Package ‘permRand’

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Title Permutation Randomization

Version 1.0.0

Description Provides randomization using permutation for applications. To provide a Quality Control (QC) check, QC samples can be randomized within strata. A second function allows for the ability to ”switch” samples to meet set requirements and perform a certain amount of minimization on these switches. The functions are flexible for users by specifying strata size and number of QC samples per strata. The randomization meets the following requirements

- QC sample requirements: QC samples not adjacent, QC samples from same mother must follow certain patterns.
- Matched sample sets must be within a single strata, and next to each other.

URL https://github.com/m-mellers/permRand

BugReports https://github.com/m-mellers/permRand/issues

Encoding UTF-8

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Repository CRAN

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Contents

`allRand` *Data Randomization*

Description

Randomizes aliquots to batches.

Usage

```
allRand(dataR, batchTot, numQC, withinN, numMatch, chkRep)
```

Arguments

`dataR`	Data for randomization.
`batchTot`	c(batchTot1, batchTot2) sizes of plates, just use one plate per batch, batch size inclusive of QC samples.
`numQC`	Number of QC samples per batch.
`withinN`	Number of samples away that the QC samples must be from each other.
`numMatch`	Number of QC samples from a single mother within a batch.
`chkRep`	Check if there is a repeat of the groups within the batches.

Value

A dataset with serum order randomized.

Examples

```
serumRand <- allRand(dataR=serumMaster3,batchTot=c(40,44), numQC=2,withinN=2,numMatch=2,chkRep=1)
```

`batchCount` *Tests the number in each batch.*

Description

Counts the number of samples that are in each of the batches.

Usage

```
batchCount(dataS, batchSizeT)
```

Arguments

`dataS`	Test dataset.
`batchSizeT`	Batch size to test for.

Value

The ID of any batch that does not contain the specified number of samples.

Examples

```
test <- batchCount(dataS=serumRand,batchSizeT=84)
```

`countQC` *Number of QC in each batch.*

Description

Count how many QC samples are in each of the batches, and if it doesn't match the number specified.

Usage

```
countQC(dataS, QCN)
```

Arguments

`dataS`	Test dataset.
`QCN`	Number of QC samples per batch.

Value

The output includes any batches that does not contain the number of QC samples specified.

Examples

```
test <- countQC(dataS=serumRand,QCN=4)
```

`emptyQC` *A dataset containing locations of empty QC samples.*

Description

A dataset containing locations of empty QC samples.

Format

Empty QC samples

serumID Serum ID

rack Rack

row Row

col Column

Author(s)

Michelle Mellers

`formatRand` *Formats data*

Description

The function `formatRand` formats the dataset for the randomization function. This function inputs serum data for both the study subjects and QC.

Usage

```
formatRand(QCdata, serumIDR, serumPack)
```

Arguments

`QCdata`	QC data.
`serumIDR`	Serum data with serumIDs.
`serumPack`	Serum data with packing lists.

Value

A dataset that is formatted and ready for the randomization file.

Examples

```
serumMaster <- formatRand(QCdata=QCMaster,serumIDR=serumIDs,serumPack=serumLoc)
```

`motherQC` *A dataset containing locations of the mother QC samples.*

Description

A dataset containing locations of the mother QC samples.

Format

Mother QC samples

serumID Serum ID

rack Rack

row Row

col Column

Author(s)

Michelle Mellers

`orderCases` *Number of single group in sequence.*

Description

Tests if a large number of cases or controls are next to each other.

Usage

```
orderCases(dataI, betW)
```

Arguments

`dataI`	Dataset to be tested.
`betW`	Number of cases or controls to check if they are next to each other.

Value

The output stores if there are any cases or controls together beyond a certain specified value.

Examples

```
test <- orderCases(dataI=serumRand,betW=4)
```

`outputLab` *Output labels.*

Description

Creates output labels for the randomized groups.

Usage

```
outputLab(dataOut, blind, origP, maxRows, maxCols, newPack)
```

Arguments

`dataOut`	Dataset to be formatted for packing list.
`blind`	Indicator 0/1 select if a blinded (1) or unblinded(0) packing list is to be generated.
`origP`	Indicator, 0/1, inclusion of the original packing location (1) or deletion of the packing location (0).
`maxRows`	Maximum row for the output dataset.
`maxCols`	Maximum column for the output dataset.
`newPack`	0/1 indicator to generate new packing locations.

Value

A dataset to be used for packing lists.

Examples

```
blind <- outputLab(dataOut=serumRand,blind=1,origP=0,maxRows=9,maxCols=9,newPack=1)
unBlindSw <- outputLab(serumSwitchP,blind=0,origP=.,maxRows=.,maxCols=.,newPack=0)
```

`QCMaster` *A dataset containing QC sample IDs and packing location.*

Description

A dataset containing QC sample IDs and packing location.

Format

QC sample IDs and Packing Location

serumID Serum ID

rack Rack

row Row

col Column

event Sample Time

motherSerumID Mother Serum ID

motherRack Mother Rack

motherRow Mother Row

motherCol Mother Column

studyID Study ID

Author(s)

Michelle Mellers

`randTest` *QC Identifiers*

Description

We first assign IDs linking mother/child and events using the function `randTest`.

Usage

```
randTest(dataMom, dataChild, maxAliq, nEvent)
```

Arguments

`dataMom`	The mother dataset.
`dataChild`	Child dataset.
`maxAliq`	Number of aliquots per mother aliquot.
`nEvent`	Number of aliquots per each of event or lab.

Value

The output of the function is a dataset with the ID links.

Examples

```
randTest(dataMom=motherQC,dataChild=emptyQC,maxAliq=4, nEvent=c(28,27,28,30))
```

`serumIDs` *A dataset containing serum sample IDs linked with studyIDs.*

Description

A dataset containing serum sample IDs linked with studyIDs.

Format

Serum Sample IDs linked with studyIDs

studyID Study Subject ID

event Sample Time

serumID Serum ID

Author(s)

Michelle Mellers

`serumLoc` *A dataset containing the a packing list with serum samples.*

Description

A dataset containing the a packing list with serum samples.

Format

Packing list of serum samples

serumID Serum ID

rack Rack

row Row

col Column

Author(s)

Michelle Mellers

`serumMaster3` *A dataset containing information for QC and serum samples.*

Description

A dataset containing information for QC and serum samples.

Format

Serum and QC sample Information

serumID Serum ID

studyID Study ID

event Sample Time

rack Rack

row Row

col Column

ccID Group ID

caseControl Case or Control Indicator

QCsamp Indicates if QC sample

Author(s)

Michelle Mellers

`serumRand` *A dataset containing randomized QC and serum samples.*

Description

A dataset containing randomized QC and serum samples.

Format

Randomized Serum and QC sample Information

serumID Serum ID

studyID Study ID

event Sample Time

rack Rack

row Row

col Column

ccID Group ID

caseControl Case or Control Indicator

QCsamp Indicates if QC sample

batchN Batch Number

loc Location

Author(s)

Michelle Mellers

`serumSwitch` *A dataset containing switched and randomized QC and serum samples.*

Description

A dataset containing switched and randomized QC and serum samples.

Format

Switched and Randomized Serum and QC sample Information

serumID Serum ID

studyID Study ID

event Sample Time

ccID Group ID

caseControl Case or Control Indicator

QCsamp Indicates if QC sample

batchN Batch Number

loc Location

outoforder Marker if Switched

Author(s)

Michelle Mellers

`serumSwitchP` *A dataset containing switched and randomized QC and serum samples with packing locations.*

Description

A dataset containing switched and randomized QC and serum samples with packing locations.

Format

Switched and Randomized Serum and QC sample Information

serumID Serum ID

rack Rack

row Row

col Column

studyID Study ID

event Sample Time

ccID Group ID

caseControl Case or Control Indicator

QCsamp Indicates if QC sample

batchN Batch Number

loc Location

outoforder Marker if Switched

Author(s)

Michelle Mellers

`switchR` *Switching Generating Function*

Description

Minimizes switches without completely re-randomizing the locations.

Usage

```
switchR(dataIn, numqc, numqcM, batchS)
```

Arguments

`dataIn`	Randomized dataset.
`numqc`	Number of QC samples per set.
`numqcM`	Numberof QC matching samples.
`batchS`	New batch size.

Value

A dataset with switches indicated.

Examples

```
serumSwitch <- switchR(dataIn=serumRand,numqc=2,numqcM=2,batchS=43)
```

`testCCAcross` *Sample groups within batches*

Description

Tests and finds sample groups that are across batches.

Usage

```
testCCAcross(dataS)
```

Arguments

`dataS`	The test dataset.

Value

The output lists all batches with not enough QC sample sets or the QC samples do not come from the same mother.

Examples

```
test <- testCCAcross(dataS=serumRand)
```

`testPair` *Ensures complete sets.*

Description

Tests if sets are next to each other. Any sets that are not next to each other are flagged.

Usage

```
testPair(dataS)
```

Arguments

`dataS`	Test dataset.

Value

The output reports any sets that are separated in the "loc".

Examples

```
test <- testPair(dataS=serumRand)
```

`testQCmatch` *Tests QC matches*

Description

Measures that every batch has at least the specified number of matching QC sample sets in a batch.

Usage

```
testQCmatch(dataS, numQCs, numMatch)
```

Arguments

`dataS`	Randomized data.
`numQCs`	Number of QCs specified per dataset.
`numMatch`	Number of QC samples form a single mother within a batch.

Value

The output lists all batches with not enough QC sample sets or the QC samples do not come from the same mother.

Examples

```
test <- testQCmatch(dataS=serumRand,numQCs=4,numMatch=2)
```

`testR` *A dataset containing the example non-randomized serum sample file.*

Description

A dataset containing the example non-randomized serum sample file.

Format

A data frame with four datasets:

serumIDs Serum Sample IDs Linked with StudyIDs

serumLoc Serum ID packing list

emptyQC Empty QC containers packing list

motherQC QC samples to be aliquoted packing list

Author(s)

Michelle Mellers

`testRand` *Test Dataset*

Description

Generates test data for the randomization functions.

Usage

```
testRand(rowSize, colSize, studySize, expNS, numCC, QCpct, child)
```

Arguments

`rowSize`	Max row size.
`colSize`	Max column size.
`studySize`	Number of cases.
`expNS`	Number of aliquots per case/control.
`numCC`	Number of controls per case.
`QCpct`	Percent of QCs for number of samples.
`child`	Number of children per "mother’ aliquot.

Value

A practice dataset.

Examples

```
testR <- testRand(rowSize=20,colSize=15,studySize=1000,expNS=7000,numCC=2,QCpct=0.05,child=4)
```

`uniqueID` *Unique IDs*

Description

Test for unique IDs.

Usage

```
uniqueID(testD, IDN)
```

Arguments

`testD`	Test dataset.
`IDN`	ID to test.

Value

Any IDs that are not unique.

Examples

```
test <- uniqueID(serumRand,"serumID")
```

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