## Package 'stjudem'

October 12, 2020
Title Microarray Data from Yeoh et al. in MACAT format
<b>Version</b> 1.28.0
<b>Date</b> 2006-9-15
<b>Depends</b> R ( $>= 2.10$ ), utils
Author Benjamin Georgi, Matthias Heinig, Sebastian Schmeier, Joern Toedling
<b>Description</b> This is a microarray data set on acute lymphoblastic leukemia, published in 2002 (Yeoh et al.Cancer Cell 2002). The experiments were conducted in the St.Jude Children's Research Hospital, Memphis, Tenessee, USA. The raw data was preprocessed by variance stabilizing normalization (Huber et al.) on probe and subsequent summarization of probe expression values into probe set expression values using median polish.
Maintainer Joern Toedling <toedling@ebi.ac.uk></toedling@ebi.ac.uk>
License LGPL (>= 2)
biocViews ExperimentData, CancerData, LeukemiaCancerData, MicroarrayData, ChipOnChipData
git_url https://git.bioconductor.org/packages/stjudem
git_branch RELEASE_3_11
git_last_commit 2cb48f9
git_last_commit_date 2020-04-27
Date/Publication 2020-10-12
R topics documented:
stjude
Index
stjude Microarry Data from St.Jude Children Research Hospital (USA)

## Description

Example for list-structure used by many functions in MACAT. It's based on the gene expression data published by Yeoh et al. in 2002. [Yeoh et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. Cancer Cell. March 2002. 1: 133-143. The data has been preprocessed using 'vsn' on probe level and the probes have been summed up using 'median polish'.

2 stjude

#### Usage

```
data(stjude)
```

#### **Format**

List of class 'MACATData' with 6 components:

geneName: Identifiers of genes/probe sets in expression data

**geneLocation:** Location of genes on their chromosome as distance from 5'end in base pairs Negative numbers denote genes on the antisense strand.

**chromosome:** Chromosome of the respective gene. Components 'geneName', 'geneLocation', and 'chromosome' are in the same order.

**expr:** expression matrix with rows = genes and columns = samples/patients

labels: (disease) subtype of each sample, has length = number of columns of expression matrix

**chip:** Identifier for Microarray used for the experiments (here for the Affymetrix HG-U95av2 Oligonucleotide GeneChip)

#### Source

Yeoh et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. Cancer Cell. March 2002. 1: 133-143.

### **Examples**

```
data(stjude)
summary(stjude)
```

# Index

```
* datasets
stjude, 1
stjude, 1
```