

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

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R topics documented:

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Vega-package

An R package for copy number data segmentation

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.

Details

Package: Vega
 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 the 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 delimited
seg <- vega(CNVdata=G519, chromosomes=c(1:22, "X", "Y"), out_file_name="G519_segmentation.txt", beta=0.5, min
```

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' the 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)
```

vega

This function computes, saves and returns the copy number segmentation 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 matrix 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, Bioinformatics.

Examples

```
# Load the 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 d
v <- vega(CNVdata=G519, chromosomes=c(8), out_file_name="G519_segmentation_chr8.txt", beta=0.5, min_region_s
```

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