

# Package ‘ecoltk’

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**Title** Meta-data and tools for E. coli

**Author** Laurent Gautier

**Maintainer** Laurent Gautier <lgautier@gmail.com>

**biocViews** Annotation, Visualization

**Depends** R (>= 2.10)

**Imports** Biobase, graphics, methods

**Suggests** ecolILeucine, ecolcdf, 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)

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ecoli.m52.genome	<i>Escherichia coli</i> data
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## 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 (beginning 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 `annBuilder`.

The environment `ecoligenomeCHRLoc` differs: two integers are associated with each key, one corresponds to the beginning 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

<http://www.genome.wisc.edu/sequencing/k12.htm> and [http://www.biostat.harvard.edu/complab/dchip/info\\_file.htm](http://www.biostat.harvard.edu/complab/dchip/info_file.htm)

## Examples

```
data(ecoli.m52.genome)
```

---

ecoligenome.operon      *Known operon in E.coli - data.frame*

---

## 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)))
```

---

`ecoligenomeBNUM`*Environment for 'bnum' identifiers*

---

**Description**

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

**Usage**

```
data(ecoligenomeBNUM)
data(ecoligenomeBNUM2SYMBOL)
data(ecoligenomeBNUM2ENZYME)
data(ecoligenomeBNUM2GENBANK)
data(ecoligenomeBNUM2GENEPRODUCT)
data(ecoligenomeSYMBOL2BNUM)
```

**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.

---

`ecoligenomeBNUM2MULTIFUN`*Environment*

---

**Description**

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

**Usage**

```
data(ecoligenomeBNUM2MULTIFUN)
```

**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	<i>function to compute gccontent</i>
-----------	--------------------------------------

---

**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 is a simple (and not particularly fast) function to compute the GC content of a 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)

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linkedmultiget	<i>A function to look for values across linked environments</i>
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---

**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.

**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 <a href="#">polygon</a> )
length, angle, code	see the corresponding parameters for the function <a href="#">arrows</a>
...	optional graphical paramaters

**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**

```

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)
}

```

**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**

```
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))
```

---

polyChrom

*Functions to plot circular chromosomes informations*

---

**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	radius
xlim, ylim	range for the plot. Can be used to zoom-in a particular region.
pos	position (nucleic base coordinate)
begin	beginning 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(ecoligenomeCHRLLOC)

## 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=ecoligenomeCHRLLOC)
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***Description**

Apply a function on a window sliding on a string.

**Usage**

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

**Arguments**

<code>x</code>	The string
<code>SIZE</code>	The size of the window (number of characters).
<code>SLIDE</code>	offset to move at each slide
<code>FUN</code>	The function to be applied
<code>...</code>	optional parameter for the function <code>FUN</code>

**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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