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ALICOR .............................. aligned and interpolated correlation for local maximum traces for two scatterplots

Description

aligned and interpolated correlation for local maximum traces from two scatterplots

Usage

allicor(x1, y1, x2, y2, bin = 50000)
ALICOR(ssr, dns = rawCD4, bin = 50000)

Arguments

x1
domain points for first scatterplot

y1
range points for first scatterplot

x2
domain points for second scatterplot

y2
range points for second scatterplot

ssr
an instance of class snpScreenResult

dns
an instance of class hg18track

bin
bin size, units are base pairs
Details

We define a scatterplot to be a pair of vectors \((x, y)\). We are interested in measuring the distance between two scatterplots, focusing on the locations of local peaks and valleys. Two scatterplots are close if their peaks and valleys in \(y\) are nearby in \(x\).

We have no restrictions on commonalities between the scatterplots, but this only makes sense if there is reasonable overlap between their \(x\) ranges.

The algorithm, implemented in low-level function `alicor`, is as follows. Use parameter `bin` to define a grid in \(x\) for each scatterplot, and compute the maximum \(y\) value in each \(x\)-grid interval. Compute a common domain for the two scatterplots based solely on \(x_1\). Linearly interpolate the maximal series for each scatterplot on the common domain. Compute the correlation coefficient for the resulting interpolated series.

The higher-level function `ALICOR` adapts this to `snpScreenResult plot_mlp display data` and to hg18 annotation track data.

Value

scalar correlation coefficient

Note

Many variations on this algorithm are possible, but the code is not very flexible at this time.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```r
data(sOSR2)
data(c19g)
juxtaPlot(c19g, sOSR2)
ALICOR(sOSR2, c19g)
```

---

**rawCd4DnaseI**

*A data frame with information on the UCSC browser track related to DNaseI hypersensitivity*

Description

A data frame with information on the UCSC browser track related to DNaseI hypersensitivity; the `rawCD4` object is an eSet extension representing the same information; `rawHelaDnaseI` is like `rawCD4` but results on Hela cells.

Usage

```r
data(rawCd4DnaseI)
data(rawHelaDnaseI)
data(rawCD4)
```
Details

Obtained from a MySQL representation of the data distributed at the Genome Browser FTP site

Value

a data.frame

Author(s)

Vince Carey &lt;stvjc@channing.harvard.edu&gt;

References

hgdownload.cse.ucsc.edu ... it appears that they do not offer the MYD/MYI representations, just the txt.gz and sql files now. So if you obtain the encodeNhgriDnaseHsChipRawCd4.txt and sql files at goldenPath/currentGenomes/Homo_Sapiens/encode/database, you can reconstruct the underlying data for this data.frame (hg18, Nov 2007).

Examples

data(rawCd4DnaseI)
dim(rawCd4DnaseI)
rawCd4DnaseI[1:5,]
library(lattice)
xyplot(dataValue~chromStart|chrom, data=rawCd4DnaseI, subset=chrom %in%
c("chr1", "chr10", "chr19", "chr20"), scales=list(x=list(relation="free")))

hgl8track-class

Class "hgl8track" container for hg18 annotation found in genome browser track files; class "chrnum" extends numeric for an indexing application on hgl8track objects.

Description

container for hg18 annotation found in genome browser track files

Objects from the Class

Objects can be created by calls of the form new("hgl8track", assayData, featureData, experimentData, annotation, dataVals, ...). These are single-sample eSet instances.

Note that demoTrk19 is a restriction of the rawCD4 structure to the interval of chromosome 19 that was assayed in the ENCODE project for DnaseI hypersensitivity.

Slots

assayData: Object of class "AssayData" ~~
phenoData: Object of class "AnnotatedDataFrame" ~~
featureData: Object of class "AnnotatedDataFrame" ~~
experimentData: Object of class "MIAME" ~~
annotation: Object of class "character" ~~
.__classVersion__: Object of class "Versions" ~
Extends

Class "eSet", directly. Class "VersionedBiobase", by class "eSet", distance 2. Class "Versioned", by class "eSet", distance 3.

Methods

[ signature(x = "hg18track")]: select using numeric, logical, or chrnum indices.

chrnum signature(object = "hg18track")]: extract numeric tokens for chromosome number at which data values are obtained; note that chrnum is also used as name of a class.

dataVals signature(object = "hg18track")]: actual data values

getTrkXY signature(object = "hg18track", type = "character")]: obtain a list with components x, y indicating location and data value respectively; location is within chromosome; default type is 'midpoint' of locations given as intervals

closeTrk signature(object = "hg18track", type = "missing")]: take default midpoint x values corresponding to data values

rangeLocs signature(object = "hg18track")]: if measures from only one chromosome are present, this returns low and high values of chromStart and chromEnd respectively, otherwise error.

closeTrk signature(obj = "hg18track", low="numeric", hi="numeric", attr="ANY")]: create a restriction of the track using an interval specification. by default the chromStart featureData component is used for coordinates to clip; if attr is non-missing, the featureData component named by attr will be used.

initialize signature(.Object = "hg18track")]: create a new instance

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

showClass("hg18track")
data(rawCD4)
rawCD4
rawCD4.chr1 = rawCD4[ chrnum(1), ]
rangeLocs(rawCD4.chr1)
plot(getTrkXY(rawCD4.chr1), ylab="data value", xlab="interval midpt on chr 1"
)
c52 = closeTrk(rawCD4[ chrnum(5), ], 1.30e8, 1.33e8 )
plot(getTrkXY(c52))

---

juxtaPlot two-panel plot with track info and snp screen t-values

description

two-panel plot with track info and snp screen t-values

Usage

juxtaPlot(trk, ssr)
**Arguments**

<table>
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<tr>
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<th>instance of <code>hg18track</code></th>
</tr>
</thead>
<tbody>
<tr>
<td>ssr</td>
<td>instance of <code>GGtools.snpScreenResult</code></td>
</tr>
</tbody>
</table>

**Details**

`xyplot` of lattice package is used.

**Value**

`xyplot` output; use `print` in Sweave.

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```r
data(sOSR2)
data(c19g)
juxtaPlot(c19g, sOSR2)
```
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