Package 'BUSpaRse'

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Type Package

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Description The kallisto | bustools pipeline is a fast and modular set of tools to convert single cell RNA-seq reads in fastq files into gene count or transcript compatibility counts (TCC) matrices for downstream analysis. Central to this pipeline is the barcode, UMI, and set (BUS) file format. This package serves the following purposes: First, this package allows users to manipulate BUS format files as data frames in R and then convert them into gene count or TCC matrices. Furthermore, since R and Rcpp code is easier to handle than pure C++ code, users are encouraged to tweak the source code of this package to experiment with new uses of BUS format and different ways to convert the BUS file into gene count matrix. Second, this package can conveniently generate files required to generate gene count matrices for spliced and unspliced transcripts for RNA velocity. Here biotypes can be filtered and scaffolds and haplotypes can be removed, and the filtered transcriptome can be extracted and written to disk. Third, this package implements utility functions to get transcripts and associated genes required to convert BUS files to gene count matrices, to write the transcript to gene information in the format required by bustools, and to read output of bustools into R as sparses matrices.

BugReports https://github.com/BUStools/BUSpaRse/issues

URL https://github.com/BUStools/BUSpaRse

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`.get_velocity_files` *Generate RNA velocity files for GRanges*

Description

Generate RNA velocity files for GRanges

Usage

```
.get_velocity_files(
  gr,
  L,
  Genome,
  Transcriptome = NULL,
  out_path = ".",
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  transcript_version = "transcript_version",
```

```
  gene_version = "gene_version",
  version_sep = ".",
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  save_filtered_gtf = FALSE,
  compress_fa = FALSE,
  width = 80L
)
```

Arguments

gr	A GRanges object for gene annotation.
L	Length of the biological read. For instance, 10xv1: 98 nt, 10xv2: 98 nt, 10xv3: 91 nt, Drop-seq: 50 nt. If in doubt check read length in a fastq file for biological reads with the bash commands: If the fastq file is gzipped, then do `zcat your_file.fastq.gz | head` on Linux. If on Mac, then `zcat < your_file.fastq.gz | head`. Then you will see lines with nucleotide bases. Copy one of those lines and determine its length with `str_length` in R or `echo -n <the sequence> | wc -c` in bash. Which file corresponds to biological reads depends on the particular technology.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
Transcriptome	A XStringSet, a path to a fasta file (can be gzipped) of the transcriptome which contains sequences of spliced transcripts, or NULL. The transcriptome here will be concatenated with the intronic sequences to give one fasta file. When NULL, the transriptome sequences will be extracted from the genome given the gene annotation, so it will be guaranteed that transcript IDs in the transcriptome and in the annotation match. Otherwise, the type of transcript ID in the transcriptome must match that in the gene annotation supplied via argument X.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
style	Formatting of chromosome names. Use genomeStyles to check which styles are supported for your organism of interest and what those styles look like. This can also be a style supported for your organism different from the style used by the annotation and the genome. Then this style will be used for both the annotation and the genome. Can take the following values: **genome** If style of the annnotation is different from that of the genome, then the style of the genome will be used. **other** Custom style, need to manually ensure that the style in annotation matches that of the genome.

Ensembl Or UCSC or NCBI, whichever is supported by your species of interest.

`isoform_action` Character, indicating action to take with different transcripts of the same gene. Must be one of the following:

collapse First, the union of all exons of different transcripts of a gene will be taken. Then the introns will be inferred from this union. Only the flanked intronic sequences are affected; isoforms will always be taken into account for spliced sequences or exon-exon junctions.

separate Introns from different transcripts will be kept separate.

`exon_option` Character, indicating how exonic sequences should be included in the kallisto index. Must be one of the following:

full The full cDNA sequences, which include the full exonic sequences, will be used. This is the default.

junction Only the exon-exon junctions, with L-1 bases on each side of the junctions, will be used.

`transcript_id` Character vector of length 1. Tag in `attribute` field corresponding to transcript IDs. This argument must be supplied and cannot be NA or NULL. Will throw error if tag indicated in this argument does not exist.

`gene_id` Character vector of length 1. Tag in `attribute` field corresponding to gene IDs. This argument must be supplied and cannot be NA or NULL. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.

`transcript_version`

Character vector of length 1. Tag in `attribute` field corresponding to *transcript* version number. If your GTF file does not include transcript version numbers, or if you do not wish to include the version number, then use NULL for this argument. To decide whether to include transcript version number, check whether version numbers are included in the `transcripts.txt` in the `kallisto` output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

`gene_version` Character vector of length 1. Tag in `attribute` field corresponding to *gene* version number. If your GTF file does not include gene version numbers, or if you do not wish to include the version number, then use NULL for this argument. Unlike transcript version number, it's up to you whether to include gene version number.

`version_sep` Character to separate bewteen the main ID and the version number. Defaults to ".", as in Ensembl.

`transcript_biotype_col`

Character vector of length 1. Tag in `attribute` field corresponding to *transcript* biotype.

`gene_biotype_col`

Character vector of length 1. Tag in `attribute` field corresponding to *gene* biotype.

`transcript_biotype_use`
: Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, `retained_intron` is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See `data("ensembl_tx_biotypes")` for all available transcript biotypes from Ensembl.

`gene_biotype_use`
: Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See `data("cellranger_biotypes")` for gene biotypes the Cell Ranger reference uses. See `data("ensembl_gene_biotypes")` for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

`chrs_only`
: Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to `TRUE`. Only applicable to species found in `genomeStyles()`.

`save_filtered_gtf`
: Logical. If filtering type, biotypes, and/or chromosomes, whether to save the filtered `GRanges` as a GTF file.

`compress_fa`
: Logical, whether to compress the output fasta file. If `TRUE`, then the fasta file will be gzipped.

`width`
: Maximum number of letters per line of sequence in the output fasta file. Must be an integer.

Value

See `get_velocity_files`

`annots_from_fa_df` *Get genome annotation from Ensembl FASTA file*

Description

Ensembl FASTA files for RNA contain much of the information contained in GTF files, such as chromosome, genome assembly version, coordinates, strand, gene ID, gene symbol, and gene description. Given such a FASTA file, this function can extract all the genome annotation information and return a data frame or a `GRanges` object.

Usage

```
annots_from_fa_df(file)

annots_from_fa_GRanges(file)
```

Arguments

file	Path to the FASTA file to be read. The file can remain gzipped.

Value

annots_from_fa_df returns a data frame and annots_from_fa_GRanges returns GRanges.

A data frame with genome annotations.

Examples

```
fn <- system.file("testdata/fasta_test.fasta", package = "BUSpaRse")
annots_from_fa_df(fn)
annots_from_fa_GRanges(fn)
```

---

annot_circular *Transfer information about circular chromosomes between genome and annotation*

Description

Internal use, called after calling subset_annot.

Usage

```
annot_circular(Genome, annot)
```

Arguments

Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
annot	Genome annotation, an object of a class with a seqlevels method, such as GRanges, TxDb, and EnsDb.

Value

If neither genome nor annotation indicates which chromosome is circular, then the input will be returned unchanged. If only one of genome and annotation has such information, then it will be transferred to the one that does not. If both do have such information, the information from the genome will be transferred to the annotation if they're different.

cellranger_biotypes *Cell Ranger gene biotypes*

Description

In the GRCh38 Cell Ranger reference package, an Ensembl human GTF file is filtered by gene biotypes. This vector includes all gene biotypes included by this Cell Ranger reference package.

Usage

```
cellranger_biotypes
```

Format

A character vector with all Cell Ranger reference package gene biotypes.

Source

https://support.10xgenomics.com/single-cell-gene-expression/software/pipelines/latest/advanced/references

See Also

ensembl_gene_biotypes ensembl_tx_biotypes

check_char1 *Check that an object is a character vector of length 1*

Description

Just in case the user passes something with length more than 1 and messes up everything thanks to vectorization.

Usage

```
check_char1(x)
```

Arguments

x	Named vector of arguments to be checked.

Value

Error if x is not a character vector with length 1.

check_genome *Check for chromosomes in genome but not annotation*

Description

Check for chromosomes in genome but not annotation

Usage

```
check_genome(chrs_use, Genome)
```

Arguments

chrs_use	Character vector of names of chromosomes present in both the annotation and the genome.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.

Value

Nothing. Will emit message if the genome contains chromosomes absent from the annotation.

check_gff *Check inputs to tr2g_gtf and tr2g_gff3*

Description

This function validates inputs to tr2g_gtf and tr2g_gff3 and throws error early if some inputs are wrong.

Usage

```
check_gff(format, file, transcript_id, gene_id)
```

Arguments

format	Whether it's gtf or gff3.
file	Path to a GTF file to be read. The file can remain gzipped. Use getGTF from the biomartr package to download GTF files from Ensembl, and use getGFF from biomartr to download GFF3 files from Ensembl and RefSeq.

transcript_id	Character vector of length 1. Tag in attribute field corresponding to transcript IDs. This argument must be supplied and cannot be NA or NULL. Will throw error if tag indicated in this argument does not exist.
gene_id	Character vector of length 1. Tag in attribute field corresponding to gene IDs. This argument must be supplied and cannot be NA or NULL. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.

Value

Nothing, will throw error if there's a problem.

---

check_tag_present *Check that a tag is present in attribute field of GTF/GFF*

Description

The attribute field of GTF/GFF files are very complicated and is very inconsistent between sources. This function is to make sure that transcript and gene IDs can be extracted properly.

Usage

```
check_tag_present(tags_use, tags, error = TRUE)
```

Arguments

tags_use	The tags to be checked.
tags	The tags present in attribute field.
error	Whether to throw an error for absent tags. If FALSE, then a warning will be given.

Value

Error or warning if tag is absent.

check_tx *Check if transcript ID in transcriptome and annotation match*

Description

This function throws an error if transcript IDs in transcriptome and annotation do not overlap. If they do overlap, this function will give a message about transcript IDs that do not agree in the transcriptome and the annotation

Usage

```
check_tx(tx_annot, tx)
```

Arguments

tx_annot	Character vector of transcript IDs from the annotation.
tx	Character vector of transcript IDs from the transcriptome.

Value

Character vector of the overlapping transcript IDs.

dl_transcriptome *Download transcriptome from Ensembl*

Description

This function downloads the cDNA fasta file from specific version of Ensembl. It can also filter the fasta file by gene and transcript biotype and remove scaffolds and haplotypes.

Usage

```
dl_transcriptome(
  species,
  out_path = ".",
  type = c("vertebrate", "metazoa", "plant", "fungus", "protist"),
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  ensembl_version = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

species	Character vector of length 1, Latin name of the species of interest.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
type	Character, must be one of "vertebrate", "metazoa", "plant", "fungus" and "protist". Passing "vertebrate" will use the default www.ensembl.org host. Gene annotation of some common invertebrate model organisms, such as *Drosophila melanogaster*, are available on www.ensembl.org so for these invertebrate model organisms, "vertebrate" can be used for this argument. Passing values other than "vertebrate" will use other Ensembl hosts. For animals absent from www.ensembl.org, try "metazoa".
transcript_biotype_use	Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, `retained_intron` is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See `data("ensembl_tx_biotypes")` for all available transcript biotypes from Ensembl.
gene_biotype_use	Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See `data("cellranger_biotypes")` for gene biotypes the Cell Ranger reference uses. See `data("ensembl_gene_biotypes")` for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.
chrs_only	Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to `TRUE`. Only applicable to species found in `genomeStyles()`.
ensembl_version	Integer version number of Ensembl (e.g. 94 for the October 2018 release). This argument defaults to `NULL`, which will use the current release of Ensembl. Use `listEnsemblArchives` to see the version number corresponding to the Ensembl release of a particular date. The version specified here must match the version of Ensembl where the transcriptome used to build the kallisto index was downloaded. This only works for vertebrates and the most common invertebrate model organisms like *Drosophila melanogaster* and *C. elegans* (i.e. www.ensembl.org and its mirrors), not the other Ensembl sites for plants, protists, fungi, and metazoa.
verbose	Whether to display progress.
...	Other arguments passed to `tr2g_fasta`.

Value

Invisibly returns the path to the fasta file. The following files are written to disk, in the `out_path` directory:

species.genome.cdna.all.fa.gz The cDNA fasta file from Ensembl, from the specified version.

cdna_filtered.fa The filtered cDNA fasta file, only keeping the desired biotypes and without scaffolds and haplotypes (if `chrs_only = TRUE`). This file will not be written if all gene and transcript biotypes are used and scaffolds and haplotypes are not removed.

tr2g.tsv The transcript to gene file, without headers so can be directly used for `bustools`.

Examples

```
dl_transcriptome("Drosophila melanogaster", gene_biotype_use = "cellranger",
                 chrs_only = FALSE)
# Clean up
file.remove("Drosophila_melanogaster.BDGP6.32.cdna.all.fa.gz")
```

`EC2gene` *Map EC Index to Genes Compatible with the EC*

Description

In the output file `output.bus`, equivalence classes (EC) are denoted by an index, which is related to the set of transcripts the EC is compatible to in the output file `matrix.ec`. This function further relates the set of transcripts to the set of genes the EC is compatible to. This function first reads in `matrix.ec`, and then translates the transcripts into genes.

Usage

```
EC2gene(tr2g, kallisto_out_path, verbose = TRUE)
```

Arguments

`tr2g`	A Data frame with columns `gene` and `transcript`, in the same order as in the transcriptome index for `kallisto`.
`kallisto_out_path`	Path to the `kallisto bus` output directory.
`verbose`	Logical, whether to display progress.

Details

The data frame passed to `tr2g` can be generated from function `transcript2gene` in this package for any organism that has gene and transcript ID on Ensembl, or from the `tr2g_*` family of function. You no longer need to use this function before running `make_sparse_matrix`; the purpose of this function is to query which genes equivalence classes map to.

Calling this function is unnessary when working with gene count matrices. However, this function is useful for finding genes the ECs map to in TCC matrices, such as when finding species-specific ECs in mixed species datasets and identifying ECs mapped to known marker genes of cell types.

Value

A data frame with 3 columns:

EC_ind Index of the EC as appearing in the `matrix.ec` file.

EC A list column each element of which is a numeric vector of the transcripts in the EC corresponding to the EC index. To learn more about list columns, see the relevant section in the R for Data Science book.

gene A list column each element of which is a character vector of genes the EC maps to.

See Also

`transcript2gene`

Examples

```
# Load toy example for testing
toy_path <- system.file("testdata", package = "BUSpaRse")
load(paste(toy_path, "toy_example.RData", sep = "/"))
EC2gene(tr2g_toy, toy_path, verbose = FALSE)
```

`ensembl_gene_biotypes` *Gene biotypes from Ensembl*

Description

These vectors are here to make it easy to look up which biotypes are available for Ensembl without having to parse GTF and fasta files every time. See this page from Ensembl for what the biotypes mean.

Usage

```
ensembl_gene_biotypes
```

Format

A character vector with all Ensembl gene biotypes.

Source

This vector is all the unique gene biotypes in the Ensembl version 99 human GTF file.

See Also

ensembl_tx_biotypes cellranger_biotypes

ensembl_gff_mcols *These are the column names of the* mcols *when the Ensembl GTF file is read into R as a* GRanges*, including* gene_id*,* transcript_id*,* biotype*,* description*, and so on, and the mandatory tags like* ID*,* Name*, and* Parent*.*

Description

These are the column names of the mcols when the Ensembl GTF file is read into R as a GRanges, including gene_id, transcript_id, biotype, description, and so on, and the mandatory tags like ID, Name, and Parent.

Usage

```
ensembl_gff_mcols
```

Format

A character vector

Source

Ensembl version 99 human GFF3 file

ensembl_gtf_mcols *Tags in the attributes field of Ensembl GTF files*

Description

These are the column names of the mcols when the Ensembl GTF file is read into R as a GRanges, including gene_id, transcript_id, gene_biotype, transcript_biotype, description, and so on.

Usage

```
ensembl_gtf_mcols
```

Format

A character vector

Source

Ensembl version 99 human GTF file

ensembl_tx_biotypes *Transcript biotypes from Ensembl*

Description

These vectors are here to make it easy to look up which biotypes are available for Ensembl without having to parse GTF and fasta files every time. See this page from Ensembl for what the biotypes mean.

Usage

```
ensembl_tx_biotypes
```

Format

A character vector with all Ensembl transcript biotypes.

Source

This vector is all the unique transcript biotypes in the Ensembl version 99 human GTF file.

See Also

ensembl_gene_biotypes cellranger_biotypes

get_intron_flanks *Get flanked intronic ranges*

Description

Get flanked intronic ranges

Usage

```
get_intron_flanks(grl, L, get_junctions)
```

Arguments

grl	A CompressedGRangesList for exonic ranges, each element for one transcript.
L	Read length.
get_junctions	Logical, whether to also return exon-exon junctions.

Value

If get_junctions is FALSE, then a GRanges object with ranges for flanked intronic regions. If get_junctions is TRUE, then in addition to the flanked intronic ranges, a CompressedGRangesList with exon-exon junction ranges and ranges for transcripts without introns.

get_knee_df *Plot the transposed knee plot and inflection point*

Description

Plot a transposed knee plot, showing the inflection point and the number of remaining cells after inflection point filtering. It's transposed since it's more generalizable to multi-modal data.

Usage

```
get_knee_df(mat)

get_inflection(df, lower = 100)

knee_plot(df, inflection)
```

Arguments

mat	Gene count matrix, a dgCMatrix.
df	The data frame from get_knee_df.
lower	Minimum total UMI counts for barcode for it to be considered when calculating the inflection point; this helps to avoid the noisy part of the curve for barcodes with very few counts.
inflection	Output of get_inflection.

Value

get_knee_df returns a tibble with two columns: total for total UMI counts for each barcode, and rank for rank of the total counts, with number 1 for the barcode with the most counts.

get_inflection returns a numeric(1) for the total UMI count at the inflection point.

knee_plot returns a ggplot2 object.

Note

Code in part adapted from barcodeRanks from DropetUtils.

Examples

```
# Download dataset already in BUS format
library(TENxBUSData)
TENxBUSData(".", dataset = "hgmm100")
tr2g <- transcript2gene(c("Homo sapiens", "Mus musculus"),
  ensembl_version = 99, kallisto_out_path = "./out_hgmm100")
m <- make_sparse_matrix("./out_hgmm100/output.sorted.txt",
  tr2g = tr2g, est_ncells = 1e5,
  est_ngenes = nrow(tr2g), TCC = FALSE)
df <- get_knee_df(m)
```

```
infl <- get_inflection(df)
knee_plot(df, infl)
# Clean up files from the example
unlink("out_hgmm100")
```

`get_velocity_files` *Get files required for RNA velocity with bustools*

Description

Computation of RNA velocity requires the number of unspliced transcripts, which can be quantified with reads containing intronic sequences. This function extracts intronic sequences flanked by L-1 bases of exonic sequences where L is the biological read length of the single cell technology of interest. The flanking exonic sequences are included for reads partially mapping to an intron and an exon.

Usage

```
get_velocity_files(
  X,
  L,
  Genome,
  Transcriptome = NULL,
  out_path = ".",
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  compress_fa = FALSE,
  width = 80L,
  ...
)

## S4 method for signature 'GRanges'
get_velocity_files(
  X,
  L,
  Genome,
  Transcriptome = NULL,
  out_path = ".",
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  compress_fa = FALSE,
  width = 80L,
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  transcript_version = "transcript_version",
```

```
  gene_version = "gene_version",
  version_sep = ".",
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  save_filtered_gtf = FALSE
)

## S4 method for signature 'character'
get_velocity_files(
  X,
  L,
  Genome,
  Transcriptome = NULL,
  out_path = ".",
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  compress_fa = FALSE,
  width = 80L,
  is_circular = NULL,
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  transcript_version = "transcript_version",
  gene_version = "gene_version",
  version_sep = ".",
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  save_filtered_gtf = FALSE
)

## S4 method for signature 'TxDb'
get_velocity_files(
  X,
  L,
  Genome,
  Transcriptome,
  out_path,
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  compress_fa = FALSE,
  width = 80L,
```

```
  chrs_only = TRUE
)

## S4 method for signature 'EnsDb'
get_velocity_files(
  X,
  L,
  Genome,
  Transcriptome,
  out_path,
  style = c("genome", "Ensembl", "UCSC", "NCBI", "other"),
  isoform_action = c("separate", "collapse"),
  exon_option = c("full", "junction"),
  compress_fa = FALSE,
  width = 80L,
  use_transcript_version = TRUE,
  use_gene_version = TRUE,
  transcript_biotype_col = "TXBIOTYPE",
  gene_biotype_col = "GENEBIOTYPE",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE
)
```

Arguments

X	Gene annotation with transcript and exon information. It can be a path to a GTF file with annotation of exon coordinates of transcripts, preferably from Ensembl. In the metadata, the following fields are required: type (e.g. whether the range of interest is a gene or transcript or exon or CDS), gene ID, and transcript ID. These fields need not to have standard names, as long as their names are specified in arguments of this function. It can also be a TxDb object, such as from the Bioconductor package `TxDb.Hsapiens.UCSC.hg38.knownGene`. It can also be a EnsDb object.
L	Length of the biological read. For instance, 10xv1: 98 nt, 10xv2: 98 nt, 10xv3: 91 nt, Drop-seq: 50 nt. If in doubt check read length in a fastq file for biological reads with the `bash` commands: If the fastq file is gzipped, then do `zcat your_file.fastq.gz | head` on Linux. If on Mac, then `zcat < your_file.fastq.gz | head`. Then you will see lines with nucleotide bases. Copy one of those lines and determine its length with `str_length` in R or `echo -n <the sequence> | wc -c` in `bash`. Which file corresponds to biological reads depends on the particular technology.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use `genomeStyles` to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.

`Transcriptome` A XStringSet, a path to a fasta file (can be gzipped) of the transcriptome which contains sequences of spliced transcripts, or NULL. The transcriptome here will be concatenated with the intronic sequences to give one fasta file. When NULL, the transriptome sequences will be extracted from the genome given the gene annotation, so it will be guaranteed that transcript IDs in the transcriptome and in the annotation match. Otherwise, the type of transcript ID in the transcriptome must match that in the gene annotation supplied via argument X.

`out_path` Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.

`style` Formatting of chromosome names. Use genomeStyles to check which styles are supported for your organism of interest and what those styles look like. This can also be a style supported for your organism different from the style used by the annotation and the genome. Then this style will be used for both the annotation and the genome. Can take the following values:

genome If style of the annnotation is different from that of the genome, then the style of the genome will be used.

other Custom style, need to manually ensure that the style in annotation matches that of the genome.

Ensembl Or UCSC or NCBI, whichever is supported by your species of interest.

`isoform_action` Character, indicating action to take with different transcripts of the same gene. Must be one of the following:

collapse First, the union of all exons of different transcripts of a gene will be taken. Then the introns will be inferred from this union. Only the flanked intronic sequences are affected; isoforms will always be taken into account for spliced sequences or exon-exon junctions.

separate Introns from different transcripts will be kept separate.

`exon_option` Character, indicating how exonic sequences should be included in the kallisto index. Must be one of the following:

full The full cDNA sequences, which include the full exonic sequences, will be used. This is the default.

junction Only the exon-exon junctions, with L-1 bases on each side of the junctions, will be used.

`compress_fa` Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.

`width` Maximum number of letters per line of sequence in the output fasta file. Must be an integer.

`...` Extra arguments for methods.

`transcript_id` Character vector of length 1. Tag in `attribute` field corresponding to transcript IDs. This argument must be supplied and cannot be NA or NULL. Will throw error if tag indicated in this argument does not exist.

`gene_id` Character vector of length 1. Tag in `attribute` field corresponding to gene IDs. This argument must be supplied and cannot be NA or NULL. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for

each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.

`transcript_version`
: Character vector of length 1. Tag in `attribute` field corresponding to *transcript* version number. If your GTF file does not include transcript version numbers, or if you do not wish to include the version number, then use `NULL` for this argument. To decide whether to include transcript version number, check whether version numbers are included in the `transcripts.txt` in the `kallisto` output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

`gene_version`
: Character vector of length 1. Tag in `attribute` field corresponding to *gene* version number. If your GTF file does not include gene version numbers, or if you do not wish to include the version number, then use `NULL` for this argument. Unlike transcript version number, it's up to you whether to include gene version number.

`version_sep`
: Character to separate bewteen the main ID and the version number. Defaults to ".", as in Ensembl.

`transcript_biotype_col`
: Character vector of length 1. Tag in `attribute` field corresponding to *transcript* biotype.

`gene_biotype_col`
: Character vector of length 1. Tag in `attribute` field corresponding to *gene* biotype.

`transcript_biotype_use`
: Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, `retained_intron` is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See `data("ensembl_tx_biotypes")` for all available transcript biotypes from Ensembl.

`gene_biotype_use`
: Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See `data("cellranger_biotypes")` for gene biotypes the Cell Ranger reference uses. See `data("ensembl_gene_biotypes")` for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

`chrs_only`
: Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to `TRUE`. Only applicable to species found in `genomeStyles()`.

`save_filtered_gtf`
: Logical. If filtering type, biotypes, and/or chromosomes, whether to save the filtered `GRanges` as a GTF file.

`is_circular` Logical vector of the same length as the number of sequences in the annotation and with the same names as the sequences, indicating whether the sequence is circular. If `NULL`, then all sequences will be assumed to be linear.

`use_transcript_version` Logical, whether to include version number in the Ensembl transcript ID.

`use_gene_version` Logical, whether to include version number in the Ensembl gene ID. Unlike transcript version number, it's up to you whether to include gene version number.

Value

The following files will be written to disk in the directory `out_path`:

cDNA_introns.fa A fasta file containing both the spliced transcripts and the flanked intronic sequences. The intronic sequences are flanked by L-1 nt of exonic sequences to capture reads from nascent transcript partially mapping to exons. If the exon is shorter than 2*(L-1) nt, then the entire exon will be included in the intronic sequence. This will be used to build the `kallisto` index.

cDNA_tx_to_capture.txt A text file of transcript IDs of spliced transcripts. If `exon_option == "junction"`, then IDs of the exon-exon junctions. These IDs will have the pattern "transcript ID"-Jx, where x is a number differentiating between different junctions of the same transcript. Here x will always be ordered from 5' to 3' as on the plus strand.

introns_tx_to_capture.txt A text file of IDs of introns. The names will have the pattern "transcript ID"-Ix, where x is a number differentiating between introns of the same transcript. If all transcripts of the same gene are collapsed before inferring intronic sequences, gene ID will be used in place of transcript ID. Here x will always be ordered from 5' to 3' as on the plus strand.

tr2g.txt A text file with two columns matching transcripts and introns to genes. The first column is transcript or intron ID, and the second column is the corresponding gene ID. The part for transcripts are generated from the gene annotation supplied.

Nothing is returned into the R session.

Examples

```
# Use toy example
toy_path <- system.file("testdata", package = "BUSpaRse")
file <- paste0(toy_path, "/velocity_annot.gtf")
genome <- Biostrings::readDNAStringSet(paste0(toy_path, "/velocity_genome.fa"))
transcriptome <- paste0(toy_path, "/velocity_tx.fa")
get_velocity_files(file, 11, genome, transcriptome, ".",
  gene_version = NULL, transcript_version = NULL)
# Clean up output of the example
file.remove("cDNA_introns.fa", "cDNA_tx_to_capture.txt",
            "introns_tx_to_capture.txt", "tr2g.txt")
```

make_sparse_matrix *Convert the Output of* kallisto bus *into Gene by Gell Matrix*

Description

This function takes the output file of kallisto bus, after being sorted and converted into text with bustools. See vignettes on the website of this package for a tutorial. The bustools output has 4 columns: barcode, UMI, equivalence class, and counts. This function converts that file into a sparse matrix that can be used in downstream analyses.

Usage

```
make_sparse_matrix(
  bus_path,
  tr2g,
  est_ncells,
  est_ngenes,
  whitelist = NULL,
  gene_count = TRUE,
  TCC = TRUE,
  single_gene = TRUE,
  verbose = TRUE,
  progress_unit = 5e+06
)
```

Arguments

bus_path	Path to the sorted text bus output file.
tr2g	A Data frame with columns gene and transcript, in the same order as in the transcriptome index for kallisto. This argument can be missing or is ignored if only the TCC matrix, not the gene count matrix, is made.
est_ncells	Estimated number of cells; providing this argument will speed up computation as it minimizes memory reallocation as vectors grow.
est_ngenes	Estimated number of genes or equivalence classes.
whitelist	A character vector with valid cell barcodes. This is an optional argument, that defaults to NULL. When it is NULL, all cell barcodes present that have some UMI assignable to genes or ECs will be included in the sparse matrix whether they are known to be valid or not. Barcodes with only UMIs that are not assignable to genes or ECs will still be excluded.
gene_count	Logical, whether the gene count matrix should be returned.
TCC	Logical, whether the TCC matrix should be returned.
single_gene	Logical, whether to use single gene mode. In single gene mode, only UMIs that can be uniquely mapped to one gene are kept. Without single gene mode, UMIs mapped to multiple genes will be evenly distributed to those genes.
verbose	Whether to display progress.

progress_unit How many iteration to print one progress update when reading in the kallisto bus file.

Details

This function can generate both the gene count matrix and the transcript compatibility count (TCC) matrix. The TCC matrix has barcodes in the columns and equivalence classes in the rows. See Ntranos et al. 2016 for more information about the RCC matrix.

For 10x data sets, you can find a barcode whitelist file that comes with CellRanger installation. You don't need to run CellRanger to get that. An example path to get the whitelist file is cellranger-2.1.0/cellranger-cs/2.1 for v2 chemistry.

Value

If both gene count and TCC matrices are returned, then this function returns a list with two matrices, each with genes/equivalence classes in the rows and barcodes in the columns. If only one of gene count and TCC matrices is returned, then a dgCMatrix with genes/equivalence classes in the rows and barcodes in the columns. These matrices are unfiltered. Please filter the empty droplets before downstream analysis.

See Also

EC2gene

Examples

```
# Load toy example for testing
toy_path <- system.file("testdata", package = "BUSpaRse")
load(paste(toy_path, "toy_example.RData", sep = "/"))
out_fn <- paste0(toy_path, "/output.sorted.txt")
# With whitelist
m <- make_sparse_matrix(out_fn, tr2g_toy, 10, 3, whitelist = whitelist,
  gene_count = TRUE, TCC = FALSE, single_gene = TRUE,
  verbose = FALSE)
```

---

match_style *Match chromosome naming styles of annotation and genome*

Description

Internal use. This function matches chromosome naming styles. It will also give the genome and the annotation the same genome slot. This function assumes that the annotation and the genome refer to the same version of genome. If more than one style, then the first element will be used.

Usage

```
match_style(Genome, annot, style)
```

Arguments

Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
annot	Genome annotation, an object of a class with a seqlevels method, such as GRanges, TxDb, and EnsDb.
style	Formatting of chromosome names. Use genomeStyles to check which styles are supported for your organism of interest and what those styles look like. This can also be a style supported for your organism different from the style used by the annotation and the genome. Then this style will be used for both the annotation and the genome. Can take the following values: **genome** If style of the annnotation is different from that of the genome, then the style of the genome will be used. **other** Custom style, need to manually ensure that the style in annotation matches that of the genome. **Ensembl** Or UCSC or NCBI, whichever is supported by your species of interest.

Value

A list of two. The first element is the genome with the proper style, and the second element is the annotation with the proper style.

---

read_count_output *Read matrix along with barcode and gene names*

Description

This function takes in a directory and name and reads the mtx file, genes, and barcodes from the output of bustools to return a sparse matrix with column names and row names.

Usage

```
read_count_output(dir, name, tcc = FALSE)
```

Arguments

dir	Directory with the bustools count outputs.
name	The files in the output directory should be "name".mtx, "name".genes.txt, and "name".barcodes.txt.
tcc	Logical, whether the matrix of interest is a TCC matrix. Defaults to FALSE.

Value

A dgCMatrix with barcodes as column names and genes as row names.

Examples

```
# Internal toy data used for unit testing
toy_path <- system.file("testdata", package = "BUSpaRse")
m <- read_count_output(toy_path, name = "genes", tcc = FALSE)
```

---

read_velocity_output *Read intronic and exonic matrices into R*

Description

Read intronic and exonic matrices into R

Usage

```
read_velocity_output(spliced_dir, unspliced_dir, spliced_name, unspliced_name)
```

Arguments

spliced_dir	Directory with mtx file for UMI counts of spliced transcripts.
unspliced_dir	Directory with mtx file for UMI counts of unspliced transcripts.
spliced_name	The files in the splicedd directory should be <spliced_name>.mtx, <spliced_name>.genes.txt, and <spliced_name>.barcodes.txt.
unspliced_name	The files in the unsplicedd directory should be <unspliced_name>.mtx, <unspliced_name>.genes.txt, and <unspliced_name>.barcodes.txt.

Value

A list of two dgCMatrix with barcodes as column names and genes as row names. The elements of the list will be spliced and unspliced.

Examples

```
# Internal toy data used for unit testing
toy_path <- system.file("testdata", package = "BUSpaRse")
m <- read_velocity_output(toy_path, toy_path,
  spliced_name = "genes",
  unspliced_name = "genes")
```

refseq_gff_mcols *Tags in the attributes field of RefSeq GFF files*

Description

These are the column names of the `mcols` when the Ensembl GTF file is read into R as a `GRanges`, including `gene`, `transcript_id`, `gene_biotype`, `description`, and so on, and the mandatory tags like `ID`, `Name`, and `Parent`.

Usage

```
refseq_gff_mcols
```

Format

A character vector

Source

Ensembl version 99 human GTF file

save_tr2g_bustools *Save transcript to gene file for use in* `bustools`

Description

This function saves the transcript to gene data frame generated by this package in whatever means in a format required by `bustools`. In order to use `bustools` to generate the gene count or TCC matrix, a file that maps transcripts to genes is required. This should be a tsv file with 2 columns: the first column for transcript ID and the second for gene ID. The order of transcripts in this file must be the same as the order in the kallisto index, and this ordering can be ensured by the function `sort_tr2g`. There must also be no headers. All columns other than `transcript` and `gene` will be discarded. To save a file with those columns, directly save the transcript to gene data frame with function like `write.table`, `readr::write_delim`.

Usage

```
save_tr2g_bustools(tr2g, file_save = "./tr2g.tsv")
```

Arguments

`tr2g`	The data frame output from the `tr2g_*` family of functions.
`file_save`	File name of the file to be saved. The directory in which the file is to be saved must exist.

Value

Nothing is returned into the R session. A tsv file of the format required by bustools with the name and directory specified will be written to disk.

Note

This function has been superseded by the new version of tr2g_* functions that can extract transcriptome for only the biotypes specified and with only the standard chromosomes. The new version of tr2g_* functions also sorts the transcriptome so the tr2g and the transcriptome have transcripts in the same order, and write the tr2g.tsv file in the bustools format.

Examples

```
toy_path <- system.file("testdata", package = "BUSpaRse")
file_use <- paste(toy_path, "gtf_test.gtf", sep = "/")
tr2g <- tr2g_gtf(file = file_use, get_transcriptome = FALSE,
  write_tr2g = FALSE, save_filtered_gtf = FALSE)
save_tr2g_bustools(tr2g, file_save = "./tr2g.tsv")
# Clean up files from the example
file.remove("tr2g.tsv")
```

---

sort_tr2g *Sort transcripts to the same order as in kallisto index*

Description

This function takes the data frame output from the tr2g_* family of functions in this package as the input, and sorts it so the transcripts are in the same order as in the kallisto index used to generate the bus file. Sorting is vital to obtain the correct sparse matrix from the bus file as equivalence class notations are based on the index of transcripts in the kallisto index.

Usage

```
sort_tr2g(tr2g, file, kallisto_out_path)
```

Arguments

tr2g	The data frame output from the tr2g_* family of functions.
file	Character vector of length 1, path to a tsv file with transcript IDs and the corresponding gene IDs, in the format required for bustools, or written by save_tr2g_bustools.
kallisto_out_path	Character vector of length 1, path to the directory for the outputs of kallisto bus.

Details

Since the attribute field of GTF and GFF3 files varies across sources, output from tr2g_gtf and tr2g_gff3 may need further clean up. You may also supply gene and transcript IDs from other sources. This function should be used after the clean up, when the transcript IDs in the cleaned up data frame have the same format as those in transcript

Value

A data frame with columns `transcript` and gene and the other columns present in `tr2g` or the data frame in `file`, with the transcript IDs sorted to be in the same order as in the kallisto index.

Note

This function has been superseded by the new version of tr2g_* functions that can extract transcriptome for only the biotypes specified and with only the standard chromosomes. The new version of tr2g_* functions also sorts the transcriptome so the tr2g and the transcriptome have transcripts in the same order.

See Also

Other functions to retrieve transcript and gene info: `tr2g_EnsDb()`, `tr2g_TxDb()`, `tr2g_ensembl()`, `tr2g_fasta()`, `tr2g_gff3()`, `tr2g_gtf()`, `transcript2gene()`

Examples

```
toy_path <- system.file("testdata", package = "BUSpaRse")
file_use <- paste(toy_path, "gtf_test.gtf", sep = "/")
tr2g <- tr2g_gtf(file = file_use, get_transcriptome = FALSE,
  write_tr2g = FALSE, save_filtered_gtf = FALSE, transcript_version = NULL)
tr2g <- sort_tr2g(tr2g, kallisto_out_path = toy_path)
```

---

species2dataset *Convert Latin species name to dataset name*

Description

This function converts Latin species name to a dataset name in biomart to query gene and transcript ID.

Usage

```
species2dataset(
  species,
  type = c("vertebrate", "metazoa", "plant", "fungus", "protist")
)
```

Arguments

`species`	A character vector of Latin names of species present in this scRNA-seq dataset. This is used to retrieve Ensembl information from biomart.
`type`	Deprecated.

Value

The appropriate dataset name for biomart.

Examples

```
species2dataset(species = "Homo sapiens")
```

---

standardize_tags *Standardize GRanges field names*

Description

To avoid introducing rlang as another dependency for tidyeval. This function will also convert exon numbers to integer.

Usage

```
standardize_tags(gr, gene_id, transcript_id)
```

Arguments

gr	A GRanges object.
gene_id	Name of the metadata field for gene ID.
transcript_id	Name of the metadata field for transcript ID.

Value

A GRanges object with standardized names: gene ID as gene_id, and transcript ID as transcript_id.

---

subset_annot *Subset genome annotation*

Description

Exclude chromosomes present in the annotation but absent from the genome and add information about circular chromosomes.

Usage

```
subset_annot(Genome, annot)

## S4 method for signature 'DNAStringSet'
subset_annot(Genome, annot)

## S4 method for signature 'BSgenome'
subset_annot(Genome, annot)
```

Arguments

Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
annot	Either a GRanges object or a TxDb object for gene annotation.

Value

A subsetted genome annotation of the same type of the input genome annotation.

Examples

```
library(BSgenome.Hsapiens.UCSC.hg38)
library(EnsDb.Hsapiens.v86)
library(GenomeInfoDb)
gn <- BSgenome.Hsapiens.UCSC.hg38
seqlevelsStyle(gn) <- "Ensembl"
subset_annot(gn, EnsDb.Hsapiens.v86)
```

---

sub_annot *Remove chromosomes in anotation absent from genome*

Description

Remove chromosomes in anotation absent from genome

Usage

```
sub_annot(chrs_use, annot)
```

Arguments

chrs_use	Character vector of names of chromosomes present in both the annotation and the genome.
annot	Either a GRanges object or a TxDb object for gene annotation.

Value

A subsetted genome annotation of the same type ofo the input genome annotation.

tr2g_EnsDb *Get transcript and gene info from EnsDb objects*

Description

Bioconductor provides Ensembl genome annotation in AnnotationHub; older versions of Ensembl annotation can be obtained from packages like EnsDb.Hsapiens.v86. This is an alternative to querying Ensembl with biomart; Ensembl's server seems to be less stable than that of Bioconductor. However, more information and species are available on Ensembl biomart than on AnnotationHub.

Usage

```
tr2g_EnsDb(
  ensdb,
  Genome = NULL,
  get_transcriptome = TRUE,
  out_path = ".",
  write_tr2g = TRUE,
  other_attrs = NULL,
  use_gene_name = TRUE,
  use_transcript_version = TRUE,
  use_gene_version = TRUE,
  transcript_biotype_col = "TXBIOTYPE",
  gene_biotype_col = "GENEBIOTYPE",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  compress_fa = FALSE,
  overwrite = FALSE
)
```

Arguments

ensdb	Ann EnsDb object, such as from AnnotationHub or EnsDb.Hsapiens.v86.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
get_transcriptome	Logical, whether to extract transcriptome from genome with the GTF file. If filtering biotypes or chromosomes, the filtered GRanges will be used to extract transcriptome.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.

write_tr2g Logical, whether to write tr2g to disk. If TRUE, then a file tr2g.tsv will be written into out_path.

other_attrs Character vector. Other attributes to get from the EnsDb object, such as gene symbol and position on the genome. Use columns to see which attributes are available.

use_gene_name Logical, whether to get gene names.

use_transcript_version
Logical, whether to include version number in the Ensembl transcript ID. To decide whether to include transcript version number, check whether version numbers are included in the transcripts.txt in the kallisto output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

use_gene_version
Logical, whether to include version number in the Ensembl gene ID. Unlike transcript version number, it's up to you whether to include gene version number.

transcript_biotype_col
Character vector of length 1. Tag in attribute field corresponding to *transcript* biotype.

gene_biotype_col
Character vector of length 1. Tag in attribute field corresponding to *gene* biotype.

transcript_biotype_use
Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, retained_intron is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See data("ensembl_tx_biotypes") for all available transcript biotypes from Ensembl.

gene_biotype_use
Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See data("cellranger_biotypes") for gene biotypes the Cell Ranger reference uses. See data("ensembl_gene_biotypes") for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().

compress_fa Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.

overwrite Logical, whether to overwrite if files with names of outputs written to disk already exist.

Value

A data frame with at least 2 columns: `gene` for gene ID, `transcript` for transcript ID, and optionally `gene_name` for gene names. If `other_attrs` has been specified, then those will also be columns in the data frame returned.

See Also

ensembl_gene_biotypes ensembl_tx_biotypes cellranger_biotypes

Other functions to retrieve transcript and gene info: `sort_tr2g()`, `tr2g_TxDb()`, `tr2g_ensembl()`, `tr2g_fasta()`, `tr2g_gff3()`, `tr2g_gtf()`, `transcript2gene()`

Examples

```
library(EnsDb.Hsapiens.v86)
tr2g_EnsDb(EnsDb.Hsapiens.v86, get_transcriptome = FALSE, write_tr2g = FALSE,
 use_transcript_version = FALSE,
 use_gene_version = FALSE)
```

---

tr2g_ensembl *Get transcript and gene info from Ensembl*

Description

This function queries Ensembl biomart to convert transcript IDs to gene IDs.

Usage

```
tr2g_ensembl(
  species,
  type = c("vertebrate", "metazoa", "plant", "fungus", "protist"),
  out_path = ".",
  write_tr2g = TRUE,
  other_attrs = NULL,
  use_gene_name = TRUE,
  use_transcript_version = TRUE,
  use_gene_version = TRUE,
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  ensembl_version = NULL,
  overwrite = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

species	Character vector of length 1, Latin name of the species of interest.
type	Character, must be one of "vertebrate", "metazoa", "plant", "fungus" and "protist". Passing "vertebrate" will use the default www.ensembl.org host. Gene annotation of some common invertebrate model organisms, such as *Drosophila melanogaster*, are available on www.ensembl.org so for these invertebrate model organisms, "vertebrate" can be used for this argument. Passing values other than "vertebrate" will use other Ensembl hosts. For animals absent from www.ensembl.org, try "metazoa".
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
write_tr2g	Logical, whether to write tr2g to disk. If TRUE, then a file tr2g.tsv will be written into out_path.
other_attrs	Character vector. Other attributes to get from Ensembl, such as gene symbol and position on the genome. Use listAttributes to see which attributes are available.
use_gene_name	Logical, whether to get gene names.
use_transcript_version	Logical, whether to include version number in the Ensembl transcript ID. To decide whether to include transcript version number, check whether version numbers are included in the transcripts.txt in the kallisto output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.
use_gene_version	Logical, whether to include version number in the Ensembl gene ID. Unlike transcript version number, it's up to you whether to include gene version number.
transcript_biotype_col	Character vector of length 1. Tag in attribute field corresponding to *transcript* biotype.
gene_biotype_col	Character vector of length 1. Tag in attribute field corresponding to *gene* biotype.
transcript_biotype_use	Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, retained_intron is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See data("ensembl_tx_biotypes") for all available transcript biotypes from Ensembl.
gene_biotype_use	Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See data("cellranger_biotypes") for gene biotypes the Cell Ranger reference uses. See data("ensembl_gene_biotypes") for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only — Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().

ensembl_version — Integer version number of Ensembl (e.g. 94 for the October 2018 release). This argument defaults to NULL, which will use the current release of Ensembl. Use listEnsemblArchives to see the version number corresponding to the Ensembl release of a particular date. The version specified here must match the version of Ensembl where the transcriptome used to build the kallisto index was downloaded. This only works for vertebrates and the most common invertebrate model organisms like *Drosophila melanogaster* and *C. elegans* (i.e. www.ensembl.org and its mirrors), not the other Ensembl sites for plants, protists, fungi, and metazoa.

overwrite — Logical, whether to overwrite if files with names of outputs written to disk already exist.

verbose — Whether to display progress.

... — Othe arguments to be passed to useMart, such as mirror. Note that setting mirrors other than the default, e.g. uswest, does not work for archived versions.

Value

A data frame with at least 2 columns: gene for gene ID, transcript for transcript ID, and optionally gene_name for gene names. If other_attrs has been specified, then those will also be columns in the data frame returned.

See Also

dl_transcriptome

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_TxDb(), tr2g_fasta(), tr2g_gff3(), tr2g_gtf(), transcript2gene()

Examples

```
tr2g <- tr2g_ensembl(species = "Danio rerio",
other_attrs = "description", write_tr2g = FALSE)
# This will use plants.ensembl.org as host instead of www.ensembl.org
tr2g <- tr2g_ensembl(species = "Arabidopsis thaliana", type = "plant",
  write_tr2g = FALSE)
```

---

tr2g_fasta *Get transcript and gene info from names in FASTA files*

Description

FASTA files, such as those for cDNA and ncRNA from Ensembl, might have genome annotation information in the name of each sequence entry. This function extracts the transcript and gene IDs from such FASTA files.

Usage

```
tr2g_fasta(
  file,
  out_path = ".",
  write_tr2g = TRUE,
  use_gene_name = TRUE,
  use_transcript_version = TRUE,
  use_gene_version = TRUE,
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  save_filtered = TRUE,
  compress_fa = FALSE,
  overwrite = FALSE
)
```

Arguments

`file`	Path to the FASTA file to be read. The file can remain gzipped.
`out_path`	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
`write_tr2g`	Logical, whether to write tr2g to disk. If `TRUE`, then a file `tr2g.tsv` will be written into `out_path`.
`use_gene_name`	Logical, whether to get gene names.
`use_transcript_version`	Logical, whether to include version number in the Ensembl transcript ID. To decide whether to include transcript version number, check whether version numbers are included in the `transcripts.txt` in the `kallisto` output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.
`use_gene_version`	Logical, whether to include version number in the Ensembl gene ID. Unlike transcript version number, it's up to you whether to include gene version number.
`transcript_biotype_use`	Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, `retained_intron` is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See `data("ensembl_tx_biotypes")` for all available transcript biotypes from Ensembl.
`gene_biotype_use`	Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See `data("cellranger_biotypes")` for gene biotypes the Cell Ranger reference uses. See `data("ensembl_gene_biotypes")` for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only	Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().
save_filtered	If filtering for biotype and chromosomes, whether to save the filtered fasta file. If TRUE, the file will be tx_filtered.fa in out_path.
compress_fa	Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.
overwrite	Logical, whether to overwrite if files with names of outputs written to disk already exist.

Details

At present, this function only works with FASTA files from Ensembl, and uses regex to extract vertebrate Ensembl IDs. Sequence names should be formatted as follows:

```
ENST00000632684.1 cdna chromosome:GRCh38:7:142786213:142786224:1
gene:ENSG00000282431.1 gene_biotype:TR_D_gene transcript_biotype:TR_D_gene
gene_symbol:TRBD1 description:T cell receptor beta diversity 1
[Source:HGNC Symbol;Acc:HGNC:12158]
```

If your FASTA file sequence names are formatted differently, then you must extract the transcript and gene IDs by some other means. The Bioconductor package Biostrings is recommended; after reading the FASTA file into R, the sequence names can be accessed by the names function.

While normally, you should call sort_tr2g to sort the transcript IDs from the output of the tr2g_* family of functions, If the FASTA file supplied here is the same as the one used to build the kallisto index, then the transcript IDs in the output of this function are in the same order as in the kallisto index, so you can skip sort_tr2g and proceed directly to EC2gene with the output of this function.

Value

A data frame with at least 2 columns: gene for gene ID, transcript for transcript ID, and optionally gene_name for gene names.

See Also

ensembl_gene_biotypes ensembl_tx_biotypes cellranger_biotypes

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_TxDb(), tr2g_ensembl(), tr2g_gff3(), tr2g_gtf(), transcript2gene()

Examples

```
toy_path <- system.file("testdata", package = "BUSpaRse")
file_use <- paste(toy_path, "fasta_test.fasta", sep = "/")
tr2g <- tr2g_fasta(file = file_use, save_filtered = FALSE, write_tr2g = FALSE)
```

tr2g_gff3 *Get transcript and gene info from GFF3 file*

Description

This function reads a GFF3 file and extracts the transcript ID and corresponding gene ID. This function assumes that the GFF3 file is properly formatted. See http://gmod.org/wiki/GFF3 for a detailed description of proper GFF3 format. Note that GTF files have a somewhat different and simpler format in the attribute field, which this function does not support. See http://mblab.wustl.edu/GTF2.html for a detailed description of proper GTF format. To extract transcript and gene information from GTF files, see the function tr2g_gtf in this package. Some files bearing the .gff3 are in fact more like the GTF format. If this is so, then change the extension to .gtf and use the function tr2g_gtf in this package instead.

Usage

```
tr2g_gff3(
  file,
  Genome = NULL,
  get_transcriptome = TRUE,
  out_path = ".",
  write_tr2g = TRUE,
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  gene_name = "Name",
  transcript_version = "version",
  gene_version = "version",
  version_sep = ".",
  transcript_biotype_col = "biotype",
  gene_biotype_col = "biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  compress_fa = FALSE,
  save_filtered_gff = TRUE,
  overwrite = FALSE,
  source = c("ensembl", "refseq")
)
```

Arguments

file	Path to a GTF file to be read. The file can remain gzipped. Use getGTF from the biomartr package to download GTF files from Ensembl, and use getGFF from biomartr to download GFF3 files from Ensembl and RefSeq.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which

styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.

`get_transcriptome`
: Logical, whether to extract transcriptome from genome with the GTF file. If filtering biotypes or chromosomes, the filtered `GRanges` will be used to extract transcriptome.

`out_path`
: Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.

`write_tr2g`
: Logical, whether to write tr2g to disk. If `TRUE`, then a file `tr2g.tsv` will be written into `out_path`.

`transcript_id`
: Character vector of length 1. Tag in `attribute` field corresponding to transcript IDs. This argument must be supplied and cannot be `NA` or `NULL`. Will throw error if tag indicated in this argument does not exist.

`gene_id`
: Character vector of length 1. Tag in `attribute` field corresponding to gene IDs. This argument must be supplied and cannot be `NA` or `NULL`. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.

`gene_name`
: Character vector of length 1. Tag in `attribute` field corresponding to gene symbols. This argument can be `NA` or `NULL` if you are fine with non-human readable gene IDs and do not wish to extract human readable gene symbols.

`transcript_version`
: Character vector of length 1. Tag in `attribute` field corresponding to *transcript* version number. If your GTF file does not include transcript version numbers, or if you do not wish to include the version number, then use `NULL` for this argument. To decide whether to include transcript version number, check whether version numbers are included in the `transcripts.txt` in the `kallisto` output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

`gene_version`
: Character vector of length 1. Tag in `attribute` field corresponding to *gene* version number. If your GTF file does not include gene version numbers, or if you do not wish to include the version number, then use `NULL` for this argument. Unlike transcript version number, it's up to you whether to include gene version number.

`version_sep`
: Character to separate bewteen the main ID and the version number. Defaults to ".", as in Ensembl.

`transcript_biotype_col`
: Character vector of length 1. Tag in `attribute` field corresponding to *transcript* biotype.

`gene_biotype_col`
: Character vector of length 1. Tag in `attribute` field corresponding to *gene* biotype.

transcript_biotype_use
: Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, `retained_intron` is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See `data("ensembl_tx_biotypes")` for all available transcript biotypes from Ensembl.

gene_biotype_use
: Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See `data("cellranger_biotypes")` for gene biotypes the Cell Ranger reference uses. See `data("ensembl_gene_biotypes")` for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only
: Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to `TRUE`. Only applicable to species found in `genomeStyles()`.

compress_fa
: Logical, whether to compress the output fasta file. If `TRUE`, then the fasta file will be gzipped.

save_filtered_gff
: Logical. If filtering type, biotypes, and/or chromosomes, whether to save the filtered `GRanges` as a GFF3 file.

overwrite
: Logical, whether to overwrite if files with names of outputs written to disk already exist.

source
: Name of the database where this GFF3 file was downloaded. Must be either "ensembl" or "refseq".

Details

Transcript and gene versions may not be present in all GTF files, so these arguments are optional. This function has arguments for transcript and gene version numbers because Ensembl IDs have version numbers. For Ensembl IDs, we recommend including the version number, since a change in version number signals a change in the entity referred to by the ID after reannotation. If a version is used, then it will be appended to the ID, separated by `version_sep`.

The transcript and gene IDs are The `attribute` field (the last field) of GTF files can be complicated and inconsistent across different sources. Please check the `attribute` tags in your GTF file and consider the arguments of this function carefully. The defaults are set according to Ensembl GTF files; defaults may not work for files from other sources. Due to the general lack of standards for the `attribute` field, you may need to further clean up the output of this function.

Value

A data frame at least 2 columns: `gene` for gene ID, `transcript` for transcript ID, and optionally, `gene_name` for gene names.

Note

The defaults here are for Ensembl GFF3 files. To see all attribute tags for Ensembl and RefSeq GFF3 files, see `data("ensembl_gff_mcols")` and `data("refseq_gff_mcols")`.

See Also

ensembl_gene_biotypes ensembl_tx_biotypes cellranger_biotypes ensembl_gtf_mcols ensembl_gff_mcols refseq_gff_mcols

Other functions to retrieve transcript and gene info: `sort_tr2g()`, `tr2g_EnsDb()`, `tr2g_TxDb()`, `tr2g_ensembl()`, `tr2g_fasta()`, `tr2g_gtf()`, `transcript2gene()`

Examples

```
toy_path <- system.file("testdata", package = "BUSpaRse")
file_use <- paste(toy_path, "gff3_test.gff3", sep = "/")
# Default
tr2g <- tr2g_gff3(file = file_use, write_tr2g = FALSE,
get_transcriptome = FALSE, save_filtered_gff = FALSE)
# Excluding version numbers
tr2g <- tr2g_gff3(file = file_use, transcript_version = NULL,
  gene_version = NULL, write_tr2g = FALSE, get_transcriptome = FALSE,
  save_filtered_gff = FALSE)
```

---

tr2g_GRanges *Get transcript and gene info from GRanges*

Description

Internal use, for GRanges from GTF files

Usage

```
tr2g_GRanges(
  gr,
  Genome = NULL,
  get_transcriptome = TRUE,
  out_path = ".",
  write_tr2g = TRUE,
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  gene_name = "gene_name",
  transcript_version = "transcript_version",
  gene_version = "gene_version",
  version_sep = ".",
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
```

```
  gene_biotype_use = "all",
  chrs_only = TRUE,
  compress_fa = FALSE,
  save_filtered_gtf = TRUE,
  overwrite = FALSE
)
```

Arguments

gr	A GRanges object. The metadata columns should be atomic vectors, not lists.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
get_transcriptome	Logical, whether to extract transcriptome from genome with the GTF file. If filtering biotypes or chromosomes, the filtered GRanges will be used to extract transcriptome.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
write_tr2g	Logical, whether to write tr2g to disk. If TRUE, then a file tr2g.tsv will be written into out_path.
transcript_id	Character vector of length 1. Tag in attribute field corresponding to transcript IDs. This argument must be supplied and cannot be NA or NULL. Will throw error if tag indicated in this argument does not exist.
gene_id	Character vector of length 1. Tag in attribute field corresponding to gene IDs. This argument must be supplied and cannot be NA or NULL. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.
gene_name	Character vector of length 1. Tag in attribute field corresponding to gene symbols. This argument can be NA or NULL if you are fine with non-human readable gene IDs and do not wish to extract human readable gene symbols.
transcript_version	Character vector of length 1. Tag in attribute field corresponding to *transcript* version number. If your GTF file does not include transcript version numbers, or if you do not wish to include the version number, then use NULL for this argument. To decide whether to include transcript version number, check whether version numbers are included in the transcripts.txt in the kallisto output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

gene_version Character vector of length 1. Tag in attribute field corresponding to *gene* version number. If your GTF file does not include gene version numbers, or if you do not wish to include the version number, then use NULL for this argument. Unlike transcript version number, it's up to you whether to include gene version number.

version_sep Character to separate bewteen the main ID and the version number. Defaults to ".", as in Ensembl.

transcript_biotype_col
Character vector of length 1. Tag in attribute field corresponding to *transcript* biotype.

gene_biotype_col
Character vector of length 1. Tag in attribute field corresponding to *gene* biotype.

transcript_biotype_use
Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl annotation, retained_intron is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See data("ensembl_tx_biotypes") for all available transcript biotypes from Ensembl.

gene_biotype_use
Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See data("cellranger_biotypes") for gene biotypes the Cell Ranger reference uses. See data("ensembl_gene_biotypes") for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().

compress_fa Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.

save_filtered_gtf
Logical. If filtering type, biotypes, and/or chromosomes, whether to save the filtered GRanges as a GTF file.

overwrite Logical, whether to overwrite if files with names of outputs written to disk already exist.

Value

A data frame at least 2 columns: gene for gene ID, transcript for transcript ID, and optionally, gene_name for gene names.

tr2g_gtf *Get transcript and gene info from GTF file*

Description

This function reads a GTF file and extracts the transcript ID and corresponding gene ID. This function assumes that the GTF file is properly formatted. See http://mblab.wustl.edu/GTF2.html for a detailed description of proper GTF format. Note that GFF3 files have a somewhat different and more complicated format in the attribute field, which this function does not support. See http://gmod.org/wiki/GFF3 for a detailed description of proper GFF3 format. To extract transcript and gene information from GFF3 files, see the function tr2g_gff3 in this package.

Usage

```
tr2g_gtf(
  file,
  Genome = NULL,
  get_transcriptome = TRUE,
  out_path = ".",
  write_tr2g = TRUE,
  transcript_id = "transcript_id",
  gene_id = "gene_id",
  gene_name = "gene_name",
  transcript_version = "transcript_version",
  gene_version = "gene_version",
  version_sep = ".",
  transcript_biotype_col = "transcript_biotype",
  gene_biotype_col = "gene_biotype",
  transcript_biotype_use = "all",
  gene_biotype_use = "all",
  chrs_only = TRUE,
  compress_fa = FALSE,
  save_filtered_gtf = TRUE,
  overwrite = FALSE
)
```

Arguments

file	Path to a GTF file to be read. The file can remain gzipped. Use getGTF from the biomartr package to download GTF files from Ensembl, and use getGFF from biomartr to download GFF3 files from Ensembl and RefSeq.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.

get_transcriptome
: Logical, whether to extract transcriptome from genome with the GTF file. If filtering biotypes or chromosomes, the filtered GRanges will be used to extract transcriptome.

out_path
: Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.

write_tr2g
: Logical, whether to write tr2g to disk. If TRUE, then a file tr2g.tsv will be written into out_path.

transcript_id
: Character vector of length 1. Tag in attribute field corresponding to transcript IDs. This argument must be supplied and cannot be NA or NULL. Will throw error if tag indicated in this argument does not exist.

gene_id
: Character vector of length 1. Tag in attribute field corresponding to gene IDs. This argument must be supplied and cannot be NA or NULL. Note that this is different from gene symbols, which do not have to be unique. This can be Ensembl or Entrez IDs. However, if the gene symbols are in fact unique for each gene, you may supply the tag for human readable gene symbols to this argument. Will throw error if tag indicated in this argument does not exist. This is typically "gene_id" for annotations from Ensembl and "gene" for refseq.

gene_name
: Character vector of length 1. Tag in attribute field corresponding to gene symbols. This argument can be NA or NULL if you are fine with non-human readable gene IDs and do not wish to extract human readable gene symbols.

transcript_version
: Character vector of length 1. Tag in attribute field corresponding to *transcript* version number. If your GTF file does not include transcript version numbers, or if you do not wish to include the version number, then use NULL for this argument. To decide whether to include transcript version number, check whether version numbers are included in the transcripts.txt in the kallisto output directory. If that file includes version numbers, then trannscript version numbers must be included here as well. If that file does not include version numbers, then transcript version numbers must not be included here.

gene_version
: Character vector of length 1. Tag in attribute field corresponding to *gene* version number. If your GTF file does not include gene version numbers, or if you do not wish to include the version number, then use NULL for this argument. Unlike transcript version number, it's up to you whether to include gene version number.

version_sep
: Character to separate bewteen the main ID and the version number. Defaults to ".", as in Ensembl.

transcript_biotype_col
: Character vector of length 1. Tag in attribute field corresponding to *transcript* biotype.

gene_biotype_col
: Character vector of length 1. Tag in attribute field corresponding to *gene* biotype.

transcript_biotype_use
: Character, can be "all" or a vector of *transcript* biotypes to be used. Transcript biotypes aren't entirely the same as gene biotypes. For instance, in Ensembl

annotation, retained_intron is a transcript biotype, but not a gene biotype. If "cellranger", then a warning will be given. See data("ensembl_tx_biotypes") for all available transcript biotypes from Ensembl.

gene_biotype_use
: Character, can be "all", "cellranger", or a vector of *gene* biotypes to be used. If "cellranger", then the biotypes used by Cell Ranger's reference are used. See data("cellranger_biotypes") for gene biotypes the Cell Ranger reference uses. See data("ensembl_gene_biotypes") for all available gene biotypes from Ensembl. Note that gene biotypes and transcript biotypes are not always the same.

chrs_only
: Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().

compress_fa
: Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.

save_filtered_gtf
: Logical. If filtering type, biotypes, and/or chromosomes, whether to save the filtered GRanges as a GTF file.

overwrite
: Logical, whether to overwrite if files with names of outputs written to disk already exist.

Details

Transcript and gene versions may not be present in all GTF files, so these arguments are optional. This function has arguments for transcript and gene version numbers because Ensembl IDs have version numbers. For Ensembl IDs, we recommend including the version number, since a change in version number signals a change in the entity referred to by the ID after reannotation. If a version is used, then it will be appended to the ID, separated by version_sep.

The transcript and gene IDs are The attribute field (the last field) of GTF files can be complicated and inconsistent across different sources. Please check the attribute tags in your GTF file and consider the arguments of this function carefully. The defaults are set according to Ensembl GTF files; defaults may not work for files from other sources. Due to the general lack of standards for the attribute field, you may need to further clean up the output of this function.

Value

A data frame at least 2 columns: gene for gene ID, transcript for transcript ID, and optionally, gene_name for gene names.

See Also

ensembl_gene_biotypes ensembl_tx_biotypes cellranger_biotypes

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_TxDb(), tr2g_ensembl(), tr2g_fasta(), tr2g_gff3(), transcript2gene()

Examples

```
toy_path <- system.file("testdata", package = "BUSpaRse")
file_use <- paste(toy_path, "gtf_test.gtf", sep = "/")
# Default
tr2g <- tr2g_gtf(file = file_use, get_transcriptome = FALSE,
  write_tr2g = FALSE, save_filtered_gtf = FALSE)
# Excluding version numbers
tr2g <- tr2g_gtf(file = file_use, transcript_version = NULL,
  gene_version = NULL, get_transcriptome = FALSE,
  write_tr2g = FALSE, save_filtered_gtf = FALSE)
```

---

tr2g_junction *tr2g for exon-exon junctions*

Description

tr2g for exon-exon junctions

Usage

```
tr2g_junction(tr2g_cdna, junction_names)
```

Arguments

tr2g_cdna	The original tr2g_cdna.
junction_names	Names of junctions internally generated.

Value

A tr2g data frame where "transcripts" are the exon-exon junctions and genes are the corresponding genes.

---

tr2g_TxDb *Get transcript and gene info from TxDb objects*

Description

The genome and gene annotations of some species can be conveniently obtained from Bioconductor packages. This is more convenient than downloading GTF files from Ensembl and reading it into R. In these packages, the gene annotation is stored in a TxDb object, which has standardized names for gene IDs, transcript IDs, exon IDs, and so on, which are stored in the metadata fields in GTF and GFF3 files, which are not standardized. This function extracts transcript and corresponding gene information from gene annotation stored in a TxDb object.

Usage

```
tr2g_TxDb(
  txdb,
  Genome = NULL,
  get_transcriptome = TRUE,
  out_path = ".",
  write_tr2g = TRUE,
  chrs_only = TRUE,
  compress_fa = FALSE,
  overwrite = FALSE
)
```

Arguments

txdb	A TxDb object with gene annotation.
Genome	Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
get_transcriptome	Logical, whether to extract transcriptome from genome with the GTF file. If filtering biotypes or chromosomes, the filtered GRanges will be used to extract transcriptome.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.
write_tr2g	Logical, whether to write tr2g to disk. If TRUE, then a file tr2g.tsv will be written into out_path.
chrs_only	Logical, whether to include chromosomes only, for GTF and GFF files can contain annotations for scaffolds, which are not incorporated into chromosomes. This will also exclude haplotypes. Defaults to TRUE. Only applicable to species found in genomeStyles().
compress_fa	Logical, whether to compress the output fasta file. If TRUE, then the fasta file will be gzipped.
overwrite	Logical, whether to overwrite if files with names of outputs written to disk already exist.

Value

A data frame with 3 columns: gene for gene ID, transcript for transcript ID, and tx_id for internal transcript IDs used to avoid duplicate transcript names. For TxDb packages from Bioconductor, gene ID is Entrez ID, while transcript IDs are Ensembl IDs with version numbers for TxDb.Hsapiens.UCSC.hg38.knownGene. In some cases, the transcript ID have duplicates, and this is resolved by adding numbers to make the IDs unique.

A data frame with 3 columns: gene for gene ID, transcript for transcript ID, and gene_name for gene names. If other_attrs has been specified, then those will also be columns in the data frame returned.

See Also

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_ensembl(), tr2g_fasta(), tr2g_gff3(), tr2g_gtf(), transcript2gene()

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_ensembl(), tr2g_fasta(), tr2g_gff3(), tr2g_gtf(), transcript2gene()

Examples

```
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
library(BSgenome.Hsapiens.UCSC.hg38)
tr2g_TxDb(TxDb.Hsapiens.UCSC.hg38.knownGene, BSgenome.Hsapiens.UCSC.hg38)
# Clean up
file.remove("transcriptome.fa", "tr2g.tsv")
```

---

transcript2gene *Map Ensembl transcript ID to gene ID*

Description

This function is a shortcut to get the correctly sorted data frame with transcript IDs and the corresponding gene IDs from Ensembl biomart or Ensembl transcriptome FASTA files. For biomart query, it calls tr2g_EnsDb and then sort_tr2g. For FASTA files, it calls tr2g_fasta and then sort_tr2g. Unlike in tr2g_EnsDb and tr2g_fasta, multiple species can be supplied if cells from different species were sequenced together. This function should only be used if the kallisto inidex was built with transcriptomes from Ensembl. Also, if querying biomart, please make sure to set ensembl_version to match the version where the transcriptomes were downloaded. tr2g_EnsDb is used now instead of tr2g_ensembl because Bioconductor's AnnotationHub keep more archive Ensembl versions than the official Ensembl website.

Usage

```
transcript2gene(
  species,
  fasta_file,
  kallisto_out_path,
  type = deprecated(),
  ensembl_version = NULL,
  ...
)
```

Arguments

species	A character vector of Latin names of species present in this scRNA-seq dataset. This is used to retrieve Ensembl information from biomart.
fasta_file	Character vector of paths to the transcriptome FASTA files used to build the kallisto index. Exactly one of species and fasta_file can be missing.
kallisto_out_path	Path to the kallisto bus output directory.
type	Deprecated.
ensembl_version	Version of Ensembl to use if fasta_file is not supplied. If NULL, then using the newest version available on AnnotationHub.
...	Other arguments passed to tr2g_ensembl such as other_attrs, arguments passed to tr2g_EnsDb, except get_transcriptome which is always set to FALSE. If fasta_files is supplied instead of species, then this will be extra arguments to tr2g_fasta, such as use_transcript_version and use_gene_version.

Value

A data frame with two columns: gene and transcript, with Ensembl gene and transcript IDs (with version number), in the same order as in the transcriptome index used in kallisto.

Note

This function has been superseded by the new version of tr2g_* functions that can extract transcriptome for only the biotypes specified and with only the standard chromosomes. The new version of tr2g_* functions also sorts the transcriptome so the tr2g and the transcriptome have transcripts in the same order.

See Also

Other functions to retrieve transcript and gene info: sort_tr2g(), tr2g_EnsDb(), tr2g_TxDb(), tr2g_ensembl(), tr2g_fasta(), tr2g_gff3(), tr2g_gtf()

Examples

```
# Download dataset already in BUS format
library(TENxBUSData)
TENxBUSData(".", dataset = "hgmm100")
tr2g <- transcript2gene(c("Homo sapiens", "Mus musculus"),
  write_tr2g = FALSE, ensembl_version = 99,
  kallisto_out_path = "./out_hgmm100")
# Clean up files from the example
unlink("out_hgmm100")
```

validate_velocity_input *Validate input to get_velocity_files*

Description

Validate input to get_velocity_files

Usage

```
validate_velocity_input(
  L,
  Genome,
  Transcriptome,
  out_path,
  compress_fa,
  width,
  exon_option
)
```

Arguments

L	Length of the biological read. For instance, 10xv1: 98 nt, 10xv2: 98 nt, 10xv3: 91 nt, Drop-seq: 50 nt. If in doubt check read length in a fastq file for biological reads with the bash commands: If the fastq file is gzipped, then do `zcat your_file.fastq.gz | head` on Linux. If on Mac, then `zcat < your_file.fastq.gz | head`. Then you will see lines with nucleotide bases. Copy one of those lines and determine its length with `str_length` in R or `echo -n <the sequence> | wc -c` in bash. Which file corresponds to biological reads depends on the particular technology.
Genome	Either a `BSgenome` or a `XStringSet` object of genomic sequences, where the intronic sequences will be extracted from. Use `genomeStyles` to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.
Transcriptome	A `XStringSet`, a path to a fasta file (can be gzipped) of the transcriptome which contains sequences of spliced transcripts, or `NULL`. The transcriptome here will be concatenated with the intronic sequences to give one fasta file. When `NULL`, the transriptome sequences will be extracted from the genome given the gene annotation, so it will be guaranteed that transcript IDs in the transcriptome and in the annotation match. Otherwise, the type of transcript ID in the transcriptome must match that in the gene annotation supplied via argument `X`.
out_path	Directory to save the outputs written to disk. If this directory does not exist, then it will be created. Defaults to the current working directory.

`compress_fa` Logical, whether to compress the output fasta file. If `TRUE`, then the fasta file will be gzipped.

`width` Maximum number of letters per line of sequence in the output fasta file. Must be an integer.

`exon_option` Character, indicating how exonic sequences should be included in the kallisto index. Must be one of the following:

full The full cDNA sequences, which include the full exonic sequences, will be used. This is the default.

junction Only the exon-exon junctions, with L-1 bases on each side of the junctions, will be used.

Value

Will throw error if validation fails. Returns a named list whose first element is the normalized path to output directory, and whose second element is the normalized path to the transcriptome file if specified.

`write_velocity_output` *Write the files for RNA velocity to disk*

Description

Write the files for RNA velocity to disk, in the specified output directory.

Usage

```
write_velocity_output(
  out_path,
  introns,
  Genome,
  Transcriptome,
  isoform_action,
  exon_option,
  tr2g_cdna,
  compress_fa,
  width
)
```

Arguments

`out_path` Directory to save the outputs written to disk. If this directory does not exist, then it will be created.

`introns` Intronic ranges plus flanking region, returned by `get_intron_flanks`.

`Genome` Either a BSgenome or a XStringSet object of genomic sequences, where the intronic sequences will be extracted from. Use genomeStyles to check which styles are supported for your organism of interest; supported styles can be interconverted. If the style in your genome or annotation is not supported, then the style of chromosome names in the genome and annotation should be manually set to be consistent.

`Transcriptome` A XStringSet, a path to a fasta file (can be gzipped) of the transcriptome which contains sequences of spliced transcripts, or `NULL`. The transcriptome here will be concatenated with the intronic sequences to give one fasta file. When `NULL`, the transriptome sequences will be extracted from the genome given the gene annotation, so it will be guaranteed that transcript IDs in the transcriptome and in the annotation match. Otherwise, the type of transcript ID in the transcriptome must match that in the gene annotation supplied via argument `X`.

`isoform_action` Character, indicating action to take with different transcripts of the same gene. Must be one of the following:

collapse First, the union of all exons of different transcripts of a gene will be taken. Then the introns will be inferred from this union. Only the flanked intronic sequences are affected; isoforms will always be taken into account for spliced sequences or exon-exon junctions.

separate Introns from different transcripts will be kept separate.

`exon_option` Character, indicating how exonic sequences should be included in the kallisto index. Must be one of the following:

full The full cDNA sequences, which include the full exonic sequences, will be used. This is the default.

junction Only the exon-exon junctions, with L-1 bases on each side of the junctions, will be used.

`tr2g_cdna` A data frame with columns `transcript` and `gene` that maps transcripts to genes for spliced transcripts.

`compress_fa` Logical, whether to compress the output fasta file. If `TRUE`, then the fasta file will be gzipped.

`width` Maximum number of letters per line of sequence in the output fasta file. Must be an integer.

Value

Nothing into the R session. The files are written to disk.

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