Package ‘neuroblastoma’

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Maintainer Toby Dylan Hocking <toby@sg.cs.titech.ac.jp>
Author Toby Dylan Hocking
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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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