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 (>= 3.0.2), methods, easyRNASeq

Suggests Rsamtools, ShortRead, BSgenome.Dmelanogaster.UCSC.dm3, GenomicAlignments, biomaRt, genomeIntervals

biocViews ExperimentData, Drosophila_melanogaster_Data, RNASeqData

NeedsCompilation no

R topics documented:

`Deprecated data` *The following data has been deprecated:*

- *annot.gff*

Description

- The annot.gff file containing exon annotation from FlyBase v5.29 (http://flybase.org, Tweedie et al., 2009) has been superseded by the Dmel-mRNA-exon-r5.52.gff3 file from FlyBase v5.52 (April 2013) containing both mRNA and exon annotation type.

`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: RnaSeqTutorial.

`RnaSeqTutorial` *An RNA-Seq tutorial*

Description

This tutorial, decribed in the attached RnaSeqTutorial vignette, introduces the core Bioconductor packages necessary for processing RNA sequencing data. It then introduces the easyRNAseq package that can simplify this task and offer different processing to be done one Next-Generation Sequencing data. It was used for various Bioconductor workshops since June 2010.

Usage

```
vignette("RnaSeqTutorial")
```

Arguments

`RnaSeqTutorial`	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. Although the corresponding gff file has been deprecated - see below - that annotation is still usable.
  - `gRngList` A file containing the Drosophila melanogaster mRNA and exon annotation retrieved from FlyBase v5.52 (April 2013) and converted into a GRangesList object.
- in extdata:
  - `ACACTG.bam, ACACTG.bam, ATGGCT.bam, TTGCGA.bam` 4 RNA-Seq samples from D. melanogaster demultiplexed, with their associated .bai indexes

  - `Dmel-mRNA-exon-r5.52.gff3` The gff3 file containing the information stored in the gRngList GRangesList object mentioned above.
  - `annot.gff` Deprecated. 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("RnaSeqTutorial")
```

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