Package ‘harbChIP’

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Title Experimental Data Package: harbChIP

Description data from a yeast ChIP-chip experiment

Version 1.14.0

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Depends R (>= 2.10.0), tools, utils, IRanges, Biobase (>= 2.5.5), Biostrings

Imports methods, stats

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biocViews ExperimentData, Saccharomyces_cerevisiae_Data, SequencingData

NeedsCompilation no

R topics documented:

| allhex             | utility function: get all hexamers in upstream sequence for an ORF |

Description
utility function: get all hexamers in upstream sequence for an ORF

Usage
allhex(orf, usobj)
**Arguments**

- **orf** character string, ORF name
- **usobj** upstreamSeqs object

**Details**

computes Biostrings Views

**Value**

computes Biostrings Views

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

```r
data(sceUpstr)
allhex("YAL001C", sceUpstr)
```

---

**Description**

workflow component – build an upstreamSeqs instance from a FASTA read

**Usage**

```r
buildUpstreamSeqs2(fastaRead, organism="sce", provenance="harmen")
```

**Arguments**

- **fastaRead** results of a readFASTA from Biostrings
- **organism** string naming organism
- **provenance** string or structure describing provenance

**Details**

generates an instance of upstreamSeqs

**Value**

generates an instance of upstreamSeqs

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>
**chkMotif4TF**

**Examples**

```r
# x = readFASTA(...)  
# y = buildUpstreamSeqs2(x)
```

**Description**

analyze relationship between motif frequency and binding intensity for selected motif and TF

**Usage**

```r
chkMotif4TF(motif, TF, chset, upstr, bthresh=2, countthresh=0)
```

**Arguments**

- **motif**: character string in alphabet known to Biostrings
- **TF**: name of a TF (sample name in the ChIP-chip data structure chset
- **chset**: an ExpressionSet instance harboring ChIP-chip data
- **upstr**: an instance of upstreamSeqs
- **bthresh**: threshold for binding intensity results to declare TF 'bound' to the upstream region
- **countthresh**: threshold for motif count to be considered 'present' in upstream region

**Details**

Uses `countPattern` to perform motif count.

**Value**

a list with elements call, table, and test, the latter providing the result of `fisher.test`

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

```r
# slow
## Not run:
data(harbChIP)  
data(sceUpstr)  
chkMotif4TF("CGGCCG", "RDS1", harbChIP, sceUpstr)
## End(Not run)
```
harbChIP  Experimental Data Package: harbChIP

Description

binding ratios and intergenic region data from a ChIP-chip experiment in yeast

Usage

data(harbChIP)

Format

The format is: An ExpressionSetObject with covariates:

• txFac: transcription factor symbol from Harbison website CSV file columnnames

Note

derived from web site jura.wi.mit.edu/young_public/regulatory_code/GWLD.html, binding ratios

Examples

data(harbChIP)
harbChIP
experimentData(harbChIP)
exprs(harbChIP)[1:6,1:7]
dim(exprs(harbChIP))
pData(featureData(harbChIP))[1:6,]

sceUpstr  Biostrings representations of S. cerevisiae upstream regions

Description

Biostrings representations of S. cerevisiae upstream regions

Usage

data(sceUpstr)

Details

environment-based S4 object with DNAstring elements

Value

environment-based S4 object with DNAstring elements
upstreamSeqs-class

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

data(sceUpstr)
sceUpstr
getUpstream("YAL001C", sceUpstr)

Description

Container for a collection of upstream sequences

Objects from the Class

Objects can be created by calls of the form new("upstreamSeqs", ...). Environments are used to store collections of DNAstrings.

Slots

seqs: Object of class "environment"
chrom: Object of class "environment"
revComp: Object of class "environment"
type: Object of class "environment"
organism: Object of class "character"
provenance: Object of class "ANY"

Methods

Nmers signature(n = "numeric", orf = "character", usobj = "upstreamSeqs"): obtain all subsequences of length n as view elements of a DNA string

keys signature(x = "upstreamSeqs"): ...
organism signature(x = "upstreamSeqs"): ...
seqs signature(x = "upstreamSeqs"): ...
show signature(object = "upstreamSeqs"): ...

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

showClass("upstreamSeqs")
data(sceUpstr)
sceUpstr
keys(sceUpstr)[1:5]
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