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Author Oskar Hansson

Maintainer Oskar Hansson <oskhan@ous-hf.no>

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BugReports https://github.com/OskarHansson/strvalidator/issues

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Suggests ResourceSelection, testthat

Description An open source platform for validation and process control. Tools to analyze data from internal validation of forensic short tandem repeat (STR) kits are provided. The tools are developed to provide the necessary data to conform with guidelines for internal validation issued by the European Network of Forensic Science Institutes (ENFSI) DNA Working Group, and the Scientific Working Group on DNA Analysis Methods (SWGDAM). A front-end graphical user interface is provided. More information about each function can be found in the respective help documentation.

License GPL-2

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Contents

strvalidator-package . . . 5
addColor . . . 6
addData . . . 7
addData_gui . . . 9
addDye_gui . . . 9
addMarker . . . 10
addMarker_gui . . . 11
addOrder . . . 12
addSize . . . 13
addSize_gui . . . 13
auditTrail . . . 14
calculateAllele . . . 16
calculateAllele_gui . . . 17
calculateAllT . . . 17
calculateAllT_gui . . . 18
calculateAT . . . 19
calculateAT6 . . . 21
calculateAT6_gui . . . 22
calculateAT_gui . . . 23
calculateCapillary . . . 24
calculateCapillary_gui . . . 25
calculateConcordance . . . 26
calculateConcordance_gui . . . 27
calculateCopies . . . 28
calculateCopies_gui . . . 29
calculateDropout . . . 29
calculateDropout_gui . . . 31
calculateHb . . . 32
calculateHb_gui . . . 33
calculateHeight . . . 34
calculateHeight_gui . . . 36
calculateLb . . . 37
calculateLb_gui . . . 39
calculateMixture . . . 40
calculateMixture_gui . . . 41
calculateOL . . . 42
calculateOL_gui . . . 43
calculateOverlap . . . 44
calculateOverlap_gui . . . 45
calculatePeaks . . . 46
calculatePeaks_gui . . . 47
calculatePullup . . . 48
calculatePullup_gui . . . 49
calculateRatio . . . 50
calculateRatio_gui . . . 51
calculateResultType . . . 52

calculateResultType_gui . . . 53
calculateSlope . . . 54
calculateSlope_gui . . . 55
calculateSpike . . . 55
calculateSpike_gui . . . 57
calculateStatistics . . . 57
calculateStatistics_gui . . . 58
calculateStutter . . . 60
calculateStutter_gui . . . 61
calculateT . . . 62
checkDataset . . . 63
checkSubset . . . 64
checkSubset_gui . . . 65
colConvert . . . 65
colNames . . . 66
columns . . . 67
columns_gui . . . 68
combine_gui . . . 69
cropData_gui . . . 69
detectKit . . . 70
editData_gui . . . 71
export . . . 72
export_gui . . . 73
filterProfile . . . 74
filterProfile_gui . . . 75
generateEPG . . . 76
generateEPG_gui . . . 77
getKit . . . 78
getSetting . . . 79
getStrings . . . 79
ggsave_gui . . . 80
guessProfile . . . 81
guessProfile_gui . . . 82
heightToPeak . . . 83
import . . . 83
import_gui . . . 85
listObjects . . . 86
manageKits_gui . . . 87
maskAT . . . 87
modelDropout_gui . . . 89
plotAT_gui . . . 91
plotBalance_gui . . . 92
plotCapillary_gui . . . 93
plotContamination_gui . . . 94
plotDistribution_gui . . . 95
plotDropout_gui . . . 96
plotEPG2 . . . 97
plotEPG2_gui . . . 98

plotGroups_gui . . . 99
plotKit_gui . . . 100
plotPeaks_gui . . . 100
plotPrecision_gui . . . 101
plotPullup_gui . . . 102
plotRatio_gui . . . 103
plotResultType_gui . . . 104
plotSlope_gui . . . 104
plotStutter_gui . . . 105
read_gene_mapper_kit . . . 106
read_gene_mapper_kit_gui . . . 107
read_gene_marker_kit . . . 107
read_gene_marker_kit_gui . . . 108
ref1 . . . 109
ref11 . . . 109
ref2 . . . 109
ref3 . . . 110
ref4 . . . 110
ref51 . . . 110
ref52 . . . 111
ref61 . . . 111
ref62 . . . 111
ref7 . . . 112
removeArtefact . . . 112
removeArtefact_gui . . . 113
removeSpike . . . 114
removeSpike_gui . . . 114
sample_tableToList . . . 115
scrambleAlleles . . . 116
set1 . . . 116
set2 . . . 117
set3 . . . 117
set4 . . . 117
set5 . . . 118
set6 . . . 118
set7 . . . 118
slim . . . 119
slim_gui . . . 119
sortMarker . . . 120
strvalidator . . . 121
trim . . . 121
trim_gui . . . 123
update_strings_with_language_file . . . 123

Index **125**

`strvalidator-package` *Process Control and Internal Validation of Forensic STR Kits*

Description

STR-validator is a free and open-source R package intended for process control and internal validation of forensic STR DNA typing kits. Its graphical user interface simplifies the analysis of data exported from software like GeneMapper, without requiring extensive knowledge about R. It provides functions to import, view, edit, and export data. After analysis, the results, generated plots, heatmaps, and data can be saved in a project for easy access. Analysis modules for stutter, balance, dropout, mixture, concordance, typing result, precision, pull-up, and analytical thresholds are available. In addition, there are functions to analyze GeneMapper bins and panels files. EPG-like plots can be generated from data. STR-validator can significantly increase the speed of validation by reducing the time and effort needed to analyze validation data. It allows exploration of the characteristics of DNA typing kits according to ENFSI and SWGDAM recommendations. This facilitates the implementation of probabilistic interpretation of DNA results.

STR-validator was written by and is maintained by Oskar Hansson, Section of Digitalization and Development, Oslo University Hospital (OUS). The work initially received external funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement no. 285487 (EUROFORGEN-NoE) but development and maintenance are now performed as part of my position at OUS, and on personal spare time.

Effort has been made to assure correct results. Refer to the main website for a list of functions specifically tested at build time.

Click `Index` at the bottom of the page to see a complete list of functions.

Created and maintained by:
Oskar Hansson, Section for Forensic Biology (OUS, Norway)

More information can be found at:
https://sites.google.com/site/forensicapps/strvalidator

Info and user community at Facebook:
https://www.facebook.com/pages/STR-validator/240891279451450?ref=tn_tnmn

https://www.facebook.com/groups/strvalidator/

The source code is hosted on GitHub:
https://github.com/OskarHansson/strvalidator

Please report bugs to:
https://github.com/OskarHansson/strvalidator/issues

Author(s)

Oskar Hansson <oskhan@ous-hf.no>

References

Recommended Minimum Criteria for the Validation of Various Aspects of the DNA Profiling Process http://enfsi.eu/wp-content/uploads/2016/09/minimum_validation_guidelines_in_dna_profiling_-_v2010_0.pdf Validation Guidelines for Forensic DNA Analysis Methods (2012) http://media.wix.com/ugd/4344b0_cbc27d16dcb64fd88cb36ab2a2a25e4c.pdf

See Also

Useful links:

- https://sites.google.com/site/forensicapps/strvalidator
- Report bugs at https://github.com/OskarHansson/strvalidator/issues

---

`addColor` *Add Color Information.*

Description

Add color information 'Color', 'Dye' or 'R Color'.

Usage

```
addColor(
  data,
  kit = NA,
  have = NA,
  need = NA,
  overwrite = FALSE,
  ignore.case = FALSE,
  debug = FALSE
)
```

Arguments

data	data frame or vector.
kit	string representing the forensic STR kit used. Default is NA, in which case 'have' must contain a valid column.
have	character string to specify color column to be matched. Default is NA, in which case color information is derived from 'kit' and added to a column named 'Color'. If 'data' is a vector 'have' must be a single string.
need	character string or string vector to specify color columns to be added. Default is NA, in which case all columns will be added. If 'data' is a vector 'need' must be a single string.
overwrite	logical if TRUE and column exist it will be overwritten.
ignore.case	logical if TRUE case in marker names will be ignored.
debug	logical indicating printing debug information.

Details

Primers in forensic STR typing kits are labeled with a fluorescent dye. The dyes are represented with single letters (Dye) in exported result files or with strings (Color) in 'panels' files. For visualization in R the R color names are used (R.Color). The function can add new color schemes matched to the existing, or it can convert a vector containing one scheme to another.

Value

data.frame with additional columns for added colors, or vector with converted values.

Examples

```
# Get marker and colors for SGM Plus.
df <- getKit("SGMPlus", what = "Color")
# Add dye color.
dfDye <- addColor(data = df, need = "Dye")
# Add all color alternatives.
dfAll <- addColor(data = df)
# Convert a dye vector to R colors
addColor(data = c("R", "G", "Y", "B"), have = "dye", need = "r.color")
```

---

addData *Adds New Data Columns to a Data Frame*

Description

Adds values from columns in 'new.data' to 'data' by keys.

Usage

```
addData(
  data,
  new.data,
  by.col,
  then.by.col = NULL,
  exact = TRUE,
  ignore.case = TRUE,
  what = NULL,
  debug = FALSE
)
```

Arguments

data	Data frame containing your main data.
new.data	Data frame containing information you want to add to 'data'.
by.col	character, primary key column.
then.by.col	character, secondary key column.
exact	logical, TRUE matches keys exact.
ignore.case	logical, TRUE ignore case.
what	character vector defining columns to add. Default is all new columns.
debug	logical indicating printing debug information.

Details

Information in columns in data frame 'new.data' is added to data frame 'data' based on primary key value in column 'by.col', and optionally on secondary key values in column 'then.by.col'.

Value

data.frame the original data frame containing additional columns.

Examples

```
# Get marker names and alleles for Promega PowerPlex ESX 17.
x <- getKit("ESX17", what = "Allele")
# Get marker names and colors for Promega PowerPlex ESX 17.
y <- getKit("ESX17", what = "Color")
# Add color information to allele information.
z <- addData(data = x, new.data = y, by.col = "Marker")
print(x)
print(y)
print(z)
```

addData_gui *Add Data*

Description

GUI wrapper for addData.

Usage

```
addData_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the addData function by providing a graphical user interface to it.

Value

TRUE

See Also

addData

addDye_gui *Add Dye Information*

Description

GUI wrapper to the addColor function.

Usage

```
addDye_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Convenience GUI for the use of addColor and addOrder to add 'Dye', 'Color', 'R.Color', and marker 'Order' to a dataset. 'Dye' is the one letter abbreviations for the fluorophores commonly used to label primers in forensic STR typing kits (e.g. R and Y), 'Color' is the corresponding color name (e.g. red and yellow), 'R.Color' is the plot color used in R (e.g. red and black). 'Order' is the marker order in the selected kit. NB! Existing columns will be overwritten.

Value

TRUE

See Also

addColor

---

addMarker *Add Missing Markers.*

Description

Add missing markers to a dataset given a set of markers.

Usage

```
addMarker(data, marker, ignore.case = FALSE, debug = FALSE)
```

Arguments

data	data.frame or vector with sample names.
marker	vector with marker names.
ignore.case	logical. TRUE ignores case in marker names.
debug	logical indicating printing debug information.

Details

Given a dataset or a vector with sample names the function loops through each sample and add any missing markers. Returns a dataframe where each sample have at least one row per marker in the specified marker vector. Use sortMarker to sort the markers according to a specified kit. Required columns are: 'Sample.Name'.

Value

data.frame.

---

addMarker_gui *Add Missing Markers*

Description

GUI wrapper for the addMarker function.

Usage

```
addMarker_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the addMarker function by providing a graphical user interface to it.

Value

TRUE

See Also

addMarker

addOrder *Add Marker Order.*

Description

Add marker order to data frame containing a column 'Marker'.

Usage

```
addOrder(
  data,
  kit = NULL,
  overwrite = FALSE,
  ignore.case = FALSE,
  debug = FALSE
)
```

Arguments

data	data frame or vector.
kit	string representing the forensic STR kit used. Default is NULL and automatic detection of kit will be attempted.
overwrite	logical if TRUE and column exist it will be overwritten.
ignore.case	logical if TRUE case in marker names will be ignored.
debug	logical indicating printing debug information.

Details

Markers in a kit appear in a certain order. Not all STR-validator functions keep the original marker order in the result. A column indicating the marker order is added to the dataset. This is especially useful when exporting the data to an external spread-sheet software and allow to quickly sort the data in the correct order.

Value

data.frame with additional numeric column 'Order'.

Examples

```
# Load a dataset containing two samples.
data("set2")
# Add marker order when kit is known.
addOrder(data = set2, kit = "SGMPlus")
```

addSize *Add Size Information.*

Description

Add size information to alleles.

Usage

```
addSize(data, kit = NA, bins = TRUE, ignore.case = FALSE, debug = FALSE)
```

Arguments

data	data.frame with at least columns 'Marker' and 'Allele'.
kit	data.frame with columns 'Marker', 'Allele', and 'Size' (for bins=TRUE) or 'Marker', 'Allele', 'Offset' and 'Repeat' (for bins=FALSE).
bins	logical TRUE alleles get size from corresponding bin. If FALSE the size is calculated from the locus offset and repeat unit.
ignore.case	logical TRUE case in marker names are ignored.
debug	logical indicating printing debug information.

Details

Adds a column 'Size' with the fragment size in base pair (bp) for each allele as estimated from kit bins OR calculated from offset and repeat. The bins option return NA for alleles not in bin. The calculate option handles all named alleles including micro variants (e.g. '9.3'). Handles 'X' and 'Y' by replacing them with '1' and '2'.

Value

data.frame with additional columns for added size.

addSize_gui *Add Size Information*

Description

GUI wrapper for the addSize function.

Usage

```
addSize_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the addSize function by providing a graphical user interface to it.

Value

TRUE

See Also

addSize

---

auditTrail *Log Audit Trail.*

Description

Adds an audit trail to a dataset.

Usage

```
auditTrail(
  obj,
  f.call = NULL,
  key = NULL,
  value = NULL,
  label = NULL,
  arguments = TRUE,
  exact = TRUE,
  remove = FALSE,
  package = NULL,
  rversion = TRUE,
  timestamp = TRUE
)
```

Arguments

obj	object to add or update the audit trail.
f.call	the function call i.e. match.call().
key	list or vector of additional keys to log.
value	list or vector of additional values to log.
label	optional label used if f.call=NULL.
arguments	logical. TRUE log function arguments.
exact	logical for exact matching of attribute name.
remove	logical. If TRUE the 'audit trail' attribute is removed.
package	character to log the package version.
rversion	logical to log the R version.
timestamp	logical to add or update timestamp.

Details

Automatically add or updates an attribute 'audit trail' with arguments and parameters extracted from the function call. To list the arguments with the default set but not overridden arguments=TRUE must be set (default). Additional custom key-value pairs can be added. The label is extracted from the function name from f.call. Specify package to include the version number of a package.

Value

object with added or updated attribute 'audit trail'.

Examples

```
# A simple function with audit trail logging.
myFunction <- function(x, a, b = 5) {
  x <- x + a + b
  x <- auditTrail(obj = x, f.call = match.call(), package = "strvalidator")
  return(x)
}
# Run the function.
myData <- myFunction(x = 10, a = 2)
# Check the audit trail.
cat(attr(myData, "audit trail"))

# Remove the audit trail.
myData <- auditTrail(myData, remove = TRUE)
# Confirm that the audit trail is removed.
cat(attr(myData, "audit trail"))
```

`calculateAllele` *Calculate Allele*

Description

Calculates summary statistics for alleles per marker over the entire dataset.

Usage

```
calculateAllele(
  data,
  threshold = NULL,
  sex.rm = FALSE,
  kit = NULL,
  debug = FALSE
)
```

Arguments

`data`	data.frame including columns 'Marker' and 'Allele', and optionally 'Height' and 'Size'.
`threshold`	numeric if not NULL only peak heights above 'threshold' will be considered.
`sex.rm`	logical TRUE removes all sex markers. Requires 'kit'.
`kit`	character for the DNA typing kit defining the sex markers.
`debug`	logical indicating printing debug information.

Details

Creates a table of the alleles in the dataset sorted by number of observations.For each allele the proportion of total observations is calculated. Using a threshold this can be used to separate likely artefacts from likely drop-in peaks. In addition the observed allele frequency is calculated. If columns 'Height' and/or 'Size' are available summary statistics is calculated. NB! The function removes NA's and OL's prior to analysis.

Value

data.frame with columns 'Marker', 'Allele', 'Peaks', 'Size.Min', 'Size.Mean', 'Size.Max', 'Height.Min', 'Height.Mean', 'Height.Max', 'Total.Peaks', 'Allele.Proportion', 'Sum.Peaks', and 'Allele.Frequency'.

See Also

`data.table`

calculateAllele_gui *Calculate Allele*

Description

GUI wrapper for the calculateAllele function.

Usage

```
calculateAllele_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateAllele function by providing a graphical user interface to it.

Value

TRUE

calculateAllT *Calculate Stochastic Thresholds*

Description

Calculates point estimates for the stochastic threshold using multiple models.

Usage

```
calculateAllT(
  data,
  kit,
  p.dropout = 0.01,
  p.conservative = 0.05,
  rm.sex = TRUE,
  debug = FALSE
)
```

Arguments

data	output from calculateDropout.
kit	character string to define the kit which is required to remove sex markers.
p.dropout	numeric accepted risk of dropout at the stochastic threshold. Default=0.01.
p.conservative	numeric accepted risk that the actual probability of dropout is >p.dropout at the conservative estimate. Default=0.05.
rm.sex	logical default=TRUE removes sex markers defined for the given kit.
debug	logical indicating printing debug information.

Details

Expects output from calculateDropout as input. The function calls calculateT repeatedly to estimate the stochastic threshold using different models. The output is a data.frame summarizing the result. Use the modelDropout_gui to plot individual models.

Explanation of the result: Explanatory_variable - Drop-out is the dependent variable. An allele in heterozygous markers in the reference profile is chosen and drop-out is scored if the other allele is not observed in the sample, i.e. below the AT. The 'Random' method chose a random allele, while the 'LMW' and 'HMW' method chose the low and high molecular weight allele, respectively. The 'Locus' method score drop-out if any of the two alleles has dropped out. As explanatory variable the peak height of the surviving allele '(Ph)', average profile peak height '(H)', the logarithm of the surviving allele 'log(Ph)', and the logarithm of the average profile peak height 'log(H)' is used. P(dropout)=x.xx@T - is the point estimate for corresponding to the specified accepted risk of drop-out. P(dropout>x.xx)<0.05@T - is the conservative point estimate corresponding to a stochastic threshold with a risk <0.05 that the actual drop-out probability is >x.xx Hosmer-Lemeshow_p - p-value from the Hosmer-Lemeshow test. A value <0.05 indicates poor fit between the model and the observations.

Value

TRUE

See Also

calculateDropout, calculateT, modelDropout_gui, plotDropout_gui

---

calculateAllT_gui *Calculate Stochastic Thresholds*

Description

GUI wrapper to the calculateAllT function.

Usage

```
calculateAllT_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Convenience GUI for the use of calculateAllT to calculate point estimates for the stochastic threshold using multiple models.

Value

TRUE

See Also

calculateAllT

---

calculateAT *Calculate Analytical Threshold*

Description

Calculate analytical thresholds estimates.

Usage

```
calculateAT(
  data,
  ref = NULL,
  mask.height = TRUE,
  height = 500,
  mask.sample = TRUE,
  per.dye = TRUE,
  range.sample = 20,
  mask.ils = TRUE,
```

```
  range.ils = 10,
  k = 3,
  rank.t = 0.99,
  alpha = 0.01,
  ignore.case = TRUE,
  word = FALSE,
  debug = FALSE
)
```

Arguments

data	a data frame containing at least 'Dye.Sample.Peak', 'Sample.File.Name', 'Marker', 'Allele', 'Height', and 'Data.Point'.
ref	a data frame containing at least 'Sample.Name', 'Marker', 'Allele'.
mask.height	logical to indicate if high peaks should be masked.
height	integer for global lower peak height threshold for peaks to be excluded from the analysis. Active if 'mask.peak=TRUE.
mask.sample	logical to indicate if sample allelic peaks should be masked.
per.dye	logical TRUE if sample peaks should be masked per dye channel. FALSE if sample peaks should be masked globally across dye channels.
range.sample	integer to specify the masking range in (+/-) data points. Active if mask.sample=TRUE.
mask.ils	logical to indicate if internal lane standard peaks should be masked.
range.ils	integer to specify the masking range in (+/-) data points. Active if mask.ils=TRUE.
k	numeric factor for the desired confidence level (method AT1).
rank.t	numeric percentile rank threshold (method AT2).
alpha	numeric one-sided confidence interval to obtain the critical value from the t-distribution (method AT4).
ignore.case	logical to indicate if sample matching should ignore case.
word	logical to indicate if word boundaries should be added before sample matching.
debug	logical to indicate if debug information should be printed.

Details

Calculate the analytical threshold (AT) according to method 1, 2, and 4 as recommended in the reference by analyzing the background signal (noise). In addition method 7, a log-normal version of method 1 has been implemented. Method 1: The average signal + 'k' * the standard deviation. Method 2: The percentile rank method. The percentage of noise peaks below 'rank.t'. Method 4: Utilize the mean and standard deviation and the critical value obtained from the t-distribution for confidence interval 'alpha' (one-sided) and observed peaks analyzed (i.e. not masked) minus one as degrees of freedom, and the number of samples. Method 7: The average natural logarithm of the signal + k * the standard deviation.

If samples containing DNA are used, a range around the allelic peaks can be masked from the analysis to discard peaks higher than the noise. Masking can be within each dye or across all dye channels. Similarly a range around the peaks of the internal lane standard (ILS) can be masked

across all dye channels. Which can bleed-through in week samples (i.e. negative controls) The mean, standard deviation, and number of peaks are calculated per dye per sample, per sample, globally across all samples, and globally across all samples per dye, for each method to estimate AT. Also the complete percentile rank list is calculated.

Value

list of three data frames. The first with result per dye per sample, per sample, globally across all samples, and globally across all samples per dye, for each method. The second is the complete percentile rank list. The third is the masked raw data used for calculation to enable manual check of the result.

References

J. Bregu et.al., Analytical thresholds and sensitivity: establishing RFU thresholds for forensic DNA analysis, J. Forensic Sci. 58 (1) (2013) 120-129, ISSN 1556-4029, DOI: 10.1111/1556-4029.12008. doi:10.1111/15564029.12008

See Also

maskAT, checkSubset

---

calculateAT6 *Calculate Analytical Threshold*

Description

Calculate analytical thresholds estimate using linear regression.

Usage

```
calculateAT6(
  data,
  ref,
  amount = NULL,
  weighted = TRUE,
  alpha = 0.05,
  ignore.case = TRUE,
  debug = FALSE
)
```

Arguments

data	data.frame containing at least columns 'Sample.Name', 'Marker', 'Allele', and 'Height'.
ref	data.frame containing at least columns 'Sample.Name', 'Marker', and 'Allele'.

amount	data.frame containing at least columns 'Sample.Name' and 'Amount'. If NULL 'data' must contain a column 'Amount'.
weighted	logical to calculate weighted linear regression (weight=1/se^2).
alpha	numeric [0,1] significance level for the t-statistic.
ignore.case	logical to indicate if sample matching should ignore case.
debug	logical to indicate if debug information should be printed.

Details

Calculate the analytical threshold (AT) according to method 6 as outlined in the reference. In short serial dilutions are analyzed and the average peak height is calculated. Linear regression or Weighted linear regression with amount of DNA as the predictor for the peak height is performed. Method 6: A simplified version of the upper limit approach. AT6 = y-intercept + t-statistic * standard error of the regression. Assumes the y-intercept is not different from the mean blank signal. The mean blank signal should be included in the confidence range ('Lower' to 'AT6' in the resulting data frame). NB! This is an indirect method to estimate AT and should be verified by other methods. From the reference: A way to determine the validity of this approach is based on whether the y-intercept +- (1-a)100 contains the mean blank signal. If the mean blank signal is included in the y-intercept band, the following relationship [i.e. AT6] can be used to determine the AT. However, it should be noted that the ATs derived in this manner need to be calculated for each color and for all preparations (i.e., different injections, sample preparation volumes, post-PCR cleanup, etc.). NB! Quality sensors must be removed prior to analysis.

Value

data.frame with columns 'Amount', 'Height', 'Sd', 'Weight', 'N', 'Alpha', 'Lower', 'Intercept', and 'AT6'.

References

J. Bregu et.al., Analytical thresholds and sensitivity: establishing RFU thresholds for forensic DNA analysis, J. Forensic Sci. 58 (1) (2013) 120-129, ISSN 1556-4029, DOI: 10.1111/1556-4029.12008. doi:10.1111/15564029.12008

See Also

calculateAT6_gui, calculateAT, calculateAT_gui, lm

---

calculateAT6_gui *Calculate Analytical Threshold*

Description

GUI wrapper for the calculateAT6 function.

Usage

```
calculateAT6_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Scores dropouts for a dataset.

Value

TRUE

See Also

calculateAT6, calculateAT, calculateAT_gui, checkSubset

---

calculateAT_gui *Calculate Analytical Threshold*

Description

GUI wrapper for the maskAT and calculateAT function.

Usage

```
calculateAT_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateAT and calculateAT function by providing a graphical user interface. In addition there are integrated control functions.

Value

TRUE

See Also

calculateAT, maskAT, checkSubset

---

calculateCapillary *Calculate Capillary Balance*

Description

Calculates the ILS inter capillary balance.

Usage

```
calculateCapillary(samples.table, plot.table, sq = 0, run = "", debug = FALSE)
```

Arguments

samples.table	data frame containing at least the columns 'Sample.File', 'Sample.Name', 'Size.Standard', 'Instrument.Type', 'Instrument.ID', 'Cap', 'Well', and 'SQ'.
plot.table	data frame containing at least the columns 'Sample.File.Name', 'Size', and 'Height'.
sq	numeric threshold for 'Sizing Quality' (SQ).
run	character string for run name.
debug	logical indicating printing debug information.

Details

Calculates the inter capillary balance for the internal lane standard (ILS). Require information from both the 'samples.table' and the 'plot.table'.

Value

data.frame with with columns 'Instrument', 'Instrument.ID', 'Run', 'Mean.Height', 'SQ', 'Injection', 'Capillary', 'Well', 'Comment'.

`calculateCapillary_gui` *Calculate Capillary Balance*

Description

GUI wrapper for the `calculateCapillary` function.

Usage

```
calculateCapillary_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateCapillary` function by providing a graphical user interface.

Value

TRUE

See Also

`calculateCapillary`

`calculateConcordance` *Calculate Concordance.*

Description

Calculates concordance and discordance for profiles in multiple datasets.

Usage

```
calculateConcordance(
  data,
  kit.name = NA,
  no.marker = "NO MARKER",
  no.sample = "NO SAMPLE",
  delimeter = ",",
  list.all = FALSE,
  debug = FALSE
)
```

Arguments

`data`	list of data frames in 'slim' format with at least columns 'Sample.Name', 'Marker', and 'Allele'.
`kit.name`	character vector for DNA typing kit names in same order and of same lengths as data sets in 'data' list. Default is NA in which case they will be numbered.
`no.marker`	character vector for string when marker is missing.
`no.sample`	character vector for string when sample is missing.
`delimeter`	character to separate the alleles in a genotype. Default is comma e.g '12,16'.
`list.all`	logical TRUE to return missing samples.
`debug`	logical indicating printing debug information.

Details

Takes a list of datasets as input. It is assumed that each unique sample name represent a result originating from the same source DNA and thus is expected to give identical DNA profiles. The function first compare the profiles for each sample across datasets and lists discordant results. Then it performs a pair-wise comparison and compiles a concordance table. The tables are returned as two data frames in a list. NB! Typing and PCR artefacts (spikes, off-ladder peaks, stutters etc.) must be removed before analysis. NB! It is expected that the unique set of marker names across a dataset is present in each sample for that dataset (a missing marker is a discordance).

Value

list of data.frames (discordance table, and pair-wise comparison).

`calculateConcordance_gui` *Calculate Concordance*

Description

GUI wrapper for the `calculateConcordance` function.

Usage

```
calculateConcordance_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateConcordance` function by providing a graphical user interface.

Value

TRUE

See Also

`calculateConcordance`

`calculateCopies` *Calculate Allele Copies*

Description

Calculates the number of alleles in each marker.

Usage

```
calculateCopies(
  data,
  observed = FALSE,
  copies = TRUE,
  heterozygous = FALSE,
  debug = FALSE
)
```

Arguments

`data`	Data frame containing at least columns 'Sample.Name', 'Marker, and 'Allele*'.
`observed`	logical indicating if a column 'Observed' should be used to count the number of unique alleles.
`copies`	logical indicating if a column 'Copies' should be used to indicate the number of allele copies with 1 for heterozygotes and 2 for homozygotes.
`heterozygous`	logical indicating if a column 'Heterozygous' should be used to indicate heterozygotes with 1 and homozygotes with 0.
`debug`	logical indicating printing debug information.

Details

Calculates the number of unique values in the 'Allele*' columns for each marker, the number of allele copies, or indicate heterozygous loci. Observed - number of unique alleles. Copies - number of allele copies, '1' for heterozygotes and '2' for homozygotes. Heterozygous - '1' for heterozygous and '0' for homozygous loci. NB! The 'copies' and 'heterozygous' option are intended for known complete profiles, while 'observed' can be used for any samples to count the number of peaks. Sample names must be unique. The result is per marker but repeated for each row of that marker. Data in 'fat' format is auto slimmed.

Value

data.frame the original data frame with optional columns 'Observed', 'Copies', and 'Heterozygous'.

calculateCopies_gui *Calculate Allele Copies*

Description

GUI wrapper for the link{calculateCopies} function.

Usage

```
calculateCopies_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateCopies function by providing a graphical user interface to it.

Value

TRUE

See Also

calculateCopies

calculateDropout *Calculate Drop-out Events*

Description

Calculate drop-out events (allele and locus) and records the surviving peak height.

Usage

```
calculateDropout(
  data,
  ref,
  threshold = NULL,
  method = c("1", "2", "X", "L"),
  ignore.case = TRUE,
  sex.rm = FALSE,
  qs.rm = TRUE,
  kit = NULL,
  debug = FALSE
)
```

Arguments

data	data frame in GeneMapper format containing at least a column 'Allele'.
ref	data frame in GeneMapper format.
threshold	numeric, threshold in RFU defining a dropout event. Default is 'NULL' and dropout is scored purely on the absence of a peak.
method	character vector, specifying which scoring method(s) to use. Method 'X' for random allele, '1' or '2' for the low/high molecular weight allele, and 'L' for the locus method (the option is case insensitive).
ignore.case	logical, default TRUE for case insensitive.
sex.rm	logical, default FALSE to include sex markers in the analysis.
qs.rm	logical, default TRUE to exclude quality sensors from the analysis.
kit	character, required if sex.rm=TRUE or qs.rm=TRUE to define the kit.
debug	logical indicating printing debug information.

Details

Calculates drop-out events. In case of allele dropout the peak height of the surviving allele is given. Homozygous alleles in the reference set can be either single or double notation (X or X X). Markers present in the reference set but not in the data set will be added to the result. NB! 'Sample.Name' in 'ref' must be unique core name of replicate sample names in 'data'. Use `checkSubset` to make sure subsetting works as intended. There are options to remove sex markers and quality sensors from analysis.

NB! There are several methods of scoring drop-out events for regression. Currently the 'MethodX', 'Method1', and 'Method2' are endorsed by the DNA commission (see Appendix B in ref 1). However, an alternative method is to consider the whole locus and score drop-out if any allele is missing.

Explanation of the methods: Dropout - all alleles are scored according to AT. This is pure observations and is not used for modeling. MethodX - a random reference allele is selected and drop-out is scored in relation to the the partner allele. Method1 - the low molecular weight allele is selected and drop-out is scored in relation to the partner allele. Method2 - the high molecular weight allele is selected and drop-out is scored in relation to the partner allele. MethodL - drop-out is scored per locus i.e. drop-out if any allele has dropped out.

Method X/1/2 records the peak height of the partner allele to be used as the explanatory variable in the logistic regression. The locus method L also do this when there has been a drop-out, if not the the mean peak height for the locus is used. Peak heights for the locus method are stored in a separate column.

Value

data.frame with columns 'Sample.Name', 'Marker', 'Allele', 'Height', 'Dropout', 'Rfu', 'Heterozygous', and 'Model'. Dropout: 0 indicate no dropout, 1 indicate allele dropout, and 2 indicate locus dropout. Rfu: height of surviving allele. Heterozygous: 1 for heterozygous and 0 for homozygous. And any of the following containing the response (or explanatory) variable used for modeling by logistic regression in function `modelDropout`: 'MethodX', 'Method1', 'Method2', 'MethodL' and 'MethodL.Ph'.

References

Peter Gill et.al., DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Science International: Genetics, Volume 6, Issue 6, December 2012, Pages 679-688, ISSN 1872-4973, 10.1016/j.fsigen.2012.06.002. doi:10.1016/j.fsigen.2012.06.002

Peter Gill, Roberto Puch-Solis, James Curran, The low-template-DNA (stochastic) threshold-Its determination relative to risk analysis for national DNA databases, Forensic Science International: Genetics, Volume 3, Issue 2, March 2009, Pages 104-111, ISSN 1872-4973, 10.1016/j.fsigen.2008.11.009. doi:10.1016/j.fsigen.2008.11.009

Examples

```
data(set4)
data(ref4)
drop <- calculateDropout(data = set4, ref = ref4, kit = "ESX17", ignore.case = TRUE)
```

---

calculateDropout_gui *Calculate Dropout Events*

Description

GUI wrapper for the `calculateDropout` function.

Usage

```
calculateDropout_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Scores dropouts for a dataset.

Value

TRUE

See Also

calculateDropout, checkSubset

---

calculateHb *Calculate Heterozygote Balance*

Description

Calculates the heterozygote (intra-locus) peak balance.

Usage

```
calculateHb(
  data,
  ref,
  hb = 1,
  kit = NULL,
  sex.rm = FALSE,
  qs.rm = FALSE,
  ignore.case = TRUE,
  exact = FALSE,
  word = FALSE,
  debug = FALSE
)
```

Arguments

data	a data frame containing at least 'Sample.Name', 'Marker', 'Height', and 'Allele'.
ref	a data frame containing at least 'Sample.Name', 'Marker', 'Allele'.
hb	numerical, definition of heterozygote balance. Default is hb=1. hb=1: HMW/LMW, hb=2: LMW/HMW, hb=3; min(Ph)/max(Ph).
kit	character defining the kit used. If NULL automatic detection is attempted.
sex.rm	logical TRUE removes sex markers defined by 'kit'.
qs.rm	logical TRUE removes quality sensors defined by 'kit'.
ignore.case	logical indicating if sample matching should ignore case.
exact	logical indicating if exact sample matching should be used.
word	logical indicating if word boundaries should be added before sample matching.
debug	logical indicating printing debug information.

Details

Calculates the heterozygote (intra-locus) peak balance for a dataset. Known allele peaks will be extracted using the reference prior to analysis. Calculates the heterozygote balance (Hb), size difference between heterozygous alleles (Delta), and mean peak height (MPH). NB! 'X' and 'Y' will be handled as '1' and '2' respectively.

Value

data.frame with with columns 'Sample.Name', 'Marker', 'Delta', 'Hb', 'MPH'.

Examples

```
data(ref2)
data(set2)
# Calculate average balances.
calculateHb(data = set2, ref = ref2)
```

---

calculateHb_gui *Calculate Heterozygote Balance*

Description

GUI wrapper for the calculateHb function.

Usage

```
calculateHb_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateHb function by providing a graphical user interface.

Value

TRUE

See Also

link{calculateHb}, link{checkSubset}

---

calculateHeight *Calculate Peak Height.*

Description

Calculate peak height metrics for samples.

Usage

```
calculateHeight(
  data,
  ref = NULL,
  na.replace = NULL,
  add = TRUE,
  exclude = NULL,
  sex.rm = FALSE,
  qs.rm = FALSE,
  kit = NULL,
  ignore.case = TRUE,
  exact = FALSE,
  word = FALSE,
  debug = FALSE
)
```

Arguments

data	data.frame with at least columns 'Sample.Name' and 'Height'.
ref	data.frame with at least columns 'Sample.Name' and 'Allele'.
na.replace	replaces NA values in the final result.
add	logical default is TRUE which will add or overwrite columns 'TPH', 'Peaks', 'H', and 'Proportion' in the provided 'data'.
exclude	character vector (case sensitive) e.g. "OL" excludes rows with "OL" in the 'Allele' column (not necessary when a reference dataset is provided).
sex.rm	logical, default FALSE to include sex markers in the analysis.
qs.rm	logical, default TRUE to exclude quality sensors from the analysis.
kit	character, required if sex.rm=TRUE or qs.rm=TRUE to define the kit.
ignore.case	logical TRUE ignores case in sample name matching.
exact	logical TRUE for exact sample name matching.
word	logical TRUE to add word boundaries to sample name matching.
debug	logical indicating printing debug information.

Details

Calculates the total peak height (TPH), and number of observed peaks (Peaks), for each sample by default. If a reference dataset is provided average peak height (H), and profile proportion (Proportion) are calculated.

H is calculated according to the formula (references [1][2]): $H = sum(peakheights)/(n[het] + 2n[hom]$ Where: n[het] = number of observed heterozygous alleles n[hom] = number of observed homozygous alleles

Important: The above formula has a drawback that when many alleles have dropped out, i.e. when only few alleles are detected, H can be overestimated. For example, if there are only 1 (homozygote) peak observed in the profile, with a height of 100 RFU, then H=100 RFU. This means that the value of H will always be between half the analytical threshold (AT/2) and the peak height of the observed allele (if only one). For this reason Tvedebrink et al. actually modified the estimate to take the number of expected alleles into account when estimating the expected peak height (reference [3]). Basically, they adjust the estimated peak height for the fact that they know how many alleles that fall below the AT, such that the expected peak height could be estimated lower than AT. In addition, they account for degradation using a log-linear relationship on peak heights and fragment length.

Tip: If it is known that all expected peaks are observed and no unexpected peaks are present, the dataset can be used as a reference for itself.

Note: If a reference dataset is provided the known alleles will be extracted from the dataset.

Value

data.frame with with at least columns 'Sample.Name', 'TPH', and 'Peaks'.

References

[1] Torben Tvedebrink, Poul Svante Eriksen, Helle Smidt Mogensen, Niels Morling, Evaluating the weight of evidence by using quantitative short tandem repeat data in DNA mixtures Journal of the Royal Statistical Society: Series C (Applied Statistics), Volume 59, Issue 5, 2010, Pages 855-874, 10.1111/j.1467-9876.2010.00722.x. doi:10.1111/j.14679876.2010.00722.x

[2] Torben Tvedebrink, Helle Smidt Mogensen, Maria Charlotte Stene, Niels Morling, Performance of two 17 locus forensic identification STR kits-Applied Biosystems's AmpFlSTR NGMSElect and Promega's PowerPlex ESI17 kits Forensic Science International: Genetics, Volume 6, Issue 5, 2012, Pages 523-531, 10.1016/j.fsigen.2011.12.006. doi:10.1016/j.fsigen.2011.12.006

[3] Torben Tvedebrink, Maria Asplund, Poul Svante Eriksen, Helle Smidt Mogensen, Niels Morling, Estimating drop-out probabilities of STR alleles accounting for stutters, detection threshold truncation and degradation Forensic Science International: Genetics Supplement Series, Volume 4, Issue 1, 2013, Pages e51-e52, 10.1016/j.fsigss.2013.10.026. doi:10.1016/j.fsigss.2013.10.026

`calculateHeight_gui` *Calculate Peak Height*

Description

GUI wrapper for the `calculateHeight` function.

Usage

```
calculateHeight_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateHeight` function by providing a graphical user interface to it.

Value

TRUE

References

Torben Tvedebrink, Poul Svante Eriksen, Helle Smidt Mogensen, Niels Morling, Evaluating the weight of evidence by using quantitative short tandem repeat data in DNA mixtures Journal of the Royal Statistical Society: Series C (Applied Statistics), Volume 59, Issue 5, 2010, Pages 855-874, 10.1111/j.1467-9876.2010.00722.x. doi:10.1111/j.14679876.2010.00722.x

See Also

`calculateHeight`

`calculateLb` *Calculate Inter-locus Balance*

Description

Calculates the inter-locus balance.

Usage

```
calculateLb(
  data,
  ref = NULL,
  option = "prop",
  by.dye = FALSE,
  ol.rm = TRUE,
  sex.rm = FALSE,
  qs.rm = FALSE,
  na = NULL,
  kit = NULL,
  ignore.case = TRUE,
  word = FALSE,
  exact = FALSE,
  debug = FALSE
)
```

Arguments

`data`	data.frame containing at least 'Sample.Name', 'Marker', and 'Height'.
`ref`	data.frame containing at least 'Sample.Name', 'Marker', 'Allele'. If provided alleles matching 'ref' will be extracted from 'data' (see `filterProfile`).
`option`	character: 'prop' for proportional Lb, 'norm' for normalized LB, 'cent' for centred Lb, 'marker' for the min and max marker peak height ratio, .and 'peak' for the min and max peak height ratio.
`by.dye`	logical. Default is FALSE for global Lb, if TRUE Lb is calculated within each dye channel.
`ol.rm`	logical. Default is TRUE indicating that off-ladder 'OL' alleles will be removed.

sex.rm	logical. Default is FALSE indicating that all markers will be considered. If TRUE sex markers will be removed.
qs.rm	logical. Default is TRUE indicating that all quality sensors will be removed.
na	numeric. Numeric to replace NA values e.g. locus dropout can be given a peak height equal to the limit of detection threshold, or zero. Default is NULL indicating that NA will be treated as missing values.
kit	character providing the kit name. Attempt to auto detect if NULL.
ignore.case	logical indicating if sample matching should ignore case. Only used if 'ref' is provided and 'data' is filtered.
word	logical indicating if word boundaries should be added before sample matching. Only used if 'ref' is provided and 'data' is filtered.
exact	logical indicating if exact sample matching should be used. Only used if 'ref' is provided and 'data' is filtered.
debug	logical indicating printing debug information.

Details

The inter-locus balance (Lb), or profile balance, can be calculated as a proportion of the whole, normalized, or as centered quantities (as in the cited paper, but using the mean total marker peak height instead of H). Lb can be calculated globally across the complete profile or within each dye channel. All markers must be present in each sample. Data can be filtered or unfiltered when the sum of peak heights by marker is used. A reference dataset is required to filter the dataset, which also adds any missing markers. A kit should be provided for filtering of known profile, sex markers, or quality sensors. If kit is not provided, automatic detection will be attempted. If 'Dye' column is missing, it will be added according to kit. Off-ladder alleles and quality sensors are by default removed from the dataset. Sex markers are optionally removed, which is recommended if the 'peak' or 'marker' option is used. Some columns in the result may vary: TPH: Total (marker) Peak Height. TPPH: Total Profile Peak Height. MTPH: Maximum (sample) Total Peak Height. MPH: Mean (marker) Peak Height.

Value

data.frame with at least columns 'Sample.Name', 'Marker', 'TPH', 'Peaks', and 'Lb'. See description for additional columns.

References

Torben Tvedebrink et.al., Performance of two 17 locus forensic identification STR kits-Applied Biosystems's AmpFlSTR NGMSElect and Promega's PowerPlex ESI17 kits, Forensic Science International: Genetics, Volume 6, Issue 5, September 2012, Pages 523-531, ISSN 1872-4973, 10.1016/j.fsigen.2011.12.006. doi:10.1016/j.fsigen.2011.12.006

Examples

```
# Load data.
data(set2)

# Calculate inter-locus balance.
```

```
res <- calculateLb(data = set2)
print(res)
```

`calculateLb_gui` *Calculate Locus Balance*

Description

GUI wrapper for the `calculateLb` function.

Usage

```
calculateLb_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateLb` function by providing a graphical user interface.

Value

TRUE

See Also

`link{calculateLb}`, `link{checkSubset}`

`calculateMixture` *Calculate Mixture.*

Description

Calculate Mx, drop-in, and

Usage

```
calculateMixture(
  data,
  ref1,
  ref2,
  ol.rm = TRUE,
  ignore.dropout = TRUE,
  debug = FALSE
)
```

Arguments

`data`	list of data frames in 'slim' format with at least columns 'Sample.Name', 'Marker', and 'Allele'.
`ref1`	data.frame with known genotypes for the major contributor.
`ref2`	data.frame with known genotypes for the minor contributor.
`ol.rm`	logical TRUE removes off-ladder alleles (OL), FALSE count OL as drop-in.
`ignore.dropout`	logical TRUE calculate Mx also if there are missing alleles.
`debug`	logical indicating printing debug information.

Details

Given a set of mixture results, reference profiles for the major component, and reference profile for the minor component the function calculates the mixture proportion (Mx), the average Mx, the absolute difference D=|Mx-AvgMx| for each marker, the percentage profile for the minor component, number of drop-ins. The observed and expected number of free alleles for the minor component (used to calculate the profile percentage) is also given.

NB! All sample names must be unique within and between each reference dataset. NB! Samples in ref1 and ref2 must be in 'sync'. The first sample in ref1 is combined with the first sample in ref2 to make a mixture sample. For example: ref1 "A" and ref2 "B" match mixture samples "A_B_1", "A_B_2" and so on. NB! If reference datasets have unequal number of unique samples the smaller dataset will limit the calculation.

Mixture proportion is calculated in accordance with:
Locus style (minor:MAJOR) | Mx
AA:AB | (A-B)/(A+B)
AB:AA | (2*B)/(A+B)
AB:AC | B/(B+C)

AA:BB | A/(A+B)
AB:CC | (A+B)/(A+B+C)
AB:CD | (A+B)/(A+B+C+D)
AB:AB | NA - cannot be calculated
AA:AA | NA - cannot be calculated

Value

data.frame with columns 'Sample.Name', 'Marker', 'Style', 'Mx', 'Average', 'Difference', 'Observed', 'Expected', 'Profile', and 'Dropin'.

References

Bright, Jo-Anne, Jnana Turkington, and John Buckleton. "Examination of the Variability in Mixed DNA Profile Parameters for the Identifiler Multiplex." Forensic Science International: Genetics 4, no. 2 (February 2010): 111-14. doi:10.1016/j.fsigen.2009.07.002. doi:10.1016/j.fsigen.2009.07.002

---

calculateMixture_gui *Calculate Mixture*

Description

GUI wrapper for the `calculateMixture` function.

Usage

```
calculateMixture_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateMixture` function by providing a graphical user interface.

Value

TRUE

See Also

calculateMixture, checkSubset

`calculateOL` *Analyze Off-ladder Alleles*

Description

Analyze the risk for off-ladder alleles.

Usage

```
calculateOL(kit, db, virtual = TRUE, limit = TRUE, debug = FALSE)
```

Arguments

`kit`	data.frame, providing kit information.
`db`	data.frame, allele frequency database.
`virtual`	logical default is TRUE, calculation includes virtual alleles.
`limit`	logical default is TRUE, limit small frequencies to 5/2N.
`debug`	logical indicating printing debug information.

Details

By analyzing the allelic ladders the risk for getting off-ladder (OL) alleles are calculated. The frequencies from a provided population database is used to calculate the risk per marker and in total for the given kit(s). Virtual alleles can be excluded from the calculation. Small frequencies can be limited to the estimate 5/2N.

Value

data.frame with columns 'Kit', 'Marker', 'Database', 'Risk', and 'Total'.

`calculateOL_gui` *Analyze Off-ladder Alleles*

Description

GUI wrapper for the `calculateOL` function.

Usage

```
calculateOL_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = TRUE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

By analysis of the allelic ladder the risk for getting off-ladder (OL) alleles are calculated. The frequencies from a provided population database is used to calculate the risk per marker and in total for the given kit(s). Virtual alleles can be excluded from the calculation. Small frequencies can be limited to the estimate 5/2N.

Value

TRUE

See Also

`calculateOL`

`calculateOverlap` *Calculate Bins Overlap*

Description

Analyses the bins overlap between colors.

Usage

```
calculateOverlap(
  data,
  db = NULL,
  penalty = NULL,
  virtual = TRUE,
  debug = FALSE
)
```

Arguments

`data`	data frame providing kit information.
`db`	data frame allele frequency database.
`penalty`	vector with factors for reducing the impact from distant dye channels. NB! Length must equal number of dyes in kit minus one.
`virtual`	logical default is TRUE meaning that overlap calculation includes virtual bins.
`debug`	logical indicating printing debug information.

Details

By analyzing the bins overlap between dye channels a measure of the risk for spectral pull-up artefacts can be obtain. The default result is a matrix with the total bins overlap in number of base pairs. If an allele frequency database is provided the overlap at each bin is multiplied with the frequency of the corresponding allele. If no frequence exist for that allele a frequency of 5/2N will be used. X and Y alleles is given the frequency 1. A penalty matrix can be supplied to reduce the effect by spectral distance, meaning that overlap with the neighboring dye can be counted in full (100 while a non neighbor dye get its overlap reduced (to e.g. 10

Value

data.frame with columns 'Kit', 'Color', [dyes], 'Sum', and 'Score'.

`calculateOverlap_gui` *Calculate Bins Overlap*

Description

GUI wrapper for the `calculateOverlap` function.

Usage

```
calculateOverlap_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = TRUE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

By analysis of the bins overlap between dye channels a measure of the risk for spectral pull-up artefacts can be obtain. The default result is a matrix with the total bins overlap in number of base pairs. If an allele frequency database is provided the overlap at each bin is multiplied with the frequency of the corresponding allele. If no frequence exist for that allele a frequency of 5/2N will be used. X and Y alleles is given the frequency 1. A scoring matrix can be supplied to reduce the effect by spectral distance, meaning that overlap with the neighboring dye can be counted in full (100 while a non neighbor dye get its overlap reduced (to e.g. 10

Value

TRUE

See Also

`calculateOverlap`

`calculatePeaks` *Calculate Peaks*

Description

Calculates the number of peaks in samples.

Usage

```
calculatePeaks(
  data,
  bins = c(0, 2, 3),
  labels = NULL,
  ol.rm = FALSE,
  by.marker = FALSE,
  debug = FALSE
)
```

Arguments

`data`	data frame containing at least the columns 'Sample.Name' and 'Height'.
`bins`	numeric vector containing the cut-off points defined as maximum number of peaks for all but the last label, which is anything above final cut-off. Must be sorted in ascending order.
`labels`	character vector defining the group labels. Length must be equal to number of bins + one label for anything above the final cut-off.
`ol.rm`	logical if TRUE, off-ladder alleles 'OL' peaks will be discarded. if FALSE, all peaks will be included in the calculations.
`by.marker`	logical if TRUE, peaks will counted per marker. if FALSE, peaks will counted per sample.
`debug`	logical indicating printing debug information.

Details

Count the number of peaks in a sample profile based on values in the 'Height' column. Each sample is labeled according to custom labels defined by the number of peaks. Peaks can be counted by sample or by marker within a sample. There is an option to discard off-ladder peaks ('OL'). The default purpose for this function is to categorize contamination in negative controls, but it can be used to simply calculating the number of peaks in any sample. NB! A column 'Peaks' for the number of peaks will be created. If present it will be overwritten. NB! A column 'Group' for the sample group will be created. If present it will be overwritten. NB! A column 'Id' will be created by combining the content in the 'Sample.Name' and 'File' column (if available). The unique entries in the 'Id' column will be the definition of a unique sample. If 'File' is present this allows for identical sample names in different batches (files) to be identified as unique samples. If 'Id' is present it will be overwritten.

Value

data.frame with with additional columns 'Peaks', 'Group', and 'Id'.

`calculatePeaks_gui` *Calculate Peaks*

Description

GUI wrapper for the `calculatePeaks` function.

Usage

```
calculatePeaks_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Counts the number of peaks in samples and markers with option to discard off-ladder peaks and to label groups according to maximum number of peaks.

Value

TRUE

See Also

`calculatePeaks`

`calculatePullup` *Calculate Spectral Pull-up*

Description

Calculates possible pull-up peaks.

Usage

```
calculatePullup(
  data,
  ref,
  pullup.range = 6,
  block.range = 12,
  ol.rm = FALSE,
  ignore.case = TRUE,
  word = FALSE,
  discard = FALSE,
  limit = 1,
  debug = FALSE
)
```

Arguments

`data`	a data frame containing at least 'Sample.Name', 'Marker', 'Height', 'Allele', 'Dye', 'Data.Point' and 'Size'.
`ref`	a data frame containing at least 'Sample.Name', 'Marker', 'Allele'.
`pullup.range`	numeric to set the analysis window to look for pull-up peaks (known allele data point +- pullup.range/2)
`block.range`	numeric to set blocking range to check for known allele overlap (known allele data point +- block.range/2).
`ol.rm`	logical TRUE if off-ladder peaks should be excluded from analysis. Default is FALSE to include off-ladder peaks.
`ignore.case`	logical indicating if sample matching should ignore case.
`word`	logical indicating if word boundaries should be added before sample matching.
`discard`	logical TRUE if known alleles with no detected pull-up should be discarded from the result. Default is FALSE to include alleles not causing pull-up.
`limit`	numeric remove ratios > limit from the result. Default is 1 to remove pull-up peaks that are higher than the source peak and hence likely not a real pull-up.
`debug`	logical indicating printing debug information.

Details

Calculates possible pull-up (aka. bleed-through) peaks in a dataset. Known alleles are identified and the analysis window range is marked. If the blocking range of known alleles overlap, they are excluded from the analysis. Pull-up peaks within the data point analysis window, around known alleles, are identified, the data point difference, and the ratio is calculated. Off-ladder ('OL') alleles are included by default but can be excluded. All known peaks included in the analysis are by default written to the result even if they did not cause any pull-up. These rows can be discarded from the result.

Value

data.frame with with columns 'Sample.Name', 'Marker', 'Dye', 'Allele', 'Height', 'Size', 'Data.Point', 'P.Marker', 'P.Dye', 'P.Allele', 'P.Height', 'P.Size', 'P.Data.Point', 'Delta', 'Ratio'.

---

calculatePullup_gui *Calculate Spectral Pull-up*

Description

GUI wrapper for the calculatePullup function.

Usage

```
calculatePullup_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculatePullup function by providing a graphical user interface.

Value

TRUE

See Also

calculatePullup, checkSubset

`calculateRatio` *Calculate Ratio*

Description

Calculates the peak height ratio between specified loci.

Usage

```
calculateRatio(
  data,
  ref = NULL,
  numerator = NULL,
  denominator = NULL,
  group = NULL,
  ol.rm = TRUE,
  ignore.case = TRUE,
  word = FALSE,
  exact = FALSE,
  debug = FALSE
)
```

Arguments

`data`	a data frame containing at least 'Sample.Name', 'Marker', 'Height', 'Allele'.
`ref`	a data frame containing at least 'Sample.Name', 'Marker', 'Allele'. If provided alleles matching 'ref' will be extracted from 'data' (see `filterProfile`).
`numerator`	character vector with marker names.
`denominator`	character vector with marker names.
`group`	character column name to group by.
`ol.rm`	logical indicating if off-ladder 'OL' alleles should be removed.
`ignore.case`	logical indicating if sample matching should ignore case.
`word`	logical indicating if word boundaries should be added before sample matching.
`exact`	logical indicating if exact sample matching should be used.
`debug`	logical indicating printing debug information.

Details

Default is to calculate the ratio between all unique pairwise combinations of markers/loci. If equal number of markers are provided in the numerator and the denominator the provided pairwise ratios will be calculated. If markers are provided in only the numerator or only the denominator the ratio of all possible combinations of the provided markers and the markers not provided will be calculated. If the number of markers provided are different in the numerator and in the denominator the shorter vector will be repeated to equal the longer vector in length. Data can be unfiltered or filtered since the sum of peak heights per marker is used. Off-ladder alleles is by default removed from the dataset before calculations.

Value

data.frame with with columns 'Sample.Name', 'Marker', 'Delta', 'Hb', 'Lb', 'MPH', 'TPH'.

Examples

```
data(set2)
# Calculate ratio between the shortest and longest marker in each dye.
numerator <- c("D3S1358", "AMEL", "D19S433")
denominator <- c("D2S1338", "D18S51", "FGA")
calculateRatio(data = set2, numerator = numerator, denominator = denominator)
calculateRatio(data = set2, numerator = NULL, denominator = "AMEL")
calculateRatio(data = set2, numerator = c("AMEL", "TH01"), denominator = NULL)
calculateRatio(data = set2, numerator = NULL, denominator = NULL)
```

---

calculateRatio_gui *Calculate Ratio*

Description

GUI wrapper for the calculateRatio function.

Usage

```
calculateRatio_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateRatio function by providing a graphical user interface.

Value

TRUE

See Also

link{calculateRatio}, link{checkSubset}

`calculateResultType` *Calculate Result Type*

Description

Calculate the result type for samples.

Usage

```
calculateResultType(
  data,
  kit = NULL,
  add.missing.marker = TRUE,
  threshold = NULL,
  mixture.limits = NULL,
  partial.limits = NULL,
  subset.name = NA,
  marker.subset = NULL,
  debug = FALSE
)
```

Arguments

`data`	a data frame containing at least the column 'Sample.Name'.
`kit`	character string or integer defining the kit.
`add.missing.marker`	logical, default is TRUE which adds missing markers.
`threshold`	integer indicating the dropout threshold.
`mixture.limits`	integer or vector indicating subtypes of 'Mixture'.
`partial.limits`	integer or vector indicating subtypes of 'Partial'.
`subset.name`	string naming the subset of 'Complete'.
`marker.subset`	string with marker names defining the subset of 'Complete'.
`debug`	logical indicating printing debug information.

Details

Calculates result types for samples in 'data'. Defined types are: 'No result', 'Mixture', 'Partial', and 'Complete'. Subtypes can be defined by parameters. An integer passed to 'threshold' defines a subtype of 'Complete' "Complete profile all peaks >threshold". An integer or vector passed to 'mixture.limits' define subtypes of 'Mixture' "> [mixture.limits] markers". An integer or vector passed to 'partial.limits' define subtypes of 'Partial' "> [partial.limits] peaks". A string with marker names separated by pipe (|) passed to 'marker.subset' and a string 'subset.name' defines a subtype of 'Partial' "Complete [subset.name]".

Value

data.frame with columns 'Sample.Name','Type', and 'Subtype'.

`calculateResultType_gui` *Calculate Result Type*

Description

GUI wrapper for the `calculateResultType` function.

Usage

```
calculateResultType_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of `calculateResultType` by providing a graphical user interface.

Value

TRUE

See Also

`calculateResultType`

`calculateSlope` *Calculate Profile Slope.*

Description

Calculate profile slope for samples.

Usage

```
calculateSlope(data, ref, conf = 0.975, kit = NULL, debug = FALSE, ...)
```

Arguments

`data`	data.frame with at least columns 'Sample.Name', 'Marker', and 'Height'.
`ref`	data.frame with at least columns 'Sample.Name', 'Marker', and 'Allele'
`conf`	numeric confidence limit to calculate a confidence interval from (Student t Distribution with 'Peaks'-2 degree of freedom). Default is 0.975 corresponding to a 95% confidence interval.
`kit`	character string or vector specifying the analysis kits used to produce the data. If length(kit) != number of groups, kit[1] will be used for all groups.
`debug`	logical indicating printing debug information.
`...`	additional arguments to the `filterProfile` function

Details

Calculates the profile slope for each sample. The slope is calculated as a linear model specified by the response (natural logarithm of peak height) by the term size (in base pair). If 'Size' is not present in the dataset, one or multiple kit names can be given as argument 'kit'. The specified kits will be used to estimate the size of each allele. If 'kit' is NULL the kit(s) will be automatically detected, and the 'Size' will be calculated.

The column 'Group' can be used to separate datasets to be compared, and if so 'kit' must be a vector of equal length as the number of groups, and in the same order. If not the first 'kit' will be recycled for all groups.

Data will be filtered using the reference profiles.

Value

data.frame with with columns 'Sample.Name', 'Kit', 'Group', 'Slope', 'Error', 'Peaks', 'Lower', and 'Upper'.

calculateSlope_gui *Calculate Profile Slope*

Description

GUI wrapper for the `calculateSlope` function.

Usage

```
calculateSlope_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateSlope` function by providing a graphical user interface.

Value

TRUE

See Also

`calculateSlope`

calculateSpike *Detect Spike*

Description

Detect samples with possible spikes in the DNA profile.

Usage

```
calculateSpike(
  data,
  threshold = NULL,
  tolerance = 2,
  kit = NULL,
  quick = FALSE,
  debug = FALSE
)
```

Arguments

data	data.frame with including columns 'Sample.Name', 'Marker', 'Size'.
threshold	numeric number of peaks of similar size in different dye channels to pass as a possible spike (NULL = number of dye channels minus one to allow for one unlabeled peak).
tolerance	numeric tolerance for Size. For the quick and dirty rounding method e.g. 1.5 rounds Size to +/- 0.75 bp. For the slower but more accurate method the value is the maximum allowed difference between peaks in a spike.
kit	string or numeric for the STR-kit used (NULL = auto detect).
quick	logical TRUE for the quick and dirty method. Default is FALSE which use a slower but more accurate method.
debug	logical indicating printing debug information.

Details

Creates a list of possible spikes by searching for peaks aligned vertically (i.e. nearly identical size). There are two methods to search. The default method (quick=FALSE) method that calculates the distance between each peak in a sample, and the quick and dirty method (quick=TRUE) that rounds the size and then group peaks with identical size. The rounding method is faster because it uses the data.table package. The accurate method is slower because it uses nested loops - the first through each sample to calculate the distance between all peaks, and the second loops through the distance matrix to identify which peaks lies within the tolerance. NB! The quick method may not catch all spikes since two peaks can be separated by rounding e.g. 200.5 and 200.6 becomes 200 and 201 respectively.

Value

data.frame

See Also

data.table

calculateSpike_gui *Detect Spike*

Description

GUI wrapper for the calculateSpike function.

Usage

```
calculateSpike_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateSpike function by providing a graphical user interface.

Value

TRUE

See Also

calculateSpike

calculateStatistics *Summary Statistics*

Description

Calculate summary statistics for the selected target and scope.

Usage

```
calculateStatistics(
  data,
  target,
  quant = 0.95,
  group = NULL,
  count = NULL,
  decimals = -1,
  debug = FALSE
)
```

Arguments

data	data.frame containing the data of interest.
target	character column to calculate summary statistics for.
quant	numeric quantile to calculate {0,1}, default 0.95.
group	character vector of column(s) to group by, if any.
count	character column to count unique values in, if any.
decimals	numeric number of decimals. Negative does not round.
debug	logical indicating printing debug information.

Details

Calculate summary statistics for the given target column ('X') across the entire dataset or grouped by one or multiple columns, and counts the number of unique values in the given count column ('Y'). Returns a data.frame with the grouped columns, number of unique values 'Y.n', number of observations 'X.n', the minimum value 'X.Min', the mean value 'X.Mean', standard deviation 'X.Stdv', and the provided percentile 'X.Perc.##'. For more details see `unique`, `min`, `mean`, `sd`, `quantile`.

Value

data.frame with summary statistics.

`calculateStatistics_gui` *Calculate Statistics*

Description

GUI wrapper for the `calculateStatistics` function.

Usage

```
calculateStatistics_gui(
  data = NULL,
  target = NULL,
  quant = 0.95,
  group = NULL,
  count = NULL,
  decimals = 4,
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

data	character preselected data.frame if provided and exist in environment.
target	character vector preselected target column.
quant	numeric quantile to calculate. Default=0.95.
group	character vector preselected column(s) to group by.
count	character vector preselected column to count unique values in.
decimals	numeric number of decimals. Negative does not round.
env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the calculateStatistics function by providing a graphical user interface. Preselected values can be provided as arguments.

Value

TRUE

See Also

link{quantile}, link{min}, link{max}, link{mean}, link{sd}

`calculateStutter` *Calculate Stutter*

Description

Calculate statistics for stutters.

Usage

```
calculateStutter(
  data,
  ref,
  back = 2,
  forward = 1,
  interference = 0,
  replace.val = NULL,
  by.val = NULL,
  debug = FALSE
)
```

Arguments

`data`	data frame with genotype data. Requires columns 'Sample.Name', 'Marker', 'Allele', 'Height'.
`ref`	data frame with the known profiles. Requires columns 'Sample.Name', 'Marker', 'Allele'.
`back`	integer for the maximal number of backward stutters (max size difference 2 = n-2 repeats).
`forward`	integer for the maximal number of forward stutters (max size difference 1 = n+1 repeats).
`interference`	integer specifying accepted level of allowed overlap.
`replace.val`	numeric vector with 'false' stutters to replace.
`by.val`	numeric vector with correct stutters.
`debug`	logical indicating printing debug information.

Details

Calculates stutter ratios based on the 'reference' data set and a defined analysis range around the true allele.

NB! Off-ladder alleles ('OL') is NOT included in the analysis. NB! Labeled pull-ups or artefacts within stutter range IS included in the analysis.

There are three levels of allowed overlap (interference). 0 = no interference (default): calculate the ratio for a stutter only if there are no overlap between the stutter or its allele with the analysis range of another allele. 1 = stutter-stutter interference: calculate the ratio for a stutter even if the

stutter or its allele overlap with a stutter within the analysis range of another allele. 2 = stutter-allele interference: calculate the ratio for a stutter even if the stutter and its allele overlap with the analysis range of another allele.

Value

data.frame with extracted result.

`calculateStutter_gui` *Calculate Stutter*

Description

GUI wrapper for the `calculateStutter` function.

Usage

```
calculateStutter_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `calculateStutter` function by providing a graphical user interface to it.

Value

TRUE

See Also

`calculateStutter`, `checkSubset`

`calculateT` *Calculate Stochastic Threshold*

Description

Calculates point estimates for the stochastic threshold.

Usage

```
calculateT(
  data,
  log.model = FALSE,
  p.dropout = 0.01,
  pred.int = 0.95,
  debug = FALSE
)
```

Arguments

`data`	data.frame with dependent and explanatory values in columns named 'Dep' and 'Exp'.
`log.model`	logical indicating if data should be log transformed. Default=FALSE.
`p.dropout`	numeric accepted risk to calculate point estimate for. Default=0.01.
`pred.int`	numeric prediction interval. Default=0.95.
`debug`	logical indicating printing debug information.

Details

Given a data.frame with observed values for the dependent variable (column 'Dep') and explanatory values (column 'Exp') point estimates corresponding to a risk level of `p.dropout` are calculated using logistic regression: `glm(Dep~Exp, family=binomial("logit"))`. A conservative estimate is calculated from the `pred.int`. In addition the model parameters B0 (intercept) and B1 (slope), Hosmer-Lemeshow test statistic (p-value), and the number of observed and dropped out alleles is returned.

Value

vector with named parameters

See Also

`calculateDropout`, `calculateAllT`, `modelDropout_gui`, `plotDropout_gui`

checkDataset *Check Dataset*

Description

Check a data.frame before analysis.

Usage

```
checkDataset(
  name,
  reqcol = NULL,
  slim = FALSE,
  slimcol = NULL,
  string = NULL,
  stringcol = NULL,
  env = parent.frame(),
  parent = NULL,
  debug = FALSE
)
```

Arguments

name	character name of data.frame.
reqcol	character vector with required column names.
slim	logical TRUE to check if 'slim' data.
slimcol	character vector with column names to check if 'slim' data.
string	character vector with invalid strings in 'stringcol', return FALSE if found.
stringcol	character vector with column names to check for 'string'.
env	environment where to look for the data frame.
parent	parent gWidget.
debug	logical indicating printing debug information.

Details

Check that the object exist, there are rows, the required columns exist, if data.frame is 'fat', and if invalid strings exist. Show error message if not.

checkSubset *Check Subset*

Description

Check the result of subsetting

Usage

```
checkSubset(
  data,
  ref,
  console = TRUE,
  ignore.case = TRUE,
  word = FALSE,
  exact = FALSE,
  debug = FALSE
)
```

Arguments

data	a data frame in GeneMapper format containing column 'Sample.Name'.
ref	a data frame in GeneMapper format containing column 'Sample.Name', OR an atomic vector e.g. a single sample name string.
console	logical, if TRUE result is printed to R console, if FALSE a string is returned.
ignore.case	logical, if TRUE case insensitive matching is used.
word	logical, if TRUE only word matching (regex).
exact	logical, if TRUE only exact match.
debug	logical indicating printing debug information.

Details

Check if ref and sample names are unique for subsetting. Prints the result to the R-prompt.

See Also

grep

checkSubset_gui *Check Subset*

Description

GUI wrapper for the checkSubset function.

Usage

```
checkSubset_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the checkSubset function by providing a graphical user interface to it.

Value

TRUE

See Also

checkSubset

colConvert *Convert Columns*

Description

Internal helper function.

Usage

```
colConvert(
  data,
  columns = "Height|Size|Data.Point",
  ignore.case = TRUE,
  fixed = FALSE,
  debug = FALSE
)
```

Arguments

data	data.frame.
columns	character string containing a regular expression (or character string for fixed = TRUE) to be matched in the given character vector (separate multiple column names by | in reg.exp).
ignore.case	logical TRUE to ignore case in matching.
fixed	logical TRUE if columns is a string to be matched as is.
debug	logical indicating printing debug information.

Details

Takes a data frame as input and return it after converting known numeric columns to numeric.

Value

data.frame.

---

colNames *Column Names*

Description

Internal helper function.

Usage

```
colNames(data, slim = TRUE, concatenate = NULL, numbered = TRUE, debug = FALSE)
```

Arguments

data	data.frame.
slim	logical, TRUE returns column names occurring once, FALSE returns column names occurring multiple times.
concatenate	string, if not NULL returns a single string with column names concatenated by the provided string instead of a vector.
numbered	logical indicating if repeated column names must have a number suffix.
debug	logical indicating printing debug information.

Details

Takes a data frame as input and return either column names occurring once or multiple times. Matching is done by the 'base name' (the substring to the left of the last period, if any). The return type is a string vector by default, or a single string of column names separated by a string 'concatenate' (see 'collapse' in `paste` for details). There is an option to limit multiple names to those with a number suffix.

Value

character, vector or string.

`columns` *Column Actions*

Description

Perform actions on columns.

Usage

```
columns(
  data,
  col1 = NA,
  col2 = NA,
  operator = "&",
  fixed = NA,
  target = NA,
  start = 1,
  stop = 1,
  debug = FALSE
)
```

Arguments

`data`	a data frame.
`col1`	character column name to perform action on.
`col2`	character optional second column name to perform action on.
`operator`	character to indicate operator: '&' concatenate, '+' add, '*' multiply, '-' subtract, '/' divide, 'substr' extract a substring.
`fixed`	character or numeric providing the second operand if 'col2' is not used.
`target`	character to specify column name for result. Default is to overwrite 'col1'. If not present it will be added.
`start`	integer, the first position to be extracted.
`stop`	integer, the last position to be extracted.
`debug`	logical to indicate if debug information should be printed.

Details

Perform actions on columns in a data frame. There are five actions: concatenate, add, multiply, subtract, divide. The selected action can be performed on two columns, or one column and a fixed value, or a new column can be added. A target column for the result is specified. NB! if the target column already exist it will be overwritten, else it will be created. A common use is to create a unique Sample.Name from the existing Sample.Name column and e.g. the File.Name or File.Time columns. It can also be used to calculate the Amount from the Concentration.

Value

data frame.

See Also

substr

Examples

```
# Get a sample dataset.
data(set2)
# Add concatenate Sample.Name and Dye.
set2 <- columns(data = set2, col1 = "Sample.Name", col2 = "Dye")
# Multiply Height by 4.
set2 <- columns(data = set2, col1 = "Height", operator = "*", fixed = 4)
# Add a new column.
set2 <- columns(data = set2, operator = "&", fixed = "1234", target = "Batch")
```

---

columns_gui *Column Actions*

Description

GUI wrapper for the columns function.

Usage

```
columns_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the columns function by providing a graphical user interface to it.

Value

TRUE

`combine_gui` *Combine Datasets*

Description

GUI for combining two datasets.

Usage

```
combine_gui(env = parent.frame(), debug = FALSE, parent = NULL)
```

Arguments

`env`	environment in which to search for data frames.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simple GUI to combine two datasets using the `rbind.fill` function. NB! Datasets must have identical column names but not necessarily in the same order.

Value

TRUE

`cropData_gui` *Crop Or Replace*

Description

GUI simplifying cropping and replacing values in data frames.

Usage

```
cropData_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select a data frame from the drop-down and a target column. To remove rows with 'NA' check the appropriate box. Select to discard or replace values and additional options. Click button to 'Apply' changes. Multiple actions can be performed on one dataset before saving as a new dataframe. NB! Check that data type is correct before click apply to avoid strange behavior. If data type is numeric any string will become a numeric 'NA'.

Value

TRUE

See Also

trim_gui, editData_gui, combine_gui

---

detectKit *Detect Kit*

Description

Finds the most likely STR kit for a dataset.

Usage

```
detectKit(data, index = FALSE, debug = FALSE)
```

Arguments

data	data frame with column 'Marker' or vector with marker names.
index	logical, returns kit index if TRUE or short name if FALSE.
debug	logical, prints debug information if TRUE.

Details

The function first check if there is a 'kit' attribute for the dataset. If there was a 'kit' attribute, and a match is found in getKit the corresponding kit or index is returned. If an attribute does not exist the function looks at the markers in the dataset and returns the most likely kit(s).

Value

integer or string indicating the detected kit.

editData_gui *Edit or View Data Frames*

Description

GUI to edit and view data frames.

Usage

```
editData_gui(
  env = parent.frame(),
  savegui = NULL,
  data = NULL,
  name = NULL,
  edit = TRUE,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
data	data.frame for instant viewing.
name	character string with the name of the provided dataset.
edit	logical TRUE to enable edit (uses gdf), FALSE to view and enable sorting by clicking a column header (uses gtable).
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select a data frame from the drop-down to view or edit a dataset. It is possible to save as a new dataframe. To enable sorting by clicking the column headers the view mode must be used (i.e. edit = FALSE). There is an option to limit the number of rows shown that can be used to preview large datasets that may otherwise cause performance problems. Attributes of the dataset can be views in a separate window.

Value

TRUE

See Also

trim_gui, cropData_gui, combine_gui

`export` *Export*

Description

Exports or saves various objects.

Usage

```
export(
  object,
  name = NA,
  use.object.name = is.na(name),
  env = parent.frame(),
  path = NA,
  ext = "auto",
  delim = "\t",
  width = 3000,
  height = 2000,
  res = 250,
  overwrite = FALSE,
  debug = FALSE
)
```

Arguments

`object`	string, list or vector containing object names to be exported.
`name`	string, list or vector containing file names. Multiple names as string must be separated by pipe '|' or comma ',', If not equal number of names as objects, first name will be used to construct names.
`use.object.name`	logical, if TRUE file name will be the same as object name.
`env`	environment where the objects exists.
`path`	string specifying the destination folder exported objects.
`ext`	string specifying file extension. Default is 'auto' for automatic .txt or .png based on object class. If .RData all objects will be exported as .RData files.
`delim`	string specifying the delimiter used as separator.
`width`	integer specifying the width of the image.
`height`	integer specifying the height of the image.
`res`	integer specifying the resolution of the image.
`overwrite`	logical, TRUE if existing files should be overwritten.
`debug`	logical indicating printing debug information.

Details

Export objects to a directory on the file system. Currently only objects of class data.frames or ggplot are supported. data.frame objects will be exported as '.txt' and ggplot objects as '.png'. .RData applies to all supported object types.

Value

NA if all objects were exported OR, data.frame with columns 'Object', 'Name', and 'New.Name' with objects that were not exported.

---

export_gui *Export*

Description

GUI wrapper for the `export` function.

Usage

```
export_gui(
  obj = listObjects(env = env, obj.class = c("data.frame", "ggplot")),
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

obj	character vector with object names.
env	environment where the objects exist. Default is the current environment.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the `export` function by providing a graphical user interface to it. Currently all available objects provided are selected by default.

Value

TRUE

See Also

`export`

`filterProfile` *Filter Profile*

Description

Filter peaks from profiles.

Usage

```
filterProfile(
  data,
  ref = NULL,
  add.missing.loci = FALSE,
  keep.na = FALSE,
  ignore.case = TRUE,
  exact = FALSE,
  word = FALSE,
  invert = FALSE,
  sex.rm = FALSE,
  qs.rm = FALSE,
  kit = NULL,
  filter.allele = TRUE,
  debug = FALSE
)
```

Arguments

`data`	data frame with genotype data in 'slim' format.
`ref`	data frame with reference profile in 'slim' format.
`add.missing.loci`	logical. TRUE add loci present in ref but not in data. Overrides keep.na=FALSE.
`keep.na`	logical. FALSE discards NA alleles. TRUE keep loci/sample even if no matching allele.
`ignore.case`	logical TRUE ignore case.
`exact`	logical TRUE use exact matching of sample names.
`word`	logical TRUE adds word boundaries when matching sample names.
`invert`	logical TRUE filter peaks NOT matching the reference.
`sex.rm`	logical TRUE removes sex markers defined by 'kit'.
`qs.rm`	logical TRUE removes quality sensors defined by 'kit'.
`kit`	character string defining the kit used. If NULL automatic detection will be attempted.
`filter.allele`	logical TRUE filter known alleles. FALSE increase the performance if only sex markers or quality sensors should be removed.
`debug`	logical indicating printing debug information.

Details

Filters out the peaks matching (or not matching) specified known profiles from typing data containing 'noise' such as stutters. If 'ref' does not contain a 'Sample.Name' column it will be used as reference for all samples in 'data'. The 'invert' option filters out peaks NOT matching the reference (e.g. drop-in peaks). Sex markers and quality sensors can be removed. NB! add.missing.loci overrides keep.na. Returns data where allele names match/not match 'ref' allele names. Required columns are: 'Sample.Name', 'Marker', and 'Allele'.

Value

data.frame with extracted result.

---

filterProfile_gui *Filter Profile*

Description

GUI wrapper for the `filterProfile` function.

Usage

```
filterProfile_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `filterProfile` function by providing a graphical user interface to it. All data not matching/matching the reference will be discarded. Useful for filtering stutters and artifacts from raw typing data or to identify drop-ins.

Value

TRUE

See Also

`filterProfile`, `checkSubset`

`generateEPG` *Generate EPG*

Description

Visualizes an EPG from DNA profiling data.

Usage

```
generateEPG(
  data,
  kit,
  title = NULL,
  wrap = TRUE,
  boxplot = FALSE,
  peaks = TRUE,
  collapse = TRUE,
  silent = FALSE,
  ignore.case = TRUE,
  at = 0,
  scale = "free",
  limit.x = TRUE,
  label.size = 3,
  label.angle = 0,
  label.vjust = 1,
  label.hjust = 0.5,
  expand = 0.1,
  debug = FALSE
)
```

Arguments

`data`	data frame containing at least columns 'Sample.Name', 'Allele', and 'Marker'.
`kit`	string or integer representing the STR typing kit.
`title`	string providing the title for the EPG.
`wrap`	logical TRUE to wrap by dye.
`boxplot`	logical TRUE to plot distributions of peak heights as boxplots.
`peaks`	logical TRUE to plot peaks for distributions using mean peak height.
`collapse`	logical TRUE to add the peak heights of identical alleles peaks within each marker. NB! Removes off-ladder alleles.
`silent`	logical FALSE to show plot.
`ignore.case`	logical FALSE for case sensitive marker names.
`at`	numeric analytical threshold (Height <= at will not be plotted).
`scale`	character "free" free x and y scale, alternatively "free_y" or "free_x".

limit.x	logical TRUE to fix x-axis to size range. To get a common x scale set scale="free_y" and limit.x=TRUE.
label.size	numeric for allele label text size.
label.angle	numeric for allele label print angle.
label.vjust	numeric for vertical justification of allele labels.
label.hjust	numeric for horizontal justification of allele labels.
expand	numeric for plot are expansion (to avoid clipping of labels).
debug	logical for printing debug information to the console.

Details

Generates a electropherogram like plot from 'data' and 'kit'. If 'Size' is not present it is estimated from kit information and allele values. If 'Height' is not present a default of 1000 RFU is used. Off-ladder alleles can be plotted if 'Size' is provided. There are various options to customize the plot scale and labels. It is also possible to plot 'distributions' of peak heights as boxplots.

Value

ggplot object.

---

generateEPG_gui *Generate EPG*

Description

GUI wrapper for the generateEPG function.

Usage

```
generateEPG_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the generateEPG function by providing a graphical user interface to it.

Value

TRUE

See Also

generateEPG

`getKit` *Get Kit*

Description

Provides information about STR kits.

Usage

```
getKit(
  kit = NULL,
  what = NA,
  show.messages = FALSE,
  .kit.info = NULL,
  debug = FALSE
)
```

Arguments

`kit`	string or integer to specify the kit.
`what`	string to specify which information to return. Default is 'NA' which return all info. Not case sensitive. Possible values: "Index", "Panel", "Short.Name", "Full.Name", "Marker, "Allele", "Size", "Virtual", "Color", "Repeat", "Range", "Offset", "Sex.Marker", "Quality.Sensor". An unsupported value returns NA and a warning.
`show.messages`	logical, default TRUE for printing messages to the R prompt.
`.kit.info`	data frame, run function on a data frame instead of the kits.txt file.
`debug`	logical indicating printing debug information.

Details

The function returns the following information for a kit specified in kits.txt: Panel name, short kit name (unique, user defined), full kit name (user defined), marker names, allele names, allele sizes (bp), minimum allele size, maximum allele size (bp), flag for virtual alleles, marker color, marker repeat unit size (bp), minimum marker size, maximum marker, marker offset (bp), flag for sex markers (TRUE/FALSE).

If no matching kit or kit index is found NA is returned. If kit='NULL' or '0' a vector of available kits is printed and NA returned.

Value

data.frame with kit information.

Examples

```
# Show all information stored for kit with short name 'ESX17'.
getKit("ESX17")
```

---

getSetting *Get Settings.*

Description

Accepts a key string and returns the corresponding value.

Usage

```
getSetting(key)
```

Arguments

key	character key for value to return.

Details

Accepts a key string and returns the corresponding value from the settings.txt file located within the package folders exdata sub folder.

Value

character the retrieved value or NA if not found.

---

getStrings *Get Language Strings*

Description

Accepts a language code and GUI. Returns the corresponding language strings.

Usage

```
getStrings(language = NA, gui = NA, key = NA, encoding = NA, about = FALSE)
```

Arguments

language	character name of the language.
gui	character the function name for the GUI to 'translate'.
key	character the key to 'translate'. Only used in combination with 'gui'.
encoding	character encoding to be assumed for input strings.
about	logical FALSE (default) to read key-value pairs, TRUE to read about file as plain text.

Details

Accepts a language code, GUI, and key. Returns the corresponding language strings for the specified GUI function or key from a text file named as the language code. Replaces backslash + n with a new line character (only if 'GUI' is specified).

Value

character vector or data.table with the retrieved values. NULL if file or GUI was not found.

---

ggsave_gui *Save Image*

Description

A simple GUI wrapper for ggsave.

Usage

```
ggsave_gui(
  ggplot = NULL,
  name = "",
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

ggplot	plot object.
name	optional string providing a file name.
env	environment where the objects exist. Default is the current environment.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	object specifying the parent widget to center the message box, and to get focus when finished.

Details

Simple GUI wrapper for ggsave.

Value

TRUE

See Also

ggsave

`guessProfile` *Guess Profile*

Description

Guesses the correct profile based on peak height.

Usage

```
guessProfile(
  data,
  ratio = 0.6,
  height = 50,
  na.rm = FALSE,
  ol.rm = TRUE,
  debug = FALSE
)
```

Arguments

`data`	a data frame containing at least 'Sample.Name', 'Marker', 'Allele', Height'.
`ratio`	numeric giving the peak height ratio threshold.
`height`	numeric giving the minimum peak height.
`na.rm`	logical indicating if rows with no peak should be discarded.
`ol.rm`	logical indicating if off-ladder alleles should be discarded.
`debug`	logical indicating printing debug information.

Details

Takes typing data from single source samples and filters out the presumed profile based on peak height and a ratio. Keeps the two highest peaks if their ratio is above the threshold, or the single highest peak if below the threshold.

Value

data.frame 'data' with genotype rows only.

Examples

```
# Load an example dataset.
data(set2)
# Filter out probable profile with criteria at least 70% Hb.
guessProfile(data = set2, ratio = 0.7)
```

---

guessProfile_gui *Guess Profile*

Description

GUI wrapper for the guessProfile function.

Usage

```
guessProfile_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the guessProfile function by providing a graphical user interface to it.

Value

TRUE

See Also

guessProfile, checkSubset

heightToPeak *Height To Peak.*

Description

Helper function to convert a peak into a plotable polygon.

Usage

```
heightToPeak(data, width = 1, keep.na = TRUE, debug = FALSE)
```

Arguments

data	data frame containing at least columns 'Height' and 'Size'.
width	numeric specifying the width of the peak in bp.
keep.na	logical. TRUE to keep empty markers.
debug	logical. TRUE prints debug information.

Details

Converts a single height and size value to a plotable 0-height-0 triangle/peak value. Makes 3 data points from each peak size for plotting a polygon representing a peak. Factors in other columns might get converted to factor level.

Value

data.frame with new values.

import *Import Data*

Description

Import text files and apply post processing.

Usage

```
import(
  folder = TRUE,
  extension = "txt",
  suffix = NA,
  prefix = NA,
  import.file = NA,
  folder.name = NA,
  file.name = TRUE,
```

```
  time.stamp = TRUE,
  separator = "\t",
  ignore.case = TRUE,
  auto.trim = FALSE,
  trim.samples = NULL,
  trim.invert = FALSE,
  auto.slim = FALSE,
  slim.na = TRUE,
  na.strings = c("NA", ""),
  debug = FALSE
)
```

Arguments

folder	logical, TRUE all files in folder will be imported, FALSE only selected file will be imported.
extension	string providing the file extension.
suffix	string, only files with specified suffix will be imported.
prefix	string, only files with specified prefix will be imported.
import.file	string if file name is provided file will be imported without showing the file open dialogue.
folder.name	string if folder name is provided files in folder will be imported without showing the select folder dialogue.
file.name	logical if TRUE the file name is written in a column 'File.Name'. NB! Any existing 'File.Name' column is overwritten.
time.stamp	logical if TRUE the file modified time stamp is written in a column 'Time'. NB! Any existing 'Time' column is overwritten.
separator	character for the delimiter used to separate columns (see 'sep' in read.table for details).
ignore.case	logical indicating if case should be ignored. Only applies to multiple file import option.
auto.trim	logical indicating if dataset should be trimmed.
trim.samples	character vector with sample names to trim.
trim.invert	logical to keep (TRUE) or remove (FALSE) samples.
auto.slim	logical indicating if dataset should be slimmed.
slim.na	logical indicating if rows without data should remain.
na.strings	character vector with strings to be replaced by NA.
debug	logical indicating printing debug information.

Details

Imports text files (e.g. GeneMapper results exported as text files) as data frames. Options to import one or multiple files. For multiple files it is possible to specify prefix, suffix, and file extension to create a file name filter. The file name and/or file time stamp can be imported. NB! Empty strings ("") and NA strings ("NA") are converted to NA. See list.files and read.table for additional details.

Value

data.frame with imported result.

See Also

trim, slim, list.files, read.table

`import_gui` *Import Data*

Description

GUI wrapper for the `import` function.

Usage

```
import_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

`env`	environment into which the object will be saved. Default is the current environment.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `import` function by providing a graphical user interface to it.

Value

TRUE

See Also

`import`

`listObjects` *List Objects*

Description

Internal helper function to list objects in an environment.

Usage

```
listObjects(
  env = parent.frame(),
  obj.class = NULL,
  sort = NULL,
  decreasing = TRUE,
  debug = FALSE
)
```

Arguments

`env`	environment in which to search for objects.
`obj.class`	character string or vector specifying the object class.
`sort`	character string "time", "alpha", "size" specifying the sorting order. Default = NULL.
`decreasing`	logical used to indicate order when sorting is not NULL. Default = TRUE.
`debug`	logical indicating printing debug information.

Details

Internal helper function to retrieve a list of objects from a workspace. Take an environment as argument and optionally an object class. Returns a list of objects of the specified class in the environment.

Value

character vector with the object names or NULL.

Examples

```
## Not run:
# List data frames in the workspace.
listObjects(obj.class = "data.frame")
# List functions in the workspace.
listObjects(obj.class = "function")

## End(Not run)
```

manageKits_gui *Manage Kits*

Description

Manage kits, import new kits, or edit the kit file through a graphical user interface.

Usage

```
manageKits_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	Environment in which to search for data frames.
savegui	Logical indicating if GUI settings should be saved in the environment (Currently not in use).
debug	Logical indicating whether to print debug information.
parent	Widget to get focus when finished.

Details

This function provides a graphical user interface (GUI) for managing kits, including the ability to import new kits, edit the short and full names of existing kits, or remove kits. The gender marker of each kit is auto-detected but can be manually adjusted. Note that the short name for each kit must be unique.

Value

TRUE if the operation completes successfully.

maskAT *Mask And Prepare Data To Analyze Analytical Threshold*

Description

Break-out function to prepare data for the function calculateAT.

Usage

```
maskAT(
  data,
  ref = NULL,
  mask.height = TRUE,
  height = 500,
  mask.sample = TRUE,
  per.dye = TRUE,
  range.sample = 20,
  mask.ils = TRUE,
  range.ils = 10,
  ignore.case = TRUE,
  word = FALSE,
  debug = FALSE
)
```

Arguments

data	a data frame containing at least 'Dye.Sample.Peak', 'Sample.File.Name', 'Marker', 'Allele', 'Height', and 'Data.Point'.
ref	a data frame containing at least 'Sample.Name', 'Marker', 'Allele'.
mask.height	logical to indicate if high peaks should be masked.
height	integer for global lower peak height threshold for peaks to be excluded from the analysis. Active if 'mask.peak=TRUE.
mask.sample	logical to indicate if sample allelic peaks should be masked.
per.dye	logical TRUE if sample peaks should be masked per dye channel. FALSE if sample peaks should be masked globally across dye channels.
range.sample	integer to specify the masking range in (+/-) data points. Active if mask.sample=TRUE.
mask.ils	logical to indicate if internal lane standard peaks should be masked.
range.ils	integer to specify the masking range in (+/-) data points. Active if mask.ils=TRUE.
ignore.case	logical to indicate if sample matching should ignore case.
word	logical to indicate if word boundaries should be added before sample matching.
debug	logical to indicate if debug information should be printed.

Details

Prepares the 'SamplePlotSizingTable' for analysis of analytical threshold. It is needed by the plot functions for control of masking. The preparation consist of converting the 'Height' and 'Data.Point' column to numeric (if needed), then dye channel information is extracted from the 'Dye.Sample.Peak' column and added to its own 'Dye' column, known fragments of the internal lane standard (marked with an asterisk '*') is flagged as 'TRUE' in a new column 'ILS'.

Value

data.frame with added columns 'Dye' and 'ILS'.

See Also

calculateAT

---

modelDropout_gui *Model And Plot Drop-out Events*

Description

Model the probability of drop-out and plot graphs.

Usage

```
modelDropout_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

calculateDropout score drop-out events relative to a user defined LDT in four different ways: (1) by reference to the low molecular weight allele (Method1), (2) by reference to the high molecular weight allele (Method2), (3) by reference to a random allele (MethodX), and (4) by reference to the locus (MethodL). Options 1-3 are recommended by the DNA commission (see reference), while option 4 is included for experimental purposes. Options 1-3 may discard many dropout events while option 4 catches all drop-out events. On the other hand options 1-3 can score events below the LDT, while option 4 cannot, making accurate predictions possible below the LDT. This is also why the number of observed drop-out events may differ between model plots and heatmap, scatterplot, and ecdf.

Method X/1/2 records the peak height of the partner allele to be used as the explanatory variable in the logistic regression. The locus method L also do this when there has been a drop-out, if not the the mean peak height for the locus is used. Peak heights for the locus method are stored in a separate column.

Using the scored drop-out events and the peak heights of the surviving alleles the probability of drop-out can be modeled by logistic regression as described in Appendix B in reference [1]. P(dropout|H) = B0 + B1*H, where 'H' is the peak height or log(peak height). This produces a plot with the predicted probabilities for a range of peak heights. There are options to print the model

parameters, mark the stochastic threshold at a specified probability of drop-out, include the underlying observations, and to calculate a specified prediction interval. A conservative estimate of the stochastic threshold can be calculated from the prediction interval: the risk of observing a drop-out probability greater than the specified threshold limit, at the conservative peak height, is less than a specified value (e.g. 1-0.95=0.05). By default the gender marker is excluded from the dataset used for modeling, and the peak height is used as explanatory variable. The logarithm of the average peak height 'H' can be used instead of the allele/locus peak height [3] (The implementation of 'H' has limitations when dropout is present. See `calculateHeight`). To evaluate the goodness of fit for the logistic regression the Hosmer-Lemeshow test is used [4]. A value below 0.05 indicates a poor fit. Alternatives to the logistic regression method are discussed in reference [5] and [6].

Explanation of the result: Dropout - all alleles are scored according to the limit of detection threshold (LDT). This is the observations and is not used for modeling. Rfu - peak height of the surviving allele. MethodX - a random reference allele is selected and drop-out is scored in relation to the the partner allele. Method1 - the low molecular weight allele is selected and drop-out is scored if the high molecular weight allele is missing. Method2 - the high molecular weight allele is selected and drop-out is scored if the low molecular weight allele is missing. MethodL - drop-out is scored per locus i.e. drop-out if any allele is missing. MethodL.Ph - peak height of the surviving allele if one allele has dropped out, or the average peak height if no drop-out.

Value

TRUE

References

[1] Peter Gill et.al., DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Science International: Genetics, Volume 6, Issue 6, December 2012, Pages 679-688, ISSN 1872-4973, 10.1016/j.fsigen.2012.06.002. doi:10.1016/j.fsigen.2012.06.002

[2] Peter Gill, Roberto Puch-Solis, James Curran, The low-template-DNA (stochastic) threshold-Its determination relative to risk analysis for national DNA databases, Forensic Science International: Genetics, Volume 3, Issue 2, March 2009, Pages 104-111, ISSN 1872-4973, 10.1016/j.fsigen.2008.11.009. doi:10.1016/j.fsigen.2008.11.009

[3] Torben Tvedebrink, Poul Svante Eriksen, Helle Smidt Mogensen, Niels Morling, Estimating the probability of allelic drop-out of STR alleles in forensic genetics, Forensic Science International: Genetics, Volume 3, Issue 4, September 2009, Pages 222-226, ISSN 1872-4973, 10.1016/j.fsigen.2009.02.002. doi:10.1016/j.fsigen.2009.02.002

[4] H. DW Jr., S. Lemeshow, Applied Logistic Regression, John Wiley & Sons, 2004.

[5] A.A. Westen, L.J.W. Grol, J. Harteveld, A.S. Matai, P. de Knijff, T. Sijen, Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM, Forensic Science International: Genetetics, Volume 6, Issue 6 December 2012, Pages 708-715, ISSN 1872-4973, 10.1016/j.fsigen.2012.05.001. doi:10.1016/j.fsigen.2012.05.001

[6] R. Puch-Solis, A.J. Kirkham, P. Gill, J. Read, S. Watson, D. Drew, Practical determination of the low template DNA threshold, Forensic Science International: Genetetics, Volume 5, Issue 5, November 2011, Pages 422-427, ISSN 1872-4973, 10.1016/j.fsigen.2010.09.001. doi:10.1016/j.fsigen.2010.09.001

See Also

calculateDropout, plotDropout_gui, hoslem.test

---

plotAT_gui *Plot Analytical Threshold*

Description

GUI simplifying the creation of plots from analytical threshold data.

Usage

```
plotAT_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select data to plot in the drop-down menu. Plot regression data Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

`plotBalance_gui` *Plot Balance*

Description

GUI simplifying the creation of plots from balance data.

Usage

```
plotBalance_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Select a dataset to plot and the typing kit used (if not automatically detected). Plot heterozygote peak balance versus the average locus peak height, the average profile peak height 'H', or by the difference in repeat units (delta). Plot inter-locus balance versus the average locus peak height, or the average profile peak height 'H'. Automatic plot titles can be replaced by custom titles. Sex markers can be excluded. It is possible to plot logarithmic ratios. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

`plotCapillary_gui` *Plot Capillary Balance*

Description

GUI simplifying the creation of plots from capillary balance data.

Usage

```
plotCapillary_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Select a dataset to plot from the drop-down menu. Plot capillary balance as a dotplot, boxplot or as a distribution. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

`plotContamination_gui` *Plot Contamination*

Description

GUI simplifying the creation of plots from negative control data.

Usage

```
plotContamination_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Select data to plot in the drop-down menu. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

References

Duncan Taylor et.al., Validating multiplexes for use in conjunction with modern interpretation strategies, Forensic Science International: Genetics, Volume 20, January 2016, Pages 6-19, ISSN 1872-4973, 10.1016/j.fsigen.2015.09.011. doi:10.1016/j.fsigen.2015.09.011

plotDistribution_gui *Plot Distribution*

Description

GUI simplifying the creation of distribution plots.

Usage

```
plotDistribution_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Plot the distribution of data as cumulative distribution function, probability density function, or count. First select a dataset, then select a group (in column 'Group' if any), finally select a column to plot the distribution of. It is possible to overlay a boxplot and to plot logarithms. Various smoothing kernels and bandwidths can be specified. The bandwidth or the number of bins can be specified for the histogram. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

log, geom_density

`plotDropout_gui` *Plot Drop-out Events*

Description

GUI simplifying the creation of plots from dropout data.

Usage

```
plotDropout_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Plot dropout data as heatmap arranged by, average peak height, amount, concentration, or sample name. It is also possible to plot the empirical cumulative distribution (ecdp) of the peak heights of surviving heterozygote alleles (with dropout of the partner allele), or a dotplot of all dropout events. The peak height of homozygote alleles can be included in the ecdp. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

References

Antoinette A. Westen, Laurens J.W. Grol, Joyce Harteveld, Anuska S.Matai, Peter de Knijff, Titia Sijen, Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM, Forensic Science International: Genetetics, Volume 6, Issue 6, December 2012, Pages 708-715, ISSN 1872-4973, 10.1016/j.fsigen.2012.05.001. doi:10.1016/j.fsigen.2012.05.001

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

plotEPG2 *plotEPG2*

Description

EPG data visualizer (interactive)

Usage

```
plotEPG2(
  mixData,
  kit,
  refData = NULL,
  AT = NULL,
  ST = NULL,
  dyeYmax = TRUE,
  plotRepsOnly = TRUE,
  options = NULL
)
```

Arguments

mixData	List of mixData[[ss]][[loc]] =list(adata,hdata), with samplenames ss, loci names loc, allele vector adata (can be strings or numeric), intensity vector hdata (must be numeric)
kit	Short name of kit: See supported kits with getKit()
refData	List of refData[[rr]][[loc]] or refData[[loc]][[rr]] to label references (flexible). Visualizer will show dropout alleles.
AT	A detection threshold can be shown in a dashed line in the plot (constant). Possibly a vector with locus column names
ST	A stochastic threshold can be shown in a dashed line in the plot (constant). Possibly a vector with locus column names
dyeYmax	Whether Y-axis should be same for all markers (FALSE) or not (TRUE this is default)
plotRepsOnly	Whether only replicate-plot is shown in case of multiple samples (TRUE is default)
options	A list of possible plot configurations. See comments below

Details

Plots peak height with corresponding allele for sample(s) for a given kit.

Value

sub A plotly widget

Author(s)

Oyvind Bleka

`plotEPG2_gui` *Plot EPG*

Description

GUI wrapper for the `plotEPG2` function.

Usage

```
plotEPG2_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `plotEPG2` function by providing a graphical user interface.

Value

TRUE

See Also

`plotEPG2`

plotGroups_gui *Plot Empirical Cumulative Distributions*

Description

GUI simplifying the creation of empirical cumulative distribution plots.

Usage

```
plotGroups_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Plot the distribution of data as cumulative distribution function for multiple groups. First select a dataset, then select columns to flat, group, and plot by. For example, if a genotype dataset is selected and data is flattened by Sample.Name the 'group by' and 'plot by' values must be identical for all rows for a given sample. Automatic plot titles can be replaced by custom titles. Group names can be changed. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

stat_ecdf

plotKit_gui *Plot Kit Marker Ranges*

Description

GUI for plotting marker ranges for kits.

Usage

```
plotKit_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Create an overview of the size range for markers in different kits. It is possible to select multiple kits, specify titles, font size, distance between two kits, distance between dye channels, and the transparency of dyes.

Value

TRUE

plotPeaks_gui *Plot Peaks*

Description

GUI simplifying the creation of plots from result type data.

Usage

```
plotPeaks_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Plot result type data. It is possible to customize titles and font size. Data can be plotted as as frequency or proportion. The values can be printed on the plot with custom number of decimals. There are several color palettes to chose from. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

---

plotPrecision_gui *Plot Precision*

Description

GUI simplifying the creation of plots from precision data.

Usage

```
plotPrecision_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Plot precision data for size, height, or data point as dotplot or boxplot. Plot per marker or all in one. Use the mean value or the allele designation as x-axis labels. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

`plotPullup_gui` *Plot Pull-up*

Description

GUI simplifying the creation of plots from pull-up data.

Usage

```
plotPullup_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames and save result.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Select a dataset to plot and the typing kit used (if not automatically detected). Plot pull-up peak ratio versus the peak height of the known allele Automatic plot titles can be replaced by custom titles. Sex markers can be excluded. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

plotRatio_gui *Plot Ratio*

Description

GUI simplifying the creation of plots from marker ratio data.

Usage

```
plotRatio_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select data to plot in the drop-down menu. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

plotResultType_gui *Plot Result Type*

Description

GUI simplifying the creation of plots from result type data.

Usage

```
plotResultType_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Plot result type data. It is possible to customize titles and font size. Data can be plotted as as frequency or proportion. The values can be printed on the plot with custom number of decimals. There are several color palettes to chose from. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

plotSlope_gui *Plot Profile Slope*

Description

GUI simplifying the creation of plots from slope data.

Usage

```
plotSlope_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select a dataset to plot. Plot slope by sample. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

---

plotStutter_gui *Plot Stutter*

Description

GUI simplifying the creation of plots from stutter data.

Usage

```
plotStutter_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select data to plot in the drop-down menu. Check that the correct kit has been detected. Plot stutter data by parent allele or by peak height. Automatic plot titles can be replaced by custom titles. A name for the result is automatically suggested. The resulting plot can be saved as either a plot object or as an image.

Value

TRUE

See Also

https://ggplot2.tidyverse.org/ for details on plot settings.

---

read_gene_mapper_kit *Read GeneMapper Kit Definition*

Description

Import kit definition from GeneMapper bins and panel files.

Usage

```
read_gene_mapper_kit(bin_files = NULL, panel_files = NULL, debug = FALSE)
```

Arguments

parent	widget to get focus when finished.

Details

Takes the GeneMapper bins and panels file and creates a kit definition data frame.

Value

data.frame

read_gene_mapper_kit_gui *Read GeneMapper Kit Definition (GUI)*

Description

Import GeneMapper kit definition files through a graphical user interface.

Usage

```
read_gene_mapper_kit_gui(
  env = globalenv(),
  savegui = TRUE,
  debug = FALSE,
  parent = NULL,
  callback = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select the kit bins and panels file using the file picker.

Value

data.frame

read_gene_marker_kit *Read GeneMarker Kit Definition*

Description

Import kit definition from GeneMarker XML-files.

Usage

```
read_gene_marker_kit(xml_file_path, panel_name)
```

Arguments

xml_file_path	the path to the XML file.
panel_name	the name of the panel to be imported.

Details

Takes the GeneMarker kit XML-file and creates a kit definition data frame.

Value

data.frame

---

read_gene_marker_kit_gui

Read GeneMarker Kit Definition

Description

Read GeneMarker kit definition file.

Usage

```
read_gene_marker_kit_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL,
  callback = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Select the kit definition XML-file using the file picker. The unique Panel Names will appear in the drop-down menu. Select the panel to import. Kit information for the selected panel will be extracted.

Value

data.frame

ref1 *ESX17 Positive Control Profile*

Description

A dataset in 'GeneMapper' format containing the DNA profile of the ESX17 positive control sample with homozygotes as one entry.

Usage

```
data(ref1)
```

Format

A data frame with 17 rows and 4 variables

ref11 *ESX17 Positive Control Profile*

Description

A dataset in 'GeneMapper' format containing the DNA profile of the ESX17 positive control sample with homozygotes as two entries.

Usage

```
data(ref11)
```

Format

A data frame with 17 rows and 4 variables

ref2 *SGMPlus Example Data*

Description

A slimmed reference dataset containing an arbitrary SGMPlus DNA profile.

Usage

```
data(ref2)
```

Format

A data frame with 16 rows and 3 variables

ref3 *ESX17 Example Data for Dropout Analysis*

Description

Reference profiles for source samples. Text file in GeneMapper format.

Format

ASCII text file

ref4 *ESX17 Example Data for Dropout Analysis*

Description

A slimmed dataset containing reference profiles for source samples in set4. Reference 'A2' has double entries for homozygotes. Reference 'F2' has single entries for homozygotes. Reference 'bc' has double entries for homozygotes, and a lower case sample name.

Usage

```
data(ref4)
```

Format

A data frame with 98 rows and 3 variables

ref51 *ESX17 Example Data for Mixture Analysis*

Description

A slimmed dataset containing the reference profile for the major component in set5.

Usage

```
data(ref51)
```

Format

A data frame with 34 rows and 3 variables

ref52 *ESX17 Example Data for Mixture Analysis*

Description

A slimmed dataset containing the reference profile for the minor component in set5.

Usage

```
data(ref52)
```

Format

A data frame with 34 rows and 3 variables

ref61 *Fusion Example Data for Dropout Analysis*

Description

A slimmed dataset containing the reference profile for the samples in set6. NB! Marker order is different from set6. NB! Reference R has a Y marker with NA.

Usage

```
data(ref61)
```

Format

A data frame with 89 rows and 3 variables

ref62 *Fusion Example Data for Dropout Analysis*

Description

A slimmed dataset containing the reference profile for the samples in set6. NB! Marker order is the same as set6. NB! Reference R has a Y marker with NA.

Usage

```
data(ref62)
```

Format

A data frame with 89 rows and 3 variables

ref7 *ESSplex SE QS Example Data for Inhibition Analysis*

Description

A slimmed dataset containing the reference profile for the samples in set7.

Usage

```
data(ref7)
```

Format

A data frame with 35 rows and 4 variables

removeArtefact *Remove Artefacts*

Description

Remove artefact peaks from data.

Usage

```
removeArtefact(
  data,
  artefact = NULL,
  marker = NULL,
  allele = NULL,
  threshold = NULL,
  na.rm = FALSE,
  debug = FALSE
)
```

Arguments

data	data.frame with data to remove spikes from.
artefact	data.frame that lists artefacts in columns 'Marker', 'Allele', optionally with 'Allele.Proportion'. Alternatively artefacts can be provided using 'marker' and 'allele'.
marker	character vector with marker names paired with values in 'allele'.
allele	character vector with allele names paired with values in 'marker'.
threshold	numeric value defining a minimum proportion for artefacts. Requires 'artefacts' including the column 'Allele.Proportion'.
na.rm	logical TRUE to preserve Allele=NA in 'data'.
debug	logical indicating printing debug information.

Details

Removes identified artefacts from the dataset. Likely artefacts can be identified using the function `calculateAllele`. The output should then be provided to the 'artefact'. Alternatively known artefacts can be provided using the 'marker' and 'allele' arguments.

Value

data.frame with spikes removed.

---

removeArtefact_gui *Remove Artefact*

Description

GUI wrapper for the `removeArtefact` function.

Usage

```
removeArtefact_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

`env`	environment in which to search for data frames.
`savegui`	logical indicating if GUI settings should be saved in the environment.
`debug`	logical indicating printing debug information.
`parent`	widget to get focus when finished.

Details

Simplifies the use of the `removeArtefact` function by providing a graphical user interface to it.

Value

TRUE

removeSpike *Remove Spikes*

Description

Remove spikes from data.

Usage

```
removeSpike(data, spike, invert = FALSE, debug = FALSE)
```

Arguments

data	data.frame with data to remove spikes from.
spike	data.frame with list of spikes.
invert	logical FALSE to remove spikes, TRUE to keep spikes.
debug	logical indicating printing debug information.

Details

Removes identified spikes from the dataset. Spikes are identified using the function calculateSpike and provided as a separate dataset. NB! Samples must have unique identifiers. Some laboratories use non-unique names for e.g. negative controls. To allow identification of specific samples when multiple batches are imported into one dataset an id is automatically created by combining the sample name and the file name. This work well as long as there is at most 1 identically named sample in each file (batch). To enable multiple identically named samples in one file, the sample names can be prefixed with the lane or well number before importing them to STR-validator.

Value

data.frame with spikes removed.

removeSpike_gui *Remove Spike*

Description

GUI wrapper for the removeSpike function.

Usage

```
removeSpike_gui(
  env = parent.frame(),
  savegui = NULL,
  debug = FALSE,
  parent = NULL
)
```

Arguments

env	environment in which to search for data frames.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the removeSpike function by providing a graphical user interface to it.

Value

TRUE

---

sample_tableToList *sample_tableToList*

Description

Converting table to list format (helpfunction)

Usage

```
sample_tableToList(table)
```

Arguments

table	A table with data (Evid or refs)

Value

outL A data list

Author(s)

Oyvind Bleka

scrambleAlleles *Scramble Alleles*

Description

Scrambles alleles in a dataset to anonymize the profile.

Usage

```
scrambleAlleles(data, db = "ESX 17 Hill")
```

Arguments

data	data.frame with columns 'Sample.Name', 'Marker', and 'Allele'.
db	character defining the allele frequency database to be used.

Details

Internal helper function to create example data. Assumes data with unique alleles per marker i.e. no duplications. This allow for sampling without replacement see sample. Sex markers are currently not scrambled i.e. they are kept intact. Alleles in the dataset is replaced with random alleles sampled from the allele database. If 'Size' is in the dataset it will be replaced by an estimated size. If 'Data.Point' is present it will be removed.

Value

data.frame with changes in 'Allele' column.

set1 *Typing Data in 'GeneMapper' Format*

Description

A dataset containing ESX17 genotyping results for 8 replicates of the positive control sample, a negative control, and a ladder.

Usage

```
data(set1)
```

Format

A data frame with 170 rows and 13 variables

set2 *SGMPlus Example Data*

Description

A slimmed dataset containing SGM Plus genotyping results for 2 replicates of 'sampleA'.

Usage

```
data(set2)
```

Format

A data frame with 32 rows and 5 variables

set3 *ESX17 Example Data for Dropout Analysis*

Description

Data from a dilution experiment for dropout analysis. Text file with exported GeneMapper genotypes table.

Format

ASCII text file

set4 *ESX17 Example Data for Dropout Analysis*

Description

A slimmed dataset containing data from a dilution experiment for dropout analysis (from set3). One sample replicate has a lower case sample name (bc9).

Usage

```
data(set4)
```

Format

A data frame with 1609 rows and 5 variables

set5 *ESX17 Example Data for Mixture Analysis*

Description

A slimmed dataset containing data from a mixture experiment for Mx analysis.

Usage

```
data(set5)
```

Format

A data frame with 1663 rows and 7 variables

set6 *Fusion Example Data for Dropout Analysis*

Description

A slimmed dataset containing data from a sensitivity experiment for dropout analysis.

Usage

```
data(set6)
```

Format

A data frame with 1848 rows and 7 variables

set7 *ESSplex SE QS Example Data for Inhibition Analysis*

Description

A slimmed dataset containing data from an inhibition experiment.

Usage

```
data(set7)
```

Format

A data frame with 883 rows and 7 variables

slim *Slim Data Frames*

Description

Slim data frames with repeated columns.

Usage

```
slim(data, fix = NULL, stack = NULL, keep.na = TRUE, debug = FALSE)
```

Arguments

data	data.frame.
fix	vector of strings with column names to keep fixed.
stack	vector of strings with column names to slim.
keep.na	logical, keep a row even if no data.
debug	logical indicating printing debug information.

Details

Stack repeated columns into single columns. For example, the following data frame: Sample.Name|Marker|Allele.1|Allele.2|S
using this command: slim(data, fix=c("Sample.Name","Marker"), stack=c("Allele","Size")) would
result in this data frame (NB! 'Data.Point' is dropped): Sample.Name|Marker|Allele|Size

Value

data.frame

slim_gui *Slim Data Frames*

Description

GUI wrapper for the slim function.

Usage

```
slim_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the slim function by providing a graphical user interface to it.

Value

TRUE

See Also

slim

`sortMarker` *Sort Markers*

Description

Sort markers and dye as they appear in the EPG.

Usage

```
sortMarker(data, kit, add.missing.levels = FALSE, debug = FALSE)
```

Arguments

`data`	data.frame containing a column 'Marker' and optionally 'Dye'.
`kit`	string or integer indicating kit.
`add.missing.levels`	logical, TRUE missing markers are added, FALSE missing markers are not added.
`debug`	logical indicating printing debug information.

Details

Change the order of factor levels for 'Marker' and 'Dye' according to 'kit'. Levels in data must be identical with kit information.

Value

data.frame with factor levels sorted according to 'kit'.

strvalidator *Graphical User Interface For The STR-validator Package*

Description

GUI simplifying the use of the strvalidator package.

Usage

```
strvalidator(debug = FALSE)
```

Arguments

debug	logical indicating printing debug information.

Details

The graphical user interface give easy access to all graphical versions of the functions available in the strvalidator package. It connects functions 'under the hood' to allow a degree of automation not available using the command based functions. In addition it provides a project based workflow.

Click Index at the bottom of the help page to see a complete list of functions.

Value

TRUE

Examples

```
# To start the graphical user interface.
## Not run:
strvalidator()

## End(Not run)
```

trim *Trim Data*

Description

Extract data from a dataset.

Usage

```
trim(
  data,
  samples = NULL,
  columns = NULL,
  word = FALSE,
  ignore.case = TRUE,
  invert.s = FALSE,
  invert.c = FALSE,
  rm.na.col = TRUE,
  rm.empty.col = TRUE,
  missing = NA,
  debug = FALSE
)
```

Arguments

data	data.frame with genotype data.
samples	string giving sample names separated by pipe (|).
columns	string giving column names separated by pipe (|).
word	logical indicating if a word boundary should be added to samples and columns.
ignore.case	logical, TRUE ignore case in sample names.
invert.s	logical, TRUE to remove matching samples from 'data', FALSE to remove samples NOT matching (i.e. keep matching samples).
invert.c	logical, TRUE to remove matching columns from 'data', FALSE to remove columns NOT matching (i.e. keep matching columns). while TRUE will remove columns NOT given.
rm.na.col	logical, TRUE columns with only NA are removed from 'data' while FALSE will preserve the columns.
rm.empty.col	logical, TRUE columns with no values are removed from 'data' while FALSE will preserve the columns.
missing	value to replace missing values with.
debug	logical indicating printing debug information.

Details

Simplifies extraction of specific data from a larger dataset. Look for samples in column named 'Sample.Name', 'Sample.File.Name', or the first column containing the string 'Sample' in mentioned order (not case sensitive). Remove unwanted columns.

Value

data.frame with extracted result.

trim_gui *Trim Data*

Description

GUI wrapper for the `trim` function.

Usage

```
trim_gui(env = parent.frame(), savegui = NULL, debug = FALSE, parent = NULL)
```

Arguments

env	environment in which to search for data frames and save result.
savegui	logical indicating if GUI settings should be saved in the environment.
debug	logical indicating printing debug information.
parent	widget to get focus when finished.

Details

Simplifies the use of the `trim` function by providing a graphical user interface to it.

Value

TRUE

See Also

`trim`

update_strings_with_language_file *Update Strings with Language File*

Description

Updates the default strings with the values from the language file.

Usage

```
update_strings_with_language_file(default_strings, language_strings)
```

Arguments

`default_strings`
: list of default strings.

`language_strings`
: list of language-specific strings.

Value

list of updated strings.

Index

∗ **datasets**
ref1, 109
ref11, 109
ref2, 109
ref3, 110
ref4, 110
ref51, 110
ref52, 111
ref61, 111
ref62, 111
ref7, 112
set1, 116
set2, 117
set3, 117
set4, 117
set5, 118
set6, 118
set7, 118
∗ **package**
strvalidator-package, 5

addColor, 6, *9, 10*
addData, 7, *9*
addData_gui, 9
addDye_gui, 9
addMarker, 10, *11*
addMarker_gui, 11
addOrder, *10*, 12
addSize, *13*, 13, *14*
addSize_gui, 13
auditTrail, 14

calculateAllele, 16, *17*, *113*
calculateAllele_gui, 17
calculateAllT, 17, *18, 19*, *62*
calculateAllT_gui, 18
calculateAT, 19, *22–24*, *89*
calculateAT6, 21, *22, 23*
calculateAT6_gui, *22*, 22
calculateAT_gui, *22, 23*, 23
calculateCapillary, 24, *25*
calculateCapillary_gui, 25
calculateConcordance, 26, *27*
calculateConcordance_gui, 27
calculateCopies, 28, *29*
calculateCopies_gui, 29
calculateDropout, *18*, 29, *31, 32*, *62*, *89*, *91*
calculateDropout_gui, 31
calculateHb, 32, *33, 34*
calculateHb_gui, 33
calculateHeight, 34, *36, 37*, *90*
calculateHeight_gui, 36
calculateLb, 37, *39*
calculateLb_gui, 39
calculateMixture, 40, *41, 42*
calculateMixture_gui, 41
calculateOL, 42, *43*
calculateOL_gui, 43
calculateOverlap, 44, *45*
calculateOverlap_gui, 45
calculatePeaks, 46, *47*
calculatePeaks_gui, 47
calculatePullup, 48, *49*
calculatePullup_gui, 49
calculateRatio, 50, *51*
calculateRatio_gui, 51
calculateResultType, 52, *53*
calculateResultType_gui, 53
calculateSlope, 54, *55*
calculateSlope_gui, 55
calculateSpike, 55, *57*, *114*
calculateSpike_gui, 57
calculateStatistics, 57, *58, 59*
calculateStatistics_gui, 58
calculateStutter, 60, *61*
calculateStutter_gui, 61
calculateT, *18*, 62
checkDataset, 63
checkSubset, *21*, *23, 24*, *32*, *42*, *49*, *61*, 64,

65, *75*, *82*
checkSubset_gui, 65
colConvert, 65
colNames, 66
columns, 67, *68*
columns_gui, 68
combine_gui, 69, *70, 71*
cropData_gui, 69, *71*

data.table, *16*, *56*
detectKit, 70

editData_gui, *70*, 71
export, 72, *73*
export_gui, 73

filterProfile, *37*, *50*, *54*, 74, *75*
filterProfile_gui, 75

gdf, *71*
generateEPG, 76, *77, 78*
generateEPG_gui, 77
geom_density, *95*
getKit, 78
getSetting, 79
getStrings, 79
ggsave, *80, 81*
ggsave_gui, 80
grep, *64*
gtable, *71*
guessProfile, 81, *82*
guessProfile_gui, 82

heightToPeak, 83
hoslem.test, *91*

import, 83, *85*
import_gui, 85

list.files, *84, 85*
listObjects, 86
lm, *22*
log, *95*

manageKits_gui, 87
maskAT, *21*, *23, 24*, 87
modelDropout_gui, *18*, *62*, 89

plotAT_gui, 91
plotBalance_gui, 92
plotCapillary_gui, 93
plotContamination_gui, 94
plotDistribution_gui, 95
plotDropout_gui, *18*, *62*, *91*, 96
plotEPG2, 97, *98*
plotEPG2_gui, 98
plotGroups_gui, 99
plotKit_gui, 100
plotPeaks_gui, 100
plotPrecision_gui, 101
plotPullup_gui, 102
plotRatio_gui, 103
plotResultType_gui, 104
plotSlope_gui, 104
plotStutter_gui, 105

rbind.fill, *69*
read.table, *84, 85*
read_gene_mapper_kit, 106
read_gene_mapper_kit_gui, 107
read_gene_marker_kit, 107
read_gene_marker_kit_gui, 108
ref1, 109
ref11, 109
ref2, 109
ref3, 110
ref4, 110
ref51, 110
ref52, 111
ref61, 111
ref62, 111
ref7, 112
removeArtefact, 112, *113*
removeArtefact_gui, 113
removeSpike, *114*, 114, *115*
removeSpike_gui, 114

sample, *116*
sample_tableToList, 115
scrambleAlleles, 116
set1, 116
set2, 117
set3, 117
set4, 117
set5, 118
set6, 118
set7, 118
slim, *85*, *119*, 119, *120*
slim_gui, 119

sortMarker, *10*, 120
stat_ecdf, *99*
strvalidator, 121
strvalidator-package, 5
substr, *68*

trim, *85*, 121, *123*
trim_gui, *70, 71*, 123

update_strings_with_language_file, 123