Package: neuroblastoma (via r-universe)

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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>.

Depends R (>= 3.5)

Repository https://tdhock.r-universe.dev

RemoteUrl https://github.com/tdhock/neuroblastoma

RemoteRef HEAD

RemoteSha a28b723f1085b9dca1fea2aaefe9856087b40c54

Contents

`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

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