R documentation

of 'ascat.GCcorrect.Rd' etc.

September 22, 2015

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ascat.GCcorrect *ascat.GCcorrect*

Description

Corrects logR of the tumour sample(s) with genomic GC content

Usage

```
ascat.GCcorrect(ASCATobj, GCcontentfile = NULL)
```

Arguments

ASCATobj	an ASCAT object
GCcontentfile	File containing the GC content around every SNP for increasing window sizes

Details

Note that probes not present in the GCcontentfile will be lost from the results

Value

ASCAT object with corrected tumour logR

ascat.aspcf *ascat.aspcf*

Description

run ASPCF segmentation

Usage

```
ascat.aspcf(ASCATobj, selectsamples = 1:length(ASCATobj$samples),
  ascat.gg = NULL, penalty = 25)
```

Arguments

ASCATobj	an ASCAT object
selectsamples	a vector containing the sample number(s) to PCF. Default = all
ascat.gg	germline genotypes (NULL if germline data is available)
penalty	penalty of introducing an additional ASPCF breakpoint (expert parameter, don't adapt unless you know what you're doing)

Details

This function can be easily parallelised by controlling the selectsamples parameter
it saves the results in LogR_PCFed[sample]_[segment].txt and BAF_PCFed[sample]_[segment].txt; if these files exist, the results are read from them.
Hence, after parallelisation, copy all the files into the current directory, and run this function to read in the results

Value

output: ascat data structure containing:
1. Tumor_LogR data matrix
2. Tumor_BAF data matrix
3. Tumor_LogR_segmented: matrix of LogR segmented values
4. Tumor_BAF_segmented: list of BAF segmented values; each element in the list is a matrix containing the segmented values for one sample (only for probes that are germline homozygous)
5. Germline_LogR data matrix
6. Germline_BAF data matrix
7. SNPpos: position of all SNPs
8. ch: a list containing vectors with the indices for each chromosome (e.g. Tumor_LogR[ch[[13]],] will output the Tumor_LogR data of chromosome 13
9. chr: a list containing vectors with the indices for each distinct part that can be segmented separately (e.g. chromosome arm, stretch of DNA between gaps in the array design)

`ascat.loadData` *ascat.loadData*

Description

Function to read in SNP array data

Usage

```
ascat.loadData(Tumor_LogR_file, Tumor_BAF_file, Germline_LogR_file = NULL,
  Germline_BAF_file = NULL, chrs = c(1:22, "X", "Y"), gender = NULL,
  sexchromosomes = c("X", "Y"))
```

Arguments

`Tumor_LogR_file`	file containing logR of tumour sample(s)
`Tumor_BAF_file`	file containing BAF of tumour sample(s)
`Germline_LogR_file`	file containing logR of germline sample(s), NULL
`Germline_BAF_file`	file containing BAF of germline sample(s), NULL
`chrs`	
`gender`	a vector of gender for each cases ("XX" or "XY"). Default = all female ("XX")
`sexchromosomes`	

Details

germline data files can be NULL - in that case these are not read in

Value

ascat data structure containing:
1. Tumor_LogR data matrix
2. Tumor_BAF data matrix
3. Tumor_LogR_segmented: placeholder, NULL
4. Tumor_BAF_segmented: placeholder, NULL
5. Germline_LogR data matrix
6. Germline_BAF data matrix
7. SNPpos: position of all SNPs
8. ch: a list containing vectors with the indices for each chromosome (e.g. Tumor_LogR[ch[[13]],] will output the Tumor_LogR data of chromosome 13
9. chr: a list containing vectors with the indices for each distinct part that can be segmented separately (e.g. chromosome arm, stretch of DNA between gaps in the array design)
10. gender: a vector of gender for each cases ("XX" or "XY"). Default = NULL: all female ("XX")

ascat.plotRawData *ascat.plotRawData*

Description

Plots SNP array data

Usage

```
ascat.plotRawData(ASCATobj)
```

Arguments

ASCATobj	an ASCAT object (e.g. data structure from ascat.loadData)

Value

Produces png files showing the logR and BAF values for tumour and germline samples

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