

Package ‘MetaGxBreast’

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Type Package

Title Transcriptomic Breast Cancer Datasets

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Description A collection of Breast Cancer Transcriptomic Datasets that are part of the MetaGxData package compendium.

License Apache License (≥ 2)

Depends R ($\geq 3.6.0$), Biobase, AnnotationHub, ExperimentHub

Imports stats, lattice, impute, SummarizedExperiment

Suggests testthat, xtable, tinytex

NeedsCompilation no

biocViews ExpressionData, ExperimentHub, CancerData,
Homo_sapiens_Data, ArrayExpress, GEO, NCI, MicroarrayData,
ExperimentData

LazyData yes

RoxygenNote 7.1.1

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 CAL

 CAL

Description

ExpressionSet for the CAL Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/17157792
  Title:
  URL: http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-158/
  PMIDs: 17157792
  No abstract available.
  notes:
    summary:
      Recurrent copy number abnormalities differ between tumor subtypes as defined by gene expression patterns. Accuracy of stratification by outcome can be improved by combining expression and copy number.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at (21169 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
  
```

Details

```

assayData: 21169 features, 118 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  1 observation deleted due to missingness
    n events median 0.95LCL 0.95UCL
  
```

117.00 77.00 8.96 8.33 9.71

 Available sample meta-data:

sample_name:

Length	Class	Mode
118	character	character

sample_type:

tumor
118

er:

negative	positive
43	75

pgr:

negative	positive	NA's
51	66	1

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.300	1.675	2.300	2.729	3.500	7.500	2

N:

0	1
51	67

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.00	44.00	51.00	55.06	66.00	88.00	1

grade:

1	2	3	NA's
10	42	61	5

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0	767	2059	2094	3336	5183	1

dmfs_status:

norecurrence	recurrence	NA's
91	26	1

days_to_tumor_recurrence:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
------	---------	--------	------	---------	------	------

```

      0      767      2059      2094      3336      5183      1

recurrence_status:
norecurrence  recurrence      NA's
           81           36           1

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
   47   1117   2234   2347   3504   5183     1

vital_status:
deceased  living
     77     41

treatment:
chemo.plus.hormono      chemotherapy      hormonotherapy      untreated
           25           36           40           14
           NA's
           3

batch:
CAL
118

uncurated_author_metadata:
  Length    Class      Mode
   118 character character

```

Source

<http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-158/>

DFHCC

DFHCC

Description

ExpressionSet for the DFHCC Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2826790/

```

```

Title:
URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19615
PMIDs: 20098429
No abstract available.
notes:
  summary:
    A small number of over-expressed and over-amplified genes were significant
ly associated with early recurrence despite adjuvant therapy. This was ve
rified in independent cohorts.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
(42447 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription

```

Details

```

assayData: 42447 features, 115 samples
Platform type:
-----
Available sample meta-data:
-----

sample_name:
  Length      Class      Mode
    115 character character

alt_sample_name:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
   6.0  155.0   230.0   293.3  398.5   828.0

sample_type:
tumor
  115

er:
negative positive
   45      70

pgr:

```

negative positive
51 64

her2:
negative positive
79 36

tumor_size:
Min. 1st Qu. Median Mean 3rd Qu. Max.
0.800 1.350 2.100 2.312 2.850 6.500

N:
0 1
62 53

age_at_initial_pathologic_diagnosis:
Min. 1st Qu. Median Mean 3rd Qu. Max.
32.00 45.00 53.00 53.89 60.00 85.00

grade:
1 2 3
23 28 64

dmfs_days:
Min. 1st Qu. Median Mean 3rd Qu. Max.
30 1500 1920 1799 2325 2640

dmfs_status:
norecurrence recurrence
101 14

treatment:
chemo.plus.hormono chemotherapy hormonotherapy untreated
42 38 22 7
NA's
6

batch:
DFHCC
115

uncurated_author_metadata:
Length Class Mode
115 character character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19615>

DFHCC2

*DFHCC2***Description**

Test the efficacy of treating TNBC with neoadjuvant cisplatin; explore biomarkers to identify predictors of response

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name:
```

```
  Laboratory:
```

```
  Contact information: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2834466/
```

```
  Title:
```

```
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18864
```

```
  PMIDs: 20100965
```

```
Abstract: A 16 word abstract is available. Use 'abstract' method.
```

```
notes:
```

```
  summary:
```

```
    A subset of the patients experienced a response induced by cisplatin and biomarkers were identified that could predict response to cisplatin.
```

```
  mapping.method:
```

```
    maxRowVariance
```

```
  mapping.group:
```

```
    EntrezGene.ID
```

```
  preprocessing:
```

```
    As published by original author.
```

```
featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
```

```
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at  
  (42447 total)
```

```
  varLabels: probeset gene EntrezGene.ID best_probe
```

```
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 84 samples
```

```
Platform type:
```

```
-----
```

```
Available sample meta-data:
```

```
-----
```



```

sample_name:
  Length  Class  Mode
    84 character character

unique_patient_ID:
  Length  Class  Mode
    84 character character

sample_type:
tumor
  84

er:
negative positive
  53      31

pgr:
negative positive
  53      31

her2:
negative positive
  66      18

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.
  29.00  45.00  53.00  52.89  59.00  85.00

grade:
  1  2  3
  10 16 58

treatment:
chemotherapy
  84

batch:
DFHCC2_CISPLATIN DFHCC2_REFERENCE
                24                60

uncurated_author_metadata:
  Length  Class  Mode
    84 character character

duplicates:
  Length  Class  Mode
    84 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18864>

DFHCC3

DFHCC3

Description

ExpressionSet for the DFHCC3 Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/16473279>

 Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3744>

 PMIDs: 16473279

 No abstract available.

 notes:

 summary:

 Basal like cancerse_often lack an inactivated X chromosome.e_Other markers found were duplication of the active X chromosome ande_nonheterochromatin ized X chromosomal DNA. A small subset of X chromosomal genes were overexp ressed. These abnormalities are thought to led to the pathogenesis of basa l like cancers.

 mapping.method:

 maxRowVariance

 mapping.group:

 EntrezGene.ID

 preprocessing:

 As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (42447 total)

 varLabels: probeset gene EntrezGene.ID best_probe

 varMetadata: labelDescription

Details

assayData: 42447 features, 40 samples

Platform type:

```

-----
Available sample meta-data:
-----

sample_name:
  Length   Class      Mode
    40     character character

alt_sample_name:
  Length   Class      Mode
    40     character character

sample_type:
tumor
  40

batch:
DFHCC3
  40

uncurated_author_metadata:
  Length   Class      Mode
    40     character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3744>

DUKE

DUKE

Description

ExpressionSet for the DUKE Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/16273092
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse3143
  PMIDs: 16273092
  No abstract available.

```

notes:

summary:

It was shown that the activation_status of several oncogenic pathways can be identified by gene expression signatures. These gene signatures identify deregulation of pathways, associations with clinically relevant outcomes, and characteristics of specific cancers and tumor subtypes.

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:

As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: 1000_at 1001_at ... AFFX-MurIL4_at (12085 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 12085 features, 171 samples

Platform type:

Overall survival time-to-event summary (in years):

Call: survfit(formula = Surv(time, cens) ~ -1)

1 observation deleted due to missingness

n	events	median	0.95LCL	0.95UCL
170.00	43.00	9.01	6.22	NA

Available sample meta-data:

sample_name:

Length	Class	Mode
171	character	character

alt_sample_name:

Length	Class	Mode
171	character	character

sample_type:

tumor
171

er:

negative positive

```

      57      114

pgr:
negative positive  NA's
      23      65      83

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.20  1.80   2.30   2.74  3.50   8.50    83

N:
  0    1 NA's
 53  36  82

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 171.0  417.0   957.5 1235.0 1852.0 4069.0    1

vital_status:
deceased  living  NA's
      43     127     1

batch:
DUKE
171

uncurated_author_metadata:
  Length    Class      Mode
  171 character character

duplicates:
DUKE.DUKE_T00.622 DUKE.DUKE_T01.052 DUKE.DUKE_T01.522 DUKE.DUKE_T01.534
              1              1              1              1
              NA's
              167

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse3143>

DUKE2

DUKE2

Description

Predicting response with gene signature

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/18024211
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse6861
  PMIDs: 18024211

  Abstract: A 5 word abstract is available. Use 'abstract' method.
  notes:
    summary:
      Retraction in Lancet Feb 2011 (21277543); Regimen specific signatures were
      able to predict pathological complete response. Selecting patients with t
      hese gene signataures could increase the proportion of patients with pCR t
      han by basing clinical decisions on clinical factors.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1053_3p_at 117_3p_at ... X79510cds_3p_s_at (45490
  total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 45490 features, 160 samples
Platform type:
-----
Available sample meta-data:
-----

sample_name:
  Length      Class      Mode
    160 character character

alt_sample_name:
  Length      Class      Mode
    160 character character

```

```

sample_type:
tumor
  160

er:
negative positive
  123      37

pgr:
negative positive  NA's
  133      25      2

N:
  0      1 NA's
58  95   7

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
26.00  43.00   49.00  49.41  56.00  70.00   35

grade:
  1      2      3 NA's
  2     37     70   51

treatment:
chemotherapy
  160

batch:
DUKE2
  160

uncurated_author_metadata:
  Length      Class      Mode
  160 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse6861>

duplicates

a list containing the names of patients that are believed to be duplicates across datasets

Description

The object is a list where each element is a patient ID that is believed to be a duplicate of a patient in another dataset. Patients are designated as duplicated if they have Spearman correlations greater than or equal to 0.98 with other patient expression profiles

Format

A list with 107 elements, each of which is a patient ID.

 EMC2

 EMC2

Description

ExpressionSet for the EMC2 Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/19421193
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse12276
  PMIDs: 19421193
  No abstract available.
  notes:
    summary:
      Genes were identified that may increase the ability of breast cancer cells
      to infiltrate the blood-brain barrier.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```


Details

assayData: 42447 features, 204 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
204	character	character

alt_sample_name:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.00	51.75	102.50	102.50	153.20	204.00

sample_type:

tumor
204

N:

0	NA's
48	156

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0	335	640	799	1098	3507

dmfs_status:

norecurrence	recurrence
19	185

treatment:

chemotherapy	untreated
156	48

batch:

EMC2
204

uncurated_author_metadata:

Length	Class	Mode
204	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse12276>

EORTC10994

*EORTC10994***Description**

ExpressionSet for the EORTC10994 Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=15897907>

 Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1561>

 PMIDs: 15897907

 No abstract available.

 notes:

 summary:

 The tumors with an apocrine gene expression profile had strong histological apocrine features. These tumors were androgen receptor positive and were all ER negative, creating further classifications of tumor cells based on steroid receptor activity- luminal which are ER and AR positive, basal that are ER and AR negative, and molecular apocrine that are ER negative and AR positive.

 mapping.method:

 maxRowVariance

 mapping.group:

 EntrezGene.ID

 preprocessing:

 As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (20967 total)

 varLabels: probeset gene EntrezGene.ID best_probe

 varMetadata: labelDescription

Details

assayData: 20967 features, 49 samples

Platform type:

Available sample meta-data:

```

-----
sample_name:
  Length   Class   Mode
    49 character character

alt_sample_name:
  Length   Class   Mode
    49 character character

sample_type:
tumor
  49

er:
negative positive
  22      27

pgr:
negative positive  NA's
  29      18      2

tumor_size:
  1  2  3  4
  4 23 14  8

N:
  0  1
19 30

grade:
  1  2  3 NA's
  4 22 20  3

batch:
EORTC10994
  49

uncurated_author_metadata:
  Length   Class   Mode
    49 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1561>

EXPO

*EXPO***Description**

ExpressionSet for the EXPO Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information:
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE2109
  PMIDs:
  No abstract available.
  notes:
  summary:
    N/A
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 42447 features, 353 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
  353 character character

```

```

alt_sample_name:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  1005  21640  101100  134700  215900  486200

sample_type:
tumor
  353

er:
negative positive  NA's
   85      161     107

pgr:
negative positive  NA's
  114      129     110

her2:
negative positive  NA's
  166       61     126

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  25.00  45.00  55.00  59.44  67.50  95.00    1

grade:
  1  2  3 NA's
  32 114 151 56

batch:
EXPO
  353

uncurated_author_metadata:
  Length    Class    Mode
  353 character character

duplicates:
EXPO.EXPO_GSM53027 EXPO.EXPO_GSM53059  NA's
                   1                   1    351

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE2109>

FNCLCC

*FNCLCC***Description**

ExpressionSet for the FNCLCC Dataset

Format

experimentData(eset):

Experiment data

Experimenter name:

Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=17659439>

Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7017>

PMIDs: 17659439

No abstract available.

notes:

summary:

A potentially more powerful clinicogenomic model was created by combining a subset of relevant genes from an already published gene expression signature and a commonly used clinical prognostic model (NPI). The genes in this model are known to have a role in breast cancer, carcinogenesis, or chemotherapy resistance.

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:

As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: UMGC_00005 UMGC_00007 ... UMGC_09018 (6064 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 6064 features, 150 samples

Platform type:

Available sample meta-data:

```
sample_name:
  Length   Class   Mode
    150 character character

alt_sample_name:
  Length   Class   Mode
    150 character character

sample_type:
tumor
  150

N:
  1
150

treatment:
chemotherapy
  150

batch:
FNCLCC
  150

uncurated_author_metadata:
  Length   Class   Mode
    150 character character
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7017>

GSE25066

GSE25066

Description

ExpressionSet for the GSE25066 Dataset

Format

```
experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information:
```

```

Title:
URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE25066
PMIDs: 21558518
No abstract available.
notes:
  summary:

  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 20967 features, 508 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
    508 character character

```

```

alt_sample_name:
  Length      Class      Mode
    508 character character

```

```

sample_type:
tumor
  508

```

```

er:
negative positive  NA's
   205      297     6

```

```

pgr:
negative positive  NA's
   258      243     7

```



```

her2:
negative positive  NA's
   485         6    17

T:
T0 T1 T2 T3 T4
  3 30 255 145 75

N:
  0  1
157 351

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  24.0   42.0   49.0   49.8   58.0   75.0

grade:
  1  2  3  4 NA's
 32 180 259 15  22

dmfs_days:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  0.0   636.5   999.9  1088.0  1500.0  2717.0

dmfs_status:
norecurrence  recurrence
           397             111

batch:
GSE25066
  508

uncurated_author_metadata:
  Length    Class      Mode
  508 character character

chemosensitivity_prediction:
Rx Insensitive  Rx Sensitive
           339             169

GGI_prediction:
High Low
 336 172

PAM50_prediction:
Basal  Her2  LumA  LumB Normal
  189   37  160   78   44

```

dlda30_prediction:

pCR RD
196 312

RCB_prediction:

RCB-0/I RCB-II/III
230 278

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE25066>

GSE32646

GSE32646

Description

ExpressionSet for the GSE32646 Dataset

Format

experimentData(eset):

Experiment data

Experimenter name:

Laboratory:

Contact information:

Title:

URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32646>

PMIDs: 22320227

No abstract available.

notes:

summary:

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:

As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: 1007_s_at 1053_at ... 91952_at (42437 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 42437 features, 115 samples
Platform type:

Available sample meta-data:

sample_name:
 Length Class Mode
 115 character character

sample_type:
tumor
 115

er:
negative positive
 44 71

pgr:
negative positive
 70 45

her2:
negative positive
 81 34

T:
 1 2 3 4
 5 87 18 5

N:
 0 1
 32 83

age_at_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max.
 27.00 45.00 51.00 51.49 59.00 73.00

grade:
 1 2 3
 16 78 21

batch:
GSE32646
 115

uncurated_author_metadata:

Length	Class	Mode
115	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32646>

GSE48091

GSE48091

Description

ExpressionSet for the GSE48091 Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information:
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE48091
  PMIDs: 26077471
  No abstract available.
notes:
  summary:

  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 100121619_TGI_at 100121620_TGI_at ... 100314044_TGI_at
  (23246 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 23246 features, 623 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
623	character	character

sample_type:

tumor
623

batch:

GSE48091
623

uncurated_author_metadata:

Length	Class	Mode
623	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE48091>

GSE58644

GSE58644

Description

ExpressionSet for the GSE58644 Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information:

 Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE58644>

 PMIDs: 25284793

 No abstract available.

 notes:

summary:

mapping.method:
maxRowVariance

mapping.group:
EntrezGene.ID

preprocessing:
As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: 7896756 7896759 ... 8180179 (21462 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 21462 features, 321 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
321	character	character

alt_sample_name:

Length	Class	Mode
321	character	character

sample_type:

tumor
321

er:

negative	positive	NA's
70	250	1

her2:

negative	positive	NA's
256	58	7

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.600	1.600	2.100	2.354	2.600	15.000

T:

1	2	3	4	NA's
43	59	13	1	205

N:

0	1	NA's
138	151	32

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
29.00	49.00	58.00	58.82	68.00	93.00

grade:

1	2	3	NA's
26	135	159	1

dmfs_status:

norecurrence	recurrence
295	26

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0	9496	17900	21620	33600	52590

treatment:

chemo.plus.hormono	chemotherapy	hormonotherapy	untreated
91	29	66	10
NA's			
125			

chemo:

0	1	NA's
105	123	93

tamoxifen:

0	1	NA's
39	157	125

herceptin:

0	1	NA's
190	12	119

batch:

GSE58644
321

uncurated_author_metadata:

Length	Class	Mode
321	character	character

```

duplicates:
  Length   Class   Mode
      321 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE58644>

HLP

HLP

Description

ExpressionSet for the HLP Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=19688261
  Title:
  URL: http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-543/
  PMIDs: 19688261
  No abstract available.
  notes:
    summary:
      The results show evidence of different patterns of genetic aberrations in
      distinct molecular subtypes of breast cancer. Patterns of copy number aber-
      rations may drive biological phenomena characteristic to each subtype.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 9g8cQB1TZtuiix.ulU fJUdX0IAn_P9VLTgJU ...
  xopB7pPn18FJ067uDs (26536 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```


Details

assayData: 26536 features, 53 samples

Platform type:

 Available sample meta-data:

sample_name:

Length	Class	Mode
53	character	character

alt_sample_name:

Length	Class	Mode
53	character	character

sample_type:

tumor
53

er:

negative	positive
28	25

pgr:

negative	positive
33	20

her2:

negative	positive
40	13

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.200	1.800	2.450	2.648	3.000	8.000	5

N:

0	1	NA's
27	25	1

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
30.00	47.50	53.50	54.96	64.25	81.00	5

grade:

3
53

batch:

HLP
53

uncurated_author_metadata:
Length Class Mode
53 character character

Source

<http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-543/>

IRB

IRB

Description

ExpressionSet for the IRB Dataset

Format

```
experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/18297396
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5460
  PMIDs: 18297396
  No abstract available.
  notes:
    summary:

    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

assayData: 42447 features, 129 samples
 Platform type:

 Available sample meta-data:

sample_name:
 Length Class Mode
 129 character character

alt_sample_name:
 Length Class Mode
 129 character character

sample_type:
 tumor
 129

er:
 negative positive
 53 76

her2:
 negative positive
 98 31

tumor_size:
 Min. 1st Qu. Median Mean 3rd Qu. Max.
 0.800 1.500 2.200 2.488 3.000 8.500

N:
 0 1
 64 65

grade:
 1 2 3
 27 32 70

treatment:
 untreated
 129

batch:
 IRB
 129

uncurated_author_metadata:

Length	Class	Mode
129	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5460>

K00

K00

Description

link does not work, in progress8

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/12747878
  Title:
  URL: Unavailable
  PMIDs: 12747878

Abstract: A 6 word abstract is available. Use 'abstract' method.
notes:
  summary:
    A new gene signature was used to accurately predict 90
n the study.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at (280
  total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 280 features, 88 samples

Platform type:

 Available sample meta-data:

sample_name:

Length	Class	Mode
88	character	character

alt_sample_name:

Length	Class	Mode
88	character	character

sample_type:

tumor
88

er:

negative	positive
15	73

pgr:

negative	positive
23	65

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.20	1.80	2.30	2.74	3.50	8.50

N:

0	1
19	69

treatment:

chemotherapy	untreated
61	27

batch:

KOO
88

uncurated_author_metadata:

Length	Class	Mode
88	character	character

duplicates:

Length	Class	Mode
88	character	character

Source

Unavailable

loadBreastDatasets	<i>Function to load breast cancer SummarizedExperiment objects from the Experiment Hub</i>
--------------------	--

Description

This function returns breast cancer datasets from the hub and a vector of patients from the datasets that are duplicates based on a spearman correlation > 0.98

Usage

```
loadBreastDatasets(
  rescale = FALSE,
  minNumberGenes = 0,
  minNumberEvents = 0,
  minSampleSize = 0,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE,
  removeDuplicates = FALSE
)
```

Arguments

rescale	apply centering and scaling to the expression sets (default FALSE)
minNumberGenes	an integer specifying to remove expression sets with less genes than this number (default 0)
minNumberEvents	an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)
minSampleSize	an integer specifying the minimum number of patients required in a summarizedExperiment (default 0)
keepCommonOnly	remove entrezIDs not common to all datasets (default FALSE)
imputeMissing	remove patients from datasets with missing expression values
removeDuplicates	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

Value

A 'list' with 2 elements. The First element named 'SummarizedExperiment's contains the datasets. The second element named duplicates contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

loadBreastEsets	<i>Function to load breast cancer expression sets from the Experiment Hub</i>
-----------------	---

Description

This function returns breast cancer datasets from the hub and a vector of patients from the datasets that are most likely duplicates

Usage

```
loadBreastEsets(
  loadString = "majority",
  removeDuplicates = TRUE,
  quantileCutoff = 0,
  rescale = FALSE,
  minNumberGenes = 0,
  minNumberEvents = 0,
  minSampleSize = 0,
  removeRetracted = TRUE,
  removeSubsets = TRUE,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE
)
```

Arguments

loadString	a character vector specifying which data will be loaded. The default is "majority", which loads in 37 of the 39 datasets. The other option is to provide a character vector of the names of the datasets to load. The metabric and tcga datasets are loaded separately as they are very large and doing so will help prevent memory allocation errors for R windows. Furthermore, these datasets are so large that they dominate statistical analyses so it is best that they are analyzed separate of the 37 smaller datasets loaded with the string majority
removeDuplicates	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)
quantileCutoff	A numeric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)
rescale	apply centering and scaling to the expression sets (default FALSE)

minNumberGenes an integer specifying to remove expression sets with less genes than this number (default 0)
minNumberEvents an integer specifying how many survival events must be in the dataset to keep the dataset (default 0)
minSampleSize an integer specifying the minimum number of patients required in an eset (default 0)
removeRetracted remove datasets from retracted papers (default TRUE, currently just PMID17290060 dataset)
removeSubsets remove datasets that are a subset of other datasets (default TRUE, currently just PMID19318476)
keepCommonOnly remove probes not common to all datasets (default FALSE)
imputeMissing remove patients from datasets with missing expression values

Value

a list with 2 elements. The first element named `esets` contains the datasets. The second element named `duplicates` contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
## Use the default loadString="majority" if you want the 37 smaller datasets
esetsAndDups <- loadBreastEsets(loadString = c("CAL", "DFHCC", "DFHCC2",
      "DFHCC3", "DUKE", "DUKE2", "EMC2"))
```

LUND

*LUND***Description**

ExpressionSet for the LUND Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=18430221
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31863
  PMIDs: 18430221
  No abstract available.
```



```

notes:
  summary:
    A significant difference was found between the ER positive subgroup and ER
    negative subgroup in the gene expression profiles.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: H200006618 H200006808 ... H300022925 (11154 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 11154 features, 143 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
    143 character character

```

```

alt_sample_name:
  Length      Class      Mode
    143 character character

```

```

sample_type:
tumor
  143

```

```

er:
negative positive
   29      114

```

```

pgr:
negative positive  NA's
   47      88      8

```

```

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.200  1.100  1.500  1.486  1.800  4.000    2

```

```

N:
  0
143

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
 27.00  47.50  56.00  54.76  63.00  73.00

batch:
LUNDS1 LUNDS2 LUNDS3 LUNDS4
   30    47    22    44

uncurated_author_metadata:
  Length      Class      Mode
   143 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31863>

LUND2

LUND2

Description

ExpressionSet for the LUND2 Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=17452630
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5325
  PMIDs: 17452630
  No abstract available.
  notes:
    summary:
      Microarray signature was able to show PTEN mRNA losse_when IHC was unable,
      even though tumors exhibited PTEN loss behavior. Stathmim was an accurate
      IHC marker of the signature and had prognostic significance.
    mapping.method:
      maxRowVariance

```

```

mapping.group:
  EntrezGene.ID
preprocessing:
  As published by original author.

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1 2 ... 27648 (22008 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 22008 features, 105 samples

Platform type:

 Available sample meta-data:

```

sample_name:
  Length      Class      Mode
    105 character character

```

```

alt_sample_name:
  Length      Class      Mode
    105 character character

```

sample_type:

```

tumor
  105

```

er:

```

negative positive
   60         45

```

treatment:

```

hormonotherapy
   105

```

batch:

```

LUND2
  105

```

uncurated_author_metadata:

```

  Length      Class      Mode
    105 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5325>

MAINZ

MAINZ

Description

ExpressionSet for the MAINZ Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=18593943>

 Title:

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

 PMIDs: 18593943

 No abstract available.

 notes:

 summary:

 Poor prognosis is noted in tumors with low ER expression, showing the highest level of proliferative activity. In some tumors with highly expressed B-cell or T-cell metagenes, metastases rarely occurred, even with high proliferation and low ER expression.

 mapping.method:

 maxRowVariance

 mapping.group:

 EntrezGene.ID

 preprocessing:

 As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

 featureNames: 1007_s_at 1053_at ... AFX-HUMISGF3A/M97935_MB_at
 (20967 total)

 varLabels: probeset gene EntrezGene.ID best_probe

 varMetadata: labelDescription

Details

assayData: 20967 features, 200 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
200	character	character

alt_sample_name:

Length	Class	Mode
200	character	character

sample_type:

tumor
200

er:

negative	positive
38	162

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.100	1.500	2.000	2.070	2.425	6.000

N:

0
200

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
25.00	50.00	60.00	59.98	69.00	90.00

grade:

1	2	3
29	136	35

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
30	1905	2715	2816	3855	7200

dmfs_status:

norecurrence	recurrence
154	46

treatment:

untreated
200

batch:

MAINZ
200

uncurated_author_metadata:
Length Class Mode
200 character character

Source

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

MAQC2	<i>MAQC2</i>
-------	--------------

Description

ExpressionSet for the MAQC2 Dataset

Format

```
experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=20064235
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20194
  PMIDs: 20064235
  No abstract available.
  notes:
    summary:
      It is possible to build multi-gene classifiers of clinical outcome. Prediction accuracy depends on training sample size and classification difficulty.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
```

varMetadata: labelDescription

Details

assayData: 20967 features, 230 samples

Platform type:

 Available sample meta-data:

sample_name:

Length	Class	Mode
230	character	character

alt_sample_name:

Length	Class	Mode
230	character	character

sample_type:

tumor
230

er:

negative	positive
89	141

pgr:

negative	positive
126	104

her2:

negative	positive
190	40

N:

0	1
66	164

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
26.00	45.00	51.00	52.02	59.00	79.00

grade:

1	2	3
13	94	123

treatment:

chemotherapy

230

batch:

MAQC2

230

uncurated_author_metadata:

Length Class Mode

230 character character

Source<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20194>

MCCC

*MCCC***Description**

ExpressionSet for the MCCC Dataset

Format

experimentData(eset):

Experiment data

Experimenter name:

Laboratory:

Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=19960244>

Title:

URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19177>

PMIDs: 19960244

No abstract available.

notes:

summary:

Overall, expression and copy number profiling of familial tumors have shown that the tumors show molecular heterogeneity similar to sporadic tumors and are defined by their molecular subtypes rather than BRCA1 or BRCA2 germline mutation status.

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:

As published by original author.

featureData(eset):


```
An object of class 'AnnotatedDataFrame'
  featureNames: probe_10017 probe_10021 ... probe_7650767 (19048 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 19048 features, 75 samples
Platform type:
```

```
-----
Available sample meta-data:
```

```
-----
sample_name:
  Length   Class   Mode
      75 character character
```

```
sample_type:
tumor
  75
```

```
batch:
MCCC
  75
```

```
uncurated_author_metadata:
  Length   Class   Mode
      75 character character
```

Source

```
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19177
```

MDA4

MDA4

Description

ExpressionSet for the MDA4 Dataset

Format

```
experimentData(eset):
Experiment data
  Experimenter name:
```

```

Laboratory:
Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=16896004
Title:
URL: http://bioinformatics.mdanderson.org/pubdata.html
PMIDs: 16896004
No abstract available.
notes:
  summary:
    The developed 30-probe set has high sensitivity and negative predictive value, accurately identifying 12 out of 13 patients with pCR and 27 out of 28 patients with residual disease.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (21169 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 21169 features, 129 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
    129 character character

```

```

unique_patient_ID:
  Length      Class      Mode
    129 character character

```

```

sample_type:
tumor
  129

```

```

er:
negative positive  NA's
    48      79      2

```

```

pgr:
negative positive  NA's
      73      54      2

her2:
negative positive
      114      15

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  0.000  0.500  1.800  2.162  3.000 10.000     8

N:
  0    1 NA's
 59  62   8

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
 28.00  43.00  51.00  51.43  61.00  73.00

treatment:
chemotherapy
      129

batch:
MDA4
      129

uncurated_author_metadata:
  Length    Class    Mode
    129 character character

duplicates:
MDA4.MDA4_M207 MDA4.MDA4_M400    NA's
              1              1    127

```

Source

<http://bioinformatics.mdanderson.org/pubdata.html>

METABRIC

METABRIC

Description

ExpressionSet for the METABRIC Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/22522925
  Title:
  URL: https://www.ebi.ac.uk/ega/studies/EGAS00000000083
  PMIDs: 22522925
  No abstract available.
notes:
  summary:

  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ILMN_1802380 ILMN_1736104 ... ILMN_1709472 (36155
    total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 36155 features, 2136 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

```

      165 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
1971.0  891.0   12.3   11.6   13.2

```

```

-----
Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
  2136 character character

```

```

alt_sample_name:

```

```

      Length      Class      Mode
      2136 character character

sample_type:
healthy  tumor
  144    1992

er:
negative positive  NA's
  440    1508    188

her2:
negative positive  NA's
  676    148    1312

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  0.000  1.700  2.300  2.621  3.000 18.200  164

N:
  0    1 NA's
1042 950 144

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 21.93  51.36  61.78  61.13  70.76  96.29  13

grade:
  1    2    3 NA's
 170  775  957  234

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
    3   1498   2632   2948   4357   9218  147

vital_status:
deceased  living  NA's
   891    1081   164

treatment:
chemo.plus.hormono  chemotherapy  hormonotherapy  untreated
                196                226                1029                685

batch:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  1.000  1.000  3.000  2.613  3.000  5.000  144

uncurated_author_metadata:

```

```

Length      Class      Mode
2136 character character

```

duplicates:

```

Length      Class      Mode
2136 character character

```

Source

<https://www.ebi.ac.uk/ega/studies/EGAS00000000083>

MSK

MSK

Description

ExpressionSet for the MSK Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=16049480
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2603
  PMIDs: 16049480
  No abstract available.
  notes:
    summary:
      A set of genes were identified that mark and mediate metastasis to the lung.
      Some genes confer growth advantages to both the breast tumor and lung environment,
      while others contribute to aggressive growth specifically in the lung.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (20967 total)

```

```
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 99 samples
Platform type:
-----
Available sample meta-data:
-----

sample_name:
  Length      Class      Mode
    99 character character

alt_sample_name:
  Length      Class      Mode
    99 character character

sample_type:
tumor
  99

er:
negative positive
  42      57

pgr:
negative positive  NA's
  55      43      1

her2:
positive  NA's
  85      14

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  1.100  2.450  3.200  3.624  4.300 10.000

N:
  0 1
34 65

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  30.00  46.50  56.00  55.81  63.50  87.00

dmfs_days:
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	245	1279	1971	1888	2575	3924	17

dmfs_status:

norecurrence	recurrence	NA's
55	27	17

batch:

MSK
99

uncurated_author_metadata:

Length	Class	Mode
99	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2603>

MUG

MUG

Description

ExpressionSet for the MUG Dataset

Format

```
experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=18592372
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse10510
  PMIDs: 18592372
  No abstract available.
notes:
  summary:
    A method was developed to separate tumor cells and their microenvironment
    to test the prognostic abilities of the immune system. Results showed that
    lymphatic infiltration is beneficial for ER negative patients, but probab
    ly not beneficial for ER positive patients.
  mapping.method:
    maxRowVariance
  mapping.group:
```



```

EntrezGene.ID
preprocessing:
  As published by original author.

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: H200000001 H200000005 ... opHsV04TC000043 (14288 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription

```

Details

```

assayData: 14288 features, 152 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length   Class      Mode
    152 character character

```

```

alt_sample_name:
  Length   Class      Mode
    152 character character

```

```

sample_type:
tumor
  152

```

```

batch:
MUG
  152

```

```

uncurated_author_metadata:
  Length   Class      Mode
    152 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse10510>

Description

ExpressionSet for the NCCS Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=18636107
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse5364
  PMIDs: 18636107
  No abstract available.
  notes:
    summary:
      48 genes were identified that displayed highly restricted levels of expres
      sion in tumors compared to normal tissues. This was validated in 11 indepe
      ndent cohorts of different cancer types.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 20967 features, 183 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
183	character	character

alt_sample_name:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
------	---------	--------	------	---------	------

1.0 46.5 92.0 92.0 137.5 183.0

sample_type:

tumor

183

batch:

NCCS

183

uncurated_author_metadata:

Length Class Mode

183 character character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse5364>

NCI

NCI

Description

ExpressionSet for the NCI Dataset

Format

experimentData(eset):

Experiment data

Experimenter name:

Laboratory:

Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=12917485>

Title:

URL: Supplemental data from paper

PMIDs: 12917485

No abstract available.

notes:

summary:

Expression patterns were strongly associated with ER status, moderately associated with grade, but not associated with menopausal state, node status, or tumor size. Genes that were significantly associated with survival were identified.

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:
As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
featureNames: AF106966 AF217974 ... Y12473 (5154 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription

Details

assayData: 5154 features, 99 samples
Platform type:

Available sample meta-data:

sample_name:
Length Class Mode
99 character character

alt_sample_name:
Min. 1st Qu. Median Mean 3rd Qu. Max.
21580 21610 21640 21650 21670 21830

sample_type:
tumor
99

er:
negative positive
34 65

tumor_size:
Min. 1st Qu. Median Mean 3rd Qu. Max.
0.80 1.80 2.50 2.82 3.00 8.00

N:
0 1
46 53

age_at_initial_pathologic_diagnosis:
Min. 1st Qu. Median Mean 3rd Qu. Max.
33.00 49.00 57.00 57.47 64.50 90.00

grade:
1 2 3
16 38 45

```

days_to_tumor_recurrence:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
      8    967    2057   1969   2930   4067

```

```

recurrence_status:
norecurrence  recurrence
           54           45

```

```

treatment:
  chemotherapy  hormonotherapy  untreated
             10             78             11

```

```

batch:
NCI
  99

```

```

uncurated_author_metadata:
  Length    Class    Mode
    99 character character

```

Source

Supplemental data from paper

NKI

NKI

Description

ExpressionSet for the NKI Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=12490681; http://www.ncbi.nlm.nih.gov
  Title:
  URL: Not available
  PMIDs: 12490681, 11823860
  No abstract available.
  notes:
  summary:
    It was found that the gene expression profile that was studied was more po

```

werful in predicting outcome of disease in younger patients than using standard clinical and pathological criteria.

```
mapping.method:
  maxRowVariance
mapping.group:
  EntrezGene.ID
preprocessing:
  As published by original author.
```

featureData(eset):

An object of class 'AnnotatedDataFrame'

```
featureNames: Contig45645_RC Contig44916_RC ... Contig62037_RC (14960
  total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
```

Details

assayData: 14960 features, 337 samples

Platform type:

Overall survival time-to-event summary (in years):

Call: survfit(formula = Surv(time, cens) ~ -1)

42 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
295	79	NA	NA	NA

Available sample meta-data:

sample_name:

Length	Class	Mode
337	character	character

alt_sample_name:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
4.0	123.0	215.0	214.1	312.0	404.0

sample_type:

```
tumor
337
```

er:

negative	positive
88	249

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.200	1.500	2.000	2.241	2.800	5.500

N:
 0 1
 193 144

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
26.0	40.0	45.0	44.2	49.0	62.0

grade:
 1 2 3
 79 109 149

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
9	1252	2414	2546	3602	6699	18

dmfs_status:

norecurrence	recurrence	NA's
210	109	18

days_to_tumor_recurrence:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
9	1252	2414	2546	3602	6699	18

recurrence_status:

norecurrence	recurrence	NA's
210	109	18

days_to_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
20	1934	2637	2870	3763	6694	42

vital_status:

deceased	living	NA's
79	216	42

treatment:

chemotherapy	hormonotherapy	untreated
90	40	207

batch:
 NKI NKI2
 117 220

uncurated_author_metadata:

Length	Class	Mode
337	character	character

Source

Not available

PNC

PNC

Description

ExpressionSet for the PNC Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=21910250
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20711
  PMIDs: GSE20711, PMID 21910250
  No abstract available.
  notes:
    summary:
      Breast tumors can be further divided than the currently known expression s
ubtypes based on DNA methylation profiles.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```


Details

assayData: 42447 features, 92 samples
 Platform type:
 Overall survival time-to-event summary (in years):
 Call: survfit(formula = Surv(time, cens) ~ -1)

4 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
88.0	25.0	NA	11.3	NA

 Available sample meta-data:

sample_name:

Length	Class	Mode
92	character	character

alt_sample_name:

Length	Class	Mode
92	character	character

sample_type:
 tumor
 92

er:

negative	positive	NA's
43	45	4

pgr:

negative	positive	NA's
43	40	9

her2:

negative	positive	NA's
64	26	2

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.900	1.700	2.500	2.758	3.000	10.000	6

N:

	0	1	NA's
	43	40	9

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
------	---------	--------	------	---------	------	------

```

32.16  48.57  53.90  55.97  64.84  82.13      4

grade:
  1    2    3 NA's
13    5   70    4

days_to_tumor_recurrence:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
    29   967   2216  2122  2931   5139    7

recurrence_status:
norecurrence  recurrence      NA's
           49           36           7

days_to_death:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
   318   1940   2372  2525  3043   5139    4

vital_status:
deceased  living  NA's
    25     63     4

batch:
PNC
92

uncurated_author_metadata:
  Length  Class  Mode
    92 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20711>

STK

STK

Description

ExpressionSet for the STK Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:

```

```

Laboratory:
Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=16280042
Title:
URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse1456
PMIDs: 16280042
No abstract available.
notes:
  summary:
    Expression profiling was able to better predict prognosis compared to histological staging.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... 244889_at (36178 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 36178 features, 159 samples
Platform type:
-----
Available sample meta-data:
-----

sample_name:
  Length      Class      Mode
    159 character character

alt_sample_name:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  1.0   67.0   136.0   138.3  208.5   277.0

sample_type:
tumor
  159

er:
negative positive
   29     130

age_at_initial_pathologic_diagnosis:

```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
31.0	48.0	56.0	57.8	68.5	87.0

grade:

1	2	3	NA's
28	58	61	12

days_to_tumor_recurrence:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
66	2022	2467	2234	2846	3099

recurrence_status:

norecurrence	recurrence
113	46

treatment:

chemotherapy	hormonotherapy	untreated
89	48	22

batch:

STK
159

uncurated_author_metadata:

Length	Class	Mode
159	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse1456>

STNO2

STNO2

Description

ExpressionSet for the STNO2 Dataset

Format

experimentData(eset):

Experiment data

Experimenter name:

Laboratory:

Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=12829800>

Title:

```

URL: http://smd.princeton.edu/cgi-bin/publication/viewPublication.pl?pub_no=248
PMIDs: 12829800
No abstract available.
notes:
  summary:
    Distinct breast cancer subtypes were determined by gene expression profile
s and were validated in other published datasets.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: IMAGE:1020315 IMAGE:1030271 ... IMAGE:971399 (3663
  total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 3663 features, 118 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

n	events	median	0.95LCL	0.95UCL
118.00	46.00	4.67	3.34	NA

```

-----
Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
  118 character character

```

```

alt_sample_name:
  Length      Class      Mode
  118 character character

```

```

sample_type:
tumor
  118

```

```

er:

```

negative	positive	NA's
31	82	5

tumor_size:				
1	2	3	4	NA's
6	13	62	32	5

N:		
0	1	NA's
34	79	5

age_at_initial_pathologic_diagnosis:					
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
21.00	46.25	58.00	58.47	71.75	85.00

grade:			
1	2	3	NA's
11	49	53	5

days_to_tumor_recurrence:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
122.0	396.0	761.0	927.9	1233.0	2800.0	23

recurrence_status:	
norecurrence	recurrence
58	60

days_to_death:					
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
91	426	898	1019	1392	5722

vital_status:	
deceased	living
46	72

treatment:		
chemotherapy	hormonotherapy	untreated
23	73	22

batch:
STN02
118

uncurated_author_metadata:		
Length	Class	Mode
118	character	character

Source

http://smd.princeton.edu/cgi-bin/publication/viewPublication.pl?pub_no=248

TCGA

TCGA

Description

ExpressionSet for the TCGA Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/23000897
  Title:
  URL: http://cancergenome.nih.gov/
  PMIDs: 23000897
  No abstract available.
  notes:
    summary:

    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:
      As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A2M ... ARHGAP11A.2 (19504 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 19504 features, 1073 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
1073.00  103.00   10.05    8.56   12.05

```

```

-----
Available sample meta-data:
-----

sample_name:
  Length   Class      Mode
  1073 character character

alt_sample_name:
  Length   Class      Mode
  1073 character character

unique_patient_ID:
  Length   Class      Mode
  1073 character character

sample_type:
tumor
  1073

er:
negative positive  NA's
  233      790      50

pgr:
negative positive  NA's
  334      686      53

her2:
negative positive  NA's
  549      161      363

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  26.00  49.00   58.00   58.48  68.00   90.00

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  -7.0  137.0  412.0   820.3 1180.0 6796.0

vital_status:
deceased  living
  103      970

batch:
TCGA
1073

```



```

uncurated_author_metadata:
  Length      Class      Mode
  1073 character character

```

Source

<http://cancergenome.nih.gov/>

TRANSBIG	<i>TRANSBIG</i>
----------	-----------------

Description

ExpressionSet for the TRANSBIG Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=17545524
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gsE7390
  PMIDs: 17545524
  No abstract available.
  notes:
  summary:
    The 76-gene signature was validated. The results supports the hypothesis t
    hat utilizing the gene signature could reduce the number of patients who r
    eceive unnecessary adjuvant therapy.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 20967 features, 198 samples
 Platform type:
 Overall survival time-to-event summary (in years):
 Call: survfit(formula = Surv(time, cens) ~ -1)

n	events	median	0.95LCL	0.95UCL
198.0	56.0	NA	17.1	NA

 Available sample meta-data:

sample_name:

Length	Class	Mode
198	character	character

sample_type:
 tumor
 198

er:
 negative positive
 64 134

tumor_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.600	1.700	2.000	2.181	2.500	5.000

N:
 0
 198

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
24.00	42.00	46.00	46.39	51.00	60.00

grade:

1	2	3	NA's
30	83	83	2

dmfs_days:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
125	2375	4384	3954	5566	9108

dmfs_status:
 norecurrence recurrence
 147 51

```

days_to_tumor_recurrence:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
   121   1528   3534   3399   5130   8711

recurrence_status:
norecurrence  recurrence
         112          86

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
   146   2744   4562   4150   5610   9108

vital_status:
deceased  living
         56    142

treatment:
untreated
         198

batch:
VDXGUYU VDXIGRU  VDXKIU VDXOXFU  VDXRHU
      36    50     51    24     37

uncurated_author_metadata:
  Length    Class      Mode
    198 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gsE7390>

UCSF

UCSF

Description

ExpressionSet for the UCSF Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:

```

Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=17428335>; <http://www.ncbi.nlm.nih.gov>

Title:

URL: Not available

PMIDs: 17428335, 14612510

No abstract available.

notes:

summary:

A gene set was identified that correctly predicted outcomes more effectively than using histological markers.

mapping.method:

maxRowVariance

mapping.group:

EntrezGene.ID

preprocessing:

As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: probe_1 probe_3 ... probe_10365 (8015 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 8015 features, 162 samples

Platform type:

Overall survival time-to-event summary (in years):

Call: survfit(formula = Surv(time, cens) ~ -1)

29 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
133.00	44.00	11.56	9.25	NA

Available sample meta-data:

sample_name:

Length	Class	Mode
162	character	character

alt_sample_name:

Length	Class	Mode
162	character	character

sample_type:

tumor
162

```

er:
negative positive NA's
   41   101    20

pgr:
negative positive NA's
   46   94    22

her2:
negative positive NA's
   35   19   108

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 0.000  1.800  2.000  2.682  3.200 11.000    7

N:
  0  1 NA's
67 82 13

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
28.00  44.00  53.00  56.61  70.00  88.00    9

grade:
  1  2  3 NA's
14 62 74 12

dmfs_days:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
   47   897   2040   2084   2992   8267    29

dmfs_status:
norecurrence  recurrence
      140           22

days_to_tumor_recurrence:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
   47   861   1865   1985   2847   8267    29

recurrence_status:
norecurrence  recurrence
      125           37

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
   47   1087   2054   2140   3087   8267    29

```

```

vital_status:
deceased  living  NA's
      54      99      9

treatment:
chemo.plus.hormono  chemotherapy  hormonotherapy  untreated
      31              38              61              22
      NA's
      10

batch:
UCSF
162

uncurated_author_metadata:
  Length  Class  Mode
    162 character character

```

Source

Not available

UNC4

UNC4

Description

ExpressionSet for the UNC4 Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=20813035
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse18229
  PMIDs: 20813035
  No abstract available.
  notes:
    summary:
      Clinically, this subtype is usually triple negative invasive ductal carcinomas with a poor prognosis. Response to standard of care preoperative chemotherapy is intermediate between basal-like and luminal tumors. The claudin

```

n-low subtype most closely resembles the mammary epithelial stem cell.

```
mapping.method:
  maxRowVariance
mapping.group:
  EntrezGene.ID
preprocessing:
  As published by original author.
```

featureData(eset):

An object of class 'AnnotatedDataFrame'

```
featureNames: probe.10 probe.12 ... probe.79701 (5420 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
```

Details

assayData: 5420 features, 305 samples

Platform type:

Overall survival time-to-event summary (in years):

Call: survfit(formula = Surv(time, cens) ~ -1)

65 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
240.00	51.00	7.73	6.82	NA

Available sample meta-data:

sample_name:

Length	Class	Mode
305	character	character

sample_type:

tumor
305

er:

negative	positive	NA's
99	154	52

pgr:

negative	positive	NA's
126	109	70

her2:

negative	positive	NA's
203	58	44

```

tumor_size:
  1  1.5  3  6 NA's
60  1 129 43 72

N:
  0  1 NA's
126 135 44

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
24.00  46.00  55.00  56.73  68.00  89.00  59

grade:
  1  2  3 NA's
25  80 138 62

days_to_tumor_recurrence:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
30.0  450.0  750.0  954.3 1380.0 3540.0 64

recurrence_status:
norecurrence  recurrence  NA's
          170           70      65

days_to_death:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
  30    540    885   1104   1590   5190   65

vital_status:
deceased  living  NA's
    51    189    65

batch:
UNC4
305

uncurated_author_metadata:
  Length  Class  Mode
    305 character character

duplicates:
K00.K00_KF_105 K00.K00_T01_514  NA's
              1              1    303

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse18229>

 UNT

 UNT

Description

ExpressionSet for the UNT Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=16478745>; <http://www.ncbi.nlm.nih.gov>

 Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2990>

 PMIDs: 16478745, 17401012

 No abstract available.

 notes:

 summary:

 A gene expression grading index (GGI) was developed. The GGI reclassified grade 2 patients into two groups with low and high risks of recurrence.

 mapping.method:

 maxRowVariance

 mapping.group:

 EntrezGene.ID

 preprocessing:

 As published by original author.

featureData(eset):

An object of class 'AnnotatedDataFrame'

 featureNames: 1007_s_at 1053_at ... 244889_at (36084 total)

 varLabels: probeset gene EntrezGene.ID best_probe

 varMetadata: labelDescription

Details

assayData: 36084 features, 133 samples

Platform type:

Available sample meta-data:

sample_name:

Length	Class	Mode
133	character	character

```

alt_sample_name:
  Length      Class      Mode
  133 character character

sample_type:
tumor
  133

er:
negative positive  NA's
  40      86      7

pgr:
negative positive  NA's
  6      56      71

tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  0.000  1.200  1.900  1.892  2.300  6.000

N:
  0
  133

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  24.00  44.00  53.00  51.79  60.00  73.00

grade:
  1  2  3 NA's
  32 51 29 21

dmfs_days:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  61  1338  2809  2724  4078  5305

dmfs_status:
norecurrence  recurrence  NA's
  97          28          8

days_to_tumor_recurrence:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  61  1338  2675  2687  3912  5305

recurrence_status:
norecurrence  recurrence  NA's
  76          49          8

```

```

treatment:
untreated
    133

batch:
KIU OXFU
    64  69

uncurated_author_metadata:
    Length      Class      Mode
    133 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2990>

UPP

UPP

Description

ExpressionSet for the UPP Dataset

Format

```

experimentData(eset):
Experiment data
  Experimenter name:
  Laboratory:
  Contact information: http://www.ncbi.nlm.nih.gov/pubmed/?term=16141321
  Title:
  URL: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse3494
  PMIDs: 16141321
  No abstract available.
  notes:
    summary:
      A 32-gene expression signature of p53 was identified that differentiates p
-53 mutant and wild-type tumors. The signature is more effective than sequ
ence-based assessments of p53 in predicting prognosis and therapeutic resp
onse.
    mapping.method:
      maxRowVariance
    mapping.group:
      EntrezGene.ID
    preprocessing:

```

As published by original author.

```
featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 1007_s_at 1053_at ... 244889_at (36178 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription
```

Details

```
assayData: 36178 features, 251 samples
Platform type:
```

```
-----
Available sample meta-data:
-----
```

```
sample_name:
  Length      Class      Mode
    251 character character
```

```
alt_sample_name:
  Length      Class      Mode
    251 character character
```

```
sample_type:
tumor
  251
```

```
er:
negative positive  NA's
    34      213      4
```

```
pgr:
negative positive
    61      190
```

```
tumor_size:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
 0.200  1.500   2.000  2.243  2.562 13.000
```

```
N:
  0      1 NA's
158  84    9
```

```
age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
28.00  52.00   64.00  62.11  72.00  93.00
```

grade:

1	2	3	NA's
67	128	54	2

days_to_tumor_recurrence:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
30	1870	3711	3007	3985	4654	17

recurrence_status:

norecurrence	recurrence	NA's
181	55	15

treatment:

hormonotherapy	untreated	NA's
80	142	29

batch:

UPPT	UPPU
80	171

uncurated_author_metadata:

Length	Class	Mode
251	character	character

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse3494>

 VDX

 VDX

Description

ExpressionSet for the VDX Dataset

Format

experimentData(eset):

Experiment data

 Experimenter name:

 Laboratory:

 Contact information: <http://www.ncbi.nlm.nih.gov/pubmed/?term=15721472>; <http://www.ncbi.nlm.nih.gov/pubmed/?term=17420468>

 Title:

 URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2034>; <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse3494>

 PMIDs: 15721472, 17420468

 No abstract available.

```

notes:
  summary:
    15721472: A gene signature was identified that can accurately predict distant metastases in node-negative cases. 17420468: Tumors with a lung metastatic gene signature were shown to be larger.
  mapping.method:
    maxRowVariance
  mapping.group:
    EntrezGene.ID
  preprocessing:
    As published by original author.

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFX-HUMISGF3A/M97935_MB_at
  (21169 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 21169 features, 344 samples
Platform type:
-----

```

```

Available sample meta-data:
-----

```

```

sample_name:
  Length      Class      Mode
    344 character character

```

```

alt_sample_name:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
   3.0  122.8   605.5   575.7  836.5  2038.0

```

```

sample_type:
tumor
  344

```

```

er:
negative positive
   135     209

```

```

tumor_size:
  1  2  3  4 NA's
146 132  5  3  58

```

```

N:

```

```

0
344

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  26.00  44.00   52.00   53.88  63.00   83.00   58

grade:
  1    2    3 NA's
  7   42  148  147

dmfs_days:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
   61   1254   2616   2377   3285   5201

dmfs_status:
norecurrence  recurrence
           226             118

treatment:
untreated
      344

batch:
 VDX VDXN
 286  58

uncurated_author_metadata:
  Length    Class      Mode
   344 character character

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse2034>; <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse5327>

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