

Package: rnaseqDTU (via r-universe)

October 4, 2026

Title RNA-seq workflow for differential transcript usage following Salmon quantification

Version 1.32.0

Date 2018-06-27

Description RNA-seq workflow for differential transcript usage (DTU) following Salmon quantification. This workflow uses Bioconductor packages tximport, DRIMSeq, and DEXSeq to perform a DTU analysis on simulated data. It also shows how to use stageR to perform two-stage testing of DTU, a statistical framework to screen at the gene level and then confirm which transcripts within the significant genes show evidence of DTU.

Depends R (>= 3.5.0), DRIMSeq, DEXSeq, stageR, DESeq2, edgeR, rafalib, devtools

License Artistic-2.0

LazyData true

VignetteBuilder knitr

biocViews Workflow, GeneExpressionWorkflow, ImmunoOncologyWorkflow

Suggests knitr, rmarkdown

NeedsCompilation no

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

Workflow TRUE

RoxygenNote 6.0.1

Config/pak/sysreqs cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev git make libharfbuzz-dev libbz2-dev libgit2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

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Contents

cts	2
dge.genes	3
disps	3
dte.genes	4
dtu.genes	4
dxr	5
dxr.g	5
fold_changes	6
frag_GC_bias	6
iso.dge	7
iso.dte	7
iso.dte.only	8
iso.dtu	8
res	9
res.txp	9
sim.counts.mat	10
sim_counts	10
tpms	11
txdf	11
txi.g	12
Index	13

cts	<i>Estimated Salmon counts (6 vs 6)</i>
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Description

The estimated Salmon counts (scaledTPM) generated as shown in the early steps in the workflow.

Usage

cts

Format

matrix

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

`dge.genes`*Genes with differential gene expression*

Description

The names of the genes in which the expression of all transcripts was multiplied by a common fold change.

Usage`dge.genes`**Format**`character`**Source**

<http://dx.doi.org/10.12688/f1000research.15398.1>

`disps`*Transcript-level dispersion parameter*

Description

The dispersion parameter used to generate the transcript-level Negative Binomial counts. Drawn from estimated dispersion from GEUVADIS project samples. Matches the transcripts in `sim_counts`.

Usage`disps`**Format**`numeric`**Source**

<http://dx.doi.org/10.12688/f1000research.15398.1>

dte.genes

Genes with differential transcript expression

Description

The names of the genes in which the expression of a single transcript was multiplied by a fold change.

Usage

dte.genes

Format

character

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

dtu.genes

Genes with differential transcript usage

Description

The names of the genes in which two transcripts had their abundance (TPM) swapped. Two expressed transcripts were chosen if possible, or one expressed and one non-expressed.

Usage

dtu.genes

Format

character

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

dxr	<i>DEXSeq transcript-level results</i>
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Description

DEXSeq transcript-level results - see workflow for details.

Usage

dxr

Format

data.frame

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

dxr.g	<i>DEXSeq gene-level results</i>
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Description

DEXSeq gene-level results - see workflow for details.

Usage

dxr.g

Format

data.frame

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

fold_changes	<i>Simulation fold changes</i>
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Description

A matrix of fold changes for group 1 and group 2, as in the format required for polyester input. The majority of the fold changes are 1. Matches the transcripts in sim_counts.

Usage

fold_changes

Format

matrix

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

frag_GC_bias	<i>Fragment GC bias</i>
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Description

The GC bias matrix as returned by plotGC in the alpine package. The columns correspond to GEUVADIS samples as indicated in this workflow publication, and each row corresponds to a percentile of GC, with 101 rows in total. The first 12 columns were used to generate realistic fragment GC bias using alpine and polyester.

Usage

frag_GC_bias

Format

matrix

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

iso.dge*Isoforms in the genes with DGE*

Description

A logical vector along all transcripts indicating which transcripts are in the genes with differential gene expression.

Usage

iso.dge

Format

logical

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

iso.dte*Isoforms with DTE*

Description

A logical vector along all transcripts indicating which transcripts are chosen for differential transcript expression.

Usage

iso.dte

Format

logical

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

iso.dte.only	<i>Isoforms with DTE and not DTU</i>
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Description

A logical vector along all transcripts indicating which transcripts are chosen for differential transcript expression, and which are the only expressed transcript in the gene, thus not participating in differential transcript usage.

Usage

iso.dte.only

Format

logical

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

iso.dtu	<i>Isoforms with DTU</i>
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Description

A logical vector along all transcripts indicating which transcripts in the genes chosen for differential transcript usage are chosen to have their abundance (TPM) swapped.

Usage

iso.dtu

Format

logical

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

res	<i>DRIMSeq gene-level results</i>
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Description

DRIMSeq gene-level results - see workflow for details.

Usage

res

Format

data.frame

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

res.txp	<i>DRIMSeq transcript-level results</i>
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Description

DRIMSeq transcript-level results - see workflow for details.

Usage

res.txp

Format

data.frame

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

sim_counts.mat	<i>Simulated counts</i>
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Description

The simulated counts for the two groups (columns). Matches the transcripts in sim_counts.

Usage

```
sim_counts.mat
```

Format

matrix

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

sim_counts	<i>Simulated counts for group 1</i>
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Description

The simulated counts as provided to polyester (representing the base line counts for group 1). The represented transcripts are a subset of all transcripts in the reference, as we do not simulate from transcripts with an expected count of 5 or more.

Usage

```
sim_counts
```

Format

numeric

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

tpms	<i>Simulated abundances</i>
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Description

The simulated abundances (TPM) for the two groups (columns). The transcripts correspond to the human transcripts from GENCODE version 28.

Usage

tpms

Format

matrix

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

txdf	<i>Transcript-to-gene data.frame</i>
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Description

A table matching transcript to gene, and providing the number of transcripts per gene. The GTF for human from GENCODE version 28 was used to generate this data.frame.

Usage

txdf

Format

data.frame

Source

<http://dx.doi.org/10.12688/f1000research.15398.1>

`txi.g`*Gene-level tximport object*

Description

The tximport object, summarized to gene level, generated as shown in the DGE section of the workflow.

Usage`txi.g`**Format**`list`**Source**

<http://dx.doi.org/10.12688/f1000research.15398.1>

Index

* datasets

- cts, [2](#)
- dge.genes, [3](#)
- disps, [3](#)
- dte.genes, [4](#)
- dtu.genes, [4](#)
- dxr, [5](#)
- dxr.g, [5](#)
- fold_changes, [6](#)
- frag_GC_bias, [6](#)
- iso.dge, [7](#)
- iso.dte, [7](#)
- iso.dte.only, [8](#)
- iso.dtu, [8](#)
- res, [9](#)
- res.txp, [9](#)
- sim.counts.mat, [10](#)
- sim_counts, [10](#)
- tpms, [11](#)
- txdf, [11](#)
- txi.g, [12](#)

sim.counts.mat, [10](#)

sim_counts, [10](#)

tpms, [11](#)

txdf, [11](#)

txi.g, [12](#)

cts, [2](#)

dge.genes, [3](#)

disps, [3](#)

dte.genes, [4](#)

dtu.genes, [4](#)

dxr, [5](#)

dxr.g, [5](#)

fold_changes, [6](#)

frag_GC_bias, [6](#)

iso.dge, [7](#)

iso.dte, [7](#)

iso.dte.only, [8](#)

iso.dtu, [8](#)

res, [9](#)

res.txp, [9](#)