USL** numeric, Customer’s upper specification limit
method string, calling the following methods:

- **Individuals Charts:** XmR,
- **Studentized Charts:** xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian

digits -
mapping Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes` = `TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
data The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.
geom The geometric object to use display the data
position Position adjustment, either as a string, or the result of a call to a position adjust-
ment function.
na.rm -
show.legend logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.
show -
direction -
type -
... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

Value

ggplot control charts.

Examples

```r
# Load Libraries -----------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data -----------------------------------------------
```
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
                      Value = rnorm(100,10,1),
                      Subgroup = rep(1:20, each=5),
                      Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
                      Value = rnorm(100,20,1),
                      Subgroup = rep(1:10, each=10),
                      Process_run_id = 101:200)
df <- rbind(Process1, Process2)

# Example 1 XmR

# You may need to use the r-studio Zoom for these plots or make the size of the
# stat_QC_cap_summary smaller with size = some number

method <- "XmR"

# Normal Histogram XmR

EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
                      show=c("TOL","DNS","Cp","Cpk","Pp","Ppk"),
                      #"LCL","X","UCL","Sig"),
                      show=c("Sig","TOL","DNS"),
                      show=c("TOL","DNS","Cp","Cpk","Pp","Ppk"),
                      color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
  ylim(0,45)
EX1.1

# Facet Histogram XmR

EX1.2 <- ggplot(df[order(df$Process_run_id),],
                 aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
                 geom_histogram(binwidth = 1) +
                 geom_hline(yintercept=0, color="grey") +
                 stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
                 stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
                 stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
                           show="ALL",
                           show=c("TOL","DNS","Cp","Cpk","Pp","Ppk"),
                           # "LCL","X","UCL","Sig"),
                           show=c("Sig","TOL","DNS"),
                           show=c("TOL","DNS","Cp","Cpk","Pp","Ppk"),
                           color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
facet_grid(~ProcessID) + ylim(0,45)
#EX1.2

# Facet Density Plot XmR ---------------------------------------------
EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    show="ALL",
    LCL", "X", "UCL", "Sig"),
    show=c("Sig","TOL", "DNS"),
    color="black", digits=2, size=4 ) +

  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)
#EX1.3

# Facet Density Plot XmR ---------------------------------------------
EX1.4 <- ggplot(df[order(df$Process_run_id),],
  aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_density(bw = .4, fill="grey", trim=TRUE ) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    show="ALL",
    LCL", "X", "UCL", "Sig"),
    show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +

  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  geom_hline(yintercept=0, color="black") +
  facet_grid(~ProcessID) + ylim(0,.5)
#EX1.4

########################################################################
## Example 2: xBar.rBar or xBar.sBar ##
########################################################################

method <- "xBar.rBar" #Alternatively Use "xBar.sBar" if desired

# Single Histogram xBar.rBar ---------------------------------------------
EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig", "TOL", "DNS"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
#EX2.1

# Faceted Histogram xBar.rBar ---------------------------------------------
EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
  facet_grid(.~ProcessID, scales="free_x")
#EX2.2

# Single Density xBar.rBar ----------------------------------------------
EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
  #EX2.3

# Faceted Density xBar.rBar ---------------------------------------------
EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
stat_QC_Capability

#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig", "TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
facet_grid(.~ProcessID, scales="free_x")

#EX2.4

###################################################
## Example 3: xBar.rMedian ##
###################################################

## Plots involving medians should give warning: "median based QC methods represent
## at best *potential* process capability"

##These plot work the same as in examples 2.X; below is an example.

method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
geom_histogram(binwidth = 1) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig", "TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))

#EX3.1

stat_QC_Capability

Auto QC Capability Stat Function

Description

Draws lines, labels and summary statistics. Works best with histogram and density plots.

Usage

stat_QC_Capability(LSL, USL, method = "xBar.rBar",
show.lines = c("LSL", "USL"), line.direction = "v",
show.line.labels = TRUE, line.label.size = 3,
show.cap.summary = c("Cp", "Cpk", "Pp", "Ppk"), cap.summary.size = 4,
px = Inf, py = -Inf, digits = 3)
Arguments

- **LSL** numeric, Customer’s lower specification limit
- **USL** numeric, Customer’s Upper specification limit
- **method** string, calling the following methods:
  - **Individuals Charts**: XmR,
  - **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian
- **show.lines** vector, indicating which lines to draw ie., c("LCL", "LSL", "X", "USL", "UCL")
  - **LCL**: Lower Control Limit
  - **LSL**: Lower Specification Limit
  - **X**: Process Center
  - **USL**: Upper Specification Limit
  - **UCL**: Upper Control Limit
- **line.direction** string "v" or "h", specifies which direction to draw lines.
- **show.line.labels** boolean, if TRUE then draw.
- **line.label.size** numeric, control the size of the line labels.
- **show.cap.summary** vector, indicating which lines to draw ie., c("TOL", "DNS", "Cp", "Cpk", "Pp", "Ppk", "LCL", "X", "UCL", "Sig"). The order given in the vector is the order presented in the graph.
  - **TOL**: Tolerance in Sigma Units (USL-LSL)/sigma
  - **DNS**: Distance to Nearest Specification Limit in Sigma Units
  - **Cp**: Cp (Within)
  - **Cpk**: Cpk (Within)
  - **Pp**: Pp (Between)
  - **Ppk**: Ppk (Between)
  - **LCL**: Lower Control Limit
  - **X**: Process Center
  - **UCL**: Upper Control Limit
  - **Sig**: Sigma from control charts
- **cap.summary.size** numeric, control the size/scale of the summary text box.
- **px** numeric, x position for summary text box. Use Inf to force label to x-limit.
- **py** numeric, y position for summary text box. Use Inf to force label to y-limits. May also need vjust parameter.
- **digits** integer, how many digits to report.

Value

capability layer for histogram and density plots.
See Also

for more control over lines, labels, and capability data see the following functions:

- `stat_QC_cap_vlabels`
- `stat_QC_cap_hlabels`
- `stat_QC_cap_vlines`
- `stat_QC_cap_hlines`
- `stat_QC_cap_summary`

Examples

```r
# Load Libraries ---------------------------------------------
require(ggQC)
require(ggplot2)
# Setup Data -----------------------------------------------
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
                        Value = rnorm(100,10,1),
                        Subgroup = rep(1:20, each=5),
                        Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
                        Value = rnorm(100,20,1),
                        Subgroup = rep(1:10, each=10),
                        Process_run_id = 101:200)
df <- rbind(Process1, Process2)

# Normal Histogram XmR --------------------------------------
EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
           geom_histogram(binwidth = 1, color="purple") +
           geom_hline(yintercept=0, color="grey") +
           stat_QC_Capability(LSL=5, USL=15, show.cap.summary = "all", method="XmR") +
           scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
           ylim(0,45)
#Ex1.1

# Facet Histogram XmR ---------------------------------------
EX1.2 <- ggplot(df[order(df$Process_run_id),],
                aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
           geom_histogram(binwidth = 1) +
           geom_hline(yintercept=0, color="grey") +
           stat_QC_Capability(LSL=5, USL=15, show.cap.summary = "all", method="XmR") +
           scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
           facet_grid(.~ProcessID, scales = "free_x") + ylim(0,45)
#Ex1.2
```
# Normal Density XmR --------------------------------------------------------
EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_Capability(LSL=5, USL=15, show.cap.summary = "all", method="XmR") +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)
#EX1.3

########################################
## Example 2: xBar.rBar or xBar.sBar ##
########################################
# Single Histogram xBar.rBar ----------------------------------------------
EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_Capability(LSL=5, USL=15, method="xBar.rBar") +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
  #EX2.1

stat_QC_cap_hlabels  horizontal Label Capability Stat

Description
Draws horizontal Lables on horizontal Capability lines

Usage
stat_QC_cap_hlabels(LSL, USL, method = "xBar.rBar", show = c("LSL", "USL"),
  mapping = NULL, data = NULL, inherit.aes = TRUE, ...)

Arguments
LSL  numeric, Customer's lower specification limit
USL  numeric, Customer’s Upper specification limit
method  string, calling the following methods:
  • Individuals Charts: XmR,
  • Studentized Charts: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar,
    xMedian.rMedian
show  vector, indicating which lines to draw ie., c("LCL", "LSL", "X", "USL", "UCL")
  • LCL: Lower Control Limit
  • LSL: Lower Specification Limit
  • X: Process Center
  • USL: Upper Specification Limit
  • UCL: Upper Control Limit
mapping  Set of aesthetic mappings created by \texttt{aes()} or \texttt{aes().} If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot().}
A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data.

\texttt{inherit.aes}  If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders().}

\texttt{...}  Other arguments passed on to \texttt{layer().} These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{colour = “red”} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

Value
horizontal lines for histogram and density plots.

Examples

```r
# Load Libraries
require(ggQC)
require(ggplot2)

# Setup Data
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
                      Value = rnorm(100,10,1),
                      Subgroup = rep(1:20, each=5),
                      Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
                      Value = rnorm(100,20, 1),
                      Subgroup = rep(1:10, each=10),
                      Process_run_id = 101:200)

df <- rbind(Process1, Process2)
```

#### Example 1 XmR

```r
method <- "XmR"
```

---

**stat_QC_cap_hlabels**

45
# Normal Histogram XmR

```r
EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,45)
```

# Facet Histogram XmR

```r
EX1.2 <- ggplot(df[order(df$Process_run_id),],
    aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_histogram(binwidth = 1) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  facet_grid(.~ProcessID) + ylim(0,45)
```

# Facet Density Plot XmR

```r
EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,5)
```
#EX1.3

# Facet Density Plot XmR ---------------------------------------------

EX1.4 <- ggplot(df[order(df$Process_run_id),],
   aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
   geom_density(bw = .4, fill="grey", trim=TRUE ) +
   stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
   #show="ALL",
   # "LCL", "X", "UCL", "Sig"),
   #show=c("Sig","TOL", "DNS"),
   color="black", digits=4, size=4) +
   scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
   facet_grid(.~ProcessID) + ylim(0,.5)
#EX1.4


# Example 2: xBar.rBar or xBar.sBar #

method <- "xBar.rBar" #Alternativly Use "xBar.sBar" if desired

# Single Histogram xBar.rBar ---------------------------------------------

EX2.1 <- ggplot(df[di$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
   geom_histogram(binwidth = 1) +
   stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
   #show="ALL",
   # "LCL", "X", "UCL", "Sig"),
   #show=c("Sig","TOL", "DNS"),
   color="black", digits=4, size=4) +
   scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
   #EX2.1

# Faceted Histogram xBar.rBar ---------------------------------------------

EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
   geom_histogram(binwidth = 1) +
   stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
   stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
```r
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +

scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+

EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +

EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +

EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +

scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+

#EX2.3

# Faceted Density xBar.rBar ---------------------------------------------

EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +

scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+

#EX2.4

# Example 3: xBar.rMedian #

# Plots involving medians should give warning: "median based QC methods represent
# at best *potential* process capability"

#These plot work the same as in examples 2.X; below is an example.
```
method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    #show=c("TOL","DNS","Cp","Cpk","Pp","Ppk",
       # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL","DNS"),
    show=c("TOL","DNS","Cp","Cpk","Pp","Ppk"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))
#EX3.1

---

stat_QC_cap_hlines  
**horizontal Line Capability Stat**

**Description**

Draws horizontal Capability Lines

**Usage**

```r
stat_QC_cap_hlines(LSL, USL, method = "xBar.rBar", show = c("LSL", "USL"), mapping = NULL, data = NULL, inherit.aes = TRUE, ...)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LSL</td>
<td>numeric, Customer's lower specification limit</td>
</tr>
<tr>
<td>USL</td>
<td>numeric, Customer's Upper specification limit</td>
</tr>
<tr>
<td>method</td>
<td>string, calling the following methods:</td>
</tr>
<tr>
<td></td>
<td>• <strong>Individuals Charts</strong>: XmR,</td>
</tr>
<tr>
<td></td>
<td>• <strong>Studentized Charts</strong>: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian</td>
</tr>
<tr>
<td>show</td>
<td>vector, indicating which lines to draw ie., c(&quot;LCL&quot;, &quot;LSL&quot;, &quot;X&quot;, &quot;USL&quot;, &quot;UCL&quot;)</td>
</tr>
<tr>
<td></td>
<td>• LCL: Lower Control Limit</td>
</tr>
<tr>
<td></td>
<td>• LSL: Lower Specification Limit</td>
</tr>
<tr>
<td></td>
<td>• X: Process Center</td>
</tr>
<tr>
<td></td>
<td>• USL: Upper Specification Limit</td>
</tr>
<tr>
<td></td>
<td>• UCL: Upper Control Limit</td>
</tr>
<tr>
<td>mapping</td>
<td>Set of aesthetic mappings created by <code>aes()</code> or <code>aes()</code>. If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply <code>mapping</code> if there is no plot mapping.</td>
</tr>
</tbody>
</table>
**data**

The data to be displayed in this layer. There are three options:

- If **NULL**, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
- A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data.

**inherit.aes**

If **FALSE**, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**...**

Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

### Value

horizontal lines for histogram and density plots.

### Examples

```r
# Load Libraries
require(ggQC)
require(ggplot2)

# Setup Data
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
                       Value = rnorm(100,10,1),
                       Subgroup = rep(1:20, each=5),
                       Process_run_id = 1:100)

set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
                       Value = rnorm(100,20,1),
                       Subgroup = rep(1:10, each=10),
                       Process_run_id = 101:200)

df <- rbind(Process1, Process2)

method <- "XmR"

# Normal Histogram XmR
```

stat_QC_cap_hlines

EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
  show="ALL",
  # "LCL", "X", "UCL", "Sig"),
  show=c("TOL", "DNS"),
  color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,45)

EX1.2 <- ggplot(df[order(df$Process_run_id),],
  aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_histogram(binwidth = 1) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
  show="ALL",
  "LCL", "X", "UCL", "Sig"),
  show=c("TOL", "DNS"),
  color="black", digits=4, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
  facet_grid(.~ProcessID) + ylim(0,45)

EX1.3 <- ggplot(df[df$ProcessID == 1,],
  aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
  show="ALL",
  "LCL", "X", "UCL", "Sig"),
  show=c("TOL", "DNS"),
  color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)

# Facet Histogram XmR -----------------------------------------------
# Facet Density Plot XmR ---------------------------------------------
# Facet Density Plot XmR ---------------------------------------------

# Ex1.1
# Ex1.2
# Ex1.3
EX1.4 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_density(bw = .4, fill="grey", trim=TRUE ) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  geom_hline(yintercept=0, color="black") +
  facet_grid(.~ProcessID) + ylim(0,.5)
#EX1.4

#########################################################################
## Example 2: xBar.rBar or xBar.sBar ##
#########################################################################

method <- "xBar.rBar" #Alternativly Use "xBar.sBar" if desired

# Single Histogram xBar.rBar -------------------------------
EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  #geom_hline(yintercept=0, color="black") +
  #EX2.1

# Faceted Histogram xBar.rBar -------------------------------
EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  #EX2.2
stat_QC_cap_hlines

```r
#show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
facet_grid(.~ProcessID, scales="free_x")
#EX2.2

# Single Density xBar.rBar ----------------------------------------------

EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))#+

# Faceted Density xBar.rBar ---------------------------------------------

EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))#+

#EX2.4

########################################################################
## Example 3: xBar.rMedian ##
########################################################################

## Plots involving medians should give warning: "median based QC methods represent
## at best *potential* process capability"

##These plot work the same as in examples 2.X; below is an example.

method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
  geom_histogram(binwidth = 1) +
```

---

# Example 3: xBar.rMedian #

---

# Plots involving medians should give warning: "median based QC methods represent
# at best *potential* process capability"

#These plot work the same as in examples 2.X; below is an example.
stat_QC_cap_summary

stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))

#EX3.1

stat_QC_cap_summary   horizontal Label Capability Stat

Description

Draws horizontal Lables on horizontal Capability lines

Usage

stat_QC_cap_summary(LSL, USL, method = "xBar.rBar", px = Inf,
py = -Inf, show = c("Cp", "Cpk", "Pp", "Ppk"), digits = 8,
mapping = NULL, data = NULL, inherit.aes = TRUE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LSL</td>
<td>numeric, Customer’s lower specification limit</td>
</tr>
<tr>
<td>USL</td>
<td>numeric, Customer’s Upper specification limit</td>
</tr>
<tr>
<td>method</td>
<td>string, calling the following methods:</td>
</tr>
<tr>
<td></td>
<td>• <strong>Individuals Charts</strong>: XmR,</td>
</tr>
<tr>
<td></td>
<td>• <strong>Studentized Charts</strong>: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian</td>
</tr>
<tr>
<td>px</td>
<td>numeric, x position for table. Use Inf to force label to x-limit.</td>
</tr>
<tr>
<td>py</td>
<td>numeric, y position for table. Use Inf to force label to y-limits. May also need vjust parameter.</td>
</tr>
<tr>
<td>show</td>
<td>vector, indicating which lines to draw ie., c(&quot;TOL&quot;,&quot;DNS&quot;, &quot;Cp&quot;, &quot;Cpk&quot;, &quot;Pp&quot;, &quot;Ppk&quot;, &quot;LCL&quot;, &quot;X&quot;, &quot;UCL&quot;, &quot;Sig&quot;). The order given in the vector is the order presented in the graph.</td>
</tr>
<tr>
<td></td>
<td>• <strong>TOL</strong>: Tolerance in Sigma Units (USL-LSL)/sigma</td>
</tr>
<tr>
<td></td>
<td>• <strong>DNS</strong>: Distance to Nearest Specification Limit in Simga Units</td>
</tr>
<tr>
<td></td>
<td>• <strong>Cp</strong>: Cp (Within)</td>
</tr>
<tr>
<td></td>
<td>• <strong>Cpk</strong>: Cpk (Within)</td>
</tr>
<tr>
<td></td>
<td>• <strong>Pp</strong>: Pp (Between)</td>
</tr>
<tr>
<td></td>
<td>• <strong>Ppk</strong>: Ppk (Between)</td>
</tr>
</tbody>
</table>
• **LCL**: Lower Control Limit
• **X**: Process Center
• **UCL**: Upper Control Limit
• **Sig**: Sigma from control charts

digits
integer, how many digits to report.

mapping
Set of aesthetic mappings created by *aes()* or *aes()*. If specified and *inherit.aes* = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply *mapping* if there is no plot mapping.

data
The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to *ggplot()*.
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See *fortify()* for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them.
This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. *borders()*.

... Other arguments passed on to *layer()*.

Value
horizontal lines for histogram and density plots.

Examples

```r
# Load Libraries ----------------------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data --------------------------------------------------------------
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
    Value = rnorm(100,10,1),
    Subgroup = rep(1:20, each=5),
    Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
    Value = rnorm(100,20,1),
    Subgroup = rep(1:10, each=10),
    Process_run_id = 101:200)

df <- rbind(Process1, Process2)
```
# Example 1 XmR

You may need to use the r-studio Zoom for these plots or make the size of the `stat_QC_cap_summary` smaller with `size = some number`.

```r
method <- "XmR"

# Normal Histogram XmR

EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
  ylim(0,45)

# Facet Histogram XmR

EX1.2 <- ggplot(df[order(df$Process_run_id),],
  aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_histogram(binwidth = 1) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, show="ALL", 
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  color="black", digits=4, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
  facet_grid(.~ProcessID) +
  ylim(0,45)

# Facet Density Plot XmR

EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, show="ALL",
```
stat_QC_cap_summary

   # "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
color="black", digits=2, size=4) +

scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)

# Facet Density Plot XmR ------------------------------------------

EX1.4 <- ggplot(df[order(df$Process_run_id),],
aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
geom_density(bw = .4, fill="grey", trim=TRUE ) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
   #show="ALL",
   # "LCL", "X", "UCL", "Sig"),
   #show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
   # geom_hline(yintercept=0, color="black") +
   facet_grid(.~ProcessID) + ylim(0,.5)

#EX1.4

####################################################
## Example 2: xBar.rBar or xBar.sBar ##
####################################################

method <- "xBar.rBar" #Alternativly Use "xBar.sBar" if desired

# Single Histogram xBar.rBar ----------------------------------

EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
geom_histogram(binwidth = 1) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
   #show="ALL",
   # "LCL", "X", "UCL", "Sig"),
   #show=c("Sig","TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
   #EX2.1
EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
geom_histogram(binwidth = 1) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig", "TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) + facet_grid(~ProcessID, scales="free_x")

EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig", "TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +

EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
geom_density(bw = .4, fill="grey", alpha=.4) +
stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig", "TOL", "DNS"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) + facet_grid(~ProcessID, scales="free_x")

# Example 3: xBar.rMedian #
# Plots involving medians should give warning: "median based QC methods represent
# at best *potential* process capability"

These plot work the same as in examples 2.X; below is an example.

```r
method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))
#EX3.1
```

---

### `stat_QC_cap_vlabels`

**Vertical Label Capability Stat**

**Description**

Draws Vertical Labels on Vertical Capability lines

**Usage**

```r
stat_QC_cap_vlabels(LSL, USL, method = "xBar.rBar", show = c("LSL", "USL"), mapping = NULL, data = NULL, inherit.aes = TRUE, ...)
```

**Arguments**

- **LSL**: numeric, Customer's lower specification limit
- **USL**: numeric, Customer's upper specification limit
- **method**: string, calling the following methods:
  - **Individuals Charts**: XmR,
  - **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian
- **show**: vector, indicating which lines to draw, e.g., c("LCL", "LSL", "X", "USL", "UCL")
  - **LCL**: Lower Control Limit
  - **LSL**: Lower Specification Limit
  - **X**: Process Center
  - **USL**: Upper Specification Limit
• **UCL:** Upper Control Limit

**mapping**
Set of aesthetic mappings created by `aes()` or `aes_()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

**data**
The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.

**inherit.aes**
If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**...**
Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

**Value**
vertical lines for histogram and density plots.

**Examples**

```r
# Load Libraries ---------------------------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data -------------------------------------------------------------------
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
                        Value = rnorm(100,10,1),
                        Subgroup = rep(1:20, each=5),
                        Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
                        Value = rnorm(100,20, 1),
                        Subgroup = rep(1:10, each=10),
                        Process_run_id = 101:200)

df <- rbind(Process1, Process2)
```

`# You may need to use the r-studio Zoom for these plots or make the size of the
# stat_QC_cap_summary smaller with size = some number"`
method <- "XmR"

# Normal Histogram XmR -----------------------------------------------

EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
                   #show= "ALL",
                   color="black", digits=2, size=4) +
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) +
  ylim(0,45)
  #EX1.1

# Facet Histogram XmR ------------------------------------------------

EX1.2 <- ggplot(df[order(df$Process_run_id),],
  aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_histogram(binwidth = 1) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
                   #show= "ALL",
                   color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  facet_grid(.~ProcessID) +
  ylim(0,45)
  #EX1.2

# Facet Density Plot XmR ---------------------------------------------

EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
                   show="ALL",
                   color="black", digits=2, size=4) +
scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)

# Facet Density Plot XmR -----------------------------------------------

EX1.4 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_density(bw = .4, fill="grey", trim=TRUE ) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  # geom_hline(yintercept=0, color="black") +
  facet_grid(.~ProcessID) + ylim(0,.5)

# Example 2: xBar.rBar or xBar.sBar 

method <- "xBar.rBar" #Alternatively Use "xBar.sBar" if desired

# Single Histogram xBar.rBar ------------------------------------------

EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
  facet_grid(.-ProcessID) + ylim(0,.5)

# Faceted Histogram xBar.rBar -----------------------------------------

EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
#show="ALL",
#show=c("TOL","DNS", "Cpk", "Pp", "Ppk",
# "LCL", "X", "UCL", "Sig"),
#show=c("Sig","TOL", "DNS"),
show=c("TOL","DNS", "Cpk", "Pp", "Ppk"),
color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
facets_grid(.~ProcessID, scales="free_x")

# Single Density xBar.rBar ----------------------------------------------
EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
  #show=c("TOL","DNS", "Cpk", "Pp", "Ppk",
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  show=c("TOL","DNS", "Cpk", "Pp", "Ppk"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))

# Faceted Density xBar.rBar ---------------------------------------------
EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
  #show="ALL",
  #show=c("TOL","DNS", "Cpk", "Pp", "Ppk",
  # "LCL", "X", "UCL", "Sig"),
  #show=c("Sig","TOL", "DNS"),
  show=c("TOL","DNS", "Cpk", "Pp", "Ppk"),
  color="black", digits=4, size=4) +
scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))+
  facet_grid(.~ProcessID, scales="free_x")

# Example 3: xBar.rMedian

# Plots involving medians should give warning: "median based QC methods represent
# at best *potential* process capability"
These plots work the same as in examples 2.X; below is an example.

```r
method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))
#EX3.1
```

---

**stat_QC_cap_vlines**  
**Vertical Line Capability Stat**

**Description**  
Draws Vertical Capability Stats

**Usage**  
```r
stat_QC_cap_vlines(LSL, USL, method = "xBar.rBar", show = c("LSL", "USL"), mapping = NULL, data = NULL, inherit.aes = TRUE, ...)  
```

**Arguments**

- **LSL**  
  numeric, Customer’s lower specification limit

- **USL**  
  numeric, Customer’s Upper specification limit

- **method**  
  string, calling the following methods:
  - **Individuals Charts**: XmR,
  - **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian

- **show**  
  vector, indicating which lines to draw ie., c("LCL", "LSL", "X", "USL", "UCL")

- **mapping**  
  Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
**data**

The data to be displayed in this layer. There are three options:

- If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
- A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data.

**inherit.aes**

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**...**

Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

**Value**

vertical lines for histogram and density plots.

**Examples**

```r
# Load Libraries -----------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data -----------------------------------------------
set.seed(5555)
Process1 <- data.frame(ProcessID = as.factor(rep(1,100)),
Value = rnorm(100,10,1),
Subgroup = rep(1:20, each=5),
Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(ProcessID = as.factor(rep(2,100)),
Value = rnorm(100,20,1),
Subgroup = rep(1:10, each=10),
Process_run_id = 101:200)
df <- rbind(Process1, Process2)

# Normal Histogram XmR -----------------------------------------------
method <- "XmR"
# You may need to use the r-studio Zoom for these plots or make the size of the
# stat_QC_cap_summary smaller with size = some number"

# Normal Histogram XmR -----------------------------------------------
```

```
stat_QC_cap_vlines

EX1.1 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1, color="purple") +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    show=c("X", "LSL", "USL"), method=method)
  scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,45)
#Ex1.1

# Facet Histogram XmR ---------------------------------------------

EX1.2 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_histogram(binwidth = 1) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    "LCL", "X", "UCL", "Sig"),
    scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) + ylim(0,45)
#EX1.2

# Facet Density Plot XmR ---------------------------------------------

EX1.3 <- ggplot(df[df$ProcessID == 1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="purple", trim=TRUE) +
  geom_hline(yintercept=0, color="grey") +
  stat_QC_cap_vlines(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, show=c("X", "LSL", "USL"), method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method,
    "LCL", "X", "UCL", "Sig"),
    scale_x_continuous(expand = expand_scale(mult = c(0.15,.8))) + ylim(0,.5)
#EX1.3

# Facet Density Plot XmR ---------------------------------------------
EX1.4 <- ggplot(df[order(df$Process_run_id),],
aes(x=Value, QC.Subgroup=Subgroup, color=ProcessID)) +
  geom_density(bw = .4, fill="grey", trim=TRUE ) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  #geom_hline(yintercept=0, color="black") +
  facet_grid(.~ProcessID) + ylim(0,.5)
#EX1.4

########################################################################
## Example 2: xBar.rBar or xBar.sBar ##
########################################################################

method <- "xBar.rBar" #Alternatively Use "xBar.sBar" if desired

# Single Histogram xBar.rBar ----------------------------------------------
EX2.1 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  #geom_hline(yintercept=0, color="black") +
  #EX2.1

# Faceted Histogram xBar.rBar ---------------------------------------------
EX2.2 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_histogram(binwidth = 1) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, #py=.3,
    #show="ALL",
    # "LCL", "X", "UCL", "Sig"),
    #show=c("Sig", "TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) +
  #EX2.2
EX2.2

```
# Single Density xBar.rBar ----------------------------------------------
EX2.3 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, py=.3,
    #show="ALL",
    #  "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
#EX2.3
```

EX2.4 <- ggplot(df[df$ProcessID==1,], aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, py=.3,
    #show="ALL",
    #  "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8))) #+
  #EX2.4

```
# Faceted Density xBar.rBar ---------------------------------------------
EX2.4 <- ggplot(df, aes(x=Value, QC.Subgroup=Subgroup)) +
  geom_density(bw = .4, fill="grey", alpha=.4) +
  stat_QC_cap_vlines(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_vlabels(LSL = 5, USL = 15, method=method) +
  stat_QC_cap_summary(LSL = 5, USL = 15, method=method, py=.3,
    #show="ALL",
    #  "LCL", "X", "UCL", "Sig"),
    #show=c("Sig","TOL", "DNS"),
    color="black", digits=4, size=4) +
  scale_x_continuous(expand = ggplot2::expand_scale(mult = c(0.15,.8)))
  #EX2.4
```

```
# Example 3: xBar.rMedian #
```

```
# Plots involving medians should give warning: "median based QC methods represent
# at best *potential* process capability"

#These plot work the same as in examples 2.X; below is an example.

method <- "xBar.rMedian"
EX3.1 <- ggplot(df[order(df$Process_run_id),], aes(x=Value, QC.Subgroup=Run)) +
  geom_histogram(binwidth = 1) +
```
stat_QC_labels

Write QC Line Labels to ggplot QC Charts.

Description
Write QC line labels to ggplot QC Charts. Useful if you want to see the value of the center line and QC limits. see method argument for methods supported.

Usage
stat_QC_labels(mapping = NULL, data = NULL, geom = "label", position = "identity", na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, n = NULL, digits = 1, method = "xBar.rBar", color.qc_limits = "red", color.qc_center = "black", text.size = 3, physical.limits = c(NA, NA), limit.txt.label = c("LCL", "UCL"), ...)

Arguments

- **mapping** Set of aesthetic mappings created by aes() or aes_.() If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

- **data** The data to be displayed in this layer. There are three options: If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data.

- **geom** The geometric object to use display the data

- **position** Position adjustment, either as a string, or the result of a call to a position adjustment function.

- **na.rm** a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

n number, for

• **Studentized Charts**, used for custom or hypothetical subgroup size.

• **np Charts**, used to specify a fixed area of opportunity.

digits integer, indicating the number of decimal places

method string, calling the following methods:

• **Individuals Charts**: mR, XmR,

• **Attribute Charts**: c, np, p, u,

• **Studentized Charts**: xBar.rBar, xBar.rMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian

• **Dispersion Charts**: rBar, rMedian, sBar.

color.qc_limits color, used to colorize the plot’s upper and lower mR control limits.

color.qc_center color, used to colorize the plot’s center line.

text.size number, size of the text label

physical.limits vector, specify lower physical boundary and upper physical boundary

limit.txt.label vector, provides option for naming or not showing the limit text labels (e.g., UCL, LCL)

• limit.txt.label = c("LCL", "UCL"): default

• limit.txt.label = c("Low", "High"): changes the label text to low and high

• limit.txt.label = NA: does not show label text.

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

Value
data need to produce the mR plot in ggplot.

Examples

```
# Example 1: mR Chart #

# Load Libraries
require(ggQC)
```
require(ggplot2)

# Setup Data -----------------------------------------------
set.seed(5555)
Process1 <- data.frame(processID = as.factor(rep(1, 100)),
                     metric_value = rnorm(100, 0, 1),
                     subgroup_sample = rep(1:20, each=5),
                     Process_run_id = 1:100)
set.seed(5556)
Process2 <- data.frame(processID = as.factor(rep(2, 100)),
                     metric_value = rnorm(100, 5, 1),
                     subgroup_sample = rep(1:10, each=10),
                     Process_run_id = 101:200)
Both_Processes <- rbind(Process1, Process2)

# Facet Plot - Both Processes ---------------------------------
EX1.1 <- ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
           geom_point() + geom_line() + stat_QC(method="XmR") +
           stat_QC_labels(method="XmR", digits = 2) +
           facet_grid(.~processID, scales = "free_x")
#EX1.1

EX1.2 <- ggplot(Both_Processes, aes(x=Process_run_id, y = metric_value)) +
           stat_mR() + ylab("Moving Range") +
           stat_QC_labels(method="mR", digits = 2) +
           facet_grid(.~processID, scales = "free_x")
#EX1.2

# Example 2: XbarR Chart #
# Facet Plot - Studentized Process ---------------------------------
EX2.1 <- ggplot(Both_Processes, aes(x=subgroup_sample,
                     y = metric_value,
                     group = processID)) +
           geom_point(alpha=.2) +
           stat_summary(fun.y = "mean", color="blue", geom=c("point")) +
           stat_summary(fun.y = "mean", color="blue", geom=c("line")) +
           stat_QC() + facet_grid(.~processID, scales = "free_x") +
           stat_QC_labels(text.size =3, label.size=.1)
#EX2.1

EX2.2 <- ggplot(Both_Processes, aes(x=subgroup_sample,
                     y = metric_value,
                     group = processID)) +
           stat_summary(fun.y = "QCrange", color="blue", geom = "point") +
           stat_summary(fun.y = "QCrange", color="blue", geom = "line") +
           stat_QC(method="rBar") +
           stat_QC_labels(digits=2, method="rBar") +
           ylab("Range") +
           facet_grid(.~processID, scales = "free_x")
stat_qc_violations

Inspect QC Violations

Description

ggplot stat function that renders a faceted plot of QC violations based on the following 4 rules:

- **Violation Same Side**: 8 or more consecutive, same-side points
- **Violation 1 Sigma**: 4 or more consecutive, same-side points exceeding 1 sigma
- **Violation 2 Sigma**: 2 or more consecutive, same-side points exceeding 2 sigma
- **Violation 3 Sigma**: any points exceeding 3 sigma

Usage

```r
stat_qc_violations(mapping = NULL, data = NULL, geom = "point",
position = "identity", show.legend = NA, inherit.aes = TRUE,
na.rm = FALSE, method = "xBar.rBar", geom_points = TRUE,
geom_line = TRUE, point.size = 1.5, point.color = "black",
violation_point.color = "red", line.color = NULL,
rule.color = "darkgreen", show.facets = c(1:4), ...)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data.
- **geom**: The geometric object to use display the data
- **position**: Position adjustment, either as a string, or the result of a call to a position adjustment function.
- **show.legend**: logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.
- **inherit.aes**: If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.
na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

method string, calling the following methods:

- **Individuals Charts**: XmR,
- **Studentized Charts**: xBar.rBar, xBarMedian, xBar.sBar, xMedian.rBar, xMedian.rMedian

geom_points boolean, draw points

geom_line boolean, draw line

point.size number, size of points on chart

point.color string, color of points on charts (e.g., "black")

violation_point.color string, color of violation points on charts (e.g., "red")

line.color string, color of lines connecting points

rule.color string, color or horizontal rules indicating distribution center and sigma levels

show.facets vector, selects violation facet 1 through 4. e.g., c(1:4), c(1,4)

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

Value

faceted plot.

Examples

#####################################
# Example 1: XmR Check Violations #
#####################################

# Load Libraries ---------------------------------------------
require(ggQC)
require(ggplot2)

# Setup Data ---------------------------------------------
set.seed(5555)
QC_XmR <- data.frame(
data = c(c(-1, 2.3, 2.4, 2.5), #Outlier Data
    sample(c(rnorm(60),5,-5), 62, replace = FALSE), #Normal Data
    c(1,-.3, -2.4,-2.6,-2.5,-2.7, .3)), #Outlier Data
Run_Order = 1:73 #Run Order
)

# Render QC Violation Plot-----------------------------------
EX1 <- ggplot(QC_XmR, aes(x = Run_Order, y = data)) +
stat_qc_violations(method = "XmR") #Makes facet graph with violations
# Example 2: Xbar Check Violations

# Setup Some Data

QC_xBar.rBar <- do.call(rbind, lapply(1:3, function(X){
  set.seed(5555+X)  #Loop over 3 seeds
  data.frame(sub_group = rep(1:42), sub_class = letters[X],
    c(c(runif(n = 5, min = 2.0,3.2)),  #Outlier Data
      sample(c(rnorm(30),5,-4), 32, replace = FALSE), #Normal Data
      c(runif(n = 5, min = -3.2, max = -2.0))  #Outlier Data
    )
})
})
colnames(QC_xBar.rBar) <- c("sub_group","sub_class", "value")

# Render QC Violation Plot

EX2 <- ggplot(QC_xBar.rBar, aes(x = sub_group, y = value)) +
  stat_qc_violations(method = "xBar.rBar")
#stat_qc_violations(method="xBar.rMedian")
#stat_qc_violations(method="xBar.sBar")
#stat_qc_violations(method="xMedian.rBar")
#stat_qc_violations(method="xMedian.rMedian")

# Example 3: Selected Facets

EX3 <- ggplot(QC_xBar.rBar, aes(x = sub_group, y = value)) +
  stat_qc_violations(method = "xBar.rBar", show.facets = c(4))

# Complete User Control - Bypass stat_qc_violation

# The code below has two options if you are looking for complete
# control over the look and feel of the graph. Use option 1 or option
# 2 as appropriate. If you want something quick and easy use examples above.

# Option 1: Setup for XmR Type Data

# QC_XmR: Defined in Example 1

QC_Vs <- QC_Violations(data = QC_XmR$data, method = "XmR")
### Option 2: Setup for xBar.rBar Type Data

```r
# QC_xBar.rBar: Defined in Example 2
QC_Vs <- QC_Violations(data = QC_xBar.rBar,
                         formula = value~sub_group,
                         method = "xBar.rBar")
QC_Stats <- QC_Lines(data = QC_xBar.rBar,
                      formula = value~sub_group,
                      method = "xBar.rBar")
MEAN <- QC_Stats$xBar_Bar
SIGMA <- QC_Stats$sigma
```  

##### Setup second table for horizontal rules

```r
FacetNames <- c("Violation Same Side",
                 "Violation 1 Sigma",
                 "Violation 2 Sigma",
                 "Violation 3 Sigma")
QC_Vs$Violation_Result <- ordered(QC_Vs$Violation_Result, levels=FacetNames)
QC_Stats_df <- data.frame(Violation_Result = factor(x = FacetNames, levels = FacetNames),
                           SigmaPlus = MEAN+SIGMA*0:3,
                           MEAN = MEAN,
                           SigmaMinus = MEAN-SIGMA*0:3)
```  

##### Make the Plot

```r
ggplot(QC_Vs, aes(x=Index, y=data, color=Violation, group=1)) +
  geom_point() + geom_line() +
  facet_grid(.~Violation_Result) +
  geom_hline(data = QC_Stats_df, aes(yintercept = c(SigmaPlus))) +
  geom_hline(data = QC_Stats_df, aes(yintercept = c(SigmaMinus))) +
  geom_hline(data = QC_Stats_df, aes(yintercept = c(MEAN)))
```  

---

**uBar**

*Mean Rate: Count Data (u-chart)*

---

**Description**

Calculates overall mean rate for count data acquired over a variable area of opportunity.

**Usage**

```r
uBar(y, n, na.rm = FALSE, ...)
```
uBar_LCL

Arguments

y Vector of counts per unit opportunity (rate). Observations may have a different area of opportunity, n.

n A vector representing the area of opportunity.

na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

... further arguments passed to or from other methods.

Value

A vector of mean rate, length equal to length of parameter y.

Examples

```r
set.seed(5555)
counts <- rpois(100, 25)
n <- rpois(100, 15)
uBar(y = counts / n, n = n)
```

uBar_LCL Lower Control Limit: Count Data (u-chart)

Description

Calculates point-wise lower control limit (LCL) for count data acquired over a variable area of opportunity.

Usage

```r
uBar_LCL(y, n, na.rm = FALSE, ...)
```

Arguments

y Vector of counts per unit opportunity (rate). Observations may have a different area of opportunity, n.

n A vector representing the area of opportunity.

na.rm a logical value indicating whether NA values should be stripped before the computation proceeds.

... further arguments passed to or from other methods.

Value

A vector; point-wise 3-sigma lower control limit (LCL)
Examples

```r
set.seed(5555)
counts <- rpois(100, 25)
n <- rpois(100, 15)
uBar_UCL(y = counts / n, n = n)
```

Description

Calculates point-wise upper control limit (UCL) for count data acquired over a variable area of opportunity.

Usage

```r
uBar_UCL(y, n, na.rm = FALSE, ...)
```

Arguments

- `y`         Vector of counts per unit opportunity (rate). Observations may have a different area of opportunity, n.
- `n`         A vector representing the area of opportunity.
- `na.rm`     a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...`       further arguments passed to or from other methods.

Value

A vector; point-wise 3-sigma upper control limit (UCL)

Examples

```r
set.seed(5555)
counts <- rpois(100, 25)
n <- rpois(100, 15)
uBar_UCL(y = counts / n, n = n)
```
**UD**  
*Calculate Distance to Upper Specification Limit*

**Description**

function to calculate a standardized distance to the Upper specification limit (sigma units)

**Usage**

\[ \text{UD}(\text{LSL}, \text{USL}, \text{QC.Center}, \text{QC.Sigma}) \]

**Arguments**

- **LSL**: number, customer’s lower specification limit.
- **USL**: number, customer’s upper specification limit.
- **QC.Center**: number, the mean or median value determined from an XmR plot or a Studentized (e.g., xBar) analysis.
- **QC.Sigma**: number, the sigma value determined from an XmR plot or a Studentized (e.g., xBar) analysis.

**Value**

numeric, standardized distance to the upper specification limit (sigma units)

---

**xBar_Bar**  
*Mean of Subgroup Means*

**Description**

Calculates the mean subgroup means used when constructing a xBar-R or xBar-S charts.

**Usage**

\[ \text{xBar.Bar}(\text{data}, \text{value}, \text{grouping}, \text{formula} = \text{NULL}, ...) \]

**Arguments**

- **data**: data frame to be processed
- **value**: numeric vector in a data frame with values of interest.
- **grouping**: single factor/variable to split the data frame "values" by.
- **formula**: a formula, such as \( y \sim x1 + x2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
- **...**: further arguments passed to or from other methods.
**Value**

A number; mean of subgroup means.

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_Bar(data = df, formula = v~g)
```

---

**Description**

Calculates the xBar_One LCL used when constructing a xBar-One chart.

**Usage**

```r
xBar_one_LCL(y, na.rm = FALSE, ...)
```

**Arguments**

- `y`: Vector of values
- `na.rm`: a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...`: further arguments passed to or from other methods.

**Value**

A number; xBar_One Lower Control Limit (LCL)

**Examples**

```r
set.seed(5555)
values <- rnorm(n = 100, mean = 25, sd = 1)
xBar_one_LCL(values)
```
**xBar_one_UCL**  
*xBar_One Upper Control Limit (UCL)*

**Description**
Calculates the xBar_One UCL used when constructing a xBar-One chart.

**Usage**
```r
xBar_one_UCL(y, na.rm = FALSE, ...)
```

**Arguments**
- `y`  
  Vector of values
- `na.rm`  
  a logical value indicating whether NA values should be stripped before the computation proceeds.
- `...`  
  further arguments passed to or from other methods.

**Value**
A number; xBar_One Upper Control Limit (UCL)

**Examples**
```r
set.seed(5555)
values <- rnorm(n = 100, mean = 25, sd = 1)
xBar_one_UCL(values)
```

---

**xBar_rBar_LCL**  
*Mean of Subgroup Means Lower Control Limit (LCL)*

**Description**
Calculates the mean of subgroup means lower control limit used when constructing a xBar-R charts.

**Usage**
```r
xBar_rBar_LCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```
**Arguments**

- **data**: data frame to be processed
- **value**: numeric vector in a data frame with values of interest.
- **grouping**: single factor/variable to split the data frame "values" by.
- **n**: a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- **natural**: logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values
- **formula**: a formula, such as \( y \sim x_1 + x_2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables

**Value**

A number; mean of subgroup means lower control limit.

**Examples**

```
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_rBar_LCL(data = df, formula = v~g)
```

---

**xBar_rBar_UCL**  
**Mean of Subgroup Means Upper Control Limit (UCL)**

**Description**

Calculates the mean of subgroup means upper control limit used when constructing a xBar-R charts.

**Usage**

```
xBar_rBar_UCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

**Arguments**

- **data**: data frame to be processed
- **value**: numeric vector in a data frame with values of interest.
- **grouping**: single factor/variable to split the data frame "values" by.
- **n**: a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- **natural**: logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values
- **formula**: a formula, such as \( y \sim x_1 + x_2 \), where the \( y \) variable is numeric data to be split into groups according to the grouping \( x \) factors/variables
**Mean of Subgroup Means Lower Control Limit (LCL) based on Median Range**

**Value**

A number; mean of subgroup means lower control limit.

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_rMedian_LCL(data = df, formula = v~g)
```

**Description**

Calculates the mean of subgroup means lower control limit based on the median range. The result is used when constructing a xBar-rMedian charts.

**Usage**

```r
xBar_rMedian_LCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

**Arguments**

- `data`: data frame to be processed
- `value`: numeric vector in a data frame with values of interest.
- `grouping`: single factor/variable to split the data frame "values" by.
- `n`: a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- `natural`: logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values.
- `formula`: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

**Value**

A number; mean of subgroup means Lower Control Limit (LCL) based on Median Range

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_rMedian_LCL(data = df, formula = v~g)
```
**xBar_rMedian_UCL**  
Mean of Subgroup Means Upper Control Limit (UCL) based on Median Range

**Description**
Calculates the mean of subgroup means upper control limit based on the median range. The result is used when constructing a xBar-rMedian charts.

**Usage**

```r
xBar_rMedian_UCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

**Arguments**
- **data**  
data frame to be processed
- **value**  
numeric vector in a data frame with values of interest.
- **grouping**  
single factor/variable to split the data frame "values" by.
- **n**  
a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- **natural**  
logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values
- **formula**  
a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

**Value**
A number; mean of subgroup means Upper Control Limit (UCL) based on Median Range

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_rMedian_UCL(data = df, formula = v-g)
```
Mean of Subgroup Means Lower Control Limit (LCL) based on Standard Deviation

Description

Calculates the mean of subgroup means lower control limit based on the standard deviation. The result is used when constructing a xBar-S charts.

Usage

```r
xBar_sBar_LCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

Arguments

- **data**: data frame to be processed
- **value**: numeric vector in a data frame with values of interest.
- **grouping**: single factor/variable to split the data frame "values" by.
- **n**: a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- **natural**: logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values.
- **formula**: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

Value

A number; mean of subgroup means Lower Control Limit (LCL) based on standard deviation

Examples

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_sBar_LCL(data = df, formula = v~g)
```
xBar_sBar_UCL  

Mean of Subgroup Means Upper Control Limit (UCL) based on Standard Deviation

Description

Calculates the mean of subgroup means upper control limit based on the standard deviation. The result is used when constructing a xBar-S charts.

Usage

xBar_sBar_UCL(data, value, grouping, n = NULL, natural = F, formula = NULL)

Arguments

data  
data frame to be processed

value  
numeric vector in a data frame with values of interest.

grouping  
single factor/variable to split the data frame "values" by.

n  
a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.

natural  
logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values

formula  
a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

Value

A number; mean of subgroup means Upper Control Limit (UCL) based on standard deviation

Examples

set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_sBar_UCL(data = df, formula = v~g)
xMedian_Bar

**Mean of Subgroup Medians**

*Description*

Calculates the mean of subgroup medians used when constructing a xMedian-R charts.

*Usage*

```r
xMedian_Bar(data, value, grouping, formula = NULL, ...)
```

*Arguments*

- `data` data frame to be processed
- `value` numeric vector in a data frame with values of interest.
- `grouping` single factor/variable to split the data frame "values" by.
- `formula` a formula, such as `y ~ x1 + x2`, where the `y` variable is numeric data to be split into groups according to the grouping `x` factors/variables
- `...` further arguments passed to or from other methods.

*Value*

A number; mean of subgroup medians.

*Examples*

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xMedian_Bar(data = df, formula = v~g)
```

---

xMedian_rBar_LCL

**Mean of Subgroup Medians Lower Control Limit (LCL) based on Mean Range**

*Description*

Calculates the mean of subgroup medians lower control limit based on the mean range. The result is used when constructing a xMedian-R charts.

*Usage*

```r
xMedian_rBar_LCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```
xMedian_rBar_UCL

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>data</code></td>
<td>data frame to be processed</td>
</tr>
<tr>
<td><code>value</code></td>
<td>numeric vector in a data frame with values of interest.</td>
</tr>
<tr>
<td><code>grouping</code></td>
<td>single factor/variable to split the data frame &quot;values&quot; by.</td>
</tr>
<tr>
<td><code>n</code></td>
<td>a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.</td>
</tr>
<tr>
<td><code>natural</code></td>
<td>logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values</td>
</tr>
<tr>
<td><code>formula</code></td>
<td>a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables</td>
</tr>
</tbody>
</table>

**Value**

A number; mean of subgroup medians Lower Control Limit (LCL) based on mean range

**Examples**

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xBar_rMedian_LCL(data = df, formula = v~g)
```

---

**xMedian_rBar_UCL**

Mean of Subgroup Medians Upper Control Limit (UCL) based on mean Range

**Description**

Calculates the mean of subgroup medians upper control limit based on the mean subgroup range. The result is used when constructing a xMedian-R charts.

**Usage**

```r
xMedian_rBar_UCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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<tr>
<td><code>data</code></td>
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<td>numeric vector in a data frame with values of interest.</td>
</tr>
<tr>
<td><code>grouping</code></td>
<td>single factor/variable to split the data frame &quot;values&quot; by.</td>
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</tr>
<tr>
<td><code>formula</code></td>
<td>a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables</td>
</tr>
</tbody>
</table>
Value

A number; mean of subgroup means Upper Control Limit (UCL) based on Median Range

Examples

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xMedian_rBar_UCL(data = df, formula = v~g)
```

**xMedian_rMedian_LCL**

Mean of Subgroup Medians Lower Control Limit (LCL) based on Median Range

Description

Calculates the mean of subgroup medians lower control limit based on the median subgroup range. The result is used when constructing a xMedian-rMedian charts.

Usage

```
xMedian_rMedian_LCL(data, value, grouping, n = NULL, natural = F, formula = NULL)
```

Arguments

- `data`: data frame to be processed
- `value`: numeric vector in a data frame with values of interest.
- `grouping`: single factor/variable to split the data frame "values" by.
- `n`: a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
- `natural`: logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values
- `formula`: a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

Value

A number; mean of subgroup median Lower Control Limit (LCL) based on Median Range

Examples

```r
set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xMedian_rMedian_LCL(data = df, formula = v~g)
```
Description

Calculates the mean of subgroup medians upper control limit based on the median subgroup range. The result is used when constructing a xMedian-rMedian charts.

Usage

xMedian_rMedian_UCL(data, value, grouping, n = NULL, natural = F, formula = NULL)

Arguments

data data frame to be processed
value numeric vector in a data frame with values of interest.
grouping single factor/variable to split the data frame "values" by.
n a number indicating a hypothetical subgroup size other than, function determined subgroup n determined by the floor length of subgroup values.
natural logical, if TRUE calculate limits for individuals (n=1) else calculate for n determined by the floor length of subgroup values
formula a formula, such as y ~ x1 + x2, where the y variable is numeric data to be split into groups according to the grouping x factors/variables

Value

A number; mean of subgroup median upper Control Limit (UCL) based on Median Range

Examples

set.seed(5555)
df <- data.frame(v=rnorm(60, 0, 1), g=rep(c("A","B","C","D","E"), each=12))
xMedian_rMedian_UCL(data = df, formula = v~g)
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