Package ‘harbChIP’

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Title Experimental Data Package: harbChIP
Description data from a yeast ChIP-chip experiment
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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

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

chkMotif4TF  
\textit{analyze relationship between motif frequency and binding intensity for selected motif and TF}

Description

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

Usage

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

Arguments

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

Details

Uses \texttt{countPattern} to perform motif count.

Value

a list with elements \texttt{call}, \texttt{table}, and \texttt{test}, the latter providing the result of \texttt{fisher.test}

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

# 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](http://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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