Package 'acnr'

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Type Package

Title Annotated Copy-Number Regions

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Description This data package contains SNP array data from different types of copy-number regions. These regions were identified manually by the authors of the package and may be used to generate realistic data sets with known truth.

License LGPL (>= 2.1)

Depends R (>= 2.10), R.utils, xtable

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acnr-package *Annotated Copy-Number Regions*

Description

This data package contains SNP array data from different types of copy-number regions. These regions were identified manually by the authors of the package and may be used to generate realistic data sets with known truth.

Details

Package:	acnr
Type:	Package
Title:	Annotated Copy-Number Regions
Version:	0.2.2
Date:	2014-09-08
Author:	Morgane Pierre-Jean and Pierre Neuvial
Maintainer:	Morgane Pierre-Jean <morgane.pierrejean@genopole.cnrs.fr>
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Suggests:	RUnit, BiocGenerics
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Author(s)

Morgane Pierre-Jean and Pierre Neuvial

loadCnRegionData *loadCnRegionData*

Description

Load real, annotated copy number data

Usage

```
loadCnRegionData(dataSet = c("GSE29172", "GSE11976"), tumorFraction = 1)
```

Arguments

dataSet	microarray dataSet from which the data was generated.
tumorFraction	proportion of tumor cells in the "tumor" sample. Should be in .3, .5, .7, 1 if dataSet=="GSE29172", and in .14,.34,.50,.79,1 when dataSet=="GSE11976".

Details

This function is a wrapper to load real genotyping array data taken from dilution series from the Affymetrix GenomeWideSNP_6 chip type (Rasmussen et al, 2011) or from the Illumina HumanCNV370v1 chip type (Staaf et al, 2008)

Value

a data.frame containing copy number data for different types of copy number regions. Columns:

c Total copy number

b Allele B fraction (a.k.a. BAF)

region a character value, annotation label for the region. Preferably encoded as `"(C1,C2)"`, where `C1` denotes the minor copy number and `C2` denotes the major copy number. For example,

- **(1,1)** Normal
- **(0,1)** Hemizygous deletion
- **(0,0)** Homozygous deletion
- **(1,2)** Single copy gain
- **(0,2)** Copy-neutral LOH
- **(2,2)** Balanced two-copy gain
- **(1,3)** Unbalanced two-copy gain
- **(0,3)** Single-copy gain with LOH

muN the (germline) genotype of SNPs. By definition, rows with missing genotypes are interpreted as non-polymorphic loci (a.k.a. copy number probes).

Author(s)

Morgane Pierre-Jean and Pierre Neuvial

References

Staaf, J., Lindgren, D., Vallon-Christersson, J., Isaksson, A., Goransson, H., Juliusson, G., ... & Ringn\'er, M. (2008). Segmentation-based detection of allelic imbalance and loss-of-heterozygosity in cancer cells using whole genome SNP arrays. Genome Biol, 9(9), R136.

GEO data set: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11976

Rasmussen, M., Sundstr\"om, M., Kultima, H. G., Botling, J., Micke, P., Birgisson, H., Glimelius, B. & Isaksson, A. (2011). Allele-specific copy number analysis of tumor samples with aneuploidy and tumor heterogeneity. Genome Biology, 12(10), R108.

GEO data sets: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE29172 http://www.ncbi.nlm.nih.gov/geo/query/acc.

Examples

```
affyDat <- loadCnRegionData(dataSet="GSE29172", tumorFraction=1)
str(affyDat)

illuDat <- loadCnRegionData(dataSet="GSE11976", tumorFraction=.79)
str(illuDat)
```

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