

Package ‘SomaDataIO’

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Type Package

Title Input/Output 'SomaScan' Data

Version 6.6.1

Description Load and export 'SomaScan' data via the 'SomaLogic Operating Co., Inc.' structured text file called an ADAT (*.adat). For file format see <https://github.com/SomaLogic/SomaLogic-Data/blob/main/README.md>. The package also exports auxiliary functions for manipulating, wrangling, and extracting relevant information from an ADAT object once in memory.

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URL <https://somallogic.github.io/SomaDataIO/>, <https://somallogic.com>

BugReports <https://github.com/SomaLogic/SomaDataIO/issues>

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Author Stu Field [aut] (ORCID: <<https://orcid.org/0000-0002-1024-5859>>),

Caleb Scheidel [cre],

SomaLogic Operating Co., Inc. [cph, fnd]

Maintainer Caleb Scheidel <calebjscheidel@gmail.com>

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Description

Retrieve elements of the HEADER attribute of a `soma_adat` object:

`getAdatVersion()` determines the the ADAT version number from a parsed ADAT header.

`getSomaScanVersion()` determines the original SomaScan assay version that generated RFU measurements within a `soma_adat` object.

`checkSomaScanVersion()` determines if the version of is a recognized version of SomaScan.

Table of SomaScan assay versions:

Version	Commercial Name	Size
V4	5k	5284
v4.1	7k	7596
v5.0	11k	11083

`getSignalSpace()` determines the current signal space of the RFU values, which may differ from the original SomaScan signal space if the data have been lifted. See `lift_adat()` and `vignette("lifting-and-bridging", package = "SomaDataIO")`.

`getSomaScanLiftCCC()` accesses the lifting Concordance Correlation Coefficients between various SomaScan versions. For more about CCC metrics see `lift_adat()`.

Usage

```
getAdatVersion(x)
```

```
getSomaScanVersion(adat)
```

```
getSignalSpace(adat)
```

```
checkSomaScanVersion(ver)
```

```
getSomaScanLiftCCC(matrix = c("plasma", "serum"))
```

Arguments

<code>x</code>	Either a <code>soma_adat</code> object with intact attributes or the attributes themselves of a <code>soma_adat</code> object.
<code>adat</code>	A <code>soma_adat</code> object (with intact attributes), typically created using <code>read_adat()</code> .
<code>ver</code>	<code>character(1)</code> . The SomaScan version as a string. Note: the "v"-prefix is case <i>insensitive</i> .
<code>matrix</code>	Character. A string of (usually) either "serum" or "plasma".

Value

`\link[=getAdatVersion]{getAdatVersion()}`
The key-value of the Version as a string.

`\link[=getSomaScanVersion]{getSomaScanVersion()}`
The key-value of the AssayVersion as a string.

`\link[=getSignalSpace]{getSignalSpace()}`
The key-value of the SignalSpace as a string.

`\link[=checkSomaScanVersion]{checkSomaScanVersion()}`
Returns NULL (invisibly) if checks pass.

`\link[=getSomaScanLiftCCC]{getSomaScanLiftCCC()}`
Returns a tibble of either the serum or plasma CCC between various versions of the SomaScan assay.

Author(s)

Stu Field

References

Lin, Lawrence I-Kuei. 1989. A Concordance Correlation Coefficient to Evaluate Reproducibility. **Biometrics**. 45:255-268.

Examples

```
getAdatVersion(example_data)

attr(example_data, "Header.Meta")$HEADER$Version <- "99.9"
getAdatVersion(example_data)

ver <- getSomaScanVersion(example_data)
ver

rfu_space <- getSignalSpace(example_data)
rfu_space

is.null(checkSomaScanVersion(ver))

# plasma (default)
getSomaScanLiftCCC()

# serum
getSomaScanLiftCCC("serum")
```

adat2eSet*Convert ADAT to ExpressionSet Object*

Description

Utility to convert a SomaLogic `soma_adat` object to an `ExpressionSet` object via the **Biobase** package from **Bioconductor**: <https://www.bioconductor.org/packages/release/bioc/html/Biobase.html>.

Usage

```
adat2eSet(adat)
```

Arguments

`adat` A `soma_adat` class object as read into the R environment using `read_adat()`.

Details

The **Biobase** package is required and must be installed from **Bioconductor** via the following at the R console:

```
if (!requireNamespace("BiocManager", quietly = TRUE)) {
  install.packages("BiocManager")
}
BiocManager::install("Biobase", version = remotes::bioc_version())
```

Value

A Bioconductor object of class `ExpressionSet`.

Author(s)

Stu Field

References

<https://bioconductor.org/install/>

See Also

Other eSet: `pivotExpressionSet()`

Examples

```
eSet <- adat2eSet(example_data)
class(eSet)
eSet

ft <- Biobase::exprs(eSet)
head(ft[, 1:10L], 10L)
```

addAttributes	<i>Add Attributes to soma_adat Objects</i>
---------------	--

Description

Adds a set of attributes, typically "Header.Meta" and "Col.Meta", to a `data.frame`, `tibble`, `soma_adat` or similar tabular object. Existing attributes data are *not* over-written. Typically untouched are:

- `names`
- `class`
- `row.names`

Usage

```
addAttributes(data, new.attrs)
```

Arguments

<code>data</code>	The <i>receiving</i> <code>data.frame</code> object for new attributes.
<code>new.attrs</code>	A <i>named</i> list object containing new attributes to add to the existing ones.

Value

A data frame object corresponding to `data` but with the attributes of `new.attrs` grafted on to it. Existing attribute names are *not* over-written.

Author(s)

Stu Field

See Also

[attr\(\)](#), [generics::setdiff\(\)](#)

addClass	<i>Add a Class to an Object</i>
----------	---------------------------------

Description

Utility to add (prepend) a class(es) to existing objects.

Usage

```
addClass(x, class)
```

Arguments

x	The object to receive new class(es).
class	Character. The name of additional class(es).

Value

An object with new classes.

Author(s)

Stu Field

See Also

[class\(\)](#), [typeof\(\)](#), [structure\(\)](#)

Examples

```
class(iris)

addClass(iris, "new") |> class()

addClass(iris, c("A", "B")) |> class() # 2 classes

addClass(iris, c("A", "data.frame")) |> class() # no duplicates

addClass(iris, c("data.frame", "A")) |> class() # re-orders if exists
```

calcOutlierMap *Calculate MAD Outlier Map*

Description

Calculate the median absolute deviation (statistical) outliers measurements and fold-change criteria from an ADAT. Two values are required for the calculation: median absolute deviation (MAD) and fold-change (FC). Outliers are determined based on the result of *both* $6 * \text{MAD}$ and $x * \text{FC}$, where x is the number of fold changes defined.

Usage

```
calcOutlierMap(
  data,
  anno_tbl = NULL,
  apt.order = c(NA, "dilution", "signal"),
  sample.order = NULL,
  fc.crit = 5
)

## S3 method for class 'outlier_map'
print(x, ...)
```

Arguments

data	A soma_adat object containing RFU feature data.
anno_tbl	An annotations table produced via getAnalyteInfo() . Used to calculate analyte dilutions for the matrix column ordering. If NULL, a table is generated internally from data (if possible), and the analytes are plotted in dilution order.
apt.order	Character. How should the columns/features be ordered? Options include: by dilution mix ("dilution"), by median overall signal ("signal"), or as-is in data (default).
sample.order	Either a character string indicating the column name with entries to be used to order the data frame rows, or a numeric vector representing the order of the data frame rows. The default (NULL) leaves the row ordering as it is in data.
fc.crit	Integer. The fold change criterion to evaluate. Defaults to 5x.
x	An object of class "outlier_map".
...	Arguments for S3 print methods.

Details

For the S3 plotting method, see [plot.Map\(\)](#).

Value

A list of class `c("outlier_map", "Map")` containing:

<code>matrix</code>	A boolean matrix of TRUE/FALSE whether each sample is an outlier according the the stated criteria.
<code>x.lab</code>	A character string containing the plot x-axis label.
<code>title</code>	A character string containing the plot title.
<code>rows.by.freq</code>	A logical indicating if the samples are ordered by outlier frequency.
<code>class.tab</code>	A table containing the frequencies of each class if input <code>sample.order</code> is defined as a categorical variable.
<code>sample.order</code>	A numeric vector representing the order of the data frame rows.
<code>legend.sub</code>	A character string containing the plot legend subtitle.

Functions

- `print(outlier_map)`: There is a S3 print method for class "outlier_map".

Author(s)

Stu Field

See Also

Other Calc Map: [getOutlierIds\(\)](#), [plot.Map\(\)](#)

Examples

```
dat <- example_data |> dplyr::filter(SampleType == "Sample")
om <- calcOutlierMap(dat)
class(om)

# S3 print method
om

# `sample.order = "frequency"` orders samples by outlier frequency
om <- calcOutlierMap(dat, sample.order = "frequency")
om$rows.by.freq
om$sample.order

# order samples field in Adat
om <- calcOutlierMap(dat, sample.order = "Sex")
om$sample.order
```

`calc_eLOD`*Calculate Estimated Limit of Detection (eLOD)*

Description

Calculate the estimated limit of detection (eLOD) for SOMAmer reagent analytes in the provided input data. The input data should be filtered to include only buffer samples desired for eLOD calculation.

Usage`calc_eLOD(data)`**Arguments**

`data` A `soma_adat`, `data.frame`, or `tibble` object including `SeqId` columns (`seq.xxxxx.xx`) containing RFU values.

Details

eLOD is calculated using the following steps:

1. For each SOMAmer, the median and adjusted median absolute deviation ($MAD_{Adjusted}$) are calculated, where

$$MAD_{Adjusted} = 1.4826 * MAD$$

The 1.4826 is a set constant used to adjust the MAD to be reflective of the standard deviation of the normal distribution.

2. For each SOMAmer, calculate

$$eLOD = median + 3.3 * MAD_{Adjusted}$$

Note: The eLOD is useful for non-core matrices, including cell lysate and CSF, but should be used carefully for evaluating background signal in plasma and serum.

Value

A `tibble` object with 2 columns: `SeqId` and `eLOD`.

Author(s)

Caleb Scheidel, Christopher Dimapasok

Examples

```

# filter data frame using vector of SampleId controls
df <- withr::with_seed(101, {
  data.frame(
    SampleType = rep(c("Sample", "Buffer"), each = 10),
    SampleId = paste0("Sample_", 1:20),
    seq.20.1.100 = runif(20, 1, 100),
    seq.21.1.100 = runif(20, 1, 100),
    seq.22.2.100 = runif(20, 1, 100)
  )
})
sample_ids <- paste0("Sample_", 11:20)
selected_samples <- df |> filter(SampleId %in% sample_ids)

selected_elod <- calc_eLOD(selected_samples)
head(selected_elod)
## Not run:
# filter `soma_adat` object to buffer samples
buffer_samples <- example_data |> filter(SampleType == "Buffer")

# calculate eLOD
buffer_elod <- calc_eLOD(buffer_samples)
head(buffer_elod)

# use eLOD to calculate signal to noise ratio of samples
samples_median <- example_data |> dplyr::filter(SampleType == "Sample") |>
  dplyr::summarise(across(starts_with("seq"), median, .names = "median_{col}") |>
    tidyr::pivot_longer(starts_with("median_"), names_to = "SeqId",
      values_to = "median_signal") |>
    dplyr::mutate(SeqId = gsub("median_seq", "seq", SeqId))

# analytes with signal to noise > 2
ratios <- samples_median |>
  dplyr::mutate(signal_to_noise = median_signal / buffer_elod$eLOD) |>
  dplyr::filter(signal_to_noise > 2) |>
  dplyr::arrange(desc(signal_to_noise))

head(ratios)

## End(Not run)

```

cleanNames

Clean Up Character String

Description

Often the names, particularly within `soma_adat` objects, are messy due to varying inputs, this function attempts to remedy this by removing the following:

- trailing/leading/internal whitespace

- non-alphanumeric strings (except underscores)
- duplicated internal dots (. .), (. . .), etc.
- SomaScan normalization scale factor format

Usage

```
cleanNames(x)
```

Arguments

x Character. String to clean up.

Value

A cleaned up character string.

Author(s)

Stu Field

See Also

[trimws\(\)](#), [gsub\(\)](#), [sub\(\)](#)

Examples

```
cleanNames("  sdkfj...sdlkfj.sdfii4994### ")
cleanNames("Hyb..Scale")
```

Col.Meta

Analyte Annotations, Col.Meta, and Row Info

Description

In a standard SomaLogic ADAT, the section of information that sits directly above the measurement data (RFU data matrix) is the column meta data (Col.Meta), which contains detailed information and annotations about the analytes, [SeqId\(\)](#)s, and their targets. See section below for further information about available fields and their descriptions. Use [getAnalyteInfo\(\)](#) to obtain an object containing this information for programmatic analyses, and use [getMeta\(\)](#) to obtain the column names representing the row-specific meta data about the samples (see section below).

Col Meta (Analyte Annotations)

Information describing the *analytes* is found to the above the data matrix in a standard SomaLogic ADAT. This information may consist of the any or all of the following:

Field	Description	Example
SeqId	SomaLogic sequence identifier	2182-54
SeqidVersion	Version of SOMAmer sequence	2
SomaId	Target identifier, of the form SLnnnnnn (8 characters in length)	SL0003
TargetFullName	Target name curated for consistency with UniProt name	Comple
Target	SomaLogic Target Name	C4b
UniProt	UniProt identifier(s)	P0C0L4
EntrezGeneID	Entrez Gene Identifier(s)	720 721
EntrezGeneSymbol	Entrez Gene Symbol names	C4A C4
Organism	Protein Source Organism	Human
Units	Relative Fluorescence Units	RFU
Type	SOMAmer target type	Protein
Dilution	Dilution mix assignment	0.01%
PlateScale_Reference	PlateScale reference value	1378.85
CalReference	Calibration sample reference value	1378.85
medNormRef_ReferenceRFU	Median normalization reference value	490.342
Cal_V4_<YY>_<SSS>_<PPP>	Calibration scale factor (for given Year_Study_Plate)	0.64
ColCheck	QC acceptance criteria across all plates/sets	PASS
QcReference_<LLLLL>	QC sample reference value (for given QC lot)	PASS
CalQcRatio_V4_<YY>_<SSS>_<PPP>	Post calibration median QC ratio to reference (for given Year_Study_Plate)	1.04

Row Meta (Sample Annotations)

Information describing the *samples* is typically found to the left of the data matrix in a standard SomaLogic ADAT. This information may consist of clinical information provided by the client, or run-specific diagnostic information included for assay quality control. Below are some examples of what may be present in this section:

Field	Description	Examples
PlateId	Plate identifier	V4-18-004_001, V4-18-004_002
ScannerID	Scanner used to analyze slide	SG12064173, SG14374437
PlatePosition	Location on 96 well plate (A1-H12)	A1, H12
SlideId	Agilent slide barcode	2.58E+11
Subarray	Agilent subarray (1 – 8)	1,8
SampleId	1st form is Subject Identifier, 2nd form (calibrators, buffers)	2031
SampleType	1st form for clinical samples (Sample), 2nd form as above	Sample, QC, Calibrator, Buffer
PercentDilution	Highest concentration the SOMAmer dilution groups	20
SampleMatrix	Sample matrix	Plasma-PPT
Barcode	1D Barcode of aliquot	S622225
Barcode2d	2D Barcode of aliquot	1.91E+08
SampleNotes	Assay team sample observation	Cloudy, Low sample volume, Reddis
SampleDescription	Supplemental sample information	Plasma QC 1
AssayNotes	Assay team run observation	Beads aspirated, Leak/Hole, Smear
TimePoint	Sample time point	Baseline
ExtIdentifier	Primary key for Subarray	EXID40000000032037
SsfExtId	Primary key for sample	EID102733
SampleGroup	Sample group	A, B

SiteId	Collection site	SomaLogic, Covance
TubeUniqueID	Unique tube identifier	1.12E+11
CLI	Cohort definition identifier	CLI6006F001
HybControlNormScale	Hybridization control scale factor	0.948304
RowCheck	Normalization acceptance criteria for all row scale factors	PASS, FLAG
NormScale_0_5	Median signal normalization scale factor (0.5% mix)	1.02718
NormScale_0_005	Median signal normalization scale factor (0.005% mix)	1.119754
NormScale_20	Median signal normalization scale factor (20% mix)	0.996148

Examples

```
# Annotations/Col.Meta
tbl <- getAnalyteInfo(example_data)
tbl

# Row/sample Meta
r_m <- getMeta(example_data)
head(r_m)

# Normalization Scale Factors
grep("NormScale", r_m, value = TRUE)

# adat subset
example_data[1:3, head(r_m)]
```

diffAdats

Diff Two ADAT Objects

Description

Diff tool for the differences between two `soma_adat` objects. When diffs of the table *values* are interrogated, **only** the intersect of the column meta data or feature data is considered

Usage

```
diffAdats(adat1, adat2, tolerance = 1e-06)
```

Arguments

`adat1, adat2` Two `soma_adat` objects to compare.

`tolerance` Numeric > 0. Differences smaller than tolerance are not triggered. See [all.equal\(\)](#).

Value

NULL, invisibly. Called for side effects.

Note

Only diffs of the column name *intersect* are reported.

Author(s)

Stu Field

Examples

```
# subset `example_data` for speed
# all SeqIds from 2000 -> 2999
seqs <- grep("^seq\\.[0-9]{3}", names(example_data), value = TRUE)
ex_data_small <- head(example_data[, c(getMeta(example_data), seqs)], 10L)
dim(ex_data_small)

# no diff to itself
diffAdats(ex_data_small, ex_data_small)

# remove random column
rm <- withr::with_seed(123, sample(1:ncol(ex_data_small), 1))
diffAdats(ex_data_small, ex_data_small[, -rm])

# randomly shuffle Subarray
diffAdats(ex_data_small, dplyr::mutate(ex_data_small, Subarray = sample(Subarray)))

# modify 2 RFUs randomly
new <- ex_data_small
new[5L, c(rm, rm + 1L)] <- 999
diffAdats(ex_data_small, new)
```

getAnalyteInfo

Get Analyte Annotation Information

Description

Uses the Col.Meta attribute (analyte annotation data that appears above the protein measurements in the *.adat text file) of a soma_adat object, adds the AptName column key, conducts a few sanity checks, and generates a "lookup table" of analyte data that can be used for simple manipulation and indexing of analyte annotation information. Most importantly, the analyte column names of the soma_adat (e.g. seq.XXXX.XX) become the AptName column of the lookup table and represents the key index between the table and soma_adat from which it comes.

Usage

```
getAnalyteInfo(adat)
```

```
getTargetNames(tbl)
```

```
getFeatureData(adat)
```

Arguments

adat	A soma_adat object (with intact attributes), typically created using <code>read_adat()</code> .
tbl	A tibble object containing analyte target annotation information. This is usually the result of a call to <code>getAnalyteInfo()</code> .

Value

A tibble object with columns corresponding to the column meta data entries in the soma_adat. One row per analyte.

Functions

- `getTargetNames()`: creates a lookup table (or dictionary) as a named list object of AptNames and Target names in key-value pairs. This is a convenient tool to quickly access a TargetName given the AptName in which the key-value pairs map the seq.XXXX.XX to its corresponding TargetName in tbl. This structure which provides a convenient auto-completion mechanism at the command line or for generating plot titles.
- `getFeatureData()`: **[Superseded]**. Please now use `getAnalyteInfo()`.

Author(s)

Stu Field

See Also

`getAnalytes()`, `is_intact_attr()`, `read_adat()`

Examples

```
# Get Aptamer table
anno_tbl <- getAnalyteInfo(example_data)
anno_tbl

# Use `dplyr::group_by()`
dplyr::tally(dplyr::group_by(anno_tbl, Dilution)) # print summary by dilution

# Columns containing "Target"
anno_tbl |>
  dplyr::select(dplyr::contains("Target"))

# Rows of "Target" starting with MMP
anno_tbl |>
  dplyr::filter(grepl("^MMP", Target))

# Target names
tg <- getTargetNames(anno_tbl)

# how to use for plotting
feats <- sample(anno_tbl$AptName, 6)
op <- par(mfrow = c(2, 3))
```

```
sapply(feats, function(.x) plot(1:10, main = tg[.x]))
par(op)
```

getAnalytes

Get Analytes

Description

Return the feature names (i.e. the column names for SOMAmer reagent analytes) from a `soma_adat`. S3 methods also exist for these classes:

```
#> [1] getAnalytes.character getAnalytes.data.frame getAnalytes.default
#> [4] getAnalytes.list       getAnalytes.matrix   getAnalytes.recipe
#> [7] getAnalytes.soma_adat
#> see '?methods' for accessing help and source code
```

`getMeta()` returns the inverse, a character vector of string names of *non*-analyte feature columns/variables, which typically correspond to the clinical ("meta") data variables. S3 methods exist for these classes:

```
#> [1] getMeta.character getMeta.data.frame getMeta.default   getMeta.list
#> [5] getMeta.matrix    getMeta.soma_adat
#> see '?methods' for accessing help and source code
```

Usage

```
getAnalytes(x, n = FALSE, rm.controls = FALSE)
```

```
getMeta(x, n = FALSE)
```

```
getFeatures(x, n = FALSE, rm.controls = FALSE)
```

Arguments

<code>x</code>	Typically a <code>soma_adat</code> class object created using <code>read_adat()</code> .
<code>n</code>	Logical. Return an integer corresponding to the <i>length</i> of the features?
<code>rm.controls</code>	Logical. Should all control and non-human analytes (e.g. HybControls, Non-Human, Non-Biotin, Spuriomer) be removed from the returned value?

Value

`getAnalytes()`: a character vector of ADAT feature ("analyte") names.

`getMeta()`: a character vector of ADAT clinical ("meta") data names.

For both, if `n = TRUE`, an integer corresponding to the **length** of the character vector.

Functions

- `getFeatures()`: **[Superseded]**. Please now use `getAnalytes()`.

Author(s)

Stu Field

See Also

`is.apr()`

Examples

```
# RFU feature variables
apts <- getAnalytes(example_data)
head(apts)
getAnalytes(example_data, n = TRUE)

# vector string
bb <- getAnalytes(names(example_data))
all.equal(apts, bb)

# create some control sequences
# ~~~~~ Spuriomer ~~~ HybControl ~~~
apts2 <- c("seq.2053.2", "seq.2171.12", head(apts))
apts2
no_ctrl <- getAnalytes(apts2, rm.controls = TRUE)
no_ctrl
setdiff(apts2, no_ctrl)

# clinical variables
mvec <- getMeta(example_data)
head(mvec, 10)
getMeta(example_data, n = TRUE)

# test 'data.frame' and 'character' S3 methods are identical
identical(getMeta(example_data), getMeta(names(example_data))) # TRUE
```

getOutlierIds

Get Flagged Ids From MAD Outlier Map

Description

Return the IDs of flagged samples for objects of the `outlier_map` class. Samples are flagged based on the percent analytes (RFU columns) for a given sample that were identified as outliers using the median absolute deviation (MAD).

Usage

```
getOutlierIds(x, flags = 0.05, data = NULL, include = NULL)
```

Arguments

x	An object of class: <ul style="list-style-type: none">• outlier_map - from <code>calcOutlierMap()</code>
flags	Numeric in $[0, 1]$. For an "outlier_map", the proportion of the analytes (columns) for a given sample that must be outliers for a flag to be placed at the right-axis, right-axis, thus flagging that sample. If NULL (default), 0.05 (5%) is selected.
data	Optional. The data originally used to create the map x. If omitted, a single column data frame is returned.
include	Optional. Character vector of column name(s) in data to include in the resulting data frame. Ignored if data = NULL.

Value

A data.frame of the indices (idx) of flagged samples, along with any additional variables as specified by include.

Author(s)

Caleb Scheidel

See Also

Other Calc Map: `calcOutlierMap()`, `plot.Map()`

Examples

```
# flagged outliers
# create a single sample outlier (12)
out_adat <- example_data
apts <- getAnalytes(out_adat)
out_adat[12, apts] <- out_adat[12, apts] * 10

om <- calcOutlierMap(out_adat)
getOutlierIds(om, out_adat, flags = 0.05, include = c("Sex", "Subarray"))
```

Description

S3 group generic methods to apply group specific prototype functions to the RFU data **only** of soma_adat objects. The clinical meta data are *not* transformed and remain unmodified in the returned object (`Math()` and `Ops()`) or are ignored for the `Summary()` group. See `groupGeneric()`.

Usage

```
## S3 method for class 'soma_adat'
Math(x, ...)

antilog(x, base = 10)

## S3 method for class 'soma_adat'
Ops(e1, e2 = NULL)

## S3 method for class 'soma_adat'
Summary(..., na.rm = FALSE)

## S3 method for class 'soma_adat'
e1 == e2
```

Arguments

x	The soma_adat class object to perform the transformation.
...	Additional arguments passed to the various group generics as appropriate.
base	A positive or complex number: the base with respect to which logarithms are computed.
e1, e2	Objects.
na.rm	Logical. Should missing values be removed?

Value

A soma_adat object with the same dimensions of the input object with the feature columns transformed by the specified generic.

Functions

- antilog(): performs the inverse or anti-log transform for a numeric vector of soma_adat object. **note:** default is base = 10, which differs from the log() default base e.
- Ops(soma_adat): performs binary mathematical operations on class soma_adat. See Ops().
- Summary(soma_adat): performs summary calculations on class soma_adat. See Summary().
- == : compares left- and right-hand sides of the operator *unless* the RHS is also a soma_adat, in which case diffAdats() is invoked.

Math

Group members:

```
#> [1] "abs"      "acos"      "acosh"     "asin"      "asinh"     "atan"
#> [7] "atanh"    "ceiling"   "cos"       "cosh"      "cospi"     "cummax"
#> [13] "cummin"   "cumprod"   "cumsum"    "digamma"   "exp"       "expm1"
#> [19] "floor"    "gamma"     "lgamma"    "log"       "log10"     "log1p"
#> [25] "log2"     "sign"      "sin"       "sinh"      "sinpi"     "sqrt"
#> [31] "tan"      "tanh"      "tanpi"     "trigamma"  "trunc"
```

Commonly used generics of this group include:

- `log()`, `log10()`, `log2()`, `antilog()`, `abs()`, `sign()`, `floor()`, `sqrt()`, `exp()`

Ops

Group members:

```
#> [1] "+" "-" "*" "^" "%" "%/%" "/" "==" ">" "<" "!=" "<="
#> [13] ">="
```

Note that for the ``==`` method if the RHS is also a `soma_adat`, `diffAdats()` is invoked which compares LHS vs. RHS. Commonly used generics of this group include:

- `+`, `-`, `*`, `/`, `^`, `==`, `>`, `<`

Summary

Group members:

```
#> [1] "all" "any" "max" "min" "prod" "range" "sum"
```

Commonly used generics of this group include:

- `max()`, `min()`, `range()`, `sum()`, `any()`

Author(s)

Stu Field

See Also

[groupGeneric\(\)](#), [getGroupMembers\(\)](#), [getGroup\(\)](#)

Examples

```
# subset `example_data` for speed
# all SeqIds from 2000 -> 2999
seqs <- grep("^seq\\.2[0-9]{3}", names(example_data), value = TRUE)
ex_data_small <- head(example_data[, c(getMeta(example_data), seqs)], 10L)
dim(ex_data_small)

ex_data_small$seq.2991.9

# Math Generics:
# -----
# log-transformation
a <- log(ex_data_small)
a$seq.2991.9

b <- log10(ex_data_small)
b$seq.2991.9
```

```
isTRUE(all.equal(b, log(ex_data_small, base = 10)))

# floor
c <- floor(ex_data_small)
c$seq.2991.9

# square-root
d <- sqrt(ex_data_small)
d$seq.2991.9

# rounding
e <- round(ex_data_small)
e$seq.2991.9

# inverse log
antilog(1:4)

alog <- antilog(b)
all.equal(ex_data_small, alog) # return `b` -> linear space

# Ops Generics:
# -----
plus1 <- ex_data_small + 1
times2 <- ex_data_small * 2

sq <- ex_data_small^2
all.equal(sqrt(sq), ex_data_small)

gt100k <- ex_data_small > 100000
gt100k

ex_data_small == ex_data_small # invokes diffAdats()

# Summary Generics:
# -----
sum(ex_data_small)

any(ex_data_small < 100) # low RFU analytes

sum(ex_data_small < 100) # how many

min(ex_data_small)

min(ex_data_small, 0)

max(ex_data_small)

max(ex_data_small, 1e+7)

range(ex_data_small)
```

is_intact_attr	<i>Are Attributes Intact?</i>
----------------	-------------------------------

Description

This function runs a series of checks to determine if a `soma_adat` object has a complete set of attributes. If not, this indicates that the object has been modified since the initial `read_adat()` call. Checks for the presence of both "Header.Meta" and "Col.Meta" in the attribute names. These entries are added during the `read_adat()` call. Specifically, within these sections it also checks for the presence of the following entries:

"Header.Meta" section: "HEADER", "COL_DATA", and "ROW_DATA"

"Col.Meta" section: "SeqId", "Target", "Units", and "Dilution"

If any of the above they are altered or missing, FALSE is returned.

`is.intact.attributes()` is **[Superseded]**. It remains for backward compatibility and may be removed in the future. You are encouraged to shift your code to `is_intact_attr()`.

Usage

```
is_intact_attr(adat, verbose = interactive())
```

```
is.intact.attributes(adat, verbose = interactive())
```

Arguments

<code>adat</code>	A <code>soma_adat</code> object to query.
<code>verbose</code>	Logical. Should diagnostic information about failures be printed to the console? If the default, see <code>interactive()</code> , is invoked, only messages via direct calls are triggered. This prohibits messages generated deep in the call stack from bubbling up to the user.

Value

Logical. TRUE if all checks pass, otherwise FALSE.

See Also

[attributes\(\)](#)

Examples

```
# checking attributes
my_adat <- example_data
is_intact_attr(my_adat) # TRUE
is_intact_attr(my_adat[, -303L]) # doesn't break atts; TRUE
attributes(my_adat)$Col.Meta$Target <- NULL # break attributes
is_intact_attr(my_adat) # FALSE (Target missing)
```

is_seqFormat *Test AptName Format*

Description

Test whether an object is in the new seq.XXXX.XX format.

Usage

```
is_seqFormat(x)
```

Arguments

x The object to be tested.

Value

A logical indicating whether x contains AptNames consistent with the new format, beginning with a seq. prefix.

Author(s)

Stu Field, Eduardo Tabacman

Examples

```
# character S3 method
is_seqFormat(names(example_data)) # no; meta data not ^seq.
is_seqFormat(tail(names(example_data), -20L)) # yes

# soma_adat S3 method
is_seqFormat(example_data)
```

lift_adat *Lift an ADAT Between Assay Versions*

Description

The SomaScan platform continually improves its technical processes between assay versions. The primary change of interest is content expansion, and other protocol changes may be implemented including: changing reagents, liquid handling equipment, and well volumes.

Table of SomaScan assay versions:

Version	Commercial Name	Size
V4	5k	5284
v4.1	7k	7596

v5.0 11k 11083

However, for a given analyte, these technical upgrades can result in minute measurement signal differences, requiring a calibration (aka "lifting" or "bridging") to bring RFUs into a comparable signal space. This is accomplished by applying an analyte-specific scalar, a linear transformation, to each analyte RFU measurement (column). If you have an annotations file (*.xlsx) and wish to examine the bridging scalars themselves, please see [read_annotations\(\)](#).

Lifting between SomaScan versions no longer requires an annotations file containing lifting scalars. We now enable users to pass a bridge parameter, indicating the direction of the bridge. For example, to "lift" between 11k -> 7k, you *must* be acting on SomaScan data in 11k RFU space and would pass `bridge = "11k_to_7k"`. Likewise, 7k -> 5k requires `bridge = "7k_to_5k"`. Lastly, you may also lift directly from 11k -> 5k (aka "double-bridge") with `bridge = "11k_to_5k"`. See below for all options for the bridge argument.

Usage

```
lift_adat(
  adat,
  bridge = c("11k_to_7k", "11k_to_5k", "7k_to_11k", "7k_to_5k", "5k_to_11k", "5k_to_7k"),
  anno.tbl = deprecated()
)

is_lifted(adat)
```

Arguments

<code>adat</code>	A <code>soma_adat</code> object (with intact attributes), typically created using read_adat() .
<code>bridge</code>	The direction of the lift (i.e. bridge).
<code>anno.tbl</code>	[Deprecated] . Please now use the bridge argument.

Details

Matched samples across assay versions are used to calculate bridging scalars. For each analyte, this scalar is computed as the ratio of population *medians* across assay versions. Please see the lifting vignette `vignette("lifting-and-bridging", package = "SomaDataIO")` for more details.

Value

[lift_adat\(\)](#): A "lifted" `soma_adat` object corresponding to the scaling requested in the bridge parameter. RFU values are rounded to 1 decimal place to match standard SomaScan delivery format.

[is_lifted\(\)](#): Logical. Whether the RFU values in a `soma_adat` have been lifted from its original signal space to a new signal space.

Lin's CCC

The Lin's Concordance Correlation Coefficient (CCC) is calculated by computing the correlation between post-lift RFU values and the RFU values generated on the original SomaScan version. This CCC estimate is a measure of how well an analyte can be bridged across SomaScan versions. See `vignette("lifting-and-bridging", package = "SomaDataIO")`. As with the lifting scalars, if you have an annotations file you may view the analyte-specific CCC values via `read_annotations()`. Alternatively, `getSomaScanLiftCCC()` retrieves these values from an internal object for both "serum" and "plasma".

Analyte Setdiff

- Newer versions of SomaScan typically have additional content, i.e. new reagents added to the multi-plex assay that bind to additional proteins. When lifting *to* a previous SomaScan version, new reagents that do *not* exist in the "earlier" assay version are scaled by 1.0, and thus maintained, unmodified in the returned object. Users may need to drop these columns in order to combine these data with a previous study from an earlier SomaScan version, e.g. with `collapseAdats()`.
- In the inverse scenario, lifting "forward" *from* a previous, lower-plex version, there will be extra reference values that are unnecessary to perform the lift, and a warning is triggered. The resulting data consists of RFU data in the "new" signal space, but with fewer analytes than would otherwise be expected (e.g. 11k space with only 5284 analytes; see example below).

References

Lin, Lawrence I-Kuei. 1989. A Concordance Correlation Coefficient to Evaluate Reproducibility. *Biometrics*. 45:255-268.

Examples

```
# `example_data` is SomaScan (V4, 5k)
adat <- head(example_data, 3L)
dim(adat)

getSomaScanVersion(adat)

getSignalSpace(adat)

# perform 'lift'
lift_11k <- lift_adat(adat, "5k_to_11k") # warning

is_lifted(lift_11k)

dim(lift_11k)

# attributes updated to reflect the 'lift'
attr(lift_11k, "Header")$HEADER$SignalSpace

attr(lift_11k, "Header")$HEADER$ProcessSteps
```

loadAdatsAsList	<i>Load ADAT files as a list</i>
-----------------	----------------------------------

Description

Load a series of ADATs and return a list of `soma_adat` objects, one for each ADAT file. `collapseAdats()` concatenates a list of ADATs from `loadAdatsAsList()`, while maintaining the relevant attribute entries (mainly the `HEADER` element). This makes writing out the final object possible without the loss of `HEADER` information.

Usage

```
loadAdatsAsList(files, collapse = FALSE, verbose = interactive(), ...)  
  
collapseAdats(x)
```

Arguments

<code>files</code>	A character string of files to load.
<code>collapse</code>	Logical. Should the resulting list of ADATs be collapsed into a single ADAT object?
<code>verbose</code>	Logical. Should the function call be run in <i>verbose</i> mode.
<code>...</code>	Additional arguments passed to <code>read_adat()</code> .
<code>x</code>	A list of <code>soma_adat</code> class objects returned from <code>loadAdatsAsList()</code> .

Details

Note 1: The default behavior is to "vertically bind" (`rbind()`) on the *intersect* of the column variables, with unique columns silently dropped.

Note 2: If "vertically binding" on the column *union* is desired, use `dplyr::bind_rows()`, however this results in NAs in non-intersecting columns. For many files with little variable intersection, a sparse RFU-matrix will result (and will likely break ADAT attributes):

```
adats <- loadAdatsAsList(files)  
union_adat <- dplyr::bind_rows(adats, .id = "SourceFile")
```

Value

A list of ADATs named by files, each a `soma_adat` object corresponding to an individual file in files. For `collapseAdats()`, a single, collapsed `soma_adat` object.

Author(s)

Stu Field

See Also[read_adat\(\)](#)Other IO: [parseHeader\(\)](#), [read_adat\(\)](#), [soma_adat](#), [write_adat\(\)](#)**Examples**

```
# only 1 file in directory
dir(system.file("extdata", package = "SomaDataIO"))

files <- system.file("extdata", package = "SomaDataIO") |>
  dir(pattern = "[.]adat$", full.names = TRUE) |> rev()

adats <- loadAdatsAsList(files)
class(adats)

# collapse into 1 ADAT
collapsed <- collapseAdats(adats)
class(collapsed)

# Alternatively use `collapse = TRUE`

loadAdatsAsList(files, collapse = TRUE)
```

medianNormalize*Perform Median Normalization on Study Samples*

Description

Performs median normalization on a `soma_adat` object that has already undergone standard data processing for array-based SomaScan studies.

Median normalization is a common, scale-based normalization technique that corrects for assay-derived technical variation by applying sample-specific linear scaling to expression measurements. Typical sources of assay variation include robotic and manual liquid handling, manufactured consumables such as buffers and plastic goods, laboratory instrument calibration, ambient environmental conditions, inter-operator differences, and other sources of technical variation. Median normalization can improve assay precision and reduce technical variation that can mask true biological signal.

The method scales each sample so that the center of the within-sample analyte distribution aligns to a defined reference, thereby correcting global intensity shifts without altering relative differences between measurements within a sample. For assay formats with multiple dilution groups (e.g., 1:5 or 20%; 1:200 or 0.5%; 1:20,000 or 0.005%), separate scale factors are calculated for each dilution because each dilution group is processed separately during the assay. For each sample, the ratio of reference RFU / observed RFU is calculated for every `SeqId`. The median ratio within each dilution group is selected as the scale factor and applied to all `SeqIds` for that sample within the associated dilution bin.

Usage

```
medianNormalize(adat, reference = NULL, by = NULL, verbose = TRUE)
```

Arguments

adat	A soma_adat object created using <code>read_adat()</code> , containing RFU values that have been hybridization normalized and plate scaled.
reference	Optional. Reference for median normalization. Can be: <ul style="list-style-type: none"> • NULL (default): Calculate an internal reference from study samples by taking the median of each SeqId within the sample grouping. • A soma_adat object: Extract reference from this ADAT • A data.frame: Use provided reference data directly When providing an external reference data.frame it must contain: <p>SeqId Character column containing the SeqId identifiers mapping to those in the soma_adat object. Must be in "10000-28" format, not "seq.10000.28" format.</p> <p>Reference Numeric column containing the reference RFU values for each SeqId.</p>
by	Character vector. Grouping variable(s) for grouped median normalization. Must be column name(s) in the ADAT. Normalization will be performed within each group separately. Default is NULL (all samples normalized together). Note that only study samples (<code>SampleType == 'Sample'</code>) are normalized; QC, Calibrator, and Buffer samples are automatically excluded.
verbose	Logical. Should progress messages be printed? Default is TRUE.

Value

A soma_adat object with median normalization applied and RFU values adjusted. The existing `NormScale_*` columns are updated to include the effects of both plate scale normalization and median normalization.

Data Requirements

This function is designed for data in standard SomaLogic deliverable formats. Specific ADAT file requirements:

1. **Intact ADAT file**, with available data processing information in the header section. Specifically, the `ProcessSteps` field must be present and correctly represent the data processing steps present in the data table.
2. **Minimal standard processing**, the function assumes a standard SomaScan data deliverable with minimally standard `HybNorm` and `PlateScale` steps applied.

Primary use cases:

- Combining data sets from the same overarching experiment or sample population and normalize to a common reference that were originally processed separately and each normalized "within study".

- Normalize fundamentally different types of samples separately (by group). For instance, lysate samples from different cell lines that will be analyzed separately should likely be median normalized within each cell type. Lysis buffer background samples would also be expected to be normalized separately.

Important Considerations

- A core assumption of median normalization is that the majority of analytes are not differentially expressed; consequently, users should validate this assumption by inspecting scale-factor distributions for systematic bias between the biological groups intended for comparison.
- Note this function does not perform the adaptive normalization by maximum likelihood (ANML) method which leverages a population-based reference that iteratively down-selects the set of analytes to include for the normalization calculation.
- This function requires unnormalized data as input. If study samples have already undergone median normalization (ANML or standard), first use `reverseMedianNormalize()` to remove existing normalization.

Examples

```
## Not run:
# Starting with unnormalized ADAT
unnormalized_adat <- read_adat("unnormalized_study_data.adat")

# Internal reference from study samples (default - all samples normalized together)
med_norm_adat <- medianNormalize(unnormalized_adat)

# Reference from another ADAT
ref_adat <- read_adat("reference_file.adat")
med_norm_adat <- medianNormalize(unnormalized_adat, reference = ref_adat)

# External reference as a data.frame - requires `SeqId` and `Reference` columns
ref_data <- read.csv("reference_file.csv")
med_norm_adat <- medianNormalize(unnormalized_adat, reference = ref_data)

# Custom grouping by biological variables
# Use when samples should be normalized separately by group
med_norm_adat <- medianNormalize(unnormalized_adat, by = "Sex")
med_norm_adat <- medianNormalize(unnormalized_adat, by = c("Sex", "Age_Group"))

# If you already have normalized data, first reverse the normalization
normalized_adat <- read_adat("normalized_study_data.adat")
unnormalized_adat <- reverseMedianNormalize(normalized_adat)
custom_norm_adat <- medianNormalize(unnormalized_adat, reference = new_reference)

## End(Not run)
```

`merge_clin`*Merge Clinical Data into SomaScan*

Description

Occasionally, additional clinical data is obtained *after* samples have been submitted to SomaLogic, or even after 'SomaScan' results have been delivered. This requires the new clinical variables, i.e. non-proteomic, data to be merged with 'SomaScan' data into a "new" ADAT prior to analysis. `merge_clin()` easily merges such clinical variables into an existing `soma_adat` object and is a simple wrapper around `dplyr::left_join()`.

Usage

```
merge_clin(x, clin_data, by = NULL, by_class = NULL, ...)
```

Arguments

<code>x</code>	A <code>soma_adat</code> object (with intact attributes), typically created using <code>read_adat()</code> .
<code>clin_data</code>	One of 2 options: <ul style="list-style-type: none">• a data frame containing clinical variables to merge into <code>x</code>, or• a path to a file, typically a <code>*.csv</code>, containing clinical variables to merge into <code>x</code>.
<code>by</code>	A character vector of variables to join by. See <code>dplyr::left_join()</code> for more details.
<code>by_class</code>	If <code>clin_data</code> is a file path, a named character vector of the variable and its class. This ensures the "by-key" is compatible for the join. For example, <code>c(SampleId = "character")</code> . See <code>read.table()</code> for details about its <code>colClasses</code> argument, and also the examples below.
<code>...</code>	Additional parameters passed to <code>dplyr::left_join()</code> .

Details

This functionality also exists as a command-line tool (R script) contained in `merge_clin.R` that lives in the `cli/merge` system file directory. Please see:

- `dir(system.file("cli/merge", package = "SomaDataIO"), full.names = TRUE)`
- `vignette("cli-merge-tool", package = "SomaDataIO")`

Value

A `soma_adat` with new clinical variables merged.

Author(s)

Stu Field

See Also

`dplyr::left_join()`

Examples

```
# retrieve clinical data
clin_file <- system.file("cli/merge", "meta.csv",
                        package = "SomaDataIO",
                        mustWork = TRUE)

clin_file

# view clinical data to be merged:
# 1) `group`
# 2) `newvar`
clin_df <- read.csv(clin_file, colClasses = c(SampleId = "character"))
clin_df

# create mini-adat
apts <- withr::with_seed(123, sample(getAnalytes(example_data), 2L))
adat <- head(example_data, 9L) |> # 9 x 2
  dplyr::select(SampleId, all_of(apts))

# merge clinical variables
merged <- merge_clin(adat, clin_df, by = "SampleId")
merged

# Alternative syntax:
# 1) pass file path
# 2) merge on different variable names
# 3) convert join type on-the-fly
clin_file2 <- system.file("cli/merge", "meta2.csv",
                          package = "SomaDataIO",
                          mustWork = TRUE)

id_type <- typeof(adat$SampleId)
merged2 <- merge_clin(adat, clin_file2, # file path
                     by = c(SampleId = "ClinKey"), # join on 2 variables
                     by_class = c(ClinKey = id_type)) # match types

merged2
```

params

Common Parameters in SomaDataIO

Description

The parameters below are commonly used throughout the **SomaDataIO** package.

Arguments

adat	A soma_adat object (with intact attributes), typically created using read_adat() .
x	A soma_adat object (with intact attributes), typically created using read_adat() .
matrix	Character. A string of (usually) either "serum" or "plasma".

Value

A soma_adat class object.

parseHeader	<i>SomaLogic ADAT parser</i>
-------------	------------------------------

Description

Parses the header section of an ADAT file.

Usage

```
parseHeader(file)
```

Arguments

file	Character. The elaborated path and file name of the *.adat file to be loaded into an R workspace environment.
------	---

Value

A list of relevant file information required by [read_adat\(\)](#) in order to complete loading the ADAT file, including:

Header.Meta	list of notes and other information about the adat
Col.Meta	list of vectors that contain the column meta data about individual analytes, includes information about the target name and calibration and QC ratios
file_specs	list of values of the file parsing specifications
row_meta	character vector of the clinical variables; assay information that is included in the adat output along with the RFU data

Author(s)

Stu Field

See Also

Other IO: [loadAdatsAsList\(\)](#), [read_adat\(\)](#), [soma_adat](#), [write_adat\(\)](#)

Examples

```
f <- system.file("extdata", "example_data10.adat",
                package = "SomaDataIO", mustWork = TRUE)
header <- parseHeader(f)
names(header)

header$header.Meta

header$file_specs

header$row_meta

head(as.data.frame(header$Col.Meta))
```

pivotExpressionSet *Convert to Long Format*

Description

Utility to convert an ExpressionSet class object from the "wide" data format to the "long" format via `tidyr::pivot_longer()`. The **Biobase** package is required for this function.

Usage

```
pivotExpressionSet(eSet)

meltExpressionSet(eSet)
```

Arguments

eSet An ExpressionSet class object, created using `adat2eSet()`.

Value

A tibble consisting of the long format conversion of an ExpressionSet object.

Functions

- `meltExpressionSet()`: **[Superseded]**. Please now use `pivotExpressionSet()`.

Author(s)

Stu Field

See Also

Other eSet: `adat2eSet()`

Examples

```
# subset into a reduced mini-ADAT object
# 10 samples (rows)
# 5 clinical variables and 3 features (cols)
sub_adat <- example_data[1:10, c(1:5, 35:37)]
ex_set <- adat2eSet(sub_adat)

# convert ExpressionSet object to long format
adat_long <- pivotExpressionSet(ex_set)
```

plot.Map

Plot Image Maps

Description

Plotting function for objects of the outlier_map class. Produces a heatmap-style image using **ggplot2** syntax, for objects produced by `calcOutlierMap()`.

Usage

```
## S3 method for class 'Map'
plot(
  x,
  color.scheme = NULL,
  legend.ticks = 7,
  gridlines = NULL,
  gridlinecol = "red",
  gridlinelwd = 0.5,
  gridlinelty = 2,
  main = NULL,
  y.lab = NULL,
  x.lab = NULL,
  flags = NULL,
  legend.width = 1,
  legend.height = 2,
  filename = NULL,
  plot.width = 14,
  plot.height = 8,
  plot.scale = 1,
  ...
)
```

Arguments

`x` An object of class: outlier_map
`color.scheme` Which color scheme to use. Typical choices include:

	<ul style="list-style-type: none"> • <code>gplots::redgreen()</code> • <code>gplots::bluered()</code> • <code>grDevices::heat.colors()</code> • <code>grDevices::terrain.colors()</code> • <code>grDevices::topo.colors()</code> • <code>RColorBrewer::brewer.pal()</code> • <code>viridis::viridis()</code> • <code>viridis::magma()</code>
<code>legend.ticks</code>	How many ticks to place on the color legend.
<code>gridlines</code>	Numeric vector or logical. Indicates where to draw the <i>horizontal</i> grid lines that can be used to separate samples (rows). This should be a vector of the cumulative sum of the horizontal lines to be drawn, typically something like <code>cumsum(table(data\$Sex))</code> . Alternatively, TRUE can be passed whereby the lines are determined by the "class.tab" element of <code>x\$class.tab</code> (if possible).
<code>gridlinecol</code>	Color of the gridlines.
<code>gridlinelwd</code>	Width of the gridlines.
<code>gridlinelty</code>	Line type of the gridlines.
<code>main</code>	Character. Main title for the plot. See <code>ggplot2::ggtitle()</code> for ggplot2 style graphics.
<code>y.lab</code>	Character. Optional string for the y-axis. Otherwise one is automatically generated (default).
<code>x.lab</code>	Character. Optional string for the x-axis. Otherwise one is automatically generated (default).
<code>flags</code>	Numeric in $[0, 1]$. For an "outlier_map", the proportion of the analytes (columns) for a given sample that must be outliers for a flag to be placed at the right-axis, right-axis, thus flagging that sample. If NULL (default), 0.05 (5%) is selected.
<code>legend.width</code>	Width for the color legend.
<code>legend.height</code>	Height for the color legend.
<code>filename</code>	Optional. If provided, the plot will be written to a file. The file name must also include the desired file type extension; this will be used to determine the file type, e.g. a file named <code>foo.png</code> will be saved as a PNG. See <code>ggplot2::ggsave()</code> for a full list of file type (device) options.
<code>plot.width</code>	If " <code>filename != NULL</code> ", the width of the plot image file.
<code>plot.height</code>	If " <code>filename != NULL</code> ", the height of the plot image file.
<code>plot.scale</code>	If " <code>filename != NULL</code> ", the scale of the plot image file.
<code>...</code>	Arguments required by the <code>plot()</code> generic. Currently unused.

Value

Plot an image of the passed matrix.

Author(s)

Stu Field, Amanda Hiser

See Also

[ggplot2::ggplot\(\)](#), [ggplot2::geom_raster\(\)](#)

Other Calc Map: [calcOutlierMap\(\)](#), [getOutlierIds\(\)](#)

Examples

```
example_data |>
  dplyr::filter(SampleType == "Sample") |>
  head(10) |>
  calcOutlierMap() |>
  plot(flags = 0.05)
```

preProcessAdat

Pre-Process an ADAT Object for Analysis

Description

Pre-process an ADAT file containing raw analyte RFU values in preparation for analysis. For more details please refer to the [pre-processing how-to article](#)

Usage

```
preProcessAdat(
  adat,
  filter.features = TRUE,
  filter.controls = TRUE,
  filter.rowcheck = TRUE,
  filter.qc = deprecated(),
  filter.outliers = FALSE,
  data.qc = NULL,
  log.10 = FALSE,
  center.scale = FALSE
)
```

Arguments

adat A `soma_adat` object created using [read_adat\(\)](#), including `SeqId` columns (`seq.xxxxx.xx`) containing raw RFU values.

filter.features Logical. Should non-human protein features (`SeqIds`) be dropped? Default is `TRUE`.

<code>filter.controls</code>	Logical. Should SomaScan technical control samples be dropped? If TRUE, this retains all samples where <code>SampleType = "Sample"</code> (study samples) and discards all others including buffer, calibrator, and QC control samples. Default is TRUE.
<code>filter.rowcheck</code>	Logical. If TRUE only samples that pass default normalization acceptance criteria will be retained. Default is TRUE.
<code>filter.qc</code>	[Deprecated] Logical. Please use <code>filter.rowcheck</code> instead. This parameter is deprecated and will be removed in a future version.
<code>filter.outliers</code>	Logical. Should the <code>adat</code> object drop outlier samples? An outlier sample is defined by $\geq 5\%$ of filtered <code>SeqIds</code> exceeding ± 6 MAD and 5x fold-change from the median signal. This filter is typically appropriate for studies on plasma, serum, and other biological matrices generally exhibiting homeostatic characteristics. For studies on matrices such as tissue homogenate, cell culture, or study designs containing client-provided background lysis buffer controls (or similar), this filter will likely not be appropriate. Default is FALSE. If set to TRUE it is highly recommended that <code>filter.controls</code> is also set to TRUE
<code>data.qc</code>	Character. Character vector of variable names for which data QC plots are desired. Default is NULL, which does not generate any QC plots. Note: These plots are for visual inspection only, no samples or features are dropped from the output <code>soma_adat</code> object.
<code>log.10</code>	Logical. Should the RFU values be log10 transformed? Default is FALSE.
<code>center.scale</code>	Logical. Should the RFU values be Z-transformed (centered and scaled)? Default is FALSE. If set to set to TRUE it is highly recommended that <code>log.10</code> is also set to TRUE

Details

The `soma_adat` object is pre-processed with the following steps:

1. Filter features -> down to human protein analytes
2. Filter samples -> by the following order and criteria: a) Retain study samples only (dropping buffer, calibrator, and QC samples) b) Only those that pass default normalization acceptance criteria c) Those not identified as outliers.
3. Data QC -> plots of normalization scale factors by clinical covariates
4. Transformations -> log10, center, and scale analyte RFU values

Value

A `soma_adat` object.

Author(s)

Caleb Scheidel

Examples

```
preProcessAdat(example_data, data.qc = c("Age", "Sex"))
```

read_adat	<i>Read (Load) SomaLogic ADATs</i>
-----------	------------------------------------

Description

The parse and load a *.adat file as a data.frame-like object into an R workspace environment. The class of the returned object is a soma_adat object.

`read.adat()` is **[Superseded]**. For backward compatibility it will likely never go away completely, but you are strongly encouraged to shift your code to use `read_adat()`.

`is.soma_adat()` checks whether an object is of class soma_adat. See `inherits()`.

Usage

```
read_adat(file, debug = FALSE, verbose = getOption("verbose"), ...)
```

```
read.adat(file, debug = FALSE, verbose = getOption("verbose"), ...)
```

```
is.soma_adat(x)
```

Arguments

file	Character. The elaborated path and file name of the *.adat file to be loaded into an R workspace.
debug	Logical. Used for debugging and development of an ADAT that fails to load, particularly out-of-spec, poorly modified, or legacy ADATs.
verbose	Logical. Should the function call be run in <i>verbose</i> mode, printing relevant diagnostic call information to the console.
...	Additional arguments passed ultimately to <code>read.delim()</code> , or additional arguments passed to either other S3 print or summary methods as required by those generics.
x	An R object to test.

Value

A data.frame-like object of class soma_adat consisting of SomaLogic RFU (feature) data and clinical meta data as columns, and samples as rows. Row names are labeled with the unique ID "SlideId_Subarray" concatenation. The sections of the ADAT header (e.g., "Header.Meta", "Col.Meta", ...) are stored as attributes (e.g. `attributes(x)$Header.Meta`).

Logical. Whether x inherits from class soma_adat.

Author(s)

Stu Field

See Also`read.delim()`Other IO: `loadAdatsAsList()`, `parseHeader()`, `soma_adat`, `write_adat()`**Examples**

```
# path to *.adat file
# replace with your file path
adat_path <- system.file("extdata", "example_data10.adat",
                        package = "SomaDataIO", mustWork = TRUE)

adat_path

my_adat <- read_adat(adat_path)

is.soma_adat(my_adat)
```

`read_annotations`*Import a SomaLogic Annotations File*

Description

Import a SomaLogic Annotations File

Usage`read_annotations(file)`**Arguments**

<code>file</code>	A path to an annotations file location. This should be a SomaLogic annotations file in *.xlsx format.
-------------------	---

ValueA tibble containing analyte-specific annotations and related (e.g. lift/bridging) information, keyed on SomaLogic [SeqId](#), the unique SomaScan analyte identifier.**Examples**

```
## Not run:
# for example
file <- "~/Downloads/SomaScan_11K_v5.0_Plasma_Serum_Annotated_Menu.xlsx"
anno_tbl <- read_annotations(file)

## End(Not run)
```

`reverseMedianNormalize`*Reverse Median Normalization from Study Samples*

Description

Reverses median normalization (including ANML) that was previously applied to study samples (`SampleType == "Sample"`). This function is designed to work with standard SomaScan deliverable ADAT files where study samples have undergone median normalization as the final processing step.

This function validates that:

1. Study samples have a median normalization step applied
2. The normalization was the last transformation applied to study samples
3. The correct reversal method is applied based on the normalization type

Usage

```
reverseMedianNormalize(adat, verbose = TRUE)
```

Arguments

<code>adat</code>	A <code>soma_adat</code> object with study samples that have been median normalized
<code>verbose</code>	Logical. Should progress messages be printed? Default is TRUE.

Value

A `soma_adat` object with median normalization reversed for study samples. QC, Calibrator, and Buffer samples retain their original normalization. The `ProcessSteps` header is updated to reflect the reversal operation, and median normalization-specific metadata fields are cleared.

Use Cases

- Converting from normalized ADAT to unnormalized ADAT for custom normalization
- Preparing normalized delivery data for use with `medianNormalize()` function
- Backing out normalization to apply different normalization strategies

Data Requirements

- ADAT file with study samples (`SampleType == "Sample"`) that have been median normalized (either standard median normalization or ANML)
- Intact header metadata with `ProcessSteps` field indicating the normalization history
- Median normalization must be the last processing step applied to study samples

Examples

```
## Not run:
# Reverse normalization from a delivered ADAT file
normalized_adat <- read_adat("normalized_study_data.adat")
unnormalized_adat <- reverseMedianNormalize(normalized_adat)

## End(Not run)
```

rownames

*Helpers for Working With Row Names***Description**

Easily move row names to a column and vice-versa without the unwanted side-effects to object class and attributes. Drop-in replacement for `tibble::rownames_to_column()` and `tibble::column_to_rownames()` which can have undesired side-effects to complex object attributes. Does not import any external packages, modify the environment, or change the object (other than the desired column). When using `col2rn()`, if explicit row names exist, they are overwritten with a warning. `add_rowid()` does *not* affect row names, which differs from `tibble::rowid_to_column()`.

Usage

```
rn2col(data, name = ".rn")

col2rn(data, name = ".rn")

has_rn(data)

rm_rn(data)

set_rn(data, value)

add_rowid(data, name = ".rowid")
```

Arguments

<code>data</code>	An object that inherits from class <code>data.frame</code> . Typically a <code>soma_adat</code> class object.
<code>name</code>	Character. The name of the column to move.
<code>value</code>	Character. The new set of names for the data frame. If duplicates exist they are modified on-the-fly via <code>make.unique()</code> .

Value

All functions attempt to return an object of the same class as the input with fully intact and unmodified attributes (aside from those required by the desired action). `has_rn()` returns a scalar logical.

Functions

- `rn2col()`: moves the row names of data to an explicit column whether they are explicit or implicit.
- `col2rn()`: is the inverse of `rn2col()`. If row names exist, they will be overwritten (with warning).
- `has_rn()`: returns a boolean indicating whether the data frame has explicit row names assigned.
- `rm_rn()`: removes existing row names, leaving only "implicit" row names.
- `set_rn()`: sets (and overwrites) existing row names for data frames only.
- `add_rowid()`: adds a sequential integer row identifier; starting at `1:nrow(data)`. It does *not* remove existing row names currently, but may in the future (please code accordingly).

Examples

```
df <- data.frame(a = 1:5, b = rnorm(5), row.names = LETTERS[1:5])
df
rn2col(df)          # default name is `.rn`
rn2col(df, "AptName") # pass `name =`

# moving columns
df$mtcars <- sample(names(mtcars), 5)
col2rn(df, "mtcars") # with a warning

# Move back and forth easily
# Leaves original object un-modified
identical(df, col2rn(rn2col(df)))

# add "id" column
add_rowid(mtcars)

# remove row names
has_rn(mtcars)
mtcars2 <- rm_rn(mtcars)
has_rn(mtcars2)
```

 SeqId

Working with SomaLogic SeqIds

Description

The SeqId is the cornerstone used to uniquely identify SomaLogic analytes. SeqIds follow the format `<Pool>-<Clone>_<Version>`, for example "1234-56_7" can be represented as:

Pool	Clone	Version
1234	56	7

See **Details** below for the definition of each sub-unit. The <Pool>-<Clone> combination is sufficient to uniquely identify a specific analyte and therefore versions are no longer provided (though they may be present in legacy ADATs). The tools below enable users to extract, test, identify, compare, and manipulate SeqIds across assay runs and/or versions.

Usage

```
getSeqId(x, trim.version = FALSE)

regexSeqId()

locateSeqId(x, trailing = TRUE)

seqid2apt(x)

apt2seqid(x)

is.apt(x)

is.SeqId(x)

is.AptName(x)

matchSeqIds(x, y, order.by.x = TRUE)

getSeqIdMatches(x, y, show = FALSE)
```

Arguments

x	Character. A vector of strings, usually analyte/feature column names, AptNames, or SeqIds. For <code>seqid2apt()</code> , a vector of SeqIds. For <code>apt2seqid()</code> , a character vector containing SeqIds. For <code>matchSeqIds()</code> , a vector of pattern matches containing SeqIds. Can be AptNames with GeneIDs, the seq.XXXX format, or even "naked" SeqIds.
trim.version	Logical. Whether to remove the version number, i.e. "1234-56_7" -> "1234-56". Primarily for legacy ADATs.
trailing	Logical. Should the regular expression explicitly specify <i>trailing</i> SeqId pattern match, i.e. "regex\$"? This is the most common case and the default.
y	Character. A second vector of AptNames containing SeqIds to match against those in contained in x. For <code>matchSeqIds()</code> these values are returned if there are matching elements.
order.by.x	Logical. Order the returned character string by the x (first) argument?
show	Logical. Return the data frame visibly?

Details

Pool: ties back to the original well during **SELEX**

Clone: ties to the specific sequence within a pool
Version: refers to custom modifications (optional/defunct)

AptName a SeqId combined with a string, usually a GeneId- or seq.-prefix, for convenient, human-readable manipulation from within R.

Value

`getSeqId()`: a character vector of SeqIds captured from a string.

`regexSeqId()`: a regular expression (regex) string pre-defined to match SomaLogic the SeqId pattern.

`locateSeqId()`: a data frame containing the start and stop integer positions for SeqId matches at each value of x.

`seqid2apt()`: a character vector with the seq.* prefix, i.e. the inverse of `getSeqId()`.

`apt2seqid()`: a character vector of SeqIds. `is.SeqId()` will return TRUE for all elements.

`is.apt()`, `is.SeqId()`: Logical. TRUE or FALSE.

`matchSeqIds()`: a character string corresponding to values in y of the intersect of x and y. If no matches are found, character(\emptyset).

`getSeqIdMatches()`: a $n \times 2$ data frame, where n is the length of the intersect of the matching SeqIds. The data frame is named by the passed arguments, x and y.

Functions

- `getSeqId()`: extracts/captures the the SeqId match from an analyte column identifier, i.e. column name of an ADAT loaded with `read_adat()`. Assumes the SeqId pattern occurs at the end of the string, which for the vast majority of cases will be true. For edge cases, see the trailing argument to `locateSeqId()`.
- `regexSeqId()`: generates a pre-formatted regular expression for matching of SeqIds. Note the *trailing* match, which is most commonly required, but `locateSeqId()` offers an alternative to mach *anywhere* in a string. Used internally in *many* utility functions
- `locateSeqId()`: generates a data frame of the positional SeqId matches. Specifically designed to facilitate SeqId extraction via `substr()`. Similar to `stringr::str_locate()`.
- `seqid2apt()`: converts a SeqId into anonymous-AptName format, i.e. 1234-56 -> seq.1234.56. Version numbers (1234-56_ver) are always trimmed when present.
- `apt2seqid()`: converts an anonymous-AptName into SeqId format, i.e. seq.1234.56 -> 1234-56. Version numbers (seq.1234.56.ver) are always trimmed when present.
- `is.apt()`: regular expression match to determine if a string *contains* a SeqId, and thus is probably an AptName format string. Both legacy EntrezGeneSymbol-SeqId combinations or newer so-called "anonymous-AptNames" formats (seq.1234.45) are matched.
- `is.SeqId()`: tests for SeqId format, i.e. values returned from `getSeqId()` will always return TRUE.
- `is.AptName()`: tests for AptName format, i.e. values returned from `seqid2apt()` will always return TRUE. This function will only match AptNames, not SeqIds, and is therefore more strict than `is.apt()`.

- `matchSeqIds()`: matches two character vectors on the basis of their intersecting SeqIds. Note that elements in `y` not containing a SeqId regular expression are silently dropped.
- `getSeqIdMatches()`: matches two character vectors on the basis of their intersecting *SeqIds* only (irrespective of the GeneID-prefix). This produces a two-column data frame which then can be used as to map between the two sets.
The final order of the matches/rows is by the input corresponding to the *first* argument (`x`).
By default the data frame is invisibly returned to avoid dumping excess output to the console (see the `show = argument`.)

Author(s)

Stu Field

See Also[generics::intersect\(\)](#)**Examples**

```
x <- c("ABDC.3948.48.2", "3948.88",
      "3948.48.2", "3948-48_2", "3948.48.2",
      "3948-48_2", "3948-88",
      "My.Favorite.Apt.3948.88.9")

tibble::tibble(orig      = x,
               SeqId     = getSeqId(x),
               SeqId_trim = getSeqId(x, TRUE),
               AptName    = seqid2apt(SeqId))

# Logical Matching
is.apt("AGR2.4959.2") # TRUE
is.apt("seq.4959.2") # TRUE
is.apt("4959-2")     # TRUE
is.apt("AGR2")       # FALSE

# SeqId Matching
x <- c("seq.4554.56", "seq.3714.49", "PlateId")
y <- c("Group", "3714-49", "Assay", "4554-56")
matchSeqIds(x, y)
matchSeqIds(x, y, order.by.x = FALSE)

# vector of features
feats <- getAnalytes(example_data)

match_df <- getSeqIdMatches(feats[1:100], feats[90:500]) # 11 overlapping
match_df

a <- utils::head(feats, 15)
b <- withr::with_seed(99, sample(getSeqId(a))) # => SeqId & shuffle
(getSeqIdMatches(a, b)) # sorted by first vector "a"
```

SomaDataIO-deprecated *Deprecated function(s) of the SomaDataIO package*

Description

These functions have either been **[Superseded]** or **[Deprecated]** in the current version of **SomaDataIO** package. They may eventually be completely removed, so please re-code your scripts accordingly based on the suggestions below:

Function		Now Use
<code>getSomamers()</code>	[Superseded]	<code>getAnalytes()</code>
<code>getSomamerData()</code>	[Superseded]	<code>getAnalyteInfo()</code>

Details

Some badges you may see in **SomaDataIO**:

[Superseded]

[Deprecated]

[Soft-deprecated]

[Stable]

SomaScanObjects *Example Data and Objects*

Description

The `example_data` object is intended to provide existing and prospective SomaLogic customers with example data to enable analysis preparation prior to receipt of SomaScan data, and also for those generally curious about the SomaScan data deliverable. It is **not** intended to be used as a control group for studies or provide any metrics for SomaScan data in general.

Format

example_data a `soma_adat` parsed via `read_adat()` containing 192 samples (see below for breakdown of sample type). There are 5318 columns containing 5284 analyte features and 34 clinical meta data fields. These data have been pre-processed via the following steps:

- hybridization normalized (all samples)
- calibrators and buffers median normalized
- plate scaled
- calibrated
- Adaptive Normalization by Maximum Likelihood (ANML) of QC and clinical samples

Note1: The Age and Sex (M/F) fields contain simulated values designed to contain biological signal.

Note2: The `SampleType` column contains sample source/type information and usually the `SampleType == Sample` represents the "client" samples.

Note3: The original source file can be found at [\url{https://github.com/SomaLogic/SomaLogic-Data}](https://github.com/SomaLogic/SomaLogic-Data).

ex_analytes character string of the analyte features contained in the `soma_adat` object, derived from a call to `getAnalytes()`.

ex_anno_tbl a lookup table corresponding to a transposed data frame of the "Col.Meta" attribute of an ADAT, with an index key field `AptName` included in column 1, derived from a call to `getAnalyteInfo()`.

ex_target_names A lookup table mapping `SeqId` feature names -> target names contained in `example_data`. This object (or one like it) is convenient at the console via auto-complete for labeling and/or creating plot titles on the fly.

ex_clin_data A table containing `SampleId`, `smoking_status`, and `alcohol_use` fields for each clinical sample in `example_data` used to demonstrate how to merge sample annotation information to an existing `soma_adat` object.

Data Description

The `example_data` object contains a SomaScan V4 study from healthy normal individuals. The RFU measurements themselves and other identifiers have been altered to protect personally identifiable information (PII), but also retain underlying biological signal as much as possible. There are 192 total EDTA-plasma samples across two 96-well plate runs which are broken down by the following types:

- 170 clinical samples (client study samples)
- 10 calibrators (replicate controls for combining data across runs)
- 6 QC samples (replicate controls used to assess run quality)
- 6 Buffer samples (no protein controls)

Data Processing

The standard V4 data normalization procedure for EDTA-plasma samples was applied to this dataset. For more details on the data standardization process see the Data Standardization and File Specification Technical Note. General details are outlined above.

Source

<https://github.com/SomaLogic/SomaLogic-Data>

SomaLogic Operating Co., Inc.

Examples

```

# S3 print method
example_data

# print header info
print(example_data, show_header = TRUE)

class(example_data)

# Features/Analytes
head(ex_analytes, 20L)

# Feature info table (annotations)
ex_anno_tbl

# Search via `filter()`
dplyr::filter(ex_anno_tbl, grepl("^MMP", Target))

# Lookup table -> targets
# MMP-9
ex_target_names$seq.2579.17

# gender hormone FSH
tapply(example_data$seq.3032.11, example_data$Sex, median)

# gender hormone LH
tapply(example_data$seq.2953.31, example_data$Sex, median)

# Target lookup
ex_target_names$seq.2953.31      # tab-completion at console

# Sample Type/Source
table(example_data$SampleType)

# Sex/Gender Variable
table(example_data$Sex)

# Age Variable
summary(example_data$Age)

```

soma_adat

The soma_adat Class and S3 Methods

Description

The `soma_adat` data structure is the primary internal R representation of SomaScan data. A `soma_adat` is automatically created via `read_adat()` when loading a `*.adat` text file. It consists of a `data.frame`-like object with leading columns as clinical variables and SomaScan RFU data as the remaining variables. Two main attributes corresponding to analyte and SomaScan run information contained in the `*.adat` file are added:

- `Header.Meta`: information about the SomaScan run, see `parseHeader()` or `attr(x, "Header.Meta")`
- `Col.Meta`: annotations information about the SomaScan reagents/analytes, see `getAnalyteInfo()` or `attr(x, "Col.Meta")`
- `file_specs`: parsing specifications for the ingested *.adat file
- `row_meta`: the names of the non-RFU fields. See `getMeta()`.

See `groupGenerics()` for a details on `Math()`, `Ops()`, and `Summary()` methods that dispatch on class `soma_adat`.

See `reexports()` for a details on re-exported S3 generics from other packages (mostly `dplyr` and `tidyr`) to enable S3 methods to be dispatched on class `soma_adat`.

Below is a list of *all* currently available S3 methods that dispatch on the `soma_adat` class:

```
#> [1] [           [[           [[<-          [<-
#> [5] ==          $           $<-          anti_join
#> [9] arrange       count        filter        full_join
#> [13] getAdatVersion getAnalytes  getMeta       group_by
#> [17] inner_join     is_seqFormat left_join     Math
#> [21] median         merge        mutate        Ops
#> [25] print          rename       right_join    row.names<-
#> [29] sample_frac   sample_n     select        semi_join
#> [33] separate      slice_sample slice          summary
#> [37] Summary       transform    ungroup       unite
#> see '?methods' for accessing help and source code
```

The S3 `print()` method returns summary information parsed from the object attributes, if present, followed by a dispatch to the `tibble::tibble()` print method. Rownames are printed as the first column in the print method only.

The S3 `summary()` method returns the following for each column of the ADAT object containing SOMAmer data (clinical meta data is *excluded*):

- Target (if available)
- Minimum value
- 1st Quantile
- Median
- Mean
- 3rd Quantile
- Maximum value
- Standard deviation
- Median absolute deviation (`mad()`)
- Interquartile range (`IQR()`)

The S3 `Extract()` method is used for sub-setting a `soma_adat` object and relies heavily on the `[` method that maintains the `soma_adat` attributes intact *and* subsets the `Col.Meta` so that it is consistent with the newly created object.

S3 extraction via `$` is fully supported, however, as opposed to the `data.frame` method, partial matching is *not* allowed for class `soma_adat`.

S3 extraction via `[[` is supported, however, we restrict the usage of `[[` for `soma_adat`. Use only a numeric index (e.g. `1L`) or a character identifying the column (e.g. `"SampleID"`). Do not use `[[i, j]]` syntax with `[[`, use `[` instead. As with `$`, partial matching is *not* allowed.

S3 assignment via `[` is supported for class `soma_adat`.

S3 assignment via `$` is fully supported for class `soma_adat`.

S3 assignment via `[[` is supported for class `soma_adat`.

S3 `median()` is *not* currently supported for the `soma_adat` class, however a dispatch is in place to direct users to alternatives.

Usage

```
## S3 method for class 'soma_adat'
print(x, show_header = FALSE, ...)

## S3 method for class 'soma_adat'
summary(object, tbl = NULL, digits = max(3L, getOption("digits") - 3L), ...)

## S3 method for class 'soma_adat'
x[i, j, drop = TRUE, ...]

## S3 method for class 'soma_adat'
x$name

## S3 method for class 'soma_adat'
x[[i, j, ..., exact = TRUE]]

## S3 replacement method for class 'soma_adat'
x[i, j, ...] <- value

## S3 replacement method for class 'soma_adat'
x$i, j, ... <- value

## S3 replacement method for class 'soma_adat'
x[[i, j, ...]] <- value

## S3 method for class 'soma_adat'
median(x, na.rm = FALSE, ...)
```

Arguments

`x, object` A `soma_adat` class object.

show_header	Logical. Should all the Header Data information be displayed instead of the data frame (tibble) object?
...	Ignored.
tbl	An annotations table. If NULL (default), annotation information is extracted from the object itself (if possible). Alternatively, the result of a call to getAnalyteInfo() , from which Target names can be extracted.
digits	Integer. Used for number formatting with signif() .
i, j	Row and column indices respectively. If j is omitted, i is used as the column index.
drop	Coerce to a vector if fetching one column via <code>tbl[, j]</code> . Default FALSE, ignored when accessing a column via <code>tbl[j]</code> .
name	A name or a string.
exact	Ignored with a warning() .
value	A value to store in a row, column, range or cell.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.

Value

The set of S3 methods above return the `soma_adat` object with the corresponding S3 method applied.

See Also

[groupGenerics\(\)](#)

Other IO: [loadAdatsAsList\(\)](#), [parseHeader\(\)](#), [read_adat\(\)](#), [write_adat\(\)](#)

Examples

```
# S3 print method
example_data

# show the header info (no RFU data)
print(example_data, show_header = TRUE)

# S3 summary method
# MMP analytes (4)
mmps <- c("seq.2579.17", "seq.2788.55", "seq.2789.26", "seq.4925.54")
mmp_adat <- example_data[, c("Sex", mmps)]
summary(mmp_adat)

# Summarize by group
mmp_adat |>
  split(mmp_adat$Sex) |>
  lapply(summary)

# Alternatively pass annotations with Target info
anno <- getAnalyteInfo(mmp_adat)
summary(mmp_adat, tbl = anno)
```

transform	<i>Scale Transform soma_adat Columns/Rows</i>
-----------	---

Description

Scale the *i*-th row or column of a `soma_adat` object by the *i*-th element of a vector. Designed to facilitate linear transformations of *only* the analyte/RFU entries by scaling the data matrix. If scaling the analytes/RFU (columns), *v* *must* have `getAnalytes(adat, n = TRUE)` elements. If scaling the samples (rows), *v* *must* have `nrow(_data)` elements.

Usage

```
## S3 method for class 'soma_adat'
transform(`_data`, v, dim = 2L, ...)
```

Arguments

<code>_data</code>	A <code>soma_adat</code> object.
<code>v</code>	A numeric vector of the appropriate length corresponding to <code>dim</code> .
<code>dim</code>	Integer. The dimension to apply elements of <code>v</code> to. 1 = rows; 2 = columns (default).
<code>...</code>	Currently not used but required by the S3 generic.

Details

Performs the following operations (quickly):

Columns:

$$M_{n \times p} = A_{n \times p} * \text{diag}(v)_{p \times p}$$

Rows:

$$M_{n \times p} = \text{diag}(v)_{n \times n} * A_{n \times p}$$

Value

A modified value of `_data` with either the rows or columns linearly transformed by `v`.

Note

This method is intentionally naive, and assumes the user has ordered `v` to match the columns/rows of `_data` appropriately. This must be done upstream.

See Also

[apply\(\)](#), [sweep\(\)](#)

Examples

```

# simplified example of underlying operations
M <- matrix(1:12, ncol = 4)
M

v <- 1:4
M %*% diag(v)  # transform columns

v <- 1:3
diag(v) %*% M  # transform rows

# dummy ADAT example:
v <- c(2, 0.5)  # double seq1; half seq2
adat <- data.frame(sample      = paste0("sample_", 1:3),
                   seq.1234.56 = c(1, 2, 3),
                   seq.9999.88 = c(4, 5, 6) * 10)

adat

# `soma_adat` to invoke S3 method dispatch
class(adat) <- c("soma_adat", "data.frame")
trans <- transform(adat, v)
data.frame(trans)

```

updateColMeta

Update Col.Meta Attribute to Match Annotations Object

Description

Utility to update a provided `soma_adat` object's column metadata to match the annotations object.

Usage

```
updateColMeta(adat, anno)
```

Arguments

adat	A <code>soma_adat</code> data object to update attributes.
anno	A tibble containing analyte-specific annotations from <code>read_annotations()</code>

Details

Attempts to update the following column metadata in the `adat`:

- SomaId
- Target
- TargetFullName
- UniProt

- Type
- Organism
- EntrezGeneSymbol
- EntrezGeneID

Value

An identical object to `adat` with `Col.Meta` updated to match those in `anno`.

Author(s)

Caleb Scheidel

Examples

```
## Not run:
anno_tbl <- read_annotations("path/to/annotations.xlsx")
adat <- read_adat("path/to/adat_file.adat")
updated_adat <- updateColMeta(adat, anno_tbl)

## End(Not run)
```

write_adat

Write an ADAT to File

Description

One can write an existing modified internal ADAT (`soma_adat` R object) to an external file. However the ADAT object itself *must* have intact attributes, see [is_intact_attr\(\)](#).

Usage

```
write_adat(x, file)
```

Arguments

<code>x</code>	A <code>soma_adat</code> object (with intact attributes), typically created using read_adat() .
<code>file</code>	Character. File path where the object should be written. For example, extensions should be <code>*.adat</code> .

Details

The ADAT specification *no longer* requires Windows end of line (EOL) characters ("`\r\n`"). The current EOL spec is "`\n`" which is commonly used in POSIX systems, like MacOS and Linux. Since the EOL affects the resulting checksum, ADATs written on other systems generate slightly differing files. Standardizing to "`\n`" attempts to solve this issue. For reference, see the EOL encoding for operating systems below:

Symbol	Platform	Character
LF	Linux	" <code>\n</code> "
CR	MacOS	" <code>\r</code> "
CRLF	DOS/Windows	" <code>\r\n</code> "

Value

Invisibly returns the input `x`.

Author(s)

Stu Field

See Also

[read_adat\(\)](#), [is_intact_attr\(\)](#)

Other IO: [loadAdatsAsList\(\)](#), [parseHeader\(\)](#), [read_adat\(\)](#), [soma_adat](#)

Examples

```
# trim to 1 sample for speed
adat_out <- head(example_data, 1L)

# attributes must(!) be intact to write
is_intact_attr(adat_out)

write_adat(adat_out, file = tempfile(fileext = ".adat"))
```

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