harbChIP

March 19, 2011

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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)
```

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buildUpstreamSeqs2 *workflow component – build an upstreamSeqs instance from a FASTA read*

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>

Examples

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

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chkMotif4TF   *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

`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

```
# 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,]
```

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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

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

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

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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", 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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