allhex

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)

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)
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("CGGCGG", "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)

data(sceUpstr)
sceUpstr
keys(sceUpstr)[1:5]

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)

who you are

Examples

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