

Package ‘cheung2010’

April 13, 2017

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

Version 0.12.0

Author Vince Carey <stvjc@channing.harvard.edu>

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

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

License Artistic-2.0

LazyLoad yes

biocViews Homo_sapiens_Data, SequencingData, RNASeqData, SNPData,
HapMap

NeedsCompilation no

R topics documented:

cheung2010-package	1
cheung2010locs	2

Index	5
--------------	----------

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 ~~~

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

Index:

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)

Vince Carey <stvjc@channing.harvard.edu>

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

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

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 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]
```

Index

*Topic **datasets**

cheung2010locs, [2](#)

cheung2010 (cheung2010-package), [1](#)

cheung2010-package, [1](#)

cheung2010locs, [2](#)

cheung_eset (cheung2010-package), [1](#)

cheung_eset_notrunc
(cheung2010-package), [1](#)

ex (cheung2010-package), [1](#)

read.HapMap.data, [4](#)