Package 'SomaDataIO'

March 26, 2024

Type Package

Title Input/Output 'SomaScan' Data

Version 6.1.0

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/master/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://somalogic.github.io/SomaDataIO/, https://somalogic.com

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

Depends R (>= 4.1.0)

Imports cli, crayon, dplyr (>= 1.0.6), lifecycle (>= 1.0.0), magrittr (>= 2.0.1), methods, readxl (>= 1.3.1), tibble (>= 3.1.2), tidyr (>= 1.1.3), usethis (>= 2.0.1)

Suggests Biobase, ggplot2, knitr, purrr, recipes, rmarkdown, spelling, testthat (>= 3.0.0), withr

VignetteBuilder knitr

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R topics documented:

adat-helpers *Helpers to Extract Information from an ADAT*

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

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

Value

`getAdatVersion()`
: The key-value of the `Version` as a string.

`getSomaScanVersion()`
: The key-value of the `AssayVersion` as a string.

`getSignalSpace()`
: The key-value of the `SignalSpace` as a string.

`checkSomaScanVersion()`
: Returns `NULL` (invisibly) if checks pass.

`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 *Add Attributes to* soma_adat *Objects*

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.atts)
```

Arguments

data	The *receiving* data.frame object for new attributes.
new.atts	A *named* 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.atts grafted on to it. Existing attribute names are *not* over-written.

Author(s)

Stu Field

See Also

attr(), setdiff()

addClass *Add a Class to an Object*

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
```

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	Examp
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\\.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)

# 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 read_adat().
tbl	A tibble object containing analyte target annotation information. This is usually the result of a call to getAnalyteInfo().

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

x	Typically a soma_adat class object created using read_adat().
n	Logical. Return an integer corresponding to the *length* of the features?
rm.controls	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.apt()

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_crtl <- getAnalytes(apts2, rm.controls = TRUE)
no_crtl
```

```
setdiff(apts2, no_crtl)

# 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
```

---

groupGenerics *Group Generics for* soma_adat *Class Objects*

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` *Are Attributes Intact?*

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

`adat`	A `soma_adat` object to query.

verbose — Logical. Should diagnostic information about failures be printed to the console? If the default, see interactive(), 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

adat	A soma_adat object (with intact attributes), typically created using read_adat().
bridge	The direction of the lift (i.e. bridge).
anno.tbl	**[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 assay 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 *Load ADAT files as a list*

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

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

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 `bind_rows()`, however this results in `NA`s 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)
```

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

`x`	A `soma_adat` object (with intact attributes), typically created using `read_adat()`.
`clin_data`	One of 2 options: • a data frame containing clinical variables to merge into `x`, or • a path to a file, typically a `*.csv`, containing clinical variables to merge into `x`.
`by`	A character vector of variables to join by. See `dplyr::left_join()` for more details.
`by_class`	If `clin_data` 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, `c(SampleId = "character")`. See `read.table()` for details about its `colClasses` argument, and also the examples below.
`...`	Additional parameters passed to `dplyr::left_join()`.

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 *SomaLogic ADAT parser*

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)
header
```

`pivotExpressionSet` *Convert to Long Format*

Description

Utility to convert an `ExpressionSet` class object from the "wide" data format to the "long" format via `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)
```

read_adat *Read (Load) SomaLogic ADATs*

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 *verbose* mode, printing relevant diagnostic call information to the console.
`...`	Additional arguments passed ultimately to `read.delim()`, 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

file	A path to an annotations file location. This is a sanctioned, versioned file provided by SomaLogic Operating Co., Inc. and should be an *unmodified* *.xlsx file.

Value

A 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 <- "~/Desktop/SomaScan_V4.1_7K_Annotated_Content_20210616.xlsx"
  anno_tbl <- read_annotations(file)

## 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

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

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)

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 seqid2apt(), a vector *of* SeqIds. For apt2seqid(), a character vector *containing* SeqIds. For matchSeqIds(), 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 *trailing* 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 matchSeqIds() 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(0).

getSeqIdMatches(): a $nx2$ 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.
- 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

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
getSomamers()	[Superseded]	getAnalytes()
getSomamerData()	[Superseded]	getAnalyteInfo()

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}.
```

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.

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()` 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 tbl[, j]. Default FALSE, ignored when accessing a column via tbl[j].
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 *Scale Transform* soma_adat *Columns/Rows*

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

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

Details

Performs the following operations (quickly):

Columns:

$$M_{nxp} = A_{nxp} * diag(v)_{pxp}$$

Rows:

$$M_{nxp} = diag(v)_{nxn} * A_{nxp}$$

Value

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

Note

This method in 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)
```

`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

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

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	`"\n"`
CR	MacOS	`"\r"`
CRLF	DOS/Windows	`"\r\n"`

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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