

Package ‘breastCancerMAINZ’

July 2, 2024

Type Package

Title Gene expression dataset published by Schmidt et al. [2008] (MAINZ).

Version 1.43.0

Date 2011-02-10

Description Gene expression data from the breast cancer study published by Schmidt et al. in 2008, provided as an eSet.

biocViews ExperimentData, CancerData, BreastCancerData, MicroarrayData, GEO

Author Markus Schroeder, Benjamin Haibe-Kains, Aedin Culhane, Christos Sotiriou, Gianluca Bontempi, John Quackenbush

Maintainer Markus Schroeder <mschroed@jimmy.harvard.edu>, Benjamin Haibe-Kains <bhaibeka@jimmy.harvard.edu>

Depends R (>= 2.5.0)

Suggests survcomp, genefu, Biobase

LazyLoad yes

License Artistic-2.0

URL <http://compbio.dfci.harvard.edu/>

git_url <https://git.bioconductor.org/packages/breastCancerMAINZ>

git_branch devel

git_last_commit e58c496

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-07-02

Contents

mainz	2
Index	4

mainz	<i>Gene expression, annotations and clinical data from Schmidt et al. 2008</i>
-------	--

Description

This dataset contains the gene expression, annotations and clinical data as published in Schmidt et al. 2008.

Usage

```
data(mainz)
```

Format

ExpressionSet with 22283 features and 200 samples, containing:

- `exprs(mainz)`: Matrix containing gene expressions as measured by Affymetrix hgu133a technology (single-channel, oligonucleotides).
- `fData(mainz)`: AnnotatedDataFrame containing annotations of Affy microarray platform hgu133a.
- `pData(mainz)`: AnnotatedDataFrame containing Clinical information of the breast cancer patients whose tumors were hybridized.
- `experimentalData(mainz)`: MIAME object containing information about the dataset.
- `annotation(mainz)`: Name of the affy chip.

Details

This dataset represents the study published by Schmidt et al. 2008.

- **Abstract:** Estrogen receptor (ER) expression and proliferative activity are established prognostic factors in breast cancer. In a search for additional prognostic motifs, we analyzed the gene expression patterns of 200 tumors of patients who were not treated by systemic therapy after surgery using a discovery approach. After performing hierarchical cluster analysis, we identified coregulated genes related to the biological process of proliferation, steroid hormone receptor expression, as well as B-cell and T-cell infiltration. We calculated metagenes as a surrogate for all genes contained within a particular cluster and visualized the relative expression in relation to time to metastasis with principal component analysis. Distinct patterns led to the hypothesis of a prognostic role of the immune system in tumors with high expression of proliferation-associated genes. In multivariate Cox regression analysis, the proliferation metagene showed a significant association with metastasis-free survival of the whole discovery cohort [hazard ratio (HR), 2.20; 95% confidence interval (95% CI), 1.40-3.46]. The B-cell metagene showed additional independent prognostic information in carcinomas with high proliferative activity (HR, 0.66; 95% CI, 0.46-0.97). A prognostic influence of the B-cell metagene was independently confirmed by multivariate analysis in a first validation cohort enriched for high-grade tumors (n = 286; HR, 0.78; 95% CI, 0.62-0.98) and a second validation cohort enriched for younger patients (n = 302; HR, 0.83; 95% CI, 0.7-0.97). Thus, we

could show in three cohorts of untreated, node-negative breast cancer patients that the humoral immune system plays a pivotal role in metastasis-free survival of carcinomas of the breast.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11121>

References

Marcus Schmidt and Daniel Boehm and Christian von Toerne and Eric Steiner and Alexander Puhl and Heryk Pilch and Hans-Anton Lehr and Jan G. Hengstler and Hainz Koelbl and Mathias Gehrmann (2008)"The Humoral Immune System Has a Key Prognostic Impact in Node-Negative Breast Cancer", *Cancer Research*, **68**(13):5405-5413

Examples

```
## load Biobase package
library(Biobase)
## load the dataset
data(mainz)
## show the first 5 rows and columns of the expression data
exprs(mainz)[1:5,1:5]
## show the first 6 rows of the phenotype data
head(pData(mainz))
## show first 20 feature names
featureNames(mainz)[1:20]
## show the experiment data summary
experimentData(mainz)
## show the used platform
annotation(mainz)
## show the abstract for this dataset
abstract(mainz)
```

Index

* **datasets**
 mainz, 2

mainz, 2