Package 'TAPS'

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Type Package

Title Tumor Abberation Prediction Suite

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Description Performs a allele-specific copy number analysis of array data.

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Depends R (>= 2.10), DNAcopy, stats, fields, affxparser

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`TAPS_call` *Tumor Abberation Prediction Suite*

Description

TAPS_call calls copynumbers and displays total and minor copynumbers of a tumor sample.

Usage

```
TAPS_call(directory=NULL,minseg=1,maxCn=12)
```

Arguments

`directory`	Default is getwd().
`minseg`	Default is 1.
`maxCn`	Default is 12.

Details

TAPS_call is the second step in TAPS analysis. It takes two things as input.
1) Your interpretation of plots which you add to the SampleData.txt file. (see homepage for further instructions at http://patchwork.r-forge.r-project.org/)
2) The .Rdata files generated by TAPS_plot().

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References

http://www.biomedcentral.com/content/pdf/gb-2011-12-10-r108.pdf

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TAPS_plot *Tumor Abberation Prediction Suite*

Description

Tumor Aberration Prediction Suite. Version 1.9, April 2013

This package contains all functions used to run (and used by) Tumor Aberration Prediction Suite (TAPS). (Developed September 2009 –> January 2011, packaged 2013) Updates: Check http://patchwork.r-forge.r-project.org/ as we intend to extend some functionality.

Usage

```
TAPS_plot(directory=NULL,bin=400)
```

Arguments

directory	Default is getwd(). Specifying to a specific samples directory will run TAPS_plot on that directory. Specifying a directory containing one or more subdirectories that are samples (and not any other subdirectories or TAPS_plot will error when trying to run them!) will iteratively run TAPS_plot on all samples.
bin	Default is 400.

Details

Instructions, allele-specific copy number analysis

Note to users:
TAPS is a tool to help you actively investigate genomic aberrations of the most complex tumor samples. TAPS visualizes samples using log-ratio and allelic imbalance ratio. If the sample is deemed suitable, it can be subjected to automated copy number calling.

Data:
Validated automatic copy number calling is available for Affymetrix SNP6, 250k/500k data and cytoscan HD. Automatic copy number calling is suitable but unvalidated for OncoScan (an Affymetrix

SNP array). If you have some other microarray data please contact us, it is possible that there is a way to make it work.

Data preparation:
Nexus (BioDiscovery): find your "Samples" folder after segmentation (SNP-rank) and normalization.

Other:
Store Log-ratio as probes.txt and allele frequency as snps.txt in one folder per sample. Do not store other folders than sample folders in your "Samples" folder. The 'Array' column in these files is uninformative and may be omitted. Optionally (recommended) also put segments.txt in your sample folder.

Workflow:
1. From the folder containing your samples (sample folders) run TAPS_plot().
2. Investigate the scatter plots generated in your sample folders.
3. To proceed with copy number calls, find and open the file "SampleData.txt".
4. For each sample, enter an interpretation of Log-Ratio @ copy number 2 ("cn2"), the difference in Log-Ratio to a deletion ("delta") and the allelic imbalance ratio of CNNLOH ("loh"). Save the file.
5. Run TAPS_call().
6. Inspect the karyotype_check images, and the new chromosome-wise images.
7. If all looks reasonable, you will find good copy number estimates in 'Copynumbers.csv'.
9. Be wary of the result on sex chromosomes which may be difficult to auto-interpret.
10. Watch all images for signs of segmentation failure and tumor cell heterogeneity.

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`TAPS_region` *Tumor Abberation Prediction Suite - Region plotter*

Description

TAPS_region allows you to look closer at a region of the genome that you specify. It also displays the known genes of the region.

Usage

```
TAPS_region(directory=NULL,chr,region,hg18=F)
```

Arguments

directory	Default is getwd().
chr	Supply the chromosome you wish to look at. ex: chr=1
region	The region of the chromosome you are interested in. ex: region=10000000:13000000
hg18	Default is FALSE, meaning the hg19 known gene list will be used. If TRUE the hg18 known gene list is used.

Details

TAPS_region takes the directory of the sample that you want to look at (defaults to current working directory if no input is given), the chromosome and the actual chromosomal coordinates as input to give you an in-depth view. Unlike any of the other plots this view also shows known genes from a gene list of your choice, hg18 or hg19.

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