

Package ‘RnaSeqTutorial’

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Title RNA-Seq Tutorial (EBI Cambridge UK, October 2011)

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Description A selection of RNA-Seq data to get familiar with the related Bioconductor core packages and the easyRNASeq package.

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Depends R (>= 2.15.0), methods, easyRNASeq

Suggests Rsamtools, Short-Read, BSgenome.Dmelanogaster.UCSC.dm3, GenomicRanges, biomaRt, genomeIntervals

biocViews ExperimentData, RNAseqData

R topics documented:

gAnnot	1
RnaSeqTutorial	2
Index	4

gAnnot *Drosophila melanogaster genic annotation retrieved from FlyBase v5.29 (June 2010)*

Description

Annotation for *D. melanogaster* retrieved as a gff file from FlyBase (Tweedie et al., 2009) and post-processed. This file should not be used for analyses purposes.

Usage

```
data(gAnnot)
```

See Also

The package vignette: `RNAseq.use.case`.

RnaSeqTutorial

An RNA-Seq tutorial

Description

This tutorial, described in the attached `RNAseq.use.case` vignette, introduces the core Bioconductor packages necessary for processing RNA sequencing data. It then shows how the `RNAseq` package can simplify this task and permit new processing to be done on Next-Generation Sequencing data. It was used during the Bioconductor workshop at the EMBL, Heidelberg, Germany in June 2010 and at the EBI, Hinxton, UK in March 2011.

Usage

```
vignette("RNAseq.use.case")
```

Arguments

`RNAseq.use.case`
The vignette containing the tutorial.

Format

The different data available are:

- in data:
 - `gAnnot` A file containing the *Drosophila melanogaster* genic annotation retrieved from FlyBase v5.29 (June 2010) and converted into a [RangedData](#) object.
- in `example_files`:
 - `ACACTG.bam`, `ACACTG.bam`, `ATGGCT.bam`, `TTGCGA.bam` 4 RNA-Seq samples from *D. melanogaster* demultiplexed, with their associated `.bai` indexes
 - `annot.gff` The `gff` file containing the information stored in the `gAnnot` [RangedData](#) object mentioned above.
 - `gapped.bam` A *D.melanogaster* RNA-Seq file containing a few examples of gapped alignment (done by `tophat`) surrounding the `Mef2` gene locus
 - `multiplex_export.txt.gz` The original export file containing the multiplexed data mentioned above.
 - `subset_export.txt.gz` A *D.melanogaster* RNA-Seq export file, restricted to 100,000 reads
 - `subset.bam` The same aligned against the reference genome (*D.melanogaster* v3).

Examples

```
## Not run: vignette("RNAseq.use.case")
```

Index

*Topic **datasets**

gAnnot, [1](#)

RnaSeqTutorial, [2](#)

gAnnot, [1](#)

RangedData, [2](#)

RnaSeqTutorial, [2](#)

vignette (RnaSeqTutorial), [2](#)