Package 'Vega'

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Type Package

Title An R package for copy number data segmentation

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Description Vega (Variational Estimator for Genomic Aberrations) is an
algorithm that adapts a very popular variational model (Mumford
and Shah) used in image segmentation so that chromosomal
aberrant regions can be efficiently detected.

Depends R (>= 2.10)

License GPL-2

LazyLoad yes

biocViews aCGH, CopyNumberVariation

R topics documented:

Vega-package   *An R package for copy number data segmentation*

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Details

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Type:	Package
Version:	1.0
License:	GPL-2
LazyLoad:	yes
biocViews:	aCGH, DNACopyNumber

Author(s)

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References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinformatics.

Examples

```
# Load tha data for Granta-519 Cell Line
data(G519);

# Start Vega segmentation on all chromosomes of G519 data and save the results in G519_segmentation.txt tab delimite
seg <- vega(CNVdata=G519, chromosomes=c(1:22, "X", "Y"), out_file_name="G519_segmentation.txt", beta=0.5, min_reg
```

G519 *Granta-519 Data*

Description

LRR for Granta-519 Cell Line data (published in DeLeeuw et al. (2004). Comprehensive whole genome array CGH profiling of mantle cell lymphoma model genomes, Human Molecular Genetics, 13(17):1827-1837).

Usage

```
data(G519)
```

Format

A matrix containing four columns: chromosome, start and end probe positions, observed Log R Ratio.

`plotSegmentation`	*Plot observations and the respective segmentation.*

Description

This function allows to plot the observed data superimposing the respective segmentation. By the parameter 'opt' he user can plot the LRR mean values of each segment or the computed aberration kind. In plot window the gain and the loss are identified by a line having value of 1 and -1 respectively.

Usage

```
plotSegmentation(CNVdata, segmentation, chromosomes, opt = 0)
```

Arguments

`CNVdata`	The data matrix.
`segmentation`	The computed segmentation.
`chromosomes`	The chromosomes that have to be plotted.
`opt`	If opt=0 (default) then the LRR mean values are plotted, if opt=1 the computed labels are plotted.

Note

If the argument opt=1 then gains and losses are identified by 1 and -1 respectively.

Author(s)

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References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinformatics.

Examples

```
# Import the data
data(G519)

# Compute the segmentation for all chromosomes
seg <- vega(G519, c(1:22, "X", "Y"))

# Plot the results for all chromosomes in terms of mean of LRRs
plotSegmentation(G519, seg, c(1:22, "X", "Y"), opt=0)
```

```
# Plot the results for all chromosomes in terms of aberration kinds
plotSegmentation(G519, seg, c(1:22, "X", "Y"), opt=1)
```

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vega   *This function computes, saves and returns the copy number segmenta-*
                              tion on the aCGH data passed as argument.

Description

This function computes the segmentation of the copy number data passed as argument. 'vega'
function returns the computed segmentation and save it as a tab delimited file. Users need just to
use this function.

Usage

```
vega(CNVdata, chromosomes, out_file_name = "", beta = 0.5, min_region_size = 2)
```

Arguments

CNVdata   This argument is matrix containing the data that have to be analyzed. This ma-
                 trix must have 4 columns:
                 - the first row indicates the chromosome;
                 - the second row indicates the start bp of the probe;
                 - the third row indicates the end bp of the probe;
                 - the fourth row reports the measured Log R Ratio;

chromosomes   This is a vector containing the chromosome sthat have to be analyzed. By using
                 c(1:22, "X", "Y") the whole genome will be segmented.

out_file_name   This is the file name used to save the computed segmentation.

beta   This argument is used for the stop condition definition.

min_region_size

                 This argument specifies the minimum size for the segmented regions.

Value

segmentation   This is a data frame containing the computed segmentation.

Author(s)

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References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinfor-
matics.

Examples

```
# Load tha data for Granta-519 Cell Line
data(G519);

# Start Vega segmentation on all chromosomes of G519 data
v <- vega(CNVdata=G519, chromosomes=c(1:22, "X", "Y"), beta=0.5, min_region_size=2);

# Start Vega segmentation on chromosomes 8 of G519 data and save the results in G519_segmentation_chr8.txt tab delim
v <- vega(CNVdata=G519, chromosomes=c(8), out_file_name="G519_segmentation_chr8.txt", beta=0.5, min_region_size=
```

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