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

Description
workflow component – build an upstreamSeqs instance from a FASTA read

Usage
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)
```
Experimental Data Package: harbChIP

**Description**

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

**Usage**

```r
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**

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

---

Biostrings representations of *S. cerevisiae* upstream regions

**Description**

Biostrings representations of *S. cerevisiae* upstream regions

**Usage**

```r
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

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

---

**upstreamSeqs-class**  
*Class* "upstreamSeqs"

**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", useobj = "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

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