Package 'neuroblastoma'

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Title Neuroblastoma copy number profiles

Description Annotated neuroblastoma copy number profiles,
a benchmark data set for change-point detection algorithms.

Depends R (>= 2.10)

Repository CRAN

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NeedsCompilation no

R topics documented:

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neuroblastoma   *Neuroblastoma copy number profiles and breakpoint annotations*

Description

Tumors from patients at the Institut Curie were assayed using array comparative genomic hybridization. Their normalized copy number profiles are available as `neuroblastoma$profiles` and the breakpoint annotations are available as `neuroblastoma$annotations`.

Usage

```
data(neuroblastoma)
```

Format

A named list of 2 data frames:

profiles A data.frame with one row for each probe, and these variables:

profile.id factor: id of copy number profile.

chromosome factor: chromosome on which the probe was mapped.

position integer: probe was mapped to this position in base pairs.

logratio numeric: normalized logratio of the probe, which should be proportional to copy number.

annotations a data.frame with one row for each annotated region, and these variables:

profile.id factor: id of copy number profile.

chromosome factor: chromosome of this annotation.

min integer: lower limit of this region in base pairs.

max integer: upper limit of this region in base pairs.

annotation factor: annotation of this region, either ″normal″ for no breakpoints or ″breakpoint″ for at least one breakpoint.

Source

Gudrun Schleiermacher and Isabelle Janoueix-Lerosey, Institut Curie.

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