

Package ‘cheung2010’

October 7, 2015

Title resources for genetics of gene expression based on Cheung et al
2010

Version 0.6.0

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Description Data resources related to the PLoS Biology paper Polymorphic
Cis- and Trans-Regulation of Human Gene
Expression, including small-footprint smlSet support for 147 hgfocus
arrays and corresponding HapMap genotypes at 1.3 million SNP;
0.0.22+ includes cheung_eset... from Leek et al RECOUNT myrna output

Depends R (>= 2.13.0), Biobase, GGtools, GenomicRanges, hgfocus.db

Imports AnnotationDbi

Suggests SNPlocs.Hsapiens.dbSNP.20120608

Enhances parallel

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License Artistic-2.0

LazyLoad yes

biocViews Homo_sapiens_Data, SequencingData, RNASeqData, SNPData,
HapMap

NeedsCompilation no

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cheung2010-package *resources for genetics of gene expression based on Cheung et al 2010*
 ~~ package title ~~

Description

Data resources related to the PLoS Biology paper Polymorphic Cis- and Trans-Regulation of Human Gene Expression, including small-footprint smlSet support for 147 hgfocus arrays and corresponding HapMap genotypes at 1.3 million SNP ~~ A concise (1-5 lines) description of the package
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Details

Package: cheung2010
Version: 0.0.16
Depends: R (>= 2.13.0), Biobase, GGtools, GenomicRanges, hgfocus.db
Imports: AnnotationDbi
Suggests: SNPlocs.Hsapiens.dbSNP.20101109
License: private
LazyLoad: yes
Packaged: 2011-04-13 16:52:30 UTC; stvjc
Built: R 2.14.0; ; 2011-06-13 16:19:18 UTC; unix

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cheung2010locs cheung2010locs gives locations for HapMap phase
 3 SNPs for CEPH CEU; addresses are for hg18
cheung_eset from RECOUNT web resource for RNA-seq <http://bowtie-bio.sourceforge.net/recount/>
cheung_eset_notrunc from RECOUNT web resource for RNA-seq

Further information is available in the following vignettes:

 cheungTrans (source, pdf)

This package assembles data relevant to Cheung et al PLoS Biology (2010; 8(9)).

Author(s)

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Maintainer: Vince Carey <stvjc@channing.harvard.edu>

cheung2010locs	<i>cheung2010locs gives locations for HapMap phase 3 SNPs for CEPH CEU</i>
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Description

cheung2010locs gives locations for HapMap phase 3 SNPs for CEPH CEU

Note: updated 29 Sept 2014 to deal with new Seqinfo structure, making explicit the reference to hg18.

The cheung2010locs seems no longer necessary (29 Sept 2014) since snplocsDefault() is targeting the 20120608 SNPlocs package, which would be in sync with the contemporaneous hgfocus.db package.

Usage

```
data(cheung2010locs)
```

Format

The format is:

Formal class 'GRangesList' [package "GenomicRanges"] with 5 slots

..@ partitioning :Formal class 'PartitioningByEnd' [package "IRanges"] with 5 slots

.. ..@ end : int [1:22] 112259 226087 320873 406401 493642 585295 660727 735268 798907 871895 ...

.. ..@ NAMES : chr [1:22] "chr1" "chr2" "chr3" "chr4" ...

.. ..@ elementType : chr "integer"

.. ..@ elementMetadata: NULL

.. ..@ metadata : list()

..@ unlistData :Formal class 'GRanges' [package "GenomicRanges"] with 6 slots

.. ..@ seqnames :Formal class 'Rle' [package "IRanges"] with 4 slots

..@ values : Factor w/ 22 levels "chr1","chr2",...: 1 2 3 4 5 6 7 8 9 10 ...

..@ lengths : int [1:22] 112259 113828 94786 85528 87241 91653 75432 74541 63639 72988 ...

..@ elementMetadata: NULL

..@ metadata : list()

.. ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots

..@ start : int [1:1365825] 554340 557616 711153 742429 742584 743268 744045 750775 751010 751595 ...

..@ width : int [1:1365825] 1 1 1 1 1 1 1 1 1 1 ...

..@ NAMES : chr [1:1365825] "rs6650104" "rs11510103" "rs12565286" "rs3094315" ...

..@ elementType : chr "integer"

..@ elementMetadata: NULL

..@ metadata : list()

.. ..@ strand :Formal class 'Rle' [package "IRanges"] with 4 slots

..@ values : Factor w/ 3 levels "+","-","*": 1

..@ lengths : int 1365825

```

.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. .. ..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 1365825
.. .. ..@ listData :List of 1
.. .. .. ..$ assignment: Factor w/ 7 levels "A/C","A/G",...: 3 3 5 3 3 2 3 6 6 ...
.. .. .. ..@ elementType : chr "ANY"
.. .. .. ..@ elementMetadata: NULL
.. .. .. ..@ metadata : list()
.. .. ..@ seqinfo :Formal class 'Seqinfo' [package "GenomicRanges"] with 3 slots
.. .. .. ..@ seqnames : chr [1:22] "chr1" "chr2" "chr3" "chr4" ...
.. .. .. ..@ seqlengths : int [1:22] NA NA NA NA NA NA NA NA NA NA ...
.. .. .. ..@ is_circular: logi [1:22] NA NA NA NA NA NA ...
.. .. ..@ metadata : list()
..@ elementType : chr "GRanges"
..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 22
.. .. ..@ listData : Named list()
.. .. ..@ elementType : chr "ANY"
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
..@ metadata : list()

```

Details

obtained as the 'support' elements after [read.HapMap.data](#) was run on the files noted below.

Source

for example,

http://hapmap.ncbi.nlm.nih.gov/downloads/genotypes/hapmap3_r3/hapmap_format/polymorphic/genotypes_chr17_CEU_phase3.3_nr.b36_fwd.txt.gz

Examples

```

data(cheung2010locs)
names(cheung2010locs)
cheung2010locs[[1]][1:3]

```

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*Topic **datasets**

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