Package 'curatedOvarianData'

September 4, 2025

Type Package

Title Clinically Annotated Data for the Ovarian Cancer Transcriptome

Version 1.47.2

Date 2025-05-05

Description The curatedOvarianData package provides data for gene expression analysis in patients with ovarian cancer.

Depends Biobase, R (>= 4.5.0)

Imports BiocGenerics

Suggests BiocStyle, futile.logger, genefilter, knitr, logging, metafor, rmarkdown, RUnit, survival, sva, xtable

License Artistic-2.0

VignetteBuilder knitr

URL http://bcb.dfci.harvard.edu/ovariancancer

biocViews ExperimentData, RNASeqData, CancerData, OvarianCancerData, MicroarrayData

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Clinically Annotated Data for the Ovarian Cancer Transcriptome

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Description

The curatedOvarianData package provides manually curated clinical data, uniformly processed expression data, and convenience functions for gene expression analysis in patients with ovarian cancer.

Details

Package:	curatedOvarianData
Type:	Package
Version:	1.47.2
Date:	2025-05-05
License:	Artistic-2.0
Depends:	R (>= 2.10.0), affy

Please see http://bcb.dfci.harvard.edu/ovariancancer for alterative versions of this package, differing in how redundant probe sets are dealt with. In the curatedOvarianData version, each gene is represented by the gene with maximum mean. In NormalizerVcuratedOvarianData, each gene is represented by the mean of the probesets after removing "noisy" probesets (see the Normalizer function of the Sleipnir library for computational biology), and in FULLVcuratedOvarianData, no collapsing of probe sets is done, but a map is provided to allow the user to do so by their method of choice through featureData(eset).

In the "Available sample meta-data" sections of each dataset, please refer to the following key.

For "sample_type": tumor / metastatic / adjacentnormal / healthy / cellline: "healthy" should be only from individuals without cancer, "adjacentnormal" from individuals with cancer, "metastatic" for non-primary tumors.

For "histological_type": ser=serous / endo=endometrioid / clearcell / mucinous, undifferentiated / other / mix. Other includes sarcomatoid, adenocarcinoma, dysgerminoma.

For "primarysite" and for "arrayedsite": ov|ft|other. ov=ovary;ft=fallopian tube

For "summarygrade": low = 1, 2, LMP. High= 3,4,23.

For "summarystage": early = 1,2, 12. late=3,4,23,34.

For "tumorstage": FIGO Stage (I-IV, but coded here as 1-4 to ensure correct ordering in factors). If multiple stages given (eg 34), use the highest.

For "substage": substage (abcd). For cases like ab, bc, use highest given.

For "grade": Grade (1-3): If multiple given, ie 12, 23, use highest given. Most ovarian cancer studies use FIGO grading, with a couple exceptions in this package (Yoshihara and Tothill).

For "pltx": (y/n): patient treated with platin.

For "tax": (y/n): patient treated with taxol.

For "neo": (y/n): patient treated with neoadjuvant treatment.

For "primary_therapy_outcome_success": completeresponse|partialresponse|progressivedisease|stabledisease: response to any kind of therapy (including radiation only).

For "days_to_tumor_recurrence": time to recurrence or last follow-up in days

For "recurrence_status": recurrence censoring variable (recurrence / norecurrence)

For "days_to_death": time to death or last follow-up in days

For "vital_status": Overall survival censoring variable (living / deceased)

For "os_binary": dichotomized overall survival variable as defined by study authors (short / long).

For "relapse_binary": dichotomized relapse variable as defined by study authors (short / long)

For "site_of_tumor_first_recurrence": (metastasis / locoregional / none / locoregional_plus_metastatic). none for no recurrence, na for unknown

For "primary_therapy_outcome_success": (completeresponse / partialresponse / progressivedisease / stabledisease) Response to any kind of therapy (including radiation only).

For "debulking": amount of residual disease (optimal = <1cm, suboptimal=>1cm).

For "percent_normal_cells": Estimated percentage of normal cells. An integer 0-100, or can be >70, <70, etc.

For "percent_stromal_cells": Estimated percentage of stromal cells. An integer 0-100, or can be >70, <70, etc.

For "percent_tumor_cells": Estimated percentage of tumor cells. An integer 0-100, or can be >70, <70, etc.

For "batch": batch variable when available. Hybridization date when Affymetrix CEL files are available.

For "uncurated_author_metadata": Original uncurated data, with each field separated by ///.

Author(s)

Benjamin F. Ganzfried, Steve Skates, Markus Riester, Victoria Wang, Thomas Risch, Benjamin Haibe-Kains, Curtis Huttenhower, Svitlana Tyekucheva, Jie Ding, Ina Jazic, Michael Birrer, Giovanni Parmigiani, Levi Waldron

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Maintainer: Levi Waldron <levi@jimmy.harvard.edu>

Examples

```
##List all datasets:
data(package="curatedOvarianData")
##
##See the actual template used for syntax checking of clinical metadata:
template.file <- system.file("extdata/template_ov.csv", package = "curatedOvarianData")
template <- read.csv(template.file, as.is=TRUE)
head(template)
```

E.MTAB.386_eset *Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.*

Description

Ovarian cancer is the fifth leading cause of cancer death for women in the U.S. and the seventh most fatal worldwide. Although ovarian cancer is notable for its initial sensitivity to platinum-based therapies, the vast majority of patients eventually develop recurrent cancer and succumb to increasingly platinum-resistant disease. Modern, targeted cancer drugs intervene in cell signaling, and identifying key disease mechanisms and pathways would greatly advance our treatment abilities. In order to shed light on the molecular diversity of ovarian cancer, we performed comprehensive transcriptional profiling on 129 advanced stage, high grade serous ovarian cancers. We implemented a, re-sampling based version of the ISIS class discovery algorithm (rISIS: robust ISIS) and applied it to the entire set of ovarian cancer transcriptional profiles. rISIS identified a previously undescribed patient stratification, further supported by micro-RNA expression profiles, and gene set enrichment analysis found strong biological support for the stratification by extracellular matrix, cell adhesion, and angiogenesis genes. The corresponding "angiogenesis signature" was validated in ten published independent ovarian cancer gene expression datasets and is significantly associated with overall survival. The subtypes we have defined are of potential translational interest as they may be relevant

for identifying patients who may benefit from the addition of anti-angiogenic therapies that are now being tested in clinical trials.

Usage

```
data( E.MTAB.386_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Bentink S, Haibe-Kains B, Risch T, Fan J-B, Hirsch MS, Holton K, Rubio R, April C
  Laboratory: Bentink, Matulonis 2012
  Contact information:
 Title: Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ov
  URL:
  PMIDs: 22348002

  Abstract: A 212 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Illumina humanRef-8 v2.0 expression beadchip
   platform_shorttitle:
      Illumina humanRef-8 v2.0
   platform_summary:
      illuminaHumanv2
   platform_manufacturer:
      Illumina
   platform_distribution:
      commercial
   platform_accession:
      GPL6104
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A2M A4GALT ... ZZEF1 (10357 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 10357 features, 129 samples
Platform type: illuminaHumanv2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 129.00  129.00  129.00   73.00    3.51    2.68    4.13
```

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

unique_patient_ID:
   Length     Class      Mode
      129 character character

sample_type:
tumor
  129

histological_type:
ser
129

primarysite:
 ov
129

summarygrade:
high
 129

summarystage:
early  late
    1   128

tumorstage:
  2   3   4
  1 109  19

substage:
   a    b    c NA's
   5   12   93   19

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   50.00   66.00   60.71   72.00   95.00

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    3.9   516.9   917.1  1007.0  1401.0  2724.0

vital_status:
deceased   living
      73       56

debulking:
   optimal suboptimal       NA's
        98         28          3
```

```
uncurated_author_metadata:
   Length     Class      Mode
      129 character character
```

GSE12418_eset *Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of survivors.*

Description

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a sub-group that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

Usage

```
data( GSE12418_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression analysis of stage III ser
  Laboratory: Partheen, Horvath 2006
  Contact information:
 Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of
  URL:
  PMIDs: 16996261

  Abstract: A 177 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      SWEGENE H_v2.1.1_27k
   platform_shorttitle:
      SWEGENE H_v2.1.1_27k
   platform_summary:
      PartheenMetaData
   platform_manufacturer:
```

```
      other
   platform_distribution:
      non-commercial
   platform_accession:
      GPL5886
   platform_technology:
      spotted oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (12681 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 12681 features, 54 samples
Platform type: PartheenMetaData
Binary overall survival summary (definitions of long and short provided by study authors):

 long short
   20    34

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

alt_sample_name:
   Length     Class      Mode
       54 character character

sample_type:
tumor
   54

histological_type:
ser
 54

primarysite:
ov
54

summarystage:
late
  54

tumorstage:
 3
54
```

```
substage:
 b  c
19 35

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  35.00   51.25   59.50   59.56   69.75   84.00

pltx:
 y
54

os_binary:
 long short
   20    34

debulking:
   optimal suboptimal
        13         41

uncurated_author_metadata:
   Length     Class      Mode
       54 character character
```

GSE12470_eset *Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subclasses and implicates ZEB2 in tumor progression and prognosis.*

Description

To elucidate the mechanisms of rapid progression of serous ovarian cancer, gene expression profiles from 43 ovarian cancer tissues comprising eight early stage and 35 advanced stage tissues were carried out using oligonucleotide microarrays of 18,716 genes. By non-negative matrix factorization analysis using 178 genes, which were extracted as stage-specific genes, 35 advanced stage cases were classified into two subclasses with superior (n = 17) and poor (n = 18) outcome evaluated by progression-free survival (log rank test, P = 0.03). Of the 178 stage-specific genes, 112 genes were identified as showing different expression between the two subclasses. Of the 48 genes selected for biological function by gene ontology analysis or Ingenuity Pathway Analysis, five genes (ZEB2, CDH1, LTBP2, COL16A1, and ACTA2) were extracted as candidates for prognostic factors associated with progression-free survival. The relationship between high ZEB2 or low CDH1 expression and shorter progression-free survival was validated by real-time RT-PCR experiments of 37 independent advanced stage cancer samples. ZEB2 expression was negatively correlated with CDH1 expression in advanced stage samples, whereas ZEB2 knockdown in ovarian adenocarcinoma SKOV3 cells resulted in an increase in CDH1 expression. Multivariate analysis showed that high ZEB2 expression was independently associated with poor prognosis. Furthermore, the prognostic effect of E-cadherin encoded by CDH1 was verified using immunohistochemical analysis of an independent advanced stage cancer samples set (n = 74). These findings suggest that the expression of epithelial-mesenchymal transition-related genes such as ZEB2 and CDH1 may play important roles in the invasion process of advanced stage serous ovarian cancer.

Usage

```
data( GSE12470_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Yoshihara K, Tajima A, Komata D, Yamamoto T, Kodama S, Fujiwara H, Suzuki M, Onis
  Laboratory: Yoshihara, Tanaka 2009
  Contact information:
 Title: Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subc
  URL:
  PMIDs: 19486012

  Abstract: A 253 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)
   platform_shorttitle:
      Agilent G4110B
   platform_summary:
      hgug4110b
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL887
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1CF ... ZZZ3 (16889 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 16889 features, 53 samples
Platform type: hgug4110b
----------------------------
Available sample meta-data:
----------------------------

alt_sample_name:
   Length     Class      Mode
       53 character character
```

```
sample_type:
healthy   tumor
     10      43

histological_type:
 ser NA's
  43   10

primarysite:
ov
53

summarystage:
early  late  NA's
    8    35    10

tumorstage:
   1 NA's
   8   45

uncurated_author_metadata:
   Length     Class      Mode
       53 character character
```

GSE13876_eset *Survival-related profile, pathways, and transcription factors in ovarian cancer.*

Description

Ovarian cancer has a poor prognosis due to advanced stage at presentation and either intrinsic or acquired resistance to classic cytotoxic drugs such as platinum and taxoids. Recent large clinical trials with different combinations and sequences of classic cytotoxic drugs indicate that further significant improvement in prognosis by this type of drugs is not to be expected. Currently a large number of drugs, targeting dysregulated molecular pathways in cancer cells have been developed and are introduced in the clinic. A major challenge is to identify those patients who will benefit from drugs targeting these specific dysregulated pathways.The aims of our study were (1) to develop a gene expression profile associated with overall survival in advanced stage serous ovarian cancer, (2) to assess the association of pathways and transcription factors with overall survival, and (3) to validate our identified profile and pathways/transcription factors in an independent set of ovarian cancers.According to a randomized design, profiling of 157 advanced stage serous ovarian cancers was performed in duplicate using approximately 35,000 70-mer oligonucleotide microarrays. A continuous predictor of overall survival was built taking into account well-known issues in microarray analysis, such as multiple testing and overfitting. A functional class scoring analysis was utilized to assess pathways/transcription factors for their association with overall survival. The prognostic value of genes that constitute our overall survival profile was validated on a fully independent, publicly available dataset of 118 well-defined primary serous ovarian cancers. Furthermore, functional class scoring analysis was also performed on this independent dataset to assess the similarities with results from our own dataset. An 86-gene overall survival profile discriminated between patients

with unfavorable and favorable prognosis (median survival, 19 versus 41 mo, respectively; permutation p-value of log-rank statistic = 0.015) and maintained its independent prognostic value in multivariate analysis. Genes that composed the overall survival profile were also able to discriminate between the two risk groups in the independent dataset. In our dataset 17/167 pathways and 13/111 transcription factors were associated with overall survival, of which 16 and 12, respectively, were confirmed in the independent dataset.Our study provides new clues to genes, pathways, and transcription factors that contribute to the clinical outcome of serous ovarian cancer and might be exploited in designing new treatment strategies.

Usage

```
data( GSE13876_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Crijns AP, Fehrmann RS, de Jong S, Gerbens F, Meersma GJ, Klip HG, Hollema H, Hof
  Laboratory: Crijns, van der Zee 2009
  Contact information:
 Title: Survival-related profile, pathways, and transcription factors in ovarian cancer.
  URL:
  PMIDs: 19192944

  Abstract: A 371 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Operon human v3 ~35K 70-mer two-color oligonucleotide microarrays
   platform_shorttitle:
      Operon v3 two-color
   platform_summary:
      OperonHumanV3
   platform_manufacturer:
      other
   platform_distribution:
      non-commercial
   platform_accession:
      GPL7759
   platform_technology:
      spotted oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1CF ... ZZZ3 (20577 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 20577 features, 157 samples
```

```
Platform type: OperonHumanV3
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 157.00  157.00  157.00  113.00    2.05    1.56    2.71

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

alt_sample_name:
 151 NA's
   1  156

unique_patient_ID:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      1      40      79      79     118     157

sample_type:
tumor
  157

histological_type:
ser
157

primarysite:
 ov
157

summarygrade:
high  low NA's
  85   59   13

summarystage:
late
 157

grade:
   1    2    3    4 NA's
  14   45   82    3   13

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   50.00   60.00   57.95   67.00   84.00

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     360     630    1100    1470    7020

vital_status:
```

```
deceased   living
     113       44

uncurated_author_metadata:
   Length     Class      Mode
      157 character character
```

GSE14764_eset *A prognostic gene expression index in ovarian cancer - validation across different independent data sets.*

Description

Ovarian carcinoma has the highest mortality rate among gynaecological malignancies. In this project, we investigated the hypothesis that molecular markers are able to predict outcome of ovarian cancer independently of classical clinical predictors, and that these molecular markers can be validated using independent data sets. We applied a semi-supervised method for prediction of patient survival. Microarrays from a cohort of 80 ovarian carcinomas (TOC cohort) were used for the development of a predictive model, which was then evaluated in an entirely independent cohort of 118 carcinomas (Duke cohort). A 300-gene ovarian prognostic index (OPI) was generated and validated in a leave-one-out approach in the TOC cohort (Kaplan-Meier analysis, p = 0.0087). In a second validation step, the prognostic power of the OPI was confirmed in an independent data set (Duke cohort, p = 0.0063). In multivariate analysis, the OPI was independent of the post-operative residual tumour, the main clinico-pathological prognostic parameter with an adjusted hazard ratio of 6.4 (TOC cohort, CI 1.8-23.5, p = 0.0049) and 1.9 (Duke cohort, CI 1.2-3.0, p = 0.0068). We constructed a combined score of molecular data (OPI) and clinical parameters (residual tumour), which was able to define patient groups with highly significant differences in survival. The integrated analysis of gene expression data as well as residual tumour can be used for optimized assessment of the prognosis of platinum-taxol-treated ovarian cancer. As traditional treatment options are limited, this analysis may be able to optimize clinical management and to identify those patients who would be candidates for new therapeutic strategies.

Usage

```
data( GSE14764_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A prognostic gene expre
  Laboratory: Denkert, Lage 2009
  Contact information:
 Title: A prognostic gene expression index in ovarian cancer - validation across different independe
  URL:
  PMIDs: 19294737

  Abstract: A 254 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
```

```
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 80 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  80.00   80.00   80.00   21.00    4.52    4.19      NA

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

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00   20.75   40.50   40.50   60.25   80.00

sample_type:
tumor
   80

histological_type:
   Length     Class      Mode
       80 character character

primarysite:
ov
80
```

```
summarygrade:
high  low
  54   26

summarystage:
early  late
    9    71

tumorstage:
 1  2  3  4
 8  1 69  2

substage:
   a    b    c NA's
   4    6   32   38

grade:
 1  2  3
 3 23 54

recurrence_status:
norecurrence   recurrence         NA's
          50           26            4

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    210     660    1050    1011    1328    2190

vital_status:
deceased   living
      21       59

batch:
   Length     Class      Mode
       80 character character

uncurated_author_metadata:
   Length     Class      Mode
       80 character character
```

GSE17260_eset *Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets.*

Description

Advanced-stage ovarian cancer patients are generally treated with platinum/taxane-based chemotherapy after primary debulking surgery. However, there is a wide range of outcomes for individual patients. Therefore, the clinicopathological factors alone are insufficient for predicting prognosis. Our aim is to identify a progression-free survival (PFS)-related molecular profile for predicting

survival of patients with advanced-stage serous ovarian cancer.Advanced-stage serous ovarian cancer tissues from 110 Japanese patients who underwent primary surgery and platinum/taxane-based chemotherapy were profiled using oligonucleotide microarrays. We selected 88 PFS-related genes by a univariate Cox model (p<0.01) and generated the prognostic index based on 88 PFS-related genes after adjustment of regression coefficients of the respective genes by ridge regression Cox model using 10-fold cross-validation. The prognostic index was independently associated with PFS time compared to other clinical factors in multivariate analysis [hazard ratio (HR), 3.72; 95% confidence interval (CI), 2.66-5.43; p<0.0001]. In an external dataset, multivariate analysis revealed that this prognostic index was significantly correlated with PFS time (HR, 1.54; 95% CI, 1.20-1.98; p = 0.0008). Furthermore, the correlation between the prognostic index and overall survival time was confirmed in the two independent external datasets (log rank test, p = 0.0010 and 0.0008).The prognostic ability of our index based on the 88-gene expression profile in ridge regression Cox hazard model was shown to be independent of other clinical factors in predicting cancer prognosis across two distinct datasets. Further study will be necessary to improve predictive accuracy of the prognostic index toward clinical application for evaluation of the risk of recurrence in patients with advanced-stage serous ovarian cancer.

Usage

```
data( GSE17260_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzuki M, Onishi Y, Hatae
  Laboratory: Yoshihara, Tanaka 2010
  Contact information:
 Title: Gene expression profile for predicting survival in advanced-stage serous ovarian cancer acro
  URL:
  PMIDs: 20300634

  Abstract: A 257 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-012391 Whole Human Genome Oligo Microarray G4112A
   platform_shorttitle:
      Agilent G4112A
   platform_summary:
      hgug4112a
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6848
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
```

```
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 20106 features, 110 samples
Platform type: hgug4112a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 110.00  110.00  110.00   46.00    4.44    4.03      NA

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

alt_sample_name:
   Length     Class      Mode
      110 character character

sample_type:
tumor
  110

histological_type:
ser
110

primarysite:
 ov
110

summarygrade:
high  low
  43   67

summarystage:
late
 110

tumorstage:
 3  4
93 17

substage:
   a    b    c NA's
   6   18   69   17

grade:
 1  2  3
```

```
26 41 43

pltx:
  y
110

tax:
  y
110

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   30.0   285.0   510.0   673.9   870.0  2250.0

recurrence_status:
norecurrence   recurrence
          34           76

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     660     915    1086    1530    2430

vital_status:
deceased   living
      46       64

debulking:
   optimal suboptimal
        57         53

uncurated_author_metadata:
   Length     Class      Mode
      110 character character
```

GSE18520_eset *A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor: microfibril-associated glycoprotein 2.*

Description

Advanced stage papillary serous tumors of the ovary are responsible for the majority of ovarian cancer deaths, yet the molecular determinants modulating patient survival are poorly characterized. Here, we identify and validate a prognostic gene expression signature correlating with survival in a series of microdissected serous ovarian tumors. Independent evaluation confirmed the association of a prognostic gene microfibril-associated glycoprotein 2 (MAGP2) with poor prognosis, whereas in vitro mechanistic analyses demonstrated its ability to prolong tumor cell survival and stimulate endothelial cell motility and survival via the alpha(V)beta(3) integrin receptor. Increased MAGP2 expression correlated with microvessel density suggesting a proangiogenic role in vivo. Thus, MAGP2 may serve as a survival-associated target.

Usage

```
data( GSE18520_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KK, Park DC, Hao K, Yi
  Laboratory: Mok, Birrer 2009
  Contact information:
 Title: A gene signature predictive for outcome in advanced ovarian cancer identifies a survival fac
  URL:
  PMIDs: 19962670

  Abstract: A 110 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 63 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
  53.00   53.00   53.00   41.00    2.05    1.48    3.70

---------------------------
```

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

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  312.0   395.0   694.0   893.3  1040.0  2237.0

sample_type:
healthy   tumor
     10      53

histological_type:
 ser NA's
  53   10

primarysite:
ov
63

summarygrade:
high NA's
  53   10

summarystage:
late NA's
  53   10

tumorstage:
   3 NA's
  53   10

grade:
   3 NA's
  53   10

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    150     450     630    1212    1440    4500      10

vital_status:
deceased   living     NA's
      41       12       10

debulking:
   optimal suboptimal       NA's
        28         11         24

percent_normal_cells:
 0
63

percent_stromal_cells:
```

```
 0
63

percent_tumor_cells:
100
 63

batch:
   Length     Class      Mode
       63 character character

uncurated_author_metadata:
   Length     Class      Mode
       63 character character
```

GSE19829.GPL570_eset *Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.*

Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC).A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA germline mutations. Association with poly-ADP ribose polymerase (PARP) inhibitor responsiveness and with radiation-induced RAD51 foci formation (a surrogate of homologous recombination) was assessed in Capan-1 cell line clones. The BRCAness profile was validated in 70 patients enriched for sporadic disease to assess its association with outcome.The BRCAness profile accurately predicted platinum responsiveness in eight out of 10 patient-derived tumor specimens, and between PARP-inhibitor sensitivity and resistance in four out of four Capan-1 clones. [corrected] When applied to the 70 patients with sporadic disease, patients with the BRCA-like (BL) profile had improved disease-free survival (34 months v 15 months; log-rank P = .013) and overall survival (72 months v 41 months; log-rank P = .006) compared with patients with a non-BRCA-like (NBL) profile, respectively. The BRCAness profile maintained independent prognostic value in multivariate analysis, which controlled for other known clinical prognostic factors.The BRCAness profile correlates with responsiveness to platinum and PARP inhibitors and identifies a subset of sporadic patients with improved outcome. Additional evaluation of this profile as a predictive tool in patients with sporadic EOC is warranted.

Usage

```
data( GSE19829.GPL570_eset )
```

Format

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

```
 Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al. Gene expression
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu133plus2
  Contact information:
 Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and
  URL:
  PMIDs: 20547991

  Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 28 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  28.00   28.00   28.00   17.00    3.95    2.71      NA

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

alt_sample_name:
   Length     Class      Mode
       28 character character

sample_type:
tumor
```

```
   28

primarysite:
ov
28

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    150     540    1050    1291    1688    3450

vital_status:
deceased   living
      17       11

batch:
2009-08-14
        28

uncurated_author_metadata:
   Length     Class      Mode
       28 character character
```

GSE19829.GPL8300_eset *Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.*

Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC).A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA germline mutations. Association with poly-ADP ribose polymerase (PARP) inhibitor responsiveness and with radiation-induced RAD51 foci formation (a surrogate of homologous recombination) was assessed in Capan-1 cell line clones. The BRCAness profile was validated in 70 patients enriched for sporadic disease to assess its association with outcome.The BRCAness profile accurately predicted platinum responsiveness in eight out of 10 patient-derived tumor specimens, and between PARP-inhibitor sensitivity and resistance in four out of four Capan-1 clones. [corrected] When applied to the 70 patients with sporadic disease, patients with the BRCA-like (BL) profile had improved disease-free survival (34 months v 15 months; log-rank P = .013) and overall survival (72 months v 41 months; log-rank P = .006) compared with patients with a non-BRCA-like (NBL) profile, respectively. The BRCAness profile maintained independent prognostic value in multivariate analysis, which controlled for other known clinical prognostic factors.The BRCAness profile correlates with responsiveness to platinum and PARP inhibitors and identifies a subset of sporadic patients with improved outcome. Additional evaluation of this profile as a predictive tool in patients with sporadic EOC is warranted.

Usage

```
data( GSE19829.GPL8300_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al. Gene expression
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
  Contact information:
 Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and
  URL:
  PMIDs: 20547991

  Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG_U95Av2] Affymetrix Human Genome U95 Version 2 Array
   platform_shorttitle:
      Affymetrix HG_U95Av2
   platform_summary:
      hgu95av2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL8300
   platform_technology:
      in situ oligonucleotide

Preprocessing: rma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: AADAC AAK1 ... ZZZ3 (8995 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 8995 features, 42 samples
Platform type: hgu95av2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  42.00   42.00   42.00   23.00    3.78    2.79      NA

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

```
---------------------------

alt_sample_name:
   Length     Class      Mode
       42 character character

sample_type:
tumor
   42

primarysite:
ov
42

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   30.0   727.5  1155.0  1089.0  1485.0  2040.0

vital_status:
deceased   living
      23       19

batch:
2001-09-14 2001-12-14 2002-08-20 2003-09-09 2003-09-18
         7          4         14         13          4

uncurated_author_metadata:
   Length     Class      Mode
       42 character character
```

GSE20565_eset *A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas in patients with a previous history of breast cancer.*

Description

The distinction between primary and secondary ovarian tumors may be challenging for pathologists. The purpose of the present work was to develop genomic and transcriptomic tools to further refine the pathological diagnosis of ovarian tumors after a previous history of breast cancer.Sixteen paired breast-ovary tumors from patients with a former diagnosis of breast cancer were collected. The genomic profiles of paired tumors were analyzed using the Affymetrix GeneChip Mapping 50 K Xba Array or Genome-Wide Human SNP Array 6.0 (for one pair), and the data were normalized with ITALICS (ITerative and Alternative normaLIzation and Copy number calling for affymetrix Snp arrays) algorithm or Partek Genomic Suite, respectively. The transcriptome of paired samples was analyzed using Affymetrix GeneChip Human Genome U133 Plus 2.0 Arrays, and the data were normalized with gc-Robust Multi-array Average (gcRMA) algorithm. A hierarchical clustering of these samples was performed, combined with a dataset of well-identified primary and secondary ovarian tumors.In 12 of the 16 paired tumors analyzed, the comparison of genomic profiles confirmed the pathological diagnosis of primary ovarian tumor (n = 5) or metastasis of breast cancer

(n = 7). Among four cases with uncertain pathological diagnosis, genomic profiles were clearly distinct between the ovarian and breast tumors in two pairs, thus indicating primary ovarian carcinomas, and showed common patterns in the two others, indicating metastases from breast cancer. In all pairs, the result of the transcriptomic analysis was concordant with that of the genomic analysis.In patients with ovarian carcinoma and a previous history of breast cancer, SNP array analysis can be used to distinguish primary and secondary ovarian tumors. Transcriptomic analysis may be used when primary breast tissue specimen is not available.

Usage

```
data( GSE20565_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, Lebigot I, Nicolas A, We
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
 Title: A genomic and transcriptomic approach for a differential diagnosis between primary and secon
  URL:
  PMIDs: 20492709

  Abstract: A 277 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 140 samples
Platform type: hgu133plus2
```

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

alt_sample_name:
   Length     Class      Mode
      140 character character

sample_type:
tumor
  140

histological_type:
   Length     Class      Mode
      140 character character

primarysite:
other    ov
   44    96

summarygrade:
high  low NA's
  63   33   44

summarystage:
early  late  NA's
   27    67    46

tumorstage:
   1    2    3    4 NA's
  18    9   52   15   46

substage:
   a    b    c NA's
  14   10   55   61

grade:
   1    2    3 NA's
   6   27   63   44

batch:
   Length     Class      Mode
      140 character character

uncurated_author_metadata:
   Length     Class      Mode
      140 character character
```

Description

EXpression Project for Oncology, International Genomics Consortium, www.intgen.org

Usage

```
data( GSE2109_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: EXpression Project for Oncology, International Genomics Consortium, www.intgen.
  Laboratory: expO, IGC 2005
  Contact information:
  Title: IGC EXpression Project for Oncology
  URL:
  PMIDs: PMID unknown

  Abstract: A 8 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 204 samples
Platform type: hgu133plus2
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
```

```
   Length     Class      Mode
      204 character character

sample_type:
    benign borderline      tumor
         2          8        194

histological_type:
   Length     Class      Mode
      204 character character

primarysite:
other    ov  NA's
   23   178     3

summarygrade:
high  low NA's
  91   31   82

summarystage:
early  late  NA's
   37    87    80

tumorstage:
   1    2    3    4 NA's
  20   14   58   18   94

substage:
   a    b    c NA's
  17   22   79   86

grade:
   1    2    3    4 NA's
  11   20   83    8   82

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  25.00   45.00   55.00   58.82   65.00   85.00

batch:
   Length     Class      Mode
      204 character character

uncurated_author_metadata:
   Length     Class      Mode
      204 character character
```

GSE26193_eset *miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.*

Description

Although there is evidence that redox regulation has an essential role in malignancies, its impact on tumor prognosis remains unclear. Here we show crosstalk between oxidative stress and the miR-200 family of microRNAs that affects tumorigenesis and chemosensitivity. miR-141 and miR-200a target p38?? and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38?? deficiency and increases tumor growth in mouse models, but it also improves the response to chemotherapeutic agents. High-grade human ovarian adenocarcinomas that accumulate miR-200a have low concentrations of p38?? and an associated oxidative stress signature. The miR200a-dependent stress signature correlates with improved survival of patients in response to treatment. Therefore, the role of miR-200a in stress could be a predictive marker for clinical outcome in ovarian cancer. In addition, although oxidative stress promotes tumor growth, it also sensitizes tumors to treatment, which could account for the limited success of antioxidants in clinical trials.

Usage

```
data( GSE26193_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-Garau X, Mechta-Gr
  Laboratory: Mateescu, Mechta-Grigoriou 2011
  Contact information:
 Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.
  URL:
  PMIDs: 22101765

  Abstract: A 149 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
```

```
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 107 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 107.00  107.00  107.00   76.00    3.05    2.50    4.56

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

alt_sample_name:
   Length     Class      Mode
      107 character character

sample_type:
tumor
  107

histological_type:
clearcell      endo  mucinous     other       ser
        6         8         8         6        79

summarygrade:
high  low
  67   40

summarystage:
early  late
   31    76

tumorstage:
 1  2  3  4
20 11 59 17

substage:
   a    b    c NA's
  16   12   62   17

grade:
 1  2  3
 7 33 67

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    3.0   340.5   584.0  1108.0  1525.0  7386.0
```

```
recurrence_status:
norecurrence   recurrence
          27           80

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      3     668    1096    1520    2220    7386

vital_status:
deceased   living
      76       31

batch:
   Length     Class      Mode
      107 character character

uncurated_author_metadata:
   Length     Class      Mode
      107 character character
```

GSE26712_eset *A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.*

Description

Despite the existence of morphologically indistinguishable disease, patients with advanced ovarian tumors display a broad range of survival end points. We hypothesize that gene expression profiling can identify a prognostic signature accounting for these distinct clinical outcomes. To resolve survival-associated loci, gene expression profiling was completed for an extensive set of 185 (90 optimal/95 suboptimal) primary ovarian tumors using the Affymetrix human U133A microarray. Cox regression analysis identified probe sets associated with survival in optimally and suboptimally debulked tumor sets at a P value of <0.01. Leave-one-out cross-validation was applied to each tumor cohort and confirmed by a permutation test. External validation was conducted by applying the gene signature to a publicly available array database of expression profiles of advanced stage suboptimally debulked tumors. The prognostic signature successfully classified the tumors according to survival for suboptimally (P = 0.0179) but not optimally debulked (P = 0.144) patients. The suboptimal gene signature was validated using the independent set of tumors (odds ratio, 8.75; P = 0.0146). To elucidate signaling events amenable to therapeutic intervention in suboptimally debulked patients, pathway analysis was completed for the top 57 survival-associated probe sets. For suboptimally debulked patients, confirmation of the predictive gene signature supports the existence of a clinically relevant predictor, as well as the possibility of novel therapeutic opportunities. Ultimately, the prognostic classifier defined for suboptimally debulked tumors may aid in the classification and enhancement of patient outcome for this high-risk population.

Usage

```
data( GSE26712_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Bonome T, Levine DA, Shih J, Randonovich M, Pise-Masison CA, Bogomolniy F, Ozbun
  Laboratory: Bonome, Birrer 2008
  Contact information:
 Title: A gene signature predicting for survival in suboptimally debulked patients with ovarian canc
  URL:
  PMIDs: 18593951

  Abstract: A 238 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 195 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 185.00  185.00  185.00  129.00    3.83    3.24    4.83

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

alt_sample_name:
```

```
   Length     Class      Mode
      195 character character

sample_type:
healthy   tumor
     10     185

histological_type:
 ser NA's
 185   10

primarysite:
 ov
195

summarygrade:
high NA's
 185   10

summarystage:
late NA's
 185   10

tumorstage:
   3    4 NA's
 146   36   13

substage:
   b    c NA's
   9  137   49

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  26.00   52.00   63.00   61.54   70.00   84.00      13

recurrence_status:
norecurrence   recurrence
          42          153

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   21.9   660.6  1164.0  1429.0  1880.0  4982.0      10

vital_status:
deceased   living     NA's
     129       56       10

debulking:
   optimal suboptimal       NA's
        90         95         10

percent_normal_cells:
```

```
20-
195

percent_stromal_cells:
20-
195

percent_tumor_cells:
80+
195

batch:
   Length     Class      Mode
      195 character character

uncurated_author_metadata:
   Length     Class      Mode
      195 character character
```

GSE30009_eset *Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.*

Description

This study assesses the ability of multidrug resistance (MDR)-associated gene expression patterns to predict survival in patients with newly diagnosed carcinoma of the ovary. The scope of this research differs substantially from that of previous reports, as a very large set of genes was evaluated whose expression has been shown to affect response to chemotherapy.We applied a customized TaqMan low density array, a highly sensitive and specific assay, to study the expression profiles of 380 MDR-linked genes in 80 tumor specimens collected at initial surgery to debulk primary serous carcinoma. The RNA expression profiles of these drug resistance genes were correlated with clinical outcomes.Leave-one-out cross-validation was used to estimate the ability of MDR gene expression to predict survival. Although gene expression alone does not predict overall survival (OS; P = 0.06), four covariates (age, stage, CA125 level, and surgical debulking) do (P = 0.03). When gene expression was added to the covariates, we found an 11-gene signature that provides a major improvement in OS prediction (log-rank statistic P < 0.003). The predictive power of this 11-gene signature was confirmed by dividing high- and low-risk patient groups, as defined by their clinical covariates, into four specific risk groups on the basis of expression levels.This study reveals an 11-gene signature that allows a more precise prognosis for patients with serous cancer of the ovary treated with carboplatin- and paclitaxel-based therapy. These 11 new targets offer opportunities for new therapies to improve clinical outcome in ovarian cancer.

Usage

```
data( GSE30009_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Gillet JP, Calcagno AM, Varma S, Davidson B et al. Multidrug resistance-linked g
  Laboratory: Gillet, Gottesman 2012
  Contact information:
 Title: Multidrug resistance-linked gene signature predicts overall survival of patients with prima
  URL:
  PMIDs: 22492981

  Abstract: A 244 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      TaqMan qRT-PCR Homo sapiens Low-Density Array 380
   platform_shorttitle:
      TaqMan qRT-PCR
   platform_summary:
      NA
   platform_manufacturer:
      TaqMan
   platform_distribution:
      custom
   platform_accession:
      GPL13728
   platform_technology:
      qRT-PCR

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ABCA1 ABCA10 ... XRCC6 (359 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 359 features, 103 samples
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 103.00  103.00  103.00   57.00    3.42    2.92    5.34

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

alt_sample_name:
   Length     Class      Mode
```

```
      103 character character

sample_type:
borderline      tumor
         1        102

histological_type:
clearcell       ser
        1       102

summarygrade:
high  low NA's
  92    9    2

summarystage:
late
 103

tumorstage:
 3  4
82 21

substage:
   b    c NA's
   2   60   41

grade:
   1    2    3 NA's
   4    5   92    2

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30.00   56.00   61.00   62.45   71.50   87.00

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     24     598    1053    1156    1568    4748

vital_status:
deceased   living
      57       46

debulking:
   optimal suboptimal
        81         22

uncurated_author_metadata:
   Length     Class      Mode
      103 character character
```

GSE30161_eset *Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.*

Description

Despite advances in radical surgery and chemotherapy delivery, ovarian cancer is the most lethal gynecologic malignancy. Standard therapy includes treatment with platinum-based combination chemotherapies yet there is no biomarker model to predict their responses to these agents. We here have developed and independently tested our multi-gene molecular predictors for forecasting patients' responses to individual drugs on a cohort of 55 ovarian cancer patients. To independently validate these molecular predictors, we performed microarray profiling on FFPE tumor samples of 55 ovarian cancer patients (UVA-55) treated with platinum-based adjuvant chemotherapy. Genome-wide chemosensitivity biomarkers were initially discovered from the in vitro drug activities and genomic expression data for carboplatin and paclitaxel, respectively. Multivariate predictors were trained with the cell line data and then evaluated with a historical patient cohort. For the UVA-55 cohort, the carboplatin, taxol, and combination predictors significantly stratified responder patients and non-responder patients (p = 0.019, 0.04, 0.014) with sensitivity = 91%, 96%, 93 and NPV = 57%, 67%, 67% in pathologic clinical response. The combination predictor also demonstrated a significant survival difference between predicted responders and non-responders with a median survival of 55.4 months vs. 32.1 months. Thus, COXEN single- and combination-drug predictors successfully stratified platinum resistance and taxane response in an independent cohort of ovarian cancer patients based on their FFPE tumor samples.

Usage

```
data( GSE30161_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Ferriss JS, Kim Y, Duska L, Birrer M, Levine DA, Moskaluk C,Theodorescu D, Lee JK
  Laboratory: Ferriss, Lee 2012
  Contact information:
 Title: Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovaria
  URL:
  PMIDs: 22348014

  Abstract: A 215 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
```

```
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 58 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  58.00   58.00   58.00   36.00    4.19    2.70    6.17

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

alt_sample_name:
   Length     Class      Mode
       58 character character

sample_type:
tumor
   58

histological_type:
   Length     Class      Mode
       58 character character

summarygrade:
high  low NA's
  33   21    4

summarystage:
late
  58

tumorstage:
 3  4
53  5

substage:
```

```
 a  b  c
 9 11 38

grade:
   1    2    3 NA's
   2   19   33    4

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  38.00   53.50   62.00   62.57   72.00   85.00

pltx:
 y
58

tax:
 n  y
 4 54

neo:
 n
58

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   12.0   255.2   386.0   742.1   768.2  4208.0

recurrence_status:
norecurrence   recurrence         NA's
           6           48            4

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   49.0   585.2  1010.0  1375.0  2131.0  4208.0

vital_status:
deceased   living
      36       22

debulking:
   optimal suboptimal       NA's
        26         30          2

batch:
2009-10-07 2009-10-08 2009-10-09 2009-10-20
        28         18          8          4

uncurated_author_metadata:
   Length     Class      Mode
       58 character character
```

GSE32062.GPL6480_eset *High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.*

Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients.In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups.An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients.This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

Usage

```
data( GSE32062.GPL6480_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk ovarian cancer b
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
 Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
   platform_shorttitle:
      Agilent G4112F
   platform_summary:
      hgug4112a
```

```
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6480
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 20106 features, 260 samples
Platform type: hgug4112a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 260.00  260.00  260.00  121.00    4.93    4.11    6.58

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

alt_sample_name:
   Length     Class      Mode
      260 character character

sample_type:
tumor
  260

histological_type:
ser
260

summarygrade:
high  low
 129  131

summarystage:
late
 260

tumorstage:
  3   4
```

```
204  56

substage:
   a    b    c NA's
   4   20  180   56

grade:
  2   3
131 129

pltx:
  y
260

tax:
  y
260

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     810    1245    1344    1710    3840

vital_status:
deceased   living
     121      139

debulking:
   optimal suboptimal
       103        157

uncurated_author_metadata:
   Length     Class      Mode
      260 character character
```

GSE32063_eset *High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.*

Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients.In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups.An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with

ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients.This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

Usage

```
data( GSE32063_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk ovarian cancer b
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
 Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
   platform_shorttitle:
      Agilent G4112F
   platform_summary:
      hgug4112a
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6480
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 20106 features, 40 samples
Platform type: hgug4112a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  40.00   40.00   40.00   22.00    4.44    3.29      NA

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

alt_sample_name:
   Length     Class      Mode
       40 character character

sample_type:
tumor
   40

histological_type:
ser
 40

summarygrade:
high  low
  17   23

summarystage:
late
  40

tumorstage:
 3  4
31  9

substage:
   b    c NA's
   3   28    9

grade:
 2  3
23 17

pltx:
 y
40

tax:
 y
40
```

```
days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    210     705    1155    1346    1792    3330

vital_status:
deceased   living
      22       18

debulking:
   optimal suboptimal
        19         21

uncurated_author_metadata:
   Length     Class      Mode
       40 character character
```

GSE44104_eset *COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.*

Description

Biomarkers that predict disease progression might assist the development of better therapeutic strategies for aggressive cancers, such as ovarian cancer. Here, we investigated the role of collagen type XI alpha 1 (COL11A1) in cell invasiveness and tumor formation and the prognostic impact of COL11A1 expression in ovarian cancer. Microarray analysis suggested that COL11A1 is a disease progression-associated gene that is linked to ovarian cancer recurrence and poor survival. Small interference RNA-mediated specific reduction in COL11A1 protein levels suppressed the invasive ability and oncogenic potential of ovarian cancer cells and decreased tumor formation and lung colonization in mouse xenografts. A combination of experimental approaches, including real-time RT-PCR, casein zymography and chromatin immunoprecipitation (ChIP) assays, showed that COL11A1 knockdown attenuated MMP3 expression and suppressed binding of Ets-1 to its putative MMP3 promoter-binding site, suggesting that the Ets-1-MMP3 axis is upregulated by COL11A1. Transforming growth factor (TGF)-beta (TGF-??1) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF-??1-triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF-??1-dependent COL11A1 activation. Analysis of 88 ovarian cancer patients indicated that high COL11A1 mRNA levels are associated with advanced disease stage. The 5-year recurrence-free and overall survival rates were significantly lower (P=0.006 and P=0.018, respectively) among patients with high expression levels of tissue COL11A1 mRNA compared with those with low expression. We conclude that COL11A1 may promote tumor aggressiveness via the TGF-??1-MMP3 axis and that COL11A1 expression can predict clinical outcome in ovarian cancer patients.

Usage

```
data( GSE44104_eset )
```

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Wu Y, Chang T, Huang Y, Huang H, Chou C
  Laboratory: Wu, Chou 2013
  Contact information:
 Title: COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.
  URL:
  PMIDs: 23934190

  Abstract: A 260 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 60 samples
Platform type: hgu133plus2
Binary overall survival summary (definitions of long and short provided by study authors):

 long short
   44    16

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

alt_sample_name:
   Length     Class      Mode
       60 character character
```

```
sample_type:
tumor
   60

histological_type:
clearcell      endo  mucinous       ser
       12        11          9        28

summarystage:
early  late
   25    35

tumorstage:
 1  2  3  4
17  8 30  5

recurrence_status:
norecurrence   recurrence
          40           20

os_binary:
 long short
   44    16

relapse_binary:
 long short
   40    20

batch:
2010-09-07 2010-09-08 2010-10-14 2010-12-10 2010-12-14
        20          2         18         16          4

uncurated_author_metadata:
   Length     Class      Mode
       60 character character
```

GSE49997_eset *Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD Consortium.*

Description

Most patients with epithelial ovarian cancer (EOC) are diagnosed at advanced stage and have a poor prognosis. However, a small proportion of these patients will survive, whereas others will die very quickly. Clinicopathological factors do not allow precise identification of these subgroups. Thus, we have validated a molecular subclassification as new prognostic factor in EOC. One hundred and ninety-four patients with Stage II-IV EOC were characterized by whole-genome expression profiling of tumor tissues and were classified using a published 112 gene set, derived from an International Federation of Gynecology and Obstetrics (FIGO) stage-directed supervised classification

approach. The 194 tumor samples were classified into two subclasses comprising 95 (Subclass 1) and 99 (Subclass 2) tumors. All nine FIGO II tumors were grouped in Subclass 1 (P = 0.001). Subclass 2 (54% of advanced-stage tumors) was significantly correlated with peritoneal carcinomatosis and non-optimal debulking. Patients with Subclass 2 tumors had a worse overall survival for both serous and non-serous histological subtypes, as revealed by univariate analysis (hazard ratios [HR] of 3.17 and 17.11, respectively; P ??? 0.001) and in models corrected for relevant clinicopathologic parameters (HR 2.87 and 12.42, respectively; P ??? 0.023). Significance analysis of microarrays revealed 2082 genes that were differentially expressed in advanced-grade serous tumors of both subclasses and the focal adhesion pathway as the most deregulated pathway. In the present validation study, we have shown that, in advanced-stage serous ovarian cancer, two approximately equally large molecular subtypes exist, independent of classical clinocopathological parameters and presenting with highly different whole-genome expression profiles and a markedly different overall survival. Similar results were obtained in a small cohort of patients with non-serous tumors.?? 2012 Japanese Cancer Association.

Usage

```
data( GSE49997_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster E, Wolf A, Sehouli J,
  Laboratory: Pils, Zeilinger 2012
  Contact information:
 Title: Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OV
  URL:
  PMIDs: 22497737

  Abstract: A 276 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      ABI Human Genome Survey Microarray Version 2
   platform_shorttitle:
      ABI Human Genome
   platform_summary:

   platform_manufacturer:
      Applied Biosystems
   platform_distribution:
      commercial
   platform_accession:
      GPL2986
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1CF ... ZZZ3 (16048 total)
  varLabels: probeset gene
```

```
  varMetadata: labelDescription
```

Details

```
assayData: 16048 features, 204 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 194.00  194.00  194.00   57.00      NA    3.67      NA

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

alt_sample_name:
   Length     Class      Mode
      204 character character

sample_type:
tumor
  204

histological_type:
other   ser  NA's
   23   171    10

summarygrade:
high  low NA's
 143   50   11

summarystage:
early  late  NA's
    9   185    10

tumorstage:
   2    3    4 NA's
   9  154   31   10

grade:
   2    3 NA's
  50  143   11

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  26.00   50.00   57.00   57.66   67.00   85.00      10

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   30.0   335.0   487.0   580.1   722.5  1461.0      10
```

```
recurrence_status:
norecurrence   recurrence         NA's
          70          124           10

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   30.0   517.0   745.5   782.9  1027.0  1491.0      10

vital_status:
deceased   living     NA's
      57      137       10

debulking:
   optimal suboptimal       NA's
       137         57         10

uncurated_author_metadata:
   Length     Class      Mode
      204 character character
```

GSE51088_eset *POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovarian cancer.*

Description

To identify molecular prognosticators and therapeutic targets for high-grade serous epithelial ovarian cancers (EOCs) using genetic analyses driven by biologic features of EOC pathogenesis.Ovarian tissue samples (n = 172; 122 serous EOCs, 30 other EOCs, 20 normal/benign) collected prospectively from sequential patients undergoing gynecologic surgery were analyzed using RNA expression microarrays. Samples were classified based on expression of genes with potential relevance in ovarian cancer. Gene sets were defined using Rosetta Similarity Search Tool (ROAST) and analysis of variance (ANOVA). Gene copy number variations were identified by array comparative genomic hybridization.No distinct subgroups of EOC could be identified by unsupervised clustering, however, analyses based on genes correlated with periostin (POSTN) and estrogen receptor-alpha (ESR1) yielded distinct subgroups. When 95 high-grade serous EOCs were grouped by genes based on ANOVA comparing ESR1/WT1 and POSTN/TGFBI samples, overall survival (OS) was significantly shorter for 43 patients with tumors expressing genes associated with POSTN/TGFBI compared to 52 patients with tumors expressing genes associated with ESR1/WT1 (median 30 versus 49 months, respectively; P = 0.022). Several targets with therapeutic potential were identified within each subgroup. BRCA germline mutations were more frequent in the ESR1/WT1 subgroup. Proliferation-associated genes and TP53 status (mutated or wild-type) did not correlate with survival. Findings were validated using independent ovarian cancer datasets.Two distinct molecular subgroups of high-grade serous EOCs based on POSTN/TGFBI and ESR1/WT1 expressions were identified with significantly different OS. Specific differentially expressed genes between these subgroups provide potential prognostic and therapeutic targets.

Usage

```
data( GSE51088_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Karlan BY, Dering J, Walsh C, Orsulic S, Lester J, Anderson LA, Ginther CL, Fejzo
  Laboratory: Karlan, Slamon 2014
  Contact information:
 Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovari
  URL:
  PMIDs: 24368280

  Abstract: A 250 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
   platform_shorttitle:
      Agilent G4110B
   platform_summary:
      hgug4110b
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL7264
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (8211 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 8211 features, 172 samples
Platform type: hgug4110b
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   20 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 152.00  152.00  152.00  112.00    4.13    3.50    4.92

---------------------------
```

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

alt_sample_name:
   Length     Class      Mode
      172 character character

sample_type:
    benign borderline    healthy metastatic      tumor
         5         12         15         17        123

histological_type:
   Length     Class      Mode
      172 character character

summarygrade:
high  low NA's
 119   30   23

summarystage:
early  late  NA's
   31   120    21

tumorstage:
   1    2    3    4 NA's
  22    9  103   17   21

substage:
   a    b    c NA's
  17   22   94   39

grade:
   0    1    2    3 NA's
   8    8   14  119   23

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   26.0    49.0    57.5    58.6    68.0    91.0

neo:
  n
172

recurrence_status:
norecurrence   recurrence         NA's
          36          111           25

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     30     791    1491    1835    2344    7001      20

vital_status:
```

```
deceased   living     NA's
     112       40       20

percent_normal_cells:
 30- NA's
 140   32

percent_stromal_cells:
 30- NA's
 140   32

percent_tumor_cells:
 70+ NA's
 140   32

uncurated_author_metadata:
   Length     Class      Mode
      172 character character
```

GSE6008_eset *Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian carcinoma and worsened prognosis.*

Description

Lysophosphatidic acid (LPA) governs a number of physiologic and pathophysiological processes. Malignant ascites fluid is rich in LPA, and LPA receptors are aberrantly expressed by ovarian cancer cells, implicating LPA in the initiation and progression of ovarian cancer. However, there is an absence of systematic data critically analyzing the transcriptional changes induced by LPA in ovarian cancer.In this study, gene expression profiling was used to examine LPA-mediated transcription by exogenously adding LPA to human epithelial ovarian cancer cells for 24 h to mimic long-term stimulation in the tumor microenvironment. The resultant transcriptional profile comprised a 39-gene signature that closely correlated to serous epithelial ovarian carcinoma. Hierarchical clustering of ovarian cancer patient specimens demonstrated that the signature is associated with worsened prognosis. Patients with LPA-signature-positive ovarian tumors have reduced disease-specific and progression-free survival times. They have a higher frequency of stage IIIc serous carcinoma and a greater proportion is deceased. Among the 39-gene signature, a group of seven genes associated with cell adhesion recapitulated the results. Out of those seven, claudin-1, an adhesion molecule and phenotypic epithelial marker, is the only independent biomarker of serous epithelial ovarian carcinoma. Knockdown of claudin-1 expression in ovarian cancer cells reduces LPA-mediated cellular adhesion, enhances suspended cells and reduces LPA-mediated migration.The data suggest that transcriptional events mediated by LPA in the tumor microenvironment influence tumor progression through modulation of cell adhesion molecules like claudin-1 and, for the first time, report an LPA-mediated expression signature in ovarian cancer that predicts a worse prognosis.

Usage

```
data( GSE6008_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Murph MM, Liu W, Yu S, Lu Y, Hall H, Hennessy BT, Lahad J, Schaner M, Helland A, K
  Laboratory: Murph, Mills 2009
  Contact information:
 Title: Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian
  URL:
  PMIDs: 19440550

  Abstract: A 247 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 103 samples
Platform type: hgu133a
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   Length     Class      Mode
      103 character character

sample_type:
healthy   tumor
      4      99
```

```
histological_type:
clearcell      endo  mucinous       ser      NA's
        8        37        13        41         4

primarysite:
 ov
103

summarygrade:
high  low NA's
  38   36   29

summarystage:
early  late  NA's
   42    53     8

tumorstage:
   1    2    3    4 NA's
  35   11   44    9    4

substage:
   a    b    c    d NA's
  19    2   54    1   27

grade:
   1    2    3 NA's
  19   17   38   29

batch:
   Length     Class      Mode
      103 character character

uncurated_author_metadata:
   Length     Class      Mode
      103 character character
```

GSE6822_eset *Classification of ovarian tumor samples*

Description

Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C, Novak J, Ge B, Hudson TJ, Tonin PN, Mes-Masson A-M: Discrimination between serous low malignant potential and invasive epithelial ovarian tumors using molecular profiling. Oncogene 2005, 24:4672-4687.

Usage

```
data( GSE6822_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C, Novak J, Ge B,
  Laboratory: Ouellet, Mes-Masson 2005
  Contact information:
  Title: Classification of ovarian tumor samples
  URL:
  PMIDs: PMID unknown

  Abstract: A 40 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [Hu6800] Affymetrix Human Full Length HuGeneFL Array
   platform_shorttitle:
      Affymetrix Hu6800
   platform_summary:
      hu6800
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL80
   platform_technology:
      in situ oligonucleotide

Preprocessing: rma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A2M AADAC ... ZYX (5251 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 5251 features, 66 samples
Platform type: hu6800
----------------------------
Available sample meta-data:
----------------------------

alt_sample_name:
   Length     Class      Mode
       66 character character

sample_type:
borderline   cellline      tumor
         6          2         58
```

```
histological_type:
   Length     Class      Mode
       66 character character

primarysite:
ov
66

summarygrade:
high  low NA's
  40   15   11

grade:
   1    2    3 NA's
   1   14   40   11

batch:
   Length     Class      Mode
       66 character character

uncurated_author_metadata:
   Length     Class      Mode
       66 character character
```

GSE8842_eset *Analysis of gene expression in early-stage ovarian cancer.*

Description

Gene expression profile was analyzed in 68 stage I and 15 borderline ovarian cancers to determine if different clinical features of stage I ovarian cancer such as histotype, grade, and survival are related to differential gene expression.Tumors were obtained directly at surgery and immediately frozen in liquid nitrogen until analysis. Glass arrays containing 16,000 genes were used in a dual-color assay labeling protocol.Unsupervised analysis identified eight major patient partitions, one of which was statistically associated to overall survival, grading, and histotype and another with grading and histotype. Supervised analysis allowed detection of gene profiles clearly associated to histotype or to degree of differentiation. No difference was found between borderline and grade 1 tumors. As to recurrence, a subset of genes able to differentiate relapsers from nonrelapsers was identified. Among these, cyclin E and minichromosome maintenance protein 5 were found particularly relevant, as their expression was inversely correlated to progression-free survival (P = 0.00033 and 0.017, respectively).Specific molecular signatures define different histotypes and prognosis of stage I ovarian cancer. Mucinous and clear cells histotypes can be distinguished from the others regardless of tumor grade. Cyclin E and minichromosome maintenance protein 5, whose expression was found previously to be related to a bad prognosis of advanced ovarian cancer, appear to be potential prognostic markers in stage I ovarian cancer too, independent of other pathologic and clinical variables.

Usage

```
data( GSE8842_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Fruscio R, Clivio L, Gar
  Laboratory: Marchini, D'Incalci 2008
  Contact information:
  Title: Analysis of gene expression in early-stage ovarian cancer.
  URL:
  PMIDs: 19047114

  Abstract: A 225 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent Human 1 cDNA Microarray (G4100A)
   platform_shorttitle:
      Agilent  G4100A cDNA
   platform_summary:
      hgug4100a
   platform_manufacturer:
      Agilent
   platform_distribution:
      custom-commerical
   platform_accession:
      GPL5689
   platform_technology:
      spotted DNA/cDNA

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A2M AADAC ... ZYX (6536 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 6536 features, 83 samples
Platform type: hgug4100a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
     83      83      83      15      NA      12      NA

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

alt_sample_name:
   Length     Class      Mode
```

```
       83 character character

sample_type:
borderline      tumor
        15         68

histological_type:
   Length     Class      Mode
       83 character character

primarysite:
ov
83

summarygrade:
high  low NA's
  35   33   15

summarystage:
early
   83

tumorstage:
 1
83

substage:
 a  b  c
25  5 53

grade:
   1    2    3 NA's
  13   20   35   15

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   43.00   50.00   51.25   61.00   87.00

recurrence_status:
norecurrence   recurrence
          62           21

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      0    1192    2248    2273    3048    5824

vital_status:
deceased   living
      15       68

uncurated_author_metadata:
   Length     Class      Mode
```

```
          83 character character
```

GSE9891_eset *Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome.*

Description

The study aim to identify novel molecular subtypes of ovarian cancer by gene expression profiling with linkage to clinical and pathologic features.Microarray gene expression profiling was done on 285 serous and endometrioid tumors of the ovary, peritoneum, and fallopian tube. K-means clustering was applied to identify robust molecular subtypes. Statistical analysis identified differentially expressed genes, pathways, and gene ontologies. Laser capture microdissection, pathology review, and immunohistochemistry validated the array-based findings. Patient survival within k-means groups was evaluated using Cox proportional hazards models. Class prediction validated k-means groups in an independent dataset. A semisupervised survival analysis of the array data was used to compare against unsupervised clustering results.Optimal clustering of array data identified six molecular subtypes. Two subtypes represented predominantly serous low malignant potential and low-grade endometrioid subtypes, respectively. The remaining four subtypes represented higher grade and advanced stage cancers of serous and endometrioid morphology. A novel subtype of high-grade serous cancers reflected a mesenchymal cell type, characterized by overexpression of N-cadherin and P-cadherin and low expression of differentiation markers, including CA125 and MUC1. A poor prognosis subtype was defined by a reactive stroma gene expression signature, correlating with extensive desmoplasia in such samples. A similar poor prognosis signature could be found using a semisupervised analysis. Each subtype displayed distinct levels and patterns of immune cell infiltration. Class prediction identified similar subtypes in an independent ovarian dataset with similar prognostic trends.Gene expression profiling identified molecular subtypes of ovarian cancer of biological and clinical importance.

Usage

```
data( GSE9891_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, Johnson DS, Trivett MK,
  Laboratory: Tothill, Bowtell 2008
  Contact information:
 Title: Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcom
  URL:
  PMIDs: 18698038

  Abstract: A 243 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
```

```
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 19816 features, 285 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   7 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 278.00  278.00  278.00  113.00    3.95    3.53    5.01

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

alt_sample_name:
   Length     Class      Mode
      285 character character

sample_type:
borderline      tumor
        18        267

histological_type:
 endo other   ser
   20     1   264

primarysite:
   ft other    ov
    8    34   243

arrayedsite:
   ft other    ov
```

```
    2    83   200

summarygrade:
high  low NA's
 163  116    6

summarystage:
early  late  NA's
   42   240     3

tumorstage:
   1    2    3    4 NA's
  24   18  218   22    3

substage:
   a    b    c NA's
  26   19  212   28

grade:
   1    2    3 NA's
  19   97  163    6

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  22.00   53.00   59.00   59.62   68.00   80.00       3

pltx:
   n    y NA's
  39  243    3

tax:
   n    y NA's
  87  195    3

neo:
   n    y NA's
 264   18    3

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   300.0   450.0   618.9   810.0  4980.0      10

recurrence_status:
norecurrence   recurrence         NA's
          94          188            3

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   547.5   855.0   955.1  1252.0  6420.0       7

vital_status:
deceased   living     NA's
```

```
      113      169        3

debulking:
   optimal suboptimal       NA's
       160         88         37

batch:
   Length     Class      Mode
      285 character character

uncurated_author_metadata:
   Length     Class      Mode
      285 character character
```

PMID15897565_eset *Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.*

Description

A better understanding of the underlying biology of invasive serous ovarian cancer is critical for the development of early detection strategies and new therapeutics. The objective of this study was to define gene expression patterns associated with favorable survival.RNA from 65 serous ovarian cancers was analyzed using Affymetrix U133A microarrays. This included 54 stage III/IV cases (30 short-term survivors who lived <3 years and 24 long-term survivors who lived >7 years) and 11 stage I/II cases. Genes were screened on the basis of their level of and variability in expression, leaving 7,821 for use in developing a predictive model for survival. A composite predictive model was developed that combines Bayesian classification tree and multivariate discriminant models. Leave-one-out cross-validation was used to select and evaluate models.Patterns of genes were identified that distinguish short-term and long-term ovarian cancer survivors. The expression model developed for advanced stage disease classified all 11 early-stage ovarian cancers as long-term survivors. The MAL gene, which has been shown to confer resistance to cancer therapy, was most highly overexpressed in short-term survivors (3-fold compared with long-term survivors, and 29-fold compared with early-stage cases). These results suggest that gene expression patterns underlie differences in outcome, and an examination of the genes that provide this discrimination reveals that many are implicated in processes that define the malignant phenotype.Differences in survival of advanced ovarian cancers are reflected by distinct patterns of gene expression. This biological distinction is further emphasized by the finding that early-stage cancers share expression patterns with the advanced stage long-term survivors, suggesting a shared favorable biology.

Usage

```
data( PMID15897565_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Berchuck A, Iversen ES, Lancaster JM, Pittman J, Luo J, Lee P, Murphy S, Dressman
  Laboratory: Berchuck, Marks 2005
```

```
  Contact information:
 Title: Patterns of gene expression that characterize long-term survival in advanced stage serous ov
  URL:
  PMIDs: 15897565

  Abstract: A 258 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide
   warnings:
      These samples are a subset of PMID17290060.

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 63 samples
Platform type: hgu133a
Binary overall survival summary (definitions of long and short provided by study authors):

 long short  NA's
   24    28    11

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

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1761    1828    1907    2001    2032    2536

sample_type:
tumor
   63
```

```
histological_type:
ser
 63

primarysite:
ov
63

summarygrade:
high  low NA's
  25   37    1

summarystage:
early  late
   11    52

tumorstage:
 1  2  3  4
 7  4 48  4

grade:
   1    2    3    4 NA's
   2   35   24    1    1

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  33.00   52.50   59.00   59.21   67.00   79.00

os_binary:
 long short  NA's
   24    28    11

debulking:
   optimal suboptimal       NA's
        24         28         11

batch:
   Length     Class      Mode
       63 character character

uncurated_author_metadata:
   Length     Class      Mode
       63 character character
```

PMID17290060_eset *An integrated genomic-based approach to individualized treatment of patients with advanced-stage ovarian cancer.*

Description

The purpose of this study was to develop an integrated genomic-based approach to personalized treatment of patients with advanced-stage ovarian cancer. We have used gene expression profiles to identify patients likely to be resistant to primary platinum-based chemotherapy and also to identify alternate targeted therapeutic options for patients with de novo platinum-resistant disease.A gene expression model that predicts response to platinum-based therapy was developed using a training set of 83 advanced-stage serous ovarian cancers and tested on a 36-sample external validation set. In parallel, expression signatures that define the status of oncogenic signaling pathways were evaluated in 119 primary ovarian cancers and 12 ovarian cancer cell lines. In an effort to increase chemotherapy sensitivity, pathways shown to be activated in platinum-resistant cancers were subject to targeted therapy in ovarian cancer cell lines.Gene expression profiles identified patients with ovarian cancer likely to be resistant to primary platinum-based chemotherapy with greater than 80% accuracy. In patients with platinum-resistant disease, we identified expression signatures consistent with activation of Src and Rb/E2F pathways, components of which were successfully targeted to increase response in ovarian cancer cell lines.We have defined a strategy for treatment of patients with advanced-stage ovarian cancer that uses therapeutic stratification based on predictions of response to chemotherapy, coupled with prediction of oncogenic pathway deregulation, as a method to direct the use of targeted agents.

Usage

```
data( PMID17290060_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Dressman HK, Berchuck A, Chan G, Zhai J, Bild A, Sayer R, Cragun J, Clarke J, Whit
  Laboratory: Dressman, Lancaster 2007
  Contact information:
 Title: An integrated genomic-based approach to individualized treatment of patients with advanced-
  URL:
  PMIDs: 17290060

  Abstract: A 223 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide
   warnings:
```

```
      This paper has been retracted.

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 117 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
 117.00  117.00  117.00   67.00    5.26    2.79    7.48

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

alt_sample_name:
   Length     Class      Mode
      117 character character

sample_type:
tumor
  117

histological_type:
ser
117

primarysite:
 ov
117

summarygrade:
high  low NA's
  57   57    3

summarystage:
early  late  NA's
    1   115     1

tumorstage:
   2    3    4 NA's
   1   98   17    1

grade:
```

```
   1    2    3    4 NA's
   4   53   56    1    3

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     510    1020    1496    2220    5550

vital_status:
deceased   living
      67       50

primary_therapy_outcome_success:
  completeresponse progressivedisease
               85                 32

debulking:
   optimal suboptimal
        63         54

batch:
   Length     Class      Mode
      117 character character

uncurated_author_metadata:
   Length     Class      Mode
      117 character character
```

PMID19318476_eset *Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable outcome.*

Description

Although few women with advanced serous ovarian cancer are cured, detection of the disease at an early stage is associated with a much higher likelihood of survival. We previously used gene expression array analysis to distinguish subsets of advanced cancers based on disease outcome. In the present study, we report on gene expression of early-stage cancers and validate our prognostic model for advanced-stage cancers.Frozen specimens from 39 stage I/II, 42 stage III/IV, and 20 low malignant potential cancers were obtained from four different sites. A linear discriminant model was used to predict survival based upon array data.We validated the late-stage survival model and show that three of the most differentially expressed genes continue to be predictive of outcome. Most early-stage cancers (38 of 39 invasive, 15 of 20 low malignant potential) were classified as long-term survivors (median probabilities 0.97 and 0.86). MAL, the most differentially expressed gene, was further validated at the protein level and found to be an independent predictor of poor survival in an unselected group of advanced serous cancers (P = 0.0004).These data suggest that serous ovarian cancers detected at an early stage generally have a favorable underlying biology similar to advanced-stage cases that are long-term survivors. Conversely, most late-stage ovarian cancers seem to have a more virulent biology. This insight suggests that if screening approaches are to succeed it will be necessary to develop approaches that are able to detect these virulent cancers at an early stage.

Usage

```
data( PMID19318476_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine DA, Boyd J, Alonso MA, S
  Laboratory: Berchuck, Lancaster 2009
  Contact information:
 Title: Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favor
  URL:
  PMIDs: 19318476

  Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   platform_technology:
      in situ oligonucleotide
   warnings:
      These samples are a subset of PMID17290060.

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 42 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
  42.00   42.00   42.00   22.00    2.79    2.30      NA
```

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

alt_sample_name:
   Length     Class      Mode
       42 character character

sample_type:
tumor
   42

histological_type:
ser
 42

summarygrade:
high  low NA's
  24   17    1

summarystage:
early  late  NA's
    2    39     1

tumorstage:
   1    2    3    4 NA's
   1    1   29   10    1

substage:
   a    b    c NA's
   1    1   29   11

grade:
   1    2    3 NA's
   2   15   24    1

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  33.00   55.00   62.00   61.46   70.00   81.00       1

recurrence_status:
norecurrence   recurrence
           6           36

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   30.0   367.5   825.0  1105.0  1050.0  3420.0

vital_status:
deceased   living
      22       20
```

```
debulking:
   optimal suboptimal       NA's
        20         21          1

batch:
   Length     Class      Mode
       42 character character

uncurated_author_metadata:
   Length     Class      Mode
       42 character character
```

TCGA.mirna.8x15kv2_eset

Integrated genomic analyses of ovarian carcinoma.

Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

Usage

```
data( TCGA.mirna.8x15kv2_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
```

```
  notes:
   platform_title:
      [miRNA-8x15k2] Agilent Human miRNA G4470B
   platform_shorttitle:
      Agilent miRNA-8x15k2 G4470B
   platform_summary:
      NA
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      NA
   platform_technology:
      in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ebv-miR-BART10 ebv-miR-BART10* ... kshv-miR-K12-9* (799
    total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 799 features, 554 samples
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 544.00  544.00  544.00  286.00    3.71    3.42    4.03

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

alt_sample_name:
   Length     Class      Mode
      554 character character

unique_patient_ID:
   Length     Class      Mode
      554 character character

sample_type:
tumor
  554

histological_type:
```

```
ser
554

primarysite:
other    ov
    4   550

summarygrade:
high  low NA's
 474   68   12

summarystage:
early  late  NA's
   39   511     4

tumorstage:
   1    2    3    4 NA's
  16   23  426   85    4

substage:
   b    c NA's
  31  434   89

grade:
   1    2    3    4 NA's
   6   62  473    1   12

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  26.00   51.00   59.00   59.81   69.00   89.00

pltx:
   n    y NA's
  19  478   57

tax:
   n    y NA's
  43  454   57

neo:
   n NA's
 497   57

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    8.0   235.2   436.0   618.7   797.0  5480.0      44

recurrence_status:
norecurrence   recurrence
         268          286

days_to_death:
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    8.0   346.0   867.5   997.7  1446.0  5480.0      10

vital_status:
deceased   living     NA's
     286      261        7

site_of_tumor_first_recurrence:
                locoregional locoregional_plus_metastatic
                        145                             3
                metastasis                          NA's
                        138                           268

primary_therapy_outcome_success:
  completeresponse    partialresponse progressivedisease      stabledisease
               308                 63                 41                 30
              NA's
               112

debulking:
   optimal suboptimal       NA's
       359        137         58

percent_normal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   2.375   0.000  55.000      10

percent_stromal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    5.00   10.00   12.78   19.00   70.00      16

percent_tumor_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   75.00   85.00   80.72   90.00  100.00      13

uncurated_author_metadata:
   Length     Class      Mode
      554 character character
```

`TCGA.RNASeqV2_eset` *Integrated genomic analyses of ovarian carcinoma.*

Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic

mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

Usage

```
data( TCGA.RNASeqV2_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [RNASeqV2] Illumina HiSeq RNA sequencing
   platform_shorttitle:
      Illumina HiSeq RNA sequencing
   platform_summary:
      NA
   platform_manufacturer:
      Illumina
   platform_distribution:
      sequencing
   platform_accession:
      NA
   platform_technology:
      RNA sequencing

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ? A1BG ... ZZZ3 (20502 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 20502 features, 261 samples
```

```
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   5 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 256.00  256.00  256.00  143.00    3.62    3.19    4.03

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

alt_sample_name:
   Length     Class      Mode
      261 character character

unique_patient_ID:
   Length     Class      Mode
      261 character character

sample_type:
tumor
  261

histological_type:
ser
261

primarysite:
other    ov
    1   260

summarygrade:
high  low NA's
 226   29    6

summarystage:
early  late  NA's
   18   242     1

tumorstage:
   2    3    4 NA's
  18  209   33    1

substage:
   b    c NA's
  16  211   34

grade:
   1    2    3    4 NA's
   1   28  225    1    6
```

```
age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  34.00   51.00   58.00   58.84   66.00   87.00

pltx:
   n    y NA's
  17  215   29

tax:
   n    y NA's
  17  215   29

neo:
   n NA's
 232   29

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0   225.0   426.5   585.3   755.0  5480.0      19

recurrence_status:
norecurrence   recurrence
         123          138

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0   341.8   878.0  1018.0  1446.0  5480.0       5

vital_status:
deceased   living     NA's
     143      114        4

site_of_tumor_first_recurrence:
locoregional   metastasis         NA's
          82           56          123

primary_therapy_outcome_success:
  completeresponse    partialresponse progressivedisease      stabledisease
               147                 30                  15                 15
             NA's
               54

debulking:
   optimal suboptimal       NA's
       171         60         30

percent_normal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   2.066   0.000  55.000       5

percent_stromal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
```

```
   0.00    5.00   10.00   11.43   15.00   70.00       4

percent_tumor_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   77.00   85.00   82.07   90.00  100.00       4

uncurated_author_metadata:
   Length     Class      Mode
      261 character character
```

TCGA_eset *Integrated genomic analyses of ovarian carcinoma.*

Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

Usage

```
data( TCGA_eset )
```

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HT_HG-U133A] Affymetrix HT Human Genome U133A Array
```

```
   platform_shorttitle:
      Affymetrix HT_HG-U133A
   platform_summary:
      hthgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL3921
   platform_technology:
      in situ oligonucleotide
   warnings:
     The following samples are likely from specimens also used in GSE26712: TCG
A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13
.0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883

Preprocessing: rma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

Details

```
assayData: 13104 features, 578 samples
Platform type: hthgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   21 observations deleted due to missingness
records   n.max n.start  events  median 0.95LCL 0.95UCL
 557.00  557.00  557.00  290.00    3.73    3.45    4.06

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

alt_sample_name:
   Length     Class      Mode
      578 character character

unique_patient_ID:
   Length     Class      Mode
      578 character character

sample_type:
healthy   tumor
      8     570

histological_type:
```

```
 ser NA's
 568   10

primarysite:
other    ov  NA's
    4   564    10

summarygrade:
high  low NA's
 480   75   23

summarystage:
early  late  NA's
   43   520    15

tumorstage:
   1    2    3    4 NA's
  16   27  436   84   15

substage:
   b    c NA's
  31  448   99

grade:
   1    2    3    4 NA's
   6   69  479    1   23

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  26.00   51.00   59.00   59.70   68.25   89.00      10

pltx:
   n    y NA's
  19  492   67

tax:
   n    y NA's
  43  468   67

neo:
   n NA's
 511   67

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    8.0   238.2   443.5   623.7   812.0  5480.0      56

recurrence_status:
norecurrence   recurrence
         279          299

days_to_death:
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      8     349     881    1010    1446    5480      21

vital_status:
deceased   living     NA's
     290      270       18

site_of_tumor_first_recurrence:
                locoregional locoregional_plus_metastatic
                         153                           3
                  metastasis                        NA's
                         143                         279

primary_therapy_outcome_success:
  completeresponse    partialresponse progressivedisease      stabledisease
               318                 65                 41                 30
              NA's
               124

debulking:
   optimal suboptimal       NA's
       367        140         71

percent_normal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   2.385   0.000  55.000      19

percent_stromal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    5.00   10.00   12.85   20.00   70.00      25

percent_tumor_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   75.00   85.00   80.64   90.00  100.00      22

batch:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   9.00   13.00   17.00   18.55   22.00   40.00       1

uncurated_author_metadata:
   Length     Class      Mode
      578 character character
```

Index