Package ‘TCGAutils’

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Title  TCGA utility functions for data management
Version 1.22.2
Description A suite of helper functions for checking and manipulating TCGA data including data obtained from the curatedTCGAData experiment package. These functions aim to simplify and make working with TCGA data more manageable. Exported functions include those that import data from flat files into Bioconductor objects, convert row annotations, and identifier translation via the GDC API.
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TCGAutils-package

**TCGAutils-package**

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**TCGAutils-package**

**TCGAutils: Helper functions for working with TCGA and MultiAssay-Experiment data**
Description

TCGAutils is a toolbox to work with TCGA specific datasets. It allows the user to manipulate and translate TCGA barcodes, conveniently convert a list of data files to GRangesList. Take datasets from GISTIC and return a SummarizedExperiment class object. The package also provides functions for working with data from the curatedTCGAData experiment data package. It provides convenience functions for extracting subtype metadata data and adding clinical data to existing MultiAssayExperiment objects.

Author(s)

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See Also

Useful links:

- Report bugs at https://github.com/waldronlab/TCGAutils/issues

builds

Utilities for working with HUMAN genome builds

Description

A few functions are available to search for build versions, either from NCBI or UCSC.

- translateBuild: translates between UCSC and NCBI build versions
- extractBuild: use grep patterns to find the first build within the string input
- uniformBuilds: replace build occurrences below a threshold level of occurrence with the alternative build
- correctBuild: Ensure that the build annotation is correct based on the NCBI/UCSC website. If not, use translateBuild with the indicated ‘style’ input
- isCorrect: Check to see if the build is exactly as annotated
Usage

translateBuild(from, to = c("UCSC", "NCBI"))

correctBuild(build, style = c("UCSC", "NCBI"))

isCorrect(build, style = c("UCSC", "NCBI"))

extractBuild(string, build = c("UCSC", "NCBI"))

uniformBuilds(builds, cutoff = 0.2, na = c("", "NA"))

Arguments

from character() A vector of build versions typically from genome() (e.g., "37"). The build vector must be homogenous (i.e., length(unique(x)) == 1L).

to character(1) The name of the desired build version (either "UCSC" or "NCBI"; default: "UCSC")

build A vector of build version names (default UCSC, NCBI)

style character(1) The annotation style, either 'UCSC' or 'NCBI'

string A single character string

builds A character vector of builds

cutoff numeric(1L) An inclusive threshold tolerance value for missing values and translating builds that are below the threshold

na character() The values to be considered as missing (default: c("", "NA"))

Details

The correctBuild function takes the input and ensures that the style specified matches the input. Otherwise, it will return the correct style for use with seqlevelsStyle. Currently, the function does not support patched builds (e.g., 'GRCh38.p13') Build names are taken from the website: https://www.ncbi.nlm.nih.gov/assembly/GCF_000001405.26/

Value

translateBuild: A character vector of translated genome builds

extractBuild: A character string of the build information available

uniformBuilds: A character vector of builds where all builds are identical `identical(length(unique(build)), 1L)`

correctBuild: A character string of the 'corrected' build name

isCorrect: A logical indicating if the build is exactly as annotated
Examples

```r
translateBuild("GRCh35", "UCSC")

correctBuild("grch38", "NCBI")
correctBuild("hg19", "NCBI")

isCorrect("GRCh38", "NCBI")
isCorrect("hg19", "UCSC")
```

```r
extractBuild("SCENA_p_TCGB29and30_SNP_N_GenomeWideSNP_6_G05_569110.nocnv_grch38.seg.txt")
```

```r
buildvec <- rep(c("GRCh37", "hg19"), times = c(5, 1))
uniformBuilds(buildvec)

navec <- c(rep(c("GRCh37", "hg19"), times = c(5, 1)), "NA")
uniformBuilds(navec)
```

---

**clinicalNames**

*Clinical dataset names in TCGA*

**Description**

A dataset of names for each of the TCGA cancer codes available. These names were obtained by the clinical datasets from `getFirehoseData`. They serve to subset the current datasets provided by `curatedTCGADataset`.

**Usage**

```r
data("clinicalNames")
```

**Format**

A `CharacterList` of names for 33 cancer codes

**Value**

The clinical dataset column names in TCGA as provided by the `RTCGAToolbox`
curatedTCGADataset

*Helper functions for managing MultiAssayExperiment from curatedTCGADataset*

**Description**

Additional helper functions for cleaning and uncovering metadata within a downloaded MultiAssayExperiment from curatedTCGADataset.

**Usage**

- `getSubtypeMap(multiassayexperiment)`
- `getClinicalNames(diseaseCode)`
- `TCGAsplitAssays(multiassayexperiment, sampleCodes = NULL, exclusive = FALSE)`
- `sampleTables(multiassayexperiment, vial = FALSE)`

**Arguments**

- `multiassayexperiment` A `MultiAssayExperiment` object
- `diseaseCode` A TCGA cancer code (e.g., "BRCA")
- `sampleCodes` character (default NULL) A string of sample type codes (refer to `data(sampleTypes)`: TCGAsplitAssays section)
- `exclusive` logical (default FALSE) Whether to return only assays that contain all codes in `sampleCodes`
- `vial` (logical default FALSE) whether to display vials in the table output

**Value**

- `getSubtypeMap`: A `data.frame` with explanatory names and their in-data variable names. They may not be present for all cancer types.
- `getClinicalNames`: A vector of common variable names that may be found across several cancer disease codes.

**getSubtypeMap**

provides a two column `data.frame` with interpreted names and in-data variable names. ‘Name’ usually refers to the `colData` row names a.k.a. the patientID.

**getClinicalNames**

provides a vector of common variable names that exist in the `colData` DataFrame of a curatedTCGADataset MultiAssayExperiment object. These variables are directly obtained from the BroadFirehose clinical data (downloaded with `getFirehoseData`) and tend to be present across cancer disease codes.
TCGAsplitAssays

Separates samples by indicated sample codes into different assays in a MultiAssayExperiment. Refer to the sampleTypes data object for a list of available codes. This operation generates n times the number of assays based on the number of sample codes entered. By default, all assays will be split by samples present in the data.

sampleTables

Display all the available samples in each of the assays

Examples

library(curatedTCGAData)

gbm <- curatedTCGAData("GBM", c("RPPA*", "CNA*"), version = "2.0.1", FALSE)

getSubtypeMap(gbm)
sampleTables(gbm)
TCGAsplitAssays(gbm, c("01", "10"))
getClinicalNames("COAD")

diseaseCodes

<table>
<thead>
<tr>
<th>Study.Abbreviation</th>
<th>Disease Code used in TCGA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Available</td>
<td>Cancer datasets available via curatedTCGAData</td>
</tr>
<tr>
<td>SubtypeData</td>
<td>Subtype curation data available via curatedTCGAData</td>
</tr>
<tr>
<td>Study.Name</td>
<td>The full length study name (i.e., type of cancer)</td>
</tr>
</tbody>
</table>

Value

The TCGA diseaseCodes table
findGRangesCols

Obtain minimum necessary names for the creation of a GRangesList object

Description
This function attempts to match chromosome, start position, end position and strand names in the given character vector. Modified helper from the GenomicRanges package.

Usage
findGRangesCols(
  df_colnames,
  seqnames.field = c("seqnames", "seqname", "chromosome", "chrom", "chr",
                     "chromosome_name", "seqid", "om"),
  start.field = "start",
  end.field = c("end", "stop"),
  strand.field = "strand",
  ignore.strand = FALSE
)

Arguments
- df_colnames: A character vector of names in a dataset
- seqnames.field: A character vector of the chromosome name
- start.field: A character vector that indicates the column name of the start positions of ranged data
- end.field: A character vector that indicates the end position of ranged data
- strand.field: A character vector of the column name that indicates the strand type
- ignore.strand: logical (default FALSE) whether to ignore the strand field in the data

Value
Index positions vector indicating columns with appropriate names

Examples
myDataColNames <- c("Start_position", "End_position", "strand",
                     "chromosome", "num_probes", "segment_mean")
findGRangesCols(myDataColNames)

Source
https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/tcga-study-abbreviations
generateMap

Description

This function helps create a sampleMap in preparation of a MultiAssayExperiment object. This especially useful when the sample identifiers are not very different, as in the case of TCGA barcodes. An idConverter function can be provided to truncate such sample identifiers and obtain patient identifiers.

Usage

```r
generateMap(
  experiments,
  colData,
  idConverter = identity,
  sampleCol,
  patientCol,
  ...
)
```

Arguments

- `experiments`: A named list of experiments compatible with the MultiAssayExperiment API
- `colData`: A data.frame of clinical data with patient identifiers as rownames
- `idConverter`: A function to be used against the sample or specimen identifiers to match those in the rownames of the colData (default NULL)
- `sampleCol`: A single string indicating the sample identifiers column in the colData dataset
- `patientCol`: A single string indicating the patient identifiers in colData, "row.names" extracts the colData row names
- `...`: Additional arguments to pass to the ‘idConverter’ function.

Value

A DataFrame class object of mapped samples and patient identifiers including assays

Author(s)

M. Ramos, M. Morgan, L. Schiffer
Examples

```r
## Minimal example
expList <- list(assay1 = matrix(1:6, ncol = 2L,
   dimnames = list(paste0("feature", 1:3), c("A-J", "B-J"))),
   assay2 = matrix(1:4, ncol = 2,
   dimnames = list(paste0("gene", 1:2), c("A-L", "B-L"))))

## Mock colData
myPheno <- data.frame(var1 = c("Yes", "No"), var2 = c("High", "Low"),
   row.names = c("a", "b"))

## A look at the identifiers
vapply(expList, colnames, character(2L))
rownames(myPheno)

## Use 'idConverter' to correspond sample names to patient identifiers
generateMap(expList, myPheno,
   idConverter = function(x) substr(tolower(x), 1L, 1L))
```

getFileName

Find the file names used in RTCGAToolbox

Description

Part of this function is from the RTCGAToolbox. It aims to extract the file name used inside of the getFirehoseData function. The arguments of the function parallel those in the getFirehoseData function. It is only available for select data types.

Usage

```r
getFileName(
   disease,
   runDate = "20160128",
   dataType = c("CNASNP", "CNVSNP", "CNAseq", "CNACGH", "Mutation")
)
```

Arguments

- **disease**: The TCGA cancer disease code, e.g., "COAD"
- **runDate**: The single string used in the getFirehoseData function (default "20160128")
- **dataType**: A single character vector (default "CNASNP") indicating the data type for which to get the source file name

Value

A single character file name
Examples

getFileName("COAD", dataType = "CNASNP")

Description

A small document for helper functions

Usage

.makeListRanges(x, gn)

getRangesOfSYMBOLS(x)

getRangesOfMir(x)

Arguments

x A SummarizedExperiment containing hsa miR IDs as rownames

 gn A GRanges object with some of its names found in x

Value

A list of length 2: unmapped (character vector) and mapped (GRanges)

list of length 2: "unmapped" is a character vector providing unmapped symbols, "mapped" is a
GRanges object with ranges of mapped symbols

ID-translation

Translate study identifiers from barcode to UUID and vice versa

Description

These functions allow the user to enter a character vector of identifiers and use the GDC API to
translate from TCGA barcodes to Universally Unique Identifiers (UUID) and vice versa. These
relationships are not one-to-one. Therefore, a data.frame is returned for all inputs. The UUID
to TCGA barcode translation only applies to file and case UUIDs. Two-way UUID translation is
available from "file_id" to "case_id" and vice versa. Please double check any results before using
these features for analysis. Case / submitter identifiers are translated by default, see the from_type
argument for details. All identifiers are converted to lower case.
Usage

UUIDtoBarcode(
  id_vector,
  from_type = c("case_id", "file_id", "aliquot_ids"),
  legacy = FALSE
)

UUIDtoUUID(id_vector, to_type = c("case_id", "file_id"), legacy = FALSE)

barcodeToUUID(barcodes, legacy = FALSE)

filenameToBarcode(filenames, legacy = FALSE, slides = FALSE)

UUIDhistory(id, endpoint = .HISTORY_ENDPOINT)

Arguments

- **id_vector** character() A vector of UUIDs corresponding to either files or cases (default assumes case_ids)
- **from_type** character(1) Either case_id or file_id indicating the type of id_vector entered (default "case_id")
- **legacy** logical(1) DEPRECATED; whether to search the legacy archives (default: FALSE)
- **to_type** character(1) The desired UUID type to obtain, can either be "case_id" (default) or "file_id"
- **barcodes** character() A vector of TCGA barcodes
- **filenames** character() A vector of file names usually obtained from a GenomicDataCommons query
- **slides** logical(1L) Whether the provided file names correspond to slides typically with an .svs extension. Note The barcodes returned correspond 1:1 with the filename inputs. Always triple check the output against the Genomic Data Commons Data Portal by searching the file name and comparing associated "Entity ID" with the submitter_id given by the function.
- **id** character(1) A UUID whose history of versions is sought
- **endpoint** character(1) Generally a constant pertaining to the location of the history api endpoint. This argument rarely needs to change.

Details

Based on the file UUID supplied, the appropriate entity_id (TCGA barcode) is returned. In previous versions of the package, the 'end_point' parameter would require the user to specify what type of barcode needed. This is no longer supported as entity_id returns the appropriate one.

Value

Generally, a data.frame of identifier mappings

UUIDhistory: A data.frame containing a list of associated UUIDs for the given input along with file_change status, data_release versions, etc.
ID-translation

Author(s)

Sean Davis, M. Ramos

Examples

## Translate UUIDs >> TCGA Barcode

```r
names <- c("b4bce3ff-7fcd-4849-880b-56f2b348ceac",
           "5ca9fa79-53bc-4e91-82cd-5715038ee23e",
           "b7c3e5ad-4ffc-4fc4-acbf-1dfcbd2e5382")

UUIDtoBarcode(names, from_type = "file_id")

UUIDtoBarcode("ae55b2d3-62a1-419e-9f9a-5ddfac356db4", from_type = "case_id")

UUIDtoBarcode("d85d8a17-8aee-49d3-8a03-8f13141c163b", "aliquot_ids")
```

## Translate file UUIDs >> case UUIDs

```r
names <- c("b4bce3ff-7fcd-4849-880b-56f2b348ceac",
           "5ca9fa79-53bc-4e91-82cd-5715038ee23e",
           "b7c3e5ad-4ffc-4fc4-acbf-1dfcbd2e5382")

UUIDtoUUID(names)
```

## Translate TCGA Barcode >> UUIDs

```r
fullBarcodes <- c("TCGA-B0-5117-11A-01D-1421-08",
                   "TCGA-B0-5094-11A-01D-1421-08",
                   "TCGA-E9-A295-10A-01D-A16D-09")

directory_path <- TCGAbarcode(fullBarcodes, sample = TRUE)

barcodeToUUID(directory_path)
```

library(GenomicDataCommons)

### Query CNV data and get file names

```r
cnv <- files() |> filter(
  ~ cases.project.project_id == "TCGA-COAD" &
  data_category == "Copy Number Variation" &
  data_type == "Copy Number Segment"
) |> results(size = 6)
```
filenameToBarcode(cnv$file_name)

### Query slides data and get file names

slides <- files() |> filter(
  ~ cases.project.project_id == "TCGA-BRCA" &
  cases.samples.sample_type == "Primary Tumor" &
  data_type == "Slide Image" &
  experimental_strategy == "Diagnostic Slide"
) |> results(size = 3)
filenameToBarcode(slides$file_name, slides = TRUE)

## Get the version history of a BAM file in TCGA-KIRC
UUIDhistory("0001801b-54b0-4551-8d7a-d66fb9429bf")

---

**imputeAssay**

*This function imputes assays values inside a MultiAssayExperiment*

### Description

These function allow the user to enter a MultiAssayExperiment and impute all the NA values inside assays.

### Usage

```r
imputeAssay(multiassayexperiment, i = 1, ...)
```

### Arguments

- `multiassayexperiment`
  - A MultiAssayExperiment with genes in the rows, samples in the columns
- `i`
  - A numeric, logical, or character vector indicating the assays to perform imputation on (default 1L)
- `...`
  - Arguments passed on to `impute::impute.knn`
- `data` An expression matrix with genes in the rows, samples in the columns
- `k` Number of neighbors to be used in the imputation (default=10)
- `rowmax` The maximum percent missing data allowed in any row (default 50%). For any rows with more than `rowmax`% missing are imputed using the overall mean per sample.
- `colmax` The maximum percent missing data allowed in any column (default 80%). If any column has more than `colmax`% missing data, the program halts and reports an error.
maxp  The largest block of genes imputed using the knn algorithm inside impute.knn (default 1500); larger blocks are divided by two-means clustering (recursively) prior to imputation. If maxp=p, only knn imputation is done.

rng.seed  The seed used for the random number generator (default 362436069) for reproducibility.

Value

MultiAssayExperiment with imputed assays values

Examples

```r
example(getSubtypeMap)
```

```r
## convert data to matrix and add as experiment
gbm <- c(gbm, RPPA_matrix = data.matrix(assay(gbm[["GBM_RPPAArray-20160128"]])))
imputeAssay(gbm, i = "RPPA_matrix")
```

---

**makeGRangesListFromCopyNumber**

*Make a GRangesList from TCGA Copy Number data*

Description

makeGRangesListFromCopyNumber allows the user to convert objects of class data.frame or DataFrame to a GRangesList. It includes additional features specific to TCGA data such as, hugo symbols, probe numbers, segment means, and ucsc build (if available).

Usage

```r
makeGRangesListFromCopyNumber(
  df, 
  split.field, 
  names.field = "Hugo_Symbol", 
  ...
)
```

Arguments

- `df` A data.frame or DataFrame class object. list class objects are coerced to data.frame or DataFrame.
- `split.field` A character vector of length one indicating the column to be used as sample identifiers
- `names.field` A character vector of length one indicating the column to be used as names for each of the ranges in the data
- `...` Additional arguments to pass on to makeGRangesListFromDataFrame
Value

A GRangesList class object

Examples

library(GenomicDataCommons)

manif <- files() |> |
  filter(~ cases.project.project_id == "TCGA-COAD" & |
    data_type == "Copy Number Segment") |> |
  manifest(size = 1)

fname <- gdcdata(manif$id)

barcode <- UUIDtoBarcode(names(fname), from_type = "file_id")
barcode <- barcode[["associated_entities.entity_submitter_id"]]

cndata <- read.delim(fname[[1L]], nrows = 10L)

cngrl <- makeGRangesListFromCopyNumber(cndata, split.field = "GDC_Aliquot", |
  keep.extra.columns = TRUE)

names(cngrl) <- barcode
GenomeInfoDb::genome(cngrl) <- extractBuild(fname[[1L]])
cngrl

makeGRangesListFromExonFiles

  Read exon-level expression files and create a GRangesList

Description

This function serves to read exon-level expression data. It works for exon quantification (raw |
counts and RPKM) and junction quantification (raw counts) file paths and represents such data as |
a GRangesList. The data files can be downloaded via the Genomic Data Commons (GDC) Legacy |
Archive.

Usage

makeGRangesListFromExonFiles(
  filepaths,
  sampleNames = NULL,
  fileNames = basename(filepaths),
  getBarcodes = TRUE,
  rangesColumn = "exon",
  nrows = Inf
)
Arguments

- **filepaths**: character() vector of file paths containing TCGA exon data usually obtained from the GDC.
- **sampleNames**: character() vector of TCGA barcodes to be used as names for the GRangesList output (default NULL).
- **fileNames**: character() vector of file names as downloaded from the Genomic Data Commons Legacy archive (default basename(filepaths)).
- **getBarcodes**: logical(1). Whether to query the GDC API with the filenameToBarcode and obtain the TCGA barcodes from the file names (default TRUE); see details.
- **rangesColumn**: character(1). The name of the column in the data containing the ranges information (default "exon"); see details.
- **nrows**: numeric(1). The number of rows to return from each of the files read in (all rows by default; default Inf).

Details

The rangesColumn name in the GDC data files is usually "exon" but can be changed with the rangesColumn argument, if different. To avoid programmatically obtaining TCGA barcodes from the GDC API, set the getBarcodes to FALSE. When getBarcodes is set to FALSE, the file names are used to name the elements of the GRangesList output.

Value

A GRangesList object

Author(s)

M. Ramos

Examples

```
## Load example file found in package
pkgDir <- system.file("extdata", package = "TCGAutils", mustWork = TRUE)
exonFile <- list.files(pkgDir, pattern = "cation\..txt\$", full.names = TRUE)

filePrefix <- "unc.edu.32741f9a-9fec-441f-96b4-e504e62c5362.1755371."

## Add actual file name manually (due to Windows OS restriction)
makeGRangesListFromExonFiles(exonFile,
   fileNames = paste0(filePrefix, basename(exonFile)),
   sampleNames = "TCGA-AA-3678-01A-01R-0905-07")
```
mergeColData  
*Take a MultiAssayExperiment and include curated variables*

**Description**

This function works on the colData of a `MultiAssayExperiment` object to merge curated variable columns or other clinical variables that would like to be added. It is recommended that the user run the scripts in the `MultiAssayExperiment-TCGA` repository that build the "enhanced" type of data but not necessary if using different clinical data. Please see the repository’s README for more information.

**Usage**

```r
mergeColData(MultiAssayExperiment, colData)
```

**Arguments**

- `MultiAssayExperiment`: A `MultiAssayExperiment` object
- `colData`: A `DataFrame` or `data.frame` to merge with clinical data in the `MultiAssayExperiment` object

**Value**

A `MultiAssayExperiment` object

**Examples**

```r
library(MultiAssayExperiment)
mergeColData(MultiAssayExperiment(), S4Vectors::DataFrame())
```

---

**oncoPrintTCGA**  
*OncoPrint for TCGA Mutation Assays*

**Description**

OncoPrint for TCGA Mutation Assays
oncoPrintTCGA

Usage

oncoPrintTCGA(
  multiassayexperiment,
  matchassay = "*_Mutation-*",
  variantCol = "Variant_Classification",
  brewerPal = "Set3",
  ntop = 25,
  incl.thresh = 0.01,
  rowcol = "Hugo_Symbol"
)

Arguments

multiassayexperiment
  A MultiAssayExperiment preferably from 'curatedTCGAData'
matchassay
  character(1) The name of the assay containing mutation data, this can be a pattern (e.g., "*_Mutation-*", the default)
variantCol
  character(1) The name of the metadata column containing the mutation categories, usually "Variant_Classification" in TCGA
brewerPal
  character(1) The name of the RColorBrewer::brewer.pal palette, (default: "Set3")
ntop
  integer(1) The number of the top N genes for displaying based on per-sample mutation frequency
incl.thresh
  double(1) The inclusion threshold for empirical mutations, mutations less frequent than this value will not be included
rowcol
  character(1) The name of the column in the metadata to annotate the rows with either "Hugo_Symbol" (default) or

Value

An oncoPrint plot of mutations

Examples

library(curatedTCGAData)

acc <- curatedTCGAData("ACC", "Mutation", version = "1.1.38", FALSE)

oncoPrintTCGA(acc)
sampleTypes  
Barcode Sample Type Table

Description
A dataset that contains the mappings for sample codes in the TCGA barcodes.

Usage
data("sampleTypes")

Format
A data frame with 19 rows and 3 variables:
- **Code**  Two digit code number found in the barcode
- **Definition**  Long name for the sample type
- **Short.Letter.Code**  Letter code for the sample type

Value
The TCGA sampleTypes table

Source
https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/sample-type-codes

simplifyTCGA  
Functions to convert rows annotations to ranges and RaggedExperiment to RangedSummarizedExperiment

Description
This group of functions will convert row annotations as either gene symbols or miRNA symbols to row ranges based on database resources 'TxDB' and 'org.Hs' packages. It will also simplify the representation of RaggedExperiment objects to RangedSummarizedExperiment.

Usage
simplifyTCGA(obj, keep.assay = FALSE, unmapped = TRUE)
symbolsToRanges(obj, keep.assay = FALSE, unmapped = TRUE)
mirToRanges(obj, keep.assay = FALSE, unmapped = TRUE)
CpGtoRanges(obj, keep.assay = FALSE, unmapped = TRUE)
qreduceTCGA(obj, keep.assay = FALSE, suffix = "_simplified")
Arguments

- `obj`: A `MultiAssayExperiment` object obtained from `curatedTCGAData`
- `keep.assay`: logical (default FALSE) Whether to keep the `SummarizedExperiment` assays that have been converted to `RangedSummarizedExperiment`
- `unmapped`: logical (default TRUE) Include an assay of data that was not able to be mapped in reference database
- `suffix`: character (default "_.simplified") A character string to append to the newly modified assay for `qreduceTCGA`.

Details

The original `SummarizedExperiment` containing either gene symbol or miR annotations is replaced or supplemented by a `RangedSummarizedExperiment` for those that could be mapped to `GRanges`, and optionally another `SummarizedExperiment` for annotations that could not be mapped to `GRanges`.

Value

A `MultiAssayExperiment` with any gene expression, miRNA, copy number, and mutations converted to `RangedSummarizedExperiment` objects

`qreduceTCGA`

Using `TxDb.Hsapiens.UCSC.hg19.knownGene` as the reference, `qreduceTCGA` reduces the data by applying either the `weightedmean` or `nonsilent` function (see below) to non-mutation or mutation data, respectively. Internally, it uses `RaggedExperiment::qreduceAssay()` to reduce the ranges to the gene-level.

`qreduceTCGA` will update `genome(x)` based on the NCBI reference annotation which includes the patch number, e.g., `GRCh37.p14`, as provided by the `seqlevelsStyle` setter, `seqlevelsStyle(gn) <- "NCBI"`. `qreduceTCGA` uses the NCBI genome annotation as the default reference.

```r
nonsilent <- function(scores, ranges, qranges) any(scores != "Silent")
```

RaggedExperiment mutation objects become a genes by patients `RangedSummarizedExperiment` object containing '1' if there is a non-silent mutation somewhere in the gene, and '0' otherwise as obtained from the `Variant_Classification` column in the data.

```r
weightedmean <- function(scores, ranges, qranges) {
  isects <- GenomicRanges::pintersect(ranges, qranges)
  sum(scores * BiocGenerics::width(isects)) / sum(BiocGenerics::width(isects))
}
```

"CNA" and "CNV" segmented copy number are reduced using a weighted mean in the rare cases of overlapping (non-disjoint) copy number regions.

These functions rely on `TxDb.Hsapiens.UCSC.hg19.knownGene` and `org.Hs.eh.db` to map to the 'hg19' NCBI build. Use the `liftOver` procedure for datasets that are provided against a different reference genome (usually 'hg18'). See an example in the vignette.
Examples

```r
library(curatedTCGAData)
library(GenomeInfoDb)

accmae <- curatedTCGAData(diseaseCode = "ACC",
assays = c("CNASNP", "Mutation", "miRNASeqGene", "GISTICT"),
version = "1.1.38",
dry.run = FALSE)

## update genome annotation
rex <- accmae["ACC_Mutation-20160128"]

## Translate build to "hg19"
tgenome <- vapply(genome(rex), translateBuild, character(1L))
genome(rex) <- tgenome

accmae["ACC_Mutation-20160128"] <- rex
simplifyTCGA(accmae)
```

---

**TCGAbarcode**

*Parse data from TCGA barcode*

**Description**

This function returns the specified snippet of information obtained from the TCGA barcode.

**Usage**

```
TCGAbarcode(
  barcodes,
  participant = TRUE,
  sample = FALSE,
  portion = FALSE,
  plate = FALSE,
  center = FALSE,
  index = NULL
)
```
TCGAbiospec

Arguments

- barcodes: A character vector of TCGA barcodes
- participant: Logical (default TRUE) participant identifier chunk
- sample: Logical (default FALSE) includes the numeric sample code of the barcode and the vial letter
- portion: Logical (default FALSE) includes the portion and analyte codes of the barcode
- plate: Logical (default FALSE) returns the plate value
- center: Logical (default FALSE) returns a matrix with the plate and center codes
- index: An optional numeric vector indicating barcode positions when split by the delimiter (i.e., hyphen '-') For example, an index of c(1, 2) corresponds to 'TCGA-ZZ' in TCGA-ZZ-A1A1.

Value

A character vector or data matrix of TCGA barcode information

Author(s)

M. Ramos

Examples

```r

## Patient identifiers
TCGAbiospec(barcodes)

## Sample identifiers
TCGAbiospec(barcodes, sample = TRUE)
```

Description

This function uses the full TCGA barcode to return a data frame of the data pertinent to laboratory variables such as vials, portions, analytes, plates and the center.

Usage

```r
TCGAbiospec(barcodes)
```
TCGApredinaryTumors

Arguments
barcodes A character vector of TCGA barcodes

Value
A dataframe with sample type, sample code, portion, plate, and center columns.

Author(s)
M. Ramos

Examples
example("TCGAbarecode")
TCGAbiospec(barcodes)

---

TCGApredinaryTumors Select primary tumors from TCGA datasets

Description
Tumor selection is decided using the sampleTypes data. For 'LAML' datasets, the primary tumor code used is "03" otherwise, "01" is used.

Usage
TCGApredinaryTumors(multiassayexperiment)

Arguments
multiassayexperiment A MultiAssayExperiment with TCGA data as obtained from curatedTCGData

Value
A MultiAssayExperiment containing only primary tumor samples

Examples
example(getSubtypeMap)
TCGApredinaryTumors(gbm)
TCGAsampleSelect

**Select samples from barcodes from lookup table**

**Description**

The TCGA barcode contains several pieces of information which can be parsed by the `TCGAbocode` function. To select a specific type of sample, enter the appropriate `sampleCode` argument from the lookup table. See lookup table in `data("sampleTypes")`. Barcode inputs can be a character vector or a `CharacterList` object.

**Usage**

```r
TCGAsampleSelect(barcodes, sampleCodes)
```

**Arguments**

- `barcodes`: Either a TCGA barcode vector or `CharacterList` containing patient identifiers, sample, portion, plate, and center codes.
- `sampleCodes`: Either a character or numeric vector of TCGA sample codes. See the `sampleType` dataset.

**Value**

A logical vector or `LogicalList` of the same length as 'barcodes' indicating sample type matches

**Examples**

```r
eval(example("TCGAbocode"))
TCGAsampleSelect(barcodes, c(11, 01))
```

---

trimColData

**Minimize the number of variables in colData**

**Description**

This function removes variables that have a high number of missing data and contain keywords.

**Usage**

```r
trimColData(
  multiassayexperiment,
  maxNAfrac = 0.2,
  keystring = c("portion", "analyte")
)
```
trimColData

Arguments

multiassayexperiment
  A MultiAssayExperiment object with colData

maxNAfrac
  (numeric default 0.2) A decimal between 0 and 1 to indicate the amount of NA values allowed per column

keystring
  (character) A vector of keywords to match and remove variables

Value

A MultiAssayExperiment object

Examples

example(getSubtypeMap)

(gbm_trimmed <- trimColData(gbm))

head(colData(gbm_trimmed))[1:5]
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