Package ‘ecolitk’

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Depends  R (>= 2.10)
Imports  Biobase, graphics, methods
Suggests ecoliLeucine, ecolicdf, graph, multtest, affy
Description Meta-data and tools to work with E. coli. The tools are mostly plotting functions to work with circular genomes. They can used with other genomes/plasmids.
License  GPL (>= 2)
NeedsCompilation no

R topics documented:

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ecoli.m52.genome

Escherichia coli data

Description

Meta-data related to Escherichia coli

Usage

data(ecoli.m52.genome)
data(ecoligenomeCHRLOC)
data(ecoligenomeSYMBOL2AFFY)
data(ecoligenomeSYMBOL)
data(ecoligenomeSTRAND)
data(ecoligenome.operon)
ecoli.len

Format

The format for ecoli.m52.genome is character with genome sequence. The format for ecoligenomeCHRLOC is an environment (as a hash table). Each key is an Affymetrix probe set ID, and each value is vector of two integers (begining and end - see the details below) The format for ecoligenomeSYMBOL2AFFY is an environment (as a hash table). Each key is a gene symbol name. The format for ecoligenomeSYMBOL is an environment (as a hash table). Each key is an Affymetrix probe set id ecoli.len is a variable containing the size of the genome in ecoli.m52.genome.

Details

The environments ecoligenomeSYMBOL2AFFY and ecoligenomeSYMBOL are like the ones in the data packages built by armBuilder.

The environment ecoligenomeCHRLOC differs: two integers are associated with each key, one corresponds to the begining of the segment the other to the end.

The environment ecoligenomeSTRAND returns a logical. TRUE means that the orientation is ‘+’, FALSE means that the orientation is ‘-’ (and NA is used when irrelevant for the key).

Source


Examples

data(ecoli.m52.genome)
Description

The known operon in the Escherichia coli genome.

Usage

data(ecoligenome.operon)

Format

A data frame with 932 observations (genes) on the following 4 variables.

gene.name  a character vector
gene.annotation  a character vector
operon.name  a factor with levels the names of the operons
operon.comments  a factor with levels the comments for the operons

Details

For some operons, the source of information specifies the existence of regulating elements such as promoter, terminator, box, etc... In those cases, the gene.name is set to "Regulation", and the gene.annotation gives what kind of regulating element it is. If volunteers, it would be neat to map those on the genome... Besides that, not much to add. The data structure is fairly straightforward.

Source

Built from the webpage: http://www.cib.nig.ac.jp/dda/backup/taitoh/ecoli.operon.html

Examples

library(Biobase)
data(ecoligenome.operon)
data(ecoligenomeSYMBOL2AFFY)

## something that might be useful when working with Affymetrix data:
## get the Affymetrix identifiers for the probe sets bundled in operons
## (see the vignette for more details)
ecoligenome.operon$affyid <-
  unname(unlist(mget(ecoligenome.operon$gene.name,
                     ecoligenomeSYMBOL2AFFY, ifnotfound=NA)))
ecoligencodeBNUM

Environments to associate Affymetrix probe set IDs with 'bnum' IDs.

Usage

- data(ecoligencodeBNUM)
- data(ecoligencodeBNUM2SYMBOL)
- data(ecoligencodeBNUM2ENZYME)
- data(ecoligencodeBNUM2GENBANK)
- data(ecoligencodeBNUM2GENEPRODUCT)
- data(ecoligencodeSYMBOL2BNUM)

Format

These are environment objects.

Details

Escherichia coli genes are sometimes identified by 'bnum's. This identifier is typically a 'b' followed by digits.

Source

BNUM numbers were parsed out of the Affymetrix identifiers. BNUM2* were obtained from the GenProtEC website.

ecoligencodeBNUM2MULTIFUN

Environment

Description

An environment to store associations between 'bnum' identifiers (key) and 'MultiFun' identifiers (or strand information).

Usage

- data(ecoligencodeBNUM2MULTIFUN)

Format

The format is: length 0 <environment> - attr(*, "comments")= chr "GenProtEC: MultiFun assignments for E. coli modules September 17th, 2003"
Details

'MultiFun' is a classification scheme. The structure is 'approximately tree-like'. Several 'MultiFun' numbers can be assigned to one 'bnum'.

Source

"http://genprotec.mbl.edu/files/MultiFun.txt"

gccontent

function to compute gccontent

Description

A simple R function to compute the GC content of a sequence

Usage

gccontent(x)

Arguments

x a vector of mode character

Details

This a simple (and not particularly fast) function to compute the GC content of sequence. When speed is an issue, one should use the function in the package matchprobes. This function only exists to avoid dependency on this package.

Value

The GC content (numeric)

linkedmultiget

A function to look for values across linked environments

Description

A function to look for values across linked environments.

Usage

linkedmultiget(x, envir.list = list(), unique = TRUE)

Arguments

x The keys in the first environment in the list.
envir.list A list of environments.
unique Simplify the list returned by ensuring that the values for each key are unique.
Details

Environments can be considered as hashtables. The keys are obviously strings, but in some cases the associated values are also strings. This is the case for annotation environments (as built with the package AnnBuilder). This function helps to look for values across several environments: the keys have associated values in a first environment, these values are used as keys in the second environments, etc...

Value

A list of length the length of x.

Author(s)

Laurent Gautier

See Also

mget

Examples

data(ecoligenomeBNUM)
data(ecoligenomeBNUM2MULTIFUN)
data(multiFun)

## get 5 Affymetrix IDs
set.seed(456)
my.affyids <- sample(ls(ecoligenomeBNUM), 5)

## get the MULTIFUN annotations for them
r <- linkedmultiget(my.affyids, list(ecoligenomeBNUM, ecoligenomeBNUM2MULTIFUN, multiFun))

print(r)

---

**multifun**

**multiFun classification**

Description

The MultiFun classification scheme

Usage

data(multiFun)
data(ecoligenomeMULTIFUN2GO)

Format

These are environments.
pointsCircle

Source

http://genprotec.mbl.edu/files/MultiFun.txt

Examples

## To be done...

pointsCircle Functions to plot circular related figures

Description

Functions to plot circular related figures

Usage

linesCircle(radius, center.x = 0, center.y = 0, edges = 300, ...)  
polygonDisk(radius, center.x = 0, center.y = 0, edges=300, ...)  
arrowsArc(theta0, theta1, radius, center.x = 0, center.y = 0, edges = 10, length = 0.25, angle = 30, code = 2, ...)  
pointsArc(theta0, theta1, radius, center.x = 0, center.y = 0, ...)  
linesArc(theta0, theta1, radius, center.x = 0, center.y = 0, ...)  
polygonArc(theta0, theta1, radius.in, radius.out, center.x = 0, center.y = 0, edges = 10, col = "black", border = NA, ...)  

Arguments

theta0, theta1 start and end angles for the arc
radius radius of the circle
radius.in inner radius
radius.out outer radius
center.x, center.y Coordinates for the center of the circle (default to (0, 0))
edges number of edges the shape is made of
col color
border border (see polygon)
length, angle, code see the corresponding parameters for the function arrows
... optional graphical parameters

Details

Details to come...for now the best to run the examples and experiment by yourself...
Value

Function only used for their border effects.

Author(s)

laurent

Examples

```r
par(mfrow=c(2,2))
n <- 10
thetas <- rev(seq(0, 2 * pi, length=n))
rhos <- rev(seq(1, n) / n)

xy <- polar2xy(rhos, thetas)
colo <- heat.colors(n)

plot(0, 0, xlim=c(-2, 2), ylim=c(-2, 2), type="n")
  for (i in 1:n)
    linesCircle(rhos[i]/2, xy$x[i], xy$y[i])

plot(0, 0, xlim=c(-2, 2), ylim=c(-2, 2), type="n")
  for (i in 1:n)
    polygonDisk(rhos[i]/2, xy$x[i], xy$y[i], col=colo[i])

plot(0, 0, xlim=c(-2, 2), ylim=c(-2, 2), type="n", xlab="", ylab="")
  for (i in 1:n)
    polygonArc(0, thetas[i],
               rhos[i]/2, rhos[i],
               center.x = xy$x[i], center.y = xy$y[i], col=colo[i])

plot(0, 0, xlim=c(-2, 2), ylim=c(-2, 2), type="n", xlab="", ylab="")
  for (i in (1:n)[-1]) {
    linesCircle(rhos[i-1], col="gray", lty=2)
    polygonArc(thetas[i-1], thetas[i],
               rhos[i-1], rhos[i], col=colo[i],
               edges=20)
    arrowsArc(thetas[i-1], thetas[i],
              rhos[i] + 1, col=colo[i],
              edges=20)
  }
```

---

**polar2xy**

*Functions to perform polar coordinate related functions*

**Description**

Functions to perform polar coordinate related functions
### Usage

- `polar2xy(rho, theta)`
- `xy2polar(x, y)`
- `rotate(x, y, alpha)`

### Arguments

- `x` cartesian coordinate
- `y` cartesian coordinate
- `rho` polar radius `rho`
- `theta` polar angle `theta`
- `alpha` angle to perform rotation

### Details

`y` and `theta` can be respectively missing. In this case, `x` and `rho` are expected to be lists with entries `x`, `y`, `rho`, `theta` respectively.

### Examples

```r
n <- 40
nn <- 2
thetas <- seq(0, nn * 2 * pi, length=n)
rhos <- seq(1, n) / n
plot(c(-1, 1), c(-1, 1), type="n")
abline(h=0, col="grey")
abline(v=0, col="grey")
xy <- polar2xy(rhos, thetas)
points(xy$x, xy$y, col=rainbow(n))
```

---

### Description

Functions to plot circular chromosomes informations

### Usage

- `cPlotCircle(radius=1, xlim=c(-2, 2), ylim=xlim, edges=300, main=NULL, main.inside, ...)`
- `chromPos2angle(pos, len.chrom, rot=pi/2, clockwise=TRUE)`
polygonChrom(begin, end, len.chrom, radius.in, radius.out, 
total.edges = 300,
edges = max(round(abs(end - begin)/len.chrom * 
total.edges), 2, na.rm = TRUE),
rot = pi/2, clockwise = TRUE, ...)

linesChrom(begin, end, len.chrom, radius, 
total.edges = 300,
edges = max(round(abs(end - begin)/len.chrom * 
total.edges), 2, na.rm = TRUE),
rot = pi/2, clockwise = TRUE, ...)

ecoli.len

Arguments

radius
xlim, ylim
range for the plot. Can be used to zoom-in a particular region.
pos
begining of the segment (nucleic base number).
end
end of the segment (nucleic base number).
len.chrom
length of the chromosome in base pairs
radius.in
inner radius
radius.out
outer radius
total.edges
total number of edges for the chromosome
edges
number of edges for the specific segment(s)
rot
rotation (default is pi / 2, bringing the angle zero at 12 o’clock)
clockwise
rotate clockwise. Default to TRUE.
main, main.inside
main titles for the plot
...
optional graphical parameters

Details

The function chromPos2angle is a convenience function. The variable ecoli.len contains the size of the Escheria coli genome considered (K12).

Value

Except chromPos2angle, the function are solely used for their border effects.

Author(s)

laurent <laurent@cbs.dtu.dk>
Examples

data(ecoligenomeSYMBOL2AFFY)
data(ecoligenomeCHRLOC)

## find the operon lactose ("lac*" genes)
lac.i <- grep("^lac", ls(ecoligenomeSYMBOL2AFFY))
lac.symbol <- ls(ecoligenomeSYMBOL2AFFY)[lac.i]
lac.affy <- unlist(lapply(lac.symbol, get, envir=ecoligenomeSYMBOL2AFFY))

beg.end <- lapply(lac.affy, get, envir=ecoligenomeCHRLOC)
beg.end <- matrix(unlist(beg.end), nc=2, byrow=TRUE)

lac.o <- order(beg.end[, 1])
lac.i <- lac.i[lac.o]
lac.symbol <- lac.symbol[lac.o]
lac.affy <- lac.affy[lac.o]
beg.end <- beg.end[lac.o, ]

lac.col <- rainbow(length(lac.affy))

par(mfrow=c(2,2))

## plot
cPlotCircle(main="lac genes")
polygonChrom(beg.end[, 1], beg.end[, 2], ecoli.len, 1, 1.2, col=lac.col)
rect(0, 0, 1.1, 1.1, border="red")
cPlotCircle(xlim=c(0, 1.2), ylim=c(0, 1.1))
polygonChrom(beg.end[, 1], beg.end[, 2], ecoli.len, 1, 1.1, col=lac.col)
rect(0.4, 0.8, 0.7, 1.1, border="red")
cPlotCircle(xlim=c(.45, .5), ylim=c(.85, 1.0))
polygonChrom(beg.end[, 1], beg.end[, 2], ecoli.len, 1, 1.03, col=lac.col)
mid.genes <- apply(beg.end, 1, mean)
mid.angles <- chromPos2angle(mid.genes, ecoli.len)
xy <- polar2xy(1.03, mid.angles)
xy.labels <- data.frame(x = seq(0.45, 0.5, length=4), y = seq(0.95, 1.0, length=4))
segments(xy$x, xy$y, xy.labels$x, xy.labels$y, col=lac.col)
text(xy.labels$x, xy.labels$y, lac.symbol, col=lac.col)

wstringapply

Apply a function on a window sliding on a string

wstringapply

Apply a function on a window sliding on a string

Description

Apply a function on a window sliding on a string.

Usage

wstringapply(x, SIZE, SLIDE, FUN, ...)

**Arguments**

- **x**: The string
- **SIZE**: The size of the window (number of characters).
- **SLIDE**: Offset to move at each slide
- **FUN**: The function to be applied
- ... Optional parameter for the function FUN

**Details**

Apply the function FUN to substrings of x of length SIZE.

**Value**

A list of size `nchar(x) - SIZE`.

**Author(s)**

L, Gautier
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