Package 'breastCancerMAINZ'

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Type Package

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

Version 1.0.5

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

biocViews ExperimentData, Cancer, GeneExpression, Microarray

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Depends R (>= 2.5.0)

Suggests survcomp, genefu, Biobase

LazyLoad yes

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

R topics documented:

mainz *Gene expression, annotations and clinical data from Schmidt et al. 2008*

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