

Package ‘neuroblastoma’

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Version 2023.9.3

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Title Neuroblastoma Copy Number Profiles

Description Annotated neuroblastoma copy number profiles,
a benchmark data set for change-point detection algorithms,
as described by Hocking et al. <[doi:10.1186/1471-2105-14-164](https://doi.org/10.1186/1471-2105-14-164)>.

Depends R (>= 3.5)

NeedsCompilation no

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R topics documented:

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| neuroblastoma | <i>Neuroblastoma copy number profiles and breakpoint annotations</i> |
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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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* **datasets**

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