

Package ‘tximeta’

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Title Transcript Quantification Import with Automatic Metadata

Description Transcript quantification import from Salmon and other quantifiers with automatic attachment of transcript ranges and release information, and other associated metadata. De novo transcriptomes can be linked to the appropriate sources with linkedTxomes and shared for computational reproducibility.

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VignetteBuilder knitr, rmarkdown

Depends R (>= 4.1.0)

Imports SummarizedExperiment (>= 1.39.1), tximport, jsonlite, S4Vectors, IRanges, GenomicRanges (>= 1.61.1), AnnotationDbi, GenomicFeatures, txdbmaker, ensemblDb, BiocFileCache, AnnotationHub, Biostrings, tibble, Seqinfo, tools, utils, methods, Matrix

Suggests knitr, rmarkdown, testthat, tximportData (>= 1.37.5), org.Dm.eg.db, DESeq2, edgeR, limma, devtools, macrophage

URL <https://github.com/thelovelab/tximeta>

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tximeta-package	<i>Import transcript quantification with metadata</i>
-----------------	---

Description

The tximeta package imports abundances (TPM), estimated counts, and effective lengths from quantification tools, and will output a *SummarizedExperiment* (SE) object. For salmon and related quantification tools, `tximeta()` will attempt to identify the correct provenance of the reference transcripts and automatically attach the transcript ranges to the *SummarizedExperiment*, to facilitate downstream integration with other datasets. The automatic identification of reference transcripts should work out-of-the-box for human or mouse transcriptomes from the sources: GENCODE, Ensembl, or RefSeq. See also `importData()` for importing data when the reference transcripts were derived from a mix of annotated (e.g. GENCODE) and novel or custom transcripts.

Details

The main functions are:

- `tximeta()` - with key argument `coldata` specifying sample information
- `summarizeToGene()` - summarize quantification to gene-level
- `importData()` - import quantification with mixed reference transcript sets

All software-related questions should be posted to the Bioconductor Support Site:

<https://support.bioconductor.org>

The code can be viewed at the GitHub repository, which also lists the contributor code of conduct:

<https://github.com/thelovelab/tximeta>

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References

- *tximeta* reference:

Michael I. Love, Charlotte Soneson, Peter F. Hickey, Lisa K. Johnson N. Tessa Pierce, Lori Shepherd, Martin Morgan, Rob Patro (2020) *Tximeta: reference sequence checksums for provenance identification in RNA-seq*. PLOS Computational Biology. <https://doi.org/10.1371/journal.pcbi.1007664>

- *tximport* reference (the effective length GLM offset and counts-from-abundance):

Charlotte Soneson, Michael I. Love, Mark D. Robinson (2015) *Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences*. F1000Research. <http://doi.org/10.12688/f1000research.7563>

See Also

Useful links:

- <https://github.com/thelovelab/tximeta>

addCDS

Add CDS to rowRanges of a transcript-level SummarizedExperiment

Description

Working similarly to [addExons](#), this function can be used to add information about CDS (coding sequence) to the SummarizedExperiment object. As not all transcripts are coding, we have CDS information for only a subset of the rows of the object. For this reason, a logical indicator for whether the transcript is coding, `mcols(se)$coding`, is added as a column to the metadata columns of the `rowRanges` of the object. An additional column, `mcols(se)$cds`, is added to the metadata columns, which is a `GRangesList` with either the CDS regions (if the transcript is coding), or the original transcript/exon ranges (if the transcript is non-coding). This is necessary, as `GRangesList` cannot have NA elements. As with [addExons](#), this function is designed only for transcript-level objects.

Usage

```
addCDS(se)
```

Arguments

`se` the SummarizedExperiment

Value

a SummarizedExperiment

addExons	<i>Add exons to rowRanges of a transcript-level SummarizedExperiment</i>
----------	--

Description

After running tximeta, the SummarizedExperiment output will have GRanges representing the transcript locations attached as rowRanges to the object. These provide the start and end of the transcript in the genomic coordinates, and strand information. However, the exonic locations are not provided. This function, addExons, swaps out the GRanges with a GRangesList, essentially a list along the rows of the SummarizedExperiment, where each element of the list is a GRanges providing the locations of the exons for that transcript.

Usage

```
addExons(se)
```

Arguments

se the SummarizedExperiment

Details

This function is designed only for transcript-level objects. This "lack of a feature" reflects a belief on the part of the package author that it makes more sense to think about exons belonging to transcripts than to genes. For users desiring exonic information alongside gene-level objects, for example, which exons are associated with a particular gene, it is recommended to pull out the relevant GRangesList for the transcripts of this gene, while the object represents transcript-level data, such that the exons are still associated with transcripts.

For an example of addExons, please see the tximeta vignette.

Value

a SummarizedExperiment

addIds	<i>Add IDs to rowRanges of a SummarizedExperiment</i>
--------	---

Description

For now this function just works with SummarizedExperiments with Ensembl gene or transcript IDs. See example of usage in tximeta vignette. For obtaining multiple matching IDs for each row of the SummarizedExperiment set multiVals="list". See select for documentation on use of multiVals.

Usage

```
addIds(se, column, fromDb = FALSE, gene = FALSE, ...)
```

Arguments

se	the SummarizedExperiment
column	the name of the new ID to add (a column of the org package database or of the TxDb/EnsDb is fromDb=TRUE)
fromDb	logical, whether to use the TxDb/EnsDb that is associated with se. Default is FALSE, and an org package is used. Currently only implemented for transcript level (gene=FALSE). Column names can be viewed with columns(retrieveDb(se))
gene	logical, whether to map by genes or transcripts (default is FALSE). if rows are genes, and easily detected as such (ENSG or ENSMUSG), it will automatically switch to TRUE. if rows are transcripts and gene=TRUE, then it will try to use a gene_id column to map IDs to column
...	arguments passed to mapIds

Value

a SummarizedExperiment

Examples

```
example(tximeta)
library(org.Dm.eg.db)
se <- addIds(se, "REFSEQ", gene=FALSE)
```

getTximetaBFC	<i>Get or set the directory of the BiocFileCache used by tximeta</i>
---------------	--

Description

Running getTximetaBFC will report the saved directory, if it has been determined, or will return NULL. Running setTximetaBFC will ask the user to specify a BiocFileCache directory for accessing and saving TxDb sqlite files. Note that tximeta's BiocFileCache can be set by the environmental variable TXIMETA_HUB_CACHE, which will reset the cache location.

Usage

```
getTximetaBFC()

setTximetaBFC(dir, quiet = FALSE)
```

Arguments

dir	the location for tximeta's BiocFileCache. can be missing in which case the function will call file.choose for choosing location interactively
quiet	whether to suppress feedback message

Value

the directory of the BiocFileCache used by tximeta (or nothing, in the case of setTximetaBFC)

Examples

```
# getting the BiocFileCache used by tximeta
# (may not be set, which uses BiocFileCache default or temp directory)
getTximetaBFC()

# don't want to actually change user settings so this is not run:
# setTximetaBFC()
```

importData	<i>Import quantification across mixed reference transcripts</i>
------------	---

Description

The *oarfis* quantification tools allows a mix of `--annotated` reference transcripts (e.g. GENCODE, Ensembl) and `--novel` or custom transcripts (e.g. de novo assembled transcripts not present in the annotated set) to be used as the index for quantification. `importData()` and associated functions facilitate import, reference identification, and addition of metadata across annotated and/or novel transcripts. The `importData()` function alone imports the data, while inspection of the recognized digests and updating of transcript metadata is handled by subsequent functions (listed in *See also* section below).

Usage

```
importData(coldata, type = "oarfish", quiet = FALSE, ...)
```

Arguments

<code>coldata</code>	data.frame with columns files and names as in <code>tximeta()</code>
<code>type</code>	what quantifier was used (see <code>tximport::tximport()</code>), for now <code>importData()</code> works for "oarfish" files
<code>quiet</code>	whether to suppress printed messages
<code>...</code>	arguments passed to <code>tximport::tximport()</code>

Value

an un-ranged SummarizedExperiment (SE) object, for use with subsequent functions described in *See also* section

See Also

`inspectDigests()` and `updateMetadata()` for subsequent tasks of inspecting digest matches and updating metadata, respectively. `makeLinkedTxome()` can be used to add custom metadata into the registry used for inspecting digests and then updating transcript data. A user may follow the workflow `importData() > inspectDigests() > makeLinkedTxome() > inspectDigests() > updateMetadata()`. See also `makeLinkedTxpData()` for a lightweight alternative of linking *GRanges* metadata to a digest.

Examples

```
# oarfish files using a mix of --annotated and --novel transcripts
dir <- system.file("extdata/oarfish", package="tximportData")
names <- paste0("rep", 2:4)
files <- file.path(dir, paste0("sgnex_h9_", names, ".quant.gz"))
coldata <- data.frame(files, names)

# returns an un-ranged SE object
se <- importData(coldata, type="oarfish")
```

inspectDigests

Inspect digest matches from importData() imported data

Description

This function takes as input a *SummarizedExperiment* as output by `importData()` and returns a tibble with information about the digest-match status of two indices (annotated and novel), with respect to *tximeta* metadata. Inspection of index digests can be run iteratively, checking if the digests used in the mixed reference transcript set have a match against 1) pre-computed digests representing standard annotated sets (e.g. GENCODE, Ensembl, etc.) or 2) digests added by the user to a local registry with `makeLinkedTxome()` (GTF file) or `makeLinkedTxpData` (*GRanges*-based metadata). Optional columns may be added if specified by `fullDigest=TRUE` (include the full digest) and/or `count=TRUE` (add matching transcript ID counts per index). Following inspection, one can run `updateMetadata()` to automatically update the transcript metadata using the sources indicated by this function.

Usage

```
inspectDigests(
  se,
  type = "oarfish",
  prefer = c("txome", "txpdata", "precomputed"),
  fullDigest = FALSE,
  count = FALSE
)
```

Arguments

<code>se</code>	the <i>SummarizedExperiment</i> output by <code>importData()</code> , or alternatively just <code>metadata(se)\$quantInfo</code> a list of metadata information from the quantification tool (assuming annotated and novel indices both used)
<code>type</code>	what quantifier was used (see <code>tximport::tximport()</code>)
<code>prefer</code>	vector of length up to 3, giving the preferred order of <i>tximeta</i> 's transcript registries to when finding matches, with elements: <code>txome</code> : <code>linkedTxome</code> , <code>txpdata</code> : <code>linkedTxpData</code> , <code>precomputed</code> : the pre-computed digests in <i>tximeta</i>
<code>fullDigest</code>	whether to include the full digest string in the output, in addition to the shortened 6-char version
<code>count</code>	whether to count the number of matching transcripts ID to each index (only possible for those indices that have matching metadata). Counting requires loading transcript data, either from locally cached databases or from GTF files.

Value

a 2-row tibble of the annotated and novel index, their matching information if available (source, organism, release), for matches, whether it is a linkedTxome or a linkedTxpData (both 'FALSE' for pre-computed) and a small 6 character version of the digest itself.

Examples

```
example(importData)
# now we have an `se` created by importData()...
inspectDigests(se)
# can then update the registry via makeLinkedTxome() and re-run inspection
```

linkedTxome	<i>Make and load linked transcriptomes (linked GTF and FASTA)</i>
-------------	---

Description

makeLinkedTxome() reads the digest associated with a salmon index at indexDir, and persistently links it to metadata (alternatively the digest string itself and an indexName can be provided). Linked metadata includes key information about the transcriptome, including the source, organism, release, and genome (these are custom character strings), as well as the locations (e.g. local, HTTP, or FTP) for one or more fasta files and one gtf file. loadLinkedTxome() loads this information from a JSON file. See *Details*.

Usage

```
makeLinkedTxome(
  digest = NULL,
  indexName,
  indexDir = NULL,
  source,
  organism,
  release,
  genome,
  fasta,
  gtf,
  write = TRUE,
  jsonFile
)

loadLinkedTxome(jsonFile)
```

Arguments

digest	the full digest as character string, (this or indexDir is required, only one should be specified)
indexName	a name for the index when storing the linkedTxome, required if providing the digest string, suggest using the basename of the FASTA file and the software used, e.g. "gencode.vXX_salmon-0.XX.Y"

indexDir	the local path to the salmon index (this or digest is required, only one should be specified)
source	the source of transcriptome (e.g. "de-novo"). Note: if you specify "GENCODE" or "Ensembl", this will trigger behavior by tximeta that may not be desired: e.g. attempts to download canonical transcriptome data from AnnotationHub (unless useHub=FALSE when running tximeta) and parsing of Ensembl GTF using ensemblDb (which may fail if the GTF file has been modified). For transcriptomes that are defined by local GTF files, it is recommended to use the terms "LocalGENCODE" or "LocalEnsembl". Setting "LocalEnsembl" will also strip version numbers from the FASTA transcript IDs to enable matching with the Ensembl GTF.
organism	organism (e.g. "Homo sapiens")
release	release number (e.g. "27")
genome	genome (e.g. "GRCh38", or "none")
fasta	location(s) for the FASTA transcript sequences (of which the transcripts used to build the index is equal or a subset). This can be a local path, or an HTTP or FTP URL
gtf	location for the GTF/GFF file (of which the transcripts used to build the index is equal or a subset). This can be a local path, or an HTTP or FTP URL. While the fasta argument can take a vector of length greater than one (more than one FASTA file containing transcripts used in indexing), the gtf argument has to be a single GTF/GFF file. This can also be a serialized GRanges object (location of a .rds file) imported with rtracklayer. If transcripts were added to a standard set of reference transcripts (e.g. fusion genes, or pathogen transcripts), it is recommended that the tximeta user would manually add these to the GTF/GFF file, and post the modified GTF/GFF publicly, such as on Zenodo. This enables consistent annotation and downstream annotation tasks, such as by summarizeToGene() .
write	logical, should a JSON file be written out which documents the transcriptome digest and metadata? (default is TRUE)
jsonFile	the path to the json file for the linkedTxome

Details

`makeLinkedTxome()` links the information about the transcriptome used for quantification in two ways:

1. the function will store a record in tximeta's cache such that future import of quantification data will automatically access and parse the GTF as if the transcriptome were one of those automatically detected by tximeta. Then all features of tximeta (e.g. summarization to gene, programmatic adding of IDs or metadata) will be available;
2. it will by default write out a JSON file that can be shared, or posted online, and which can be read by `loadLinkedTxome()` which will store the information in tximeta's cache. This should make the full quantification-import pipeline computationally reproducible / auditable even for transcriptomes which differ from those provided by references (GENCODE, Ensembl, RefSeq).

For further details please see the "Linked transcriptomes" section of the tximeta vignette.

This function can be used in combination with `inspectDigests()` and oarfish data from `importData()`, when multiple reference transcript sets have been indexed. See also `makeLinkedTxpData()`.

Value

nothing, the function is run for its side effects

Examples

```
# point to a salmon quantification file with an additional artificial transcript
dir <- system.file("extdata/salmon_dm", package="tximportData")
file <- file.path(dir, "SRR1197474.plus", "quant.sf")
coldata <- data.frame(files=file, names="SRR1197474", sample="1",
                      stringsAsFactors=FALSE)

# now point to the salmon index itself to create a linkedTxome
# as the index will not match a known txome
indexDir <- file.path(dir, "Dm.BDGP6.22.98.plus_salmon-0.14.1")

# point to the source FASTA and GTF:
baseFTP <- "ftp://ftp.ensembl.org/pub/release-98/fasta/drosophila_melanogaster/"
fastaFTP <- c(
  paste0(baseFTP,
    c("cdna/Drosophila_melanogaster.BDGP6.22.cdna.all.fa.gz",
      "ncrna/Drosophila_melanogaster.BDGP6.22.ncrna.fa.gz")),
  "extra_transcript.fa.gz"
)
gtfPath <- file.path(dir, "Drosophila_melanogaster.BDGP6.22.98.plus.gtf.gz")

# now create a linkedTxome, linking the salmon index to its FASTA and GTF sources
makeLinkedTxome(indexDir=indexDir, source="LocalEnsembl", organism="Drosophila melanogaster",
                release="98", genome="BDGP6.22", fasta=fastaFTP, gtf=gtfPath, write=FALSE)

# to clear the entire linkedTxome table
# (don't run unless you want to clear this table!)
# bfcloc <- getTximetaBFC()
# bfc <- BiocFileCache(bfcloc)
# bfcremove(bfc, bfcquery(bfc, "linkedTxomeTbl")$rid)
```

linkedTxpData

Make linked transcript data (linked GRanges)

Description

linkedTxpData allows the user to save relevant *GRanges* transcript data for identifying and updating transcript metadata in a persistent manner across R sessions. It can be used in combination with `inspectDigests()` and `updateMetadata()`. This is a lightweight version of linkedTxome (see `makeLinkedTxome()`), which requires specifying a GTF file for building a *TxDB* and optionally a FASTA file for sequence retrieval.)

Usage

```
makeLinkedTxpData(
  digest,
  digestType = "sha256",
  indexName,
```

```
txpData,
source,
organism,
release,
genome
)
```

Arguments

digest	character string of the full digest of the reference transcripts, see inspectDigests() with fullDigest=TRUE
digestType	character string of the digest, default "sha256"
indexName	a name for the index when storing the linkedTxpData,
txpData	<i>GRanges</i> providing information about ranges representing the transcript sequences linked to digest
source	the source of transcriptome, e.g. denovo. See makeLinkedTxome() for more information on specifying source
organism	organism (e.g. "Homo sapiens")
release	release number (e.g. "27")
genome	genome (e.g. "GRCh38", or "none")

Details

The txpData object is saved in the getTximetaBFC() location, appended with a 32-character substring of digest. The tibble listing all linkedTxpData is named linkedTxpDataTbl and is listed in the same location.

Value

nothing, the function is run for its side effects

Examples

```
novel <- data.frame(seqnames = paste0("chr", rep(1:22, each=500)),
  start = 1e6 + 1 + 0:499 * 1000, end = 1e6 + 1 + 0:499 * 1000 + 1000 - 1,
  strand = "+", tx_name = paste0("novel", 1:(22*500)),
  gene_id = paste0("novel_gene", rep(1:(22*10), each=500)),
  type = "protein_coding")
novel_gr <- as(novel, "GRanges")
names(novel_gr) <- novel$tx_name

makeLinkedTxpData(
  digest = "43158f2c8e88e3acd77c22aee557625a6f1b6a5038cfc7deb5e64903892d8070",
  digestType = "sha256",
  indexName = "my_novel_txps",
  txpData = novel_gr,
  source = "novel", organism="Homo sapiens",
  release="v1", genome="GRCh38"
)

# to clear the entire linkedTxome table
# (don't run unless you want to clear this table!)
# bfcloc <- getTximetaBFC()
```

```
# bfc <- BiocFileCache(bfcloc)
# bfcremove(bfc, bfcquery(bfc, "linkedTxpDataTbl")$rid)
```

makeDGEList	<i>Make a DGEList from tximeta output</i>
-------------	---

Description

A simple wrapper function for constructing a DGEList for use with edgeR. See vignette for an example. Requires installation of the edgeR package from Bioconductor.

Usage

```
makeDGEList(se)
```

Arguments

se a SummarizedExperiment produced by tximeta

Value

a DGEList

retrieveCDNA	<i>Retrieve the cDNA transcript sequence for a SummarizedExperiment</i>
--------------	---

Description

This helper function retrieves the cDNA sequence of the transcripts used for expression quantification. This function either downloads or loads the transcript sequence from cache, it does not re-order or check against the rows of the SummarizedExperiment (which could be already summarized to genes for example).

Usage

```
retrieveCDNA(se, quiet = FALSE)
```

Arguments

se the SummarizedExperiment
quiet logical, suppress messages

Value

a DNASTringSet object

Examples

```
## Not run:
# this example is not run because it requires access to Ensembl ftp
example(tximeta)
cdna <- retrieveCDNA(se)

## End(Not run)
```

retrieveDb

Retrieve the TxDb or EnsDb associated with a SummarizedExperiment

Description

SummarizedExperiment objects returned by `tximeta` have associated TxDb or EnsDb databases which are cached locally and used to perform various metadata related tasks. This helper function retrieves the database itself for the user to perform any additional operations.

Usage

```
retrieveDb(se)
```

Arguments

`se` the SummarizedExperiment

Value

a database object

Examples

```
example(tximeta)
edb <- retrieveDb(se)
```

splitSE

Split SummarizedExperiment by gene categories

Description

Construct a new SummarizedExperiment by splitting one of the assays into a list of assays, each of which contains features of a given 'type'. It is assumed that there is a one-to-one correspondence between feature sets of different types; for example, these can be spliced and unspliced variants of the same transcripts. The type of each feature in the original SummarizedExperiment, and the correspondence between the features of different types, are given in a `data.frame`.

Usage

```
splitSE(se, splitDf, assayName)
```

Arguments

<code>se</code>	A SummarizedExperiment object.
<code>splitDf</code>	A data.frame with feature IDs. Each column represents a separate feature type, and the features in a given row are considered representatives of the same feature (and will be represented as one feature in the output object).
<code>assayName</code>	A character scalar, indicating the assay of <code>se</code> that will be split. Must be one of <code>assayNames(se)</code> .

Value

A SummarizedExperiment object with the same columns as the input object, and the same number of assays as the number of columns in `splitDf`. The assays will be named by the column names of `splitDf`. The `colData` and `metadata` of the input SummarizedExperiment object are copied to the output object. The row names are set to the feature IDs in the first column of `splitDf`.

Examples

```
se <- SummarizedExperiment::SummarizedExperiment(
  assays = S4Vectors::SimpleList(
    counts = as(matrix(1:15, nrow = 5), "sparseMatrix"),
    logcounts = log2(matrix(1:15, nrow = 5))
  ),
  colData = S4Vectors::DataFrame(sID = paste0("S", 1:3),
                                condition = c("A", "A", "B")),
  metadata = list(md1 = "annotation")
)
rownames(se) <- paste0("G", 1:5)
colnames(se) <- paste0("P", 1:3)
splitDf <- data.frame(spliced = c("G1", "G2", "G6"),
                     unspliced = c("G3", "G5", "G4"),
                     stringsAsFactors = FALSE)

splse <- splitSE(se = se, splitDf = splitDf, assayName = "counts")
```

summarizeToGene, SummarizedExperiment-method

Summarize estimated quantities to gene-level

Description

Summarizes abundances, counts, lengths, (and inferential replicates or variance) from transcript-to gene-level. Transcript IDs are stored as a CharacterList in the `mcols` of the output object. This function operates on SummarizedExperiment objects, and will automatically access the relevant TxDb (by either finding it in the BiocFileCache or by building it from an ftp location). This function uses the tximport package to perform summarization, where a method is defined that works on simple lists.

Usage

```
## S4 method for signature 'SummarizedExperiment'
summarizeToGene(
  object,
  assignRanges = c("range", "abundant"),
  varReduce = FALSE,
  skipRanges = FALSE,
  ...
)
```

Arguments

<code>object</code>	a <code>SummarizedExperiment</code> produced by <code>tximeta</code>
<code>assignRanges</code>	"range" or "abundant", this argument controls the way that the <code>rowRanges</code> of the output object are assigned (note that this argument does not affect data aggregation at all). The default is to just output the entire range of the gene, i.e. the leftmost basepair to the rightmost basepair across all isoforms. Alternatively, for expressed genes, one can obtain the start and end of the most abundant isoform (averaging over all samples). Non-expressed genes will have range-based positions. For abundant, for expressed genes, the name of the range-assigned isoform, <code>max_prop</code> (maximum isoform proportion), and <code>iso_prop</code> (numeric values for isoform proportions) are also returned in <code>mcols</code>
<code>varReduce</code>	whether to reduce per-sample inferential replicates information into a matrix of sample variances <code>variance</code> (default <code>FALSE</code>)
<code>skipRanges</code>	whether to skip making use of, or outputting, <code>rowRanges</code> (default <code>FALSE</code>)
<code>...</code>	arguments passed to <code>tximport</code>

Value

a `SummarizedExperiment` with summarized quantifications and transcript IDs as a `CharacterList` in the `mcols`

Examples

```
example(tximeta)
gse <- summarizeToGene(se)
```

tximeta

Import transcript quantification with metadata

Description

`tximeta` leverages the digest of the reference transcripts that were indexed in order to identify metadata from the output of quantification tools. A computed digest (a hash value) can be used to uniquely identify the collection of reference sequences, and associate the dataset with other useful metadata. After identification, `tximeta` uses a number of core Bioconductor packages (`GenomicFeatures`, `ensembldb`, `AnnotationHub`, `Seqinfo`, `BiocFileCache`) to automatically populate metadata for the user.

Usage

```
tximeta(
  coldata,
  type = NULL,
  txOut = TRUE,
  skipMeta = FALSE,
  skipSeqinfo = FALSE,
  useHub = TRUE,
  markDuplicateTxps = FALSE,
  cleanDuplicateTxps = FALSE,
  customMetaInfo = NULL,
  skipFtp = FALSE,
  ...
)
```

Arguments

<code>coldata</code>	a data.frame with at least two columns (others will propagate to object): • <code>files</code> - character, paths of quantification files • <code>names</code> - character, sample names if <code>coldata</code> is a vector, it is assumed to be the paths of quantification files and unique sample names are created
<code>type</code>	what quantifier was used, see <code>tximport::tximport()</code>
<code>txOut</code>	whether to output transcript-level data. <code>tximeta</code> is designed to have transcript-level output with salmon, so default is TRUE, and it's recommended to use <code>summarizeToGene</code> following <code>tximeta</code> for gene-level summarization. For an alevin file, <code>tximeta</code> will import the gene level counts ignoring this argument (alevin produces only gene-level quantification).
<code>skipMeta</code>	whether to skip metadata generation (e.g. to avoid errors if not connected to internet). This calls <code>tximport</code> directly and so either <code>txOut=TRUE</code> or <code>tx2gene</code> should be specified.
<code>skipSeqinfo</code>	whether to skip the addition of <code>Seqinfo</code> , which requires an internet connection to download the relevant chromosome information table from UCSC
<code>useHub</code>	whether to first attempt to download a <code>TxDb/EnsDb</code> object from AnnotationHub, rather than creating from a GTF file from FTP (default is TRUE). If FALSE, it will force <code>tximeta</code> to download and parse the GTF
<code>markDuplicateTxps</code>	whether to mark the status (<code>hasDuplicate</code>) and names of duplicate transcripts (duplicates) in the <code>rowData</code> of the <code>SummarizedExperiment</code> output. Subsequent summarization to gene level will keep track of the number of transcripts sets per gene (<code>numDupSets</code>)
<code>cleanDuplicateTxps</code>	whether to try to clean duplicate transcripts (exact sequence duplicates) by replacing the transcript names that do not appear in the GTF with those that do appear in the GTF
<code>customMetaInfo</code>	the relative path to a custom metadata information JSON file, relative to the paths in files of <code>coldata</code> . For example, <code>customMetaInfo="meta_info.json"</code> would indicate that in the same directory as the quantification files in <code>files</code> , there are custom metadata information JSON files. These should contain the SHA-256 hash of the reference transcripts with the <code>index_seq_hash</code> tag (see details in vignette).

skipFtp	whether to avoid ftp:// in case of firewall, default is FALSE
...	arguments passed to tximport

Details

Most of the code in tximeta works to add metadata and transcript ranges when the quantification was performed with salmon or related tools. However, tximeta can be used with any quantification type that is supported by `tximport::tximport()`, where it will return a non-ranged SummarizedExperiment. For other quantification tools see also the `customMetaInfo` argument below. This behavior can also be triggered with `skipMeta=TRUE`.

tximeta performs a lookup of the digest (or hash value) of the index stored in an auxiliary information directory of the quantification tool's output against a database of known transcriptomes, which is stored within the tximeta package (`extdata/hashtable.csv`) and is continually updated to match Ensembl and GENCODE releases, with updates pushed to Bioconductor current release branch. In addition, tximeta performs a lookup of the digest against a locally stored table of linkedTxome references, see `makeLinkedTxome()`. If tximeta detects a match in either source, it will automatically populate the transcript locations, the transcriptome release, the genome with correct chromosome lengths, and connect the SE object to locally cached derived metadata. tximeta also facilitates automatic summarization of transcript-level quantifications to the gene-level via `summarizeToGene``` without the need to manually build the correct `tx2gene` table for the reference used for indexing.

tximeta on the first run will ask where the `BiocFileCache::BiocFileCache()` location for this package (*tximeta*) should be kept, either using a default location or a temporary directory. At any point, the user can specify a location using `setTximetaBFC()` and this choice will be saved for future sessions. Multiple users can point to the same BiocFileCache, such that transcript databases (TxDb or EnsDb) associated with certain salmon indices and linkedTxomes can be accessed by different users without additional effort or time spent downloading and building the relevant TxDb / EnsDb. Note that, if the TxDb or EnsDb is present in AnnotationHub, tximeta will use this object instead of downloading and building a TxDb/EnsDb from GTF (to disable this set `useHub=FALSE`).

In order to allow that multiple users can read and write to the same location, one should set the BiocFileCache directory to have group write permissions (`g+w`).

Value

a SummarizedExperiment with metadata on the `rowRanges`. (if the hashed digest in the salmon or Sailfish index does not match any known transcriptomes, or any locally saved linkedTxome, tximeta will just return a non-ranged SummarizedExperiment)

Examples

```
# point to a salmon quantification file:
dir <- system.file("extdata/salmon_dm", package="tximportData")
files <- file.path(dir, "SRR1197474", "quant.sf")
coldata <- data.frame(files, names="SRR1197474", condition="A", stringsAsFactors=FALSE)

# normally we would just run the following which would download the appropriate metadata
# se <- tximeta(coldata)

# for this example, we instead point to a local path where the GTF can be found
# by making a linkedTxome:
indexDir <- file.path(dir, "Dm.BDGP6.22.98_salmon-0.14.1")
fastaFTP <- c("ftp://ftp.ensembl.org/pub/release-98/fasta/drosophila_melanogaster/cdna/Drosophila_melanogaster",
             "ftp://ftp.ensembl.org/pub/release-98/fasta/drosophila_melanogaster/ncrna/Drosophila_melanogaster")
```

```
gtfPath <- file.path(dir, "Drosophila_melanogaster.BDGP6.22.98.gtf.gz")
makeLinkedTxome(indexDir=indexDir, source="LocalEnsembl", organism="Drosophila melanogaster",
                release="98", genome="BDGP6.22", fasta=fastaFTP, gtf=gtfPath, write=FALSE)
se <- tximeta(coldata)

# to clear the entire linkedTxome table
# (don't run unless you want to clear this table!)
# bfcloc <- getTximetaBFC()
# bfc <- BiocFileCache(bfcloc)
# bfcremove(bfc, bfcquery(bfc, "linkedTxomeTbl")$rid)
```

updateMetadata

Update transcript metadata for importData() imported data

Description

This function takes as input a *SummarizedExperiment* as output by `importData()`, and will update the metadata on the transcripts when possible (updating `rowData` and/or `rowRanges` depending on the value of `ranges`). `importData()` uses metadata pulled from digest matches in registries used by *tximeta* (linkedTxome, linkedTxpData, and the pre-computed digests). Additionally, *GRanges* or *data.frame*-type data can be provided on a one-time basis via the argument `txpData`, which will annotate transcripts with `index="user"`. See `inspectDigests()` for how to inspect which indices have matching digests, and how to link data to local metadata in a persistent manner.

Usage

```
updateMetadata(
  se,
  txpData = NULL,
  ranges = FALSE,
  prefer = c("txome", "txpdata", "precomputed"),
  order = c("annotated", "novel", "user"),
  key = c(annotated = "tx_name", novel = "tx_name", user = "tx_name")
)
```

Arguments

<code>se</code>	the <i>SummarizedExperiment</i> (SE) output by <code>importData()</code>
<code>txpData</code>	either <i>GRanges</i> or <i>data.frame</i> -type object to use if there is not a match based on digest. This is used on a one-time basis, and transcripts will be marked in metadata columns as <code>index = "user"</code> . See <code>makeLinkedTxome()</code> or <code>makeLinkedTxpData()</code> for persistent metadata storage/retrieval
<code>ranges</code>	logical, whether to add <code>rowRanges</code> (or just <code>rowData</code>)
<code>prefer</code>	vector of length up to 3, giving the preferred order of <i>tximeta</i> 's transcript registries to when finding matches, with elements: <code>txome</code> : linkedTxome, <code>txpdata</code> : linkedTxpData, <code>precomputed</code> : the pre-computed digests in <i>tximeta</i>
<code>order</code>	order of index, in which to update the metadata, by default the order is <code>annotation</code> , then <code>novel</code> , then <code>user</code> , info supplied here as <code>txpData</code>

key a named character vector of length 3. For each index (annotated, novel, and user) key is the name of the column to use for merging metadata with rownames(se). The user index corresponds to data provided here as txpData Defaults to "tx_name" which often matches the transcript names in GENCODE

Value

a *SummarizedExperiment* with new rowData, or a *RangedSummarizedExperiment* with new meta-data

Examples

```
example(importData)

# build custom novel GRanges data
library(GenomicRanges)
novel <- data.frame(
  seqnames = paste0("chr", rep(1:22, each=500)),
  start = 1e6 + 1 + 0:499 * 1000, end = 1e6 + 1 + 0:499 * 1000 + 1000 - 1,
  strand = "+", tx_name = paste0("novel", 1:(22*500)),
  gene_id = paste0("novel_gene", rep(1:(22*10), each=50)), type = "protein_coding"
)
novel_gr <- as(novel, "GRanges")
names(novel_gr) <- novel$tx_name

# now update the metadata + ranges:
## Not run:
# this requires connection to internet (will download GENCODE GTF via FTP)
se_with_ranges <- updateMetadata(
  se, txpData=novel_gr, ranges=TRUE
)
mcols(se_with_ranges)

## End(Not run)
```

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