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

```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

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,]

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 DNA strings.

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)

~who you are~

Examples

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