Package: flowTrans (via r-universe)

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Type Package

Title Parameter Optimization for Flow Cytometry Data Transformation

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Author Greg Finak <gfinak@fredhutch.org>, Juan Manuel-Perez <jperez@ircm.qc.ca>, Raphael Gottardo <rgottard@fredhutch.org>

Maintainer Greg Finak <gfinak@fredhutch.org>

Description Profile maximum likelihood estimation of parameters for flow cytometry data transformations.

License Artistic-2.0

LazyLoad yes

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Imports flowCore, methods, flowViz, stats, flowClust

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`flowTrans-package` *Parameter Optimization for Flow Cytometry Data Transformation*

Description

Maximum likelihood estimation of parameters for common flow cytometry data transformations.

Details

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Index:

`flowTrans`	`Optimizing transformations for flow cytometry data`

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Juan Manuel-Perez <jperez@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

Maintainer: Greg Finak <greg.finak@ircm.qc.ca>

References

Finak G, Perez J M, Weng A, Gottardo R. Optimizing Transformations for Flow Cytometry. (Submitted)

Examples

```
#Load some data
data(GvHD)
#transform the first sample, forward and side scatter.
result<-flowTrans(GvHD[[1]],"mclMultivArcSinh",colnames(GvHD[[1]])[1:2],n2f=FALSE,parameters.only=FALSE);
plot(result$result);
summary(result);
```

`extractParams` *Extract the transformation parameters from a flowTransResult*

Description

Extracts the transformation parameters from a `flowTransResult` object

Usage

```
extractParams(x, dims = NULL)
```

Arguments

`x`	An object of type `flowTransResult` returned by a call to `flowTrans`
`dims`	A character vector specifying the dimensions for which to extract transformation parameters.

Value

A list of length `length(dims)`. Each element contains a vector of parameters for transforming the particular dimension.The names of the list elements correspond to the names of the dimensions.

Note

`flowTrans` estimates common transformation parameters.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

References

Finak G, Perez JM, Weng A, Gottardo R. Optimizing Data Transformation for Flow Cytometry. (Submitted)

See Also

`summary`, `flowTrans`, `flowTransResult`

Examples

```
m <- t(matrix(rnorm(10000),2))
colnames(m) <- c("A","B")
m <- flowFrame(m)
res <- flowTrans(m,"mclMultivBoxCox", c("A","B"), n2f=FALSE,
                 parameters.only=FALSE)
summary(res)
extractParams(res)
```

---

flowTrans *Optimizing transformations for flow cytometry data.*

Description

This is the principal function in the package. The function takes data, a transformation function name, dimension names, and optional preselection parameter as input, and runs the maximum likelihood optimization on the data, performs the transformation, and returns the transformed data together with a list of transformation paramters for each dimension. The optimization is set to maximize the likelihood of the parameters given the data, such that the transformed data is normally distributed. An optional parameter `n2f=[T,F]` allows an automated preselection of an approximately bivariate normal population via the `norm2Filter` function. The transformation parameters are then optimized for this preselected region, and finally applied globally to the entire range of data. The optional argument `parameters.only=[T,F]` specifies whether to return the parameters or the transformed data.

Usage

```
flowTrans(dat, fun, dims, n2f,parameters.only)
```

Arguments

`dat`	The data to be transformed, should be a `flowFrame` object.
`fun`	A character string naming the transformation function to be applied. Can be one of: `mclMultivBiexp`, `mclMultivBoxCox`,`mclMultivArcSinh`, and `mclMultivLinLog`. The `Multiv` series of functions estimate common transformation parameters for all dimensions.
`dims`	A character vector identifying the dimensions to be transformed.
`n2f`	An optional `TRUE`, `FALSE` value identifying whether the data should be prefiltered with `norm2Filter` to select a region of the data for which to optimize the transformation. Default is `FALSE`.
`parameters.only`	A logical specifying whether to return only the parameters, and not the transformed data. `mclMultivArcSinh` a, b, c; c=0 `mclMultivBiexp` a, b, c, d, f, w; f=0 `mclMultivBoxCox` theta `mclMultivLinLog` theta

Details

The transformation functions are multivariate, common parameter transformations. The implementation utilizes a look up table to call optimization routines for the different transformations as well as optional `flowCore` and `flowClust` transformation implementations to optimize parameters and transform data from a single interface. Parameters are optimized such that the transformed data is multivariate-normal.

Value

if `parameters.only` = `FALSE` then:

`flowTransResult`
: A `flowTransResult` object

If `parameters.only=TRUE` the returned value will be a vector of common transformation parameters: if `mclMultivArcSinh` is called, the returned vector will contain a, b, and c=0; if `mclMultivBiexp` is called, the returned vector will contain a, b, c, d, w; if `mclMultivBoxCox` is called, the returned vector will contain theta; if `mclMultivLinLog` is called, the returned vector will contain theta.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

References

Finak G, Perez J M, Weng A, Gottardo R. Optimizing Transformations for Flow Cytometry. (Submitted)

Examples

```
data(GvHD)
result <- flowTrans(GvHD[[1]], "mclMultivArcSinh",
          colnames(GvHD[[1]])[1:2], n2f=FALSE, parameters.only=FALSE)
par(mfrow=c(1,2))
contour(GvHD[[1]][,1:2], main="Untransformed FSC vs SSC")
contour(result$result[,1:2], main="Transformed FSC vs SSC")
summary(result)
```

`flowTrans-methods` *S4 method for optimizing parameters of a flow transformation and optionally transforming a flowFrame*

Description

Transforms a flowFrame and optimizes the parameters for the selected transformation.

Methods

dat = "flowFrame", fun = "character", dims = "character", n2f = "logical", parameters.only = "logical"
Transforms the flowFrame using the function fun over the dimensions dims, with optional bivaraite normal prefiltering. Parameters are optimized to make the transformed data multivariate normal depending on the selected transformation

---

flowTransResult-class *Class "flowTransResult"*

Description

Class that contains the results of a call to `flowTrans` on a `flowFrame`

Objects from the Class

Objects can be created by calls of the form `new("flowTransResult", ...)`. The object contains three slots: the transformed flowFrame, a `transform` object from which the parameters can be extracted, and a `dims` slot containing a character vector of the dimensions that have been transformed.

Slots

`result`: Object of class `"flowFrame"`. The transformed data.

`trans`: Object of class `"transform"`. The transform applied to the flowFrame. Parameters can be extracted via `summary(trans)`.

`dims`: Object of class `"character"`. The names of the dimensions that have been transformed.

Methods

summary `signature(object = "flowTransResult")`: Summarize the transformed data.

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>.

References

Finak G, Perez JM, Weng A, Gottardo R. Optimizing Data Transformation for Flow Cytometry.

See Also

`extractParams` `summary`

Examples

```
m <- t(matrix(rnorm(10000),2))
colnames(m) <- c("A","B")
m <- flowFrame(m)
res <- flowTrans(m,"mclMultivBoxCox", c("A","B"),
                 n2f=FALSE, parameters.only=FALSE)
summary(res)
extractParams(res)
```

`summary-methods` *Summarize a flowTransResult object*

Description

Print a summary of the contents of a `flowTransResult` object.

Methods

object = "flowTransResult" Prints a summary of the flowTransResult object

---

`summary.flowTransResult`
Summarize a flowTransResult object

Description

Print a summary of the contents of a `flowTransResult` object, including the type of transformation, the transformed data frame, and the transformed dimensions and transformation parameters.

Usage

```
summary.flowTransResult(object, ...)
```

Arguments

`object`	An object of `flowTransResult` returned by a call to `flowTrans`
`...`	Additional parameters passed through.

Value

No return value

Author(s)

Greg Finak <greg.finak@ircm.qc.ca>, Raphael Gottardo <raphael.gottardo@ircm.qc.ca>

References

Finak G, Perez JM, Weng A, Gottardo R. Optimizing Transformations for Flow Cytometry. (Submitted)

See Also

extractParams, flowTransResult

Examples

```
m <- t(matrix(rnorm(10000),2))
colnames(m) <- c("A","B")
m <- flowFrame(m)
res <- flowTrans(m, "mclMultivBoxCox", c("A","B"),
                 n2f=FALSE, parameters.only=FALSE)
summary(res)
```

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