Package 'focalCall'

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Type Package

Title Detection of focal aberrations in DNA copy number data

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Depends R(>= 2.10.0), CGHcall

Suggests RUnit, BiocGenerics

URL https://github.com/OscarKrijgsman/focalCall

Description Detection of genomic focal aberrations in high-resolution DNA copy number data

License GPL-2

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R topics documented:

`BierkensCNA` *Cervical cancer arrayCGH data*

Description

Example dataset with arrayCGH data of cervical pre-cancer lesions. OF NOTE: this set contains only 8 samples from the data and only the complete probeset for chromosome 2. Complete dataset is available from GEO (GSE34575).

Usage

```
BierkensCNA
```

Format

This dataset contain three files:

CGHset a CGHcall object containing 8 cervical pre-curses cancer lesions. These samples were taken from Bierkens et al. 2013 and available under GEO accession number GSE34575.

CNVset a bed file with CNV locations as provided by `http://dgv.tcag.ca/.`

calls_focals Complete results file after running focalCall on the example data from Bierkens et al. 2013.

CGHset: A CGHcall object containing the following 8 samples:

hgCIN.2.10_16 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.10_16.

hgCIN.2.13_16 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.13_16.

hgCIN.2.8_31 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.8_31.

hgCIN.2.16_31 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.16_31.

CIN3.1.2_16 Cervical Intra-epithelial Neoplasia sample: CIN3.1.2_16.

hgCIN.2.4_16 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.4_16.

CIN3.1.8_16 Cervical Intra-epithelial Neoplasia sample: CIN3.1.8_16.

hgCIN.2.19_58 high-grade Cervical Intra-epithelial Neoplasia sample: hgCIN.2.19_58.

CNVset: A bed file containing the following columns:

CNV ID Identification ID for copy number variation (CNV)

start Basepair position that indicates start of CNV

end Basepair position that indicates end of CNV

calls_focals: results file after running focalCall on the samples described above:

calls_focals results file of class `cghCall`

Value

Three datasets are returned as described in the section above.

Source

Bierkens, M., Krijgsman, O., Wilting, S.M., Bosch, L., Jaspers, A., Meijer, G.A., Meijer, C.J., Snijders, P.J., Ylstra, B., Steenbergen, R.D. (2013). Focal aberrations indicate EYA2 and hsa-miR-375 as oncogene and tumor suppressor in cervical carcinogenesis. *Genes Chromosomes Cancer 52*,56-68.

Examples

```
# Load the data file
data(BierkensCNA)
```

`focalCall` *Detection genomic focal aberrations*

Description

Detection of genomic focal copy number aberrations from high-resolution arrayCGH data or shallow-Seq copy number data.

Usage

```
focalCall(CGHset, CNVset , focalSize = 3, minFreq=2)
```

Arguments

`CGHset`	Object of class `cghCall`, contains CGHcall output of tumor data.
`CNVset`	Object of class `cghCall`, contains CGHcall output of matched normal data or .bed file with CNV locations.
`focalSize`	Threshold for the function `focalCall`. Sets max size of a focal aberration/
`minFreq`	Threshold for the function `focalCall`. Sets minimal number of samples that contain the aberration/

Details

focalCall is applied to the calls of an object of class `cghCall` (as returned by CGHcall version 1.2.0 or higher). FocalCall extract all focal aberrations from the tumor copy number data and

Value

Two files are returned - an object of class `cghCall` and a text files with all focal aberrations detected in all sample.

- "focalCall.Rdata" is an object of class `cghCall` and contains all DNA copy number information including the focal aberrations.
- "focalList_sampleName.txt" is a text file with all focal aberrations detected in the set of sample.

Author(s)

Oscar Krijgsman: `<o.krijgsman@vumc.nl>`

References

Krijgsman O., Benner C., Meijer G.A., Van de Wiel, M.A., Ylstra, B. (2013), "FocalCall: an R-package to detect genomic focal aberrations.", *Submitted*

See Also

`focalCall`, `CGHcall`

Examples

```
# Generate object of cghCall class object and input files
data(BierkensCNA)

# Extract focal aberrations and distinguish somatic from germ-line copy number aberrations (CNA)
ExampleRun<-focalCall(CGHset, CNVset, focalSize=3, minFreq=2)
```

`FreqPlot` *frequency plot copy number aberrations.*

Description

Frequency plot of all aberrations in the dataset.

Usage

```
FreqPlot(calls, header)
```

Arguments

`calls`	Object of class `focalCall`, contains focalCall output.
`header`	String with header name of frequencyPlot.

Details

FreqPlot is applied to the calls of an object of class `cghCall` (as returned by focalCall).

Value

A single plot is returned with the frequency of aberrations in the complete dataset. The x-axis represents the chromosomes, the y-axis the percentage of samples with a gain or loss at that genomic position.

Author(s)

Oscar Krijgsman: `<o.krijgsman@vumc.nl>`

References

Krijgsman O., Benner C., Meijer G.A., Van de Wiel, M.A., Ylstra, B. (2013), "FocalCall: an R-package to detect genomic focal aberrations.", *Submitted*

See Also

focalCall, CGHcall

Examples

```
# Load example data
data(BierkensCNA)

# generate frequency plot of copy number data
FreqPlot(calls_focals, "FrequencyPlot_BierkensSamples")
```

FreqPlotfocal *frequency plot focal copy number aberrations.*

Description

Frequency plot of focal aberrations in the dataset.

Usage

```
FreqPlotfocal(calls, header)
```

Arguments

calls	Object of class focalCall, contains focalCall output.
header	String with header name of frequencyPlot.

Details

FreqPlot is applied to the calls of an object of class cghCall (as returned by focalCall version 0.0.99 or higher).

Value

A single plot is returned with the frequency of focal aberrations in the complete dataset. The x-axis represents the chromosomes, the y-axis the percentage of samples with a focal gain or focal loss at that genomic position. CNVs are also plotted but in grey.

Author(s)

Oscar Krijgsman: <o.krijgsman@vumc.nl>

References

Krijgsman O., Benner C., Meijer G.A., Van de Wiel, M.A., Ylstra, B. (2013), "FocalCall: an R-package to detect genomic focal aberrations.", *Submitted*

See Also

focalCall, CGHcall

Examples

```
# Load example data
data(BierkensCNA)

# generate frequency plot of copy number data for focal aberrations only
FreqPlotfocal(calls_focals, "FrequencyPlot_focals_BierkensSamples")
```

`igvFiles` *Match Ensembl genes to focal aberrations.*

Description

Generates three tracks that can be loaded into IGV (). 1) Segmented data per sample 2) frequency plot based on the calls from CGHcall 3) Frequency plot of focal aberrations as generated with focalCall.

Usage

```
igvFiles(CGHset)
```

Arguments

`CGHset`	Object of class `focalCall`, contains focalCall output.

Details

igvFocal is applied to a (as returned by focalCall version 0.0.99 or higher).

Value

Three IGV readable files are returned - Frequency aberrations, Frequency focal aberrations and all segmented values for all samples.

- "FrequencyPlot.igv" is a IGV readable files and contains the frequency plot of all samples and all aberrations.
- "FrequencyPlotfocals.igv" is a IGV readable files and contains the frequency plot of all samples and all focal aberrations.
- "Overview_segments.igv" is a IGV readable files and contains the segmentation log2ratio values.

Author(s)

Oscar Krijgsman: <o.krijgsman@nki.nl>

References

Krijgsman O., Benner C., Meijer G.A., Van de Wiel, M.A., Ylstra, B. (2013), "FocalCall: an R-package to detect genomic focal aberrations.", *Submitted*

See Also

`focalCall`, `CGHcall`

Examples

```
data(BierkensCNA)

# generate IGV readable files
igvFiles(calls_focals)
```

`singleSample` *Detection focal aberrations with 1 sample only*

Description

Detection and plotting of focal aberrations and distinguish somatic from germ-line in a single sample. This function, as `focalCall` can be used for samples with and without patient matched normal data.

Usage

```
singleSample(CGHset, CNVset, focalSize=3, OverlapPerc=0.2)
```

Arguments

`CGHset`	Object of class `cghCall`, contains CGHcall output of tumor data.
`CNVset`	Object of class `cghCall`, contains CGHcall output of matched normal data or .bed file with CNV locations.
`focalSize`	Threshold for the function `singleSample`. Sets max size of a focal aberration/
`OverlapPerc`	Threshold for the function `singleSample`. sets minimal overlap of focal aberration with CNVs from in CNdata.normal to be classified as germ-line./

Details

singleSample is applied to the calls of an object of class `cghCall`.

Value

Three files are returned - an object of class `cghCall`, a text files with all focal aberrations listed and a plot with the genomic aberrations in the sample.

- "focalCall_sampleName.Rdata" is an object of class `cghCall` and contains all DNA copy number information including the focal aberrations.
- "focalList_sampleName.txt" is a text file with all focal aberrations detected in the sample.
- "sampleName.png" is a plot with the genomic aberrations in the sample.

Author(s)

Oscar Krijgsman: `<o.krijgsman@vumc.nl>`

References

Krijgsman O., Benner C., Meijer G.A., Van de Wiel, M.A., Ylstra, B. (2013), "FocalCall: an R-package to detect genomic focal aberrations.", *Submitted*

See Also

focalCall, CGHcall

Examples

```
# generate object of cghCall class object and input files
data(BierkensCNA)

# Extract focal aberrations and distinguish somatic from germ-line copy number aberrations (CNA) in a single s
singleSample(CGHset[,1], CNVset, focalSize=3)
```

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