

Package ‘curatedTCGAData’

May 23, 2019

Type Package

Title Curated Data From The Cancer Genome Atlas (TCGA) as
MultiAssayExperiment Objects

Version 1.6.0

Description This package provides publicly available data from The Cancer Genome Atlas (TCGA) as MultiAssayExperiment objects. MultiAssayExperiment integrates multiple assays (e.g., RNA-seq, copy number, mutation, microRNA, protein, and others) with clinical / pathological data. It also links assay barcodes with patient identifiers, enabling harmonized subsetting of rows (features) and columns (patients / samples) across the entire multi-'omics experiment.

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Depends R (>= 3.5.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, HDF5Array, S4Vectors, stats,
SummarizedExperiment, utils

Suggests BiocStyle, knitr, readr, rmarkdown, TCGAutils, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData,
ExperimentHub

BugReports <https://github.com/waldronlab/curatedTCGAData/issues>

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curatedTCGAData-package

Description

The curatedTCGAData package provides a convenient and user-friendly interface for The Cancer Genome Atlas data from the Firehose GDAC Pipeline. Please note that *_most_* of the data from the GDAC Firehose pipeline uses the ‘hg19’ reference genome (except for a few cancers; refer to <https://confluence.broadinstitute.org/display/GDAC/FAQ>).

It is highly recommended to use the 'TCGAutils' companion package. It provides convenience functions for manipulating curatedTCGAData objects. See package for more details (<http://bioconductor.org/packages/TCGAutils>).

diseaseCodes

The following are the TCGA disease codes and full names as posted on the official website (<https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/tcga-study-abbreviations>).

| Study Abbreviation | Study Name |
|--------------------|--|
| 1 ACC | Adrenocortical Carcinoma |
| 2 BLCA | Bladder Urothelial Carcinoma |
| 3 BRCA | Breast Invasive Carcinoma |
| 4 CESC | Cervical Squamous Cell Carcinoma And Endocervical Adenocarcinoma |
| 5 CHOL | Cholangiocarcinoma |
| 6 CNTL | Controls |
| 7 COAD | Colon Adenocarcinoma |
| 8 DLBC | Lymphoid Neoplasm Diffuse Large B-cell Lymphoma |
| 9 ESCA | Esophageal Carcinoma |
| 10 GBM | Glioblastoma Multiforme |
| 11 HNSC | Head And Neck Squamous Cell Carcinoma |
| 12 KICH | Kidney Chromophobe |
| 13 KIRC | Kidney Renal Clear Cell Carcinoma |
| 14 KIRP | Kidney Renal Papillary Cell Carcinoma |
| 15 LAML | Acute Myeloid Leukemia |
| 16 LGG | Brain Lower Grade Glioma |
| 17 LIHC | Liver Hepatocellular Carcinoma |
| 18 LUAD | Lung Adenocarcinoma |
| 19 LUSC | Lung Squamous Cell Carcinoma |
| 20 MESO | Mesothelioma |
| 21 OV | Ovarian Serous Cystadenocarcinoma |
| 22 PAAD | Pancreatic Adenocarcinoma |
| 23 PCPG | Pheochromocytoma And Paraganglioma |
| 24 PRAD | Prostate Adenocarcinoma |
| 25 READ | Rectum Adenocarcinoma |
| 26 SARC | Sarcoma |
| 27 SKCM | Skin Cutaneous Melanoma |
| 28 STAD | Stomach Adenocarcinoma |
| 29 TGCT | Testicular Germ Cell Tumors |
| 30 THCA | Thyroid Carcinoma |
| 31 THYM | Thymoma |
| 32 UCEC | Uterine Corpus Endometrial Carcinoma |
| 33 UCS | Uterine Carcinosarcoma |
| 34 UVM | Uveal Melanoma |

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See Also

Useful links:

- Report bugs at <https://github.com/waldronlab/curatedTCGAData/issues>

Examples

```
help(package = "curatedTCGAData")
```

ACC

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 10:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [4] ACC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 42 rows and 90 columns
 [5] ACC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [6] ACC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [7] ACC_Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
 [8] ACC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [9] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
 [10] ACC_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( ACC )
CharacterList of length 10
[["ACC_CNASNP-20160128"]] character(0)
[["ACC_CNVSNP-20160128"]] character(0)
[["ACC_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["ACC_GISTIC_Peaks-20160128"]] chr1:8403012-8925111 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["ACC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ACC_Mutation-20160128"]] character(0)
[["ACC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["ACC_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["ACC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( ACC )
CharacterList of length 10
[["ACC_CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_Peaks-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
[["ACC_Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["ACC_RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["ACC_RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...
[["ACC_Methylation-20160128"]] TCGA-OR-A5J1-01A-11D-A29J-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | ACC_CNASNP-20160128 | 2.2 Mb |
| 2 | ACC_CNVSNP-20160128 | 0.6 Mb |
| 3 | ACC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | ACC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | ACC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | ACC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | ACC_Mutation-20160128 | 12.6 Mb |
| 8 | ACC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | ACC_RPPAArray-20160128 | 0 Mb |
| 10 | ACC_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
58 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
34.00 34.00 1.51 1.34 3.03
```

Available sample meta-data:

```
years_to_birth:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
 14.00 35.50 48.50 47.16 60.00 83.00
```

```
vital_status:
 0 1
58 34
```

```
days_to_death:
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 399.0 | 551.5 | 854.6 | 1202.2 | 2405.0 | 58 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|--------|---------|--------|------|
| 383.0 | 917.8 | 1453.5 | 1781.6 | 2339.2 | 4673.0 | 34 |

tumor_tissue_site:

adrenal
92

pathologic_stage:

| stage i | stage ii | stage iii | stage iv | NA's |
|---------|----------|-----------|----------|------|
| 9 | 44 | 19 | 18 | 2 |

pathology_T_stage:

| t1 | t2 | t3 | t4 | NA's |
|----|----|----|----|------|
| 9 | 49 | 11 | 21 | 2 |

pathology_N_stage:

| n0 | n1 | NA's |
|----|----|------|
| 80 | 10 | 2 |

gender:

| female | male |
|--------|------|
| 60 | 32 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1997 | 2005 | 2008 | 2007 | 2011 | 2012 |

radiation_therapy:

| no | yes | NA's |
|----|-----|------|
| 71 | 18 | 3 |

histological_type:

| | |
|--|----|
| adrenocortical carcinoma- myxoid type | 1 |
| adrenocortical carcinoma- oncocytic type | 4 |
| adrenocortical carcinoma- usual type | 87 |

residual_tumor:

| r0 | r1 | r2 | rx | NA's |
|----|----|----|----|------|
| 64 | 7 | 12 | 6 | 3 |

number_of_lymph_nodes:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 0.000 | 0.000 | 0.000 | 2.548 | 0.500 | 52.000 | 61 |

race:

| | |
|---|-------|
| asian black or african american | white |
| 2 | 1 |
| NA's | 78 |
| 11 | |
| ethnicity: | |
| hispanic or latino not hispanic or latino | NA's |
| 8 | 40 |
| | 44 |

Including an additional 806 columns

BLCA

Bladder Urothelial Carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( BLCA )
ExperimentList class object of length 12:
 [1] BLCA_CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
 [2] BLCA_CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
 [3] BLCA_CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
 [4] BLCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [5] BLCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 71 rows and 408 columns
 [6] BLCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [7] BLCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
 [8] BLCA_Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
 [9] BLCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 427 columns
 [10] BLCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns
 [11] BLCA_RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns
 [12] BLCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns

> rownames( BLCA )
CharacterList of length 12
[["BLCA_CNASeq-20160128"]] character(0)
[["BLCA_CNASNP-20160128"]] character(0)
[["BLCA_CNVSNP-20160128"]] character(0)
[["BLCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["BLCA_GISTIC_Peaks-20160128"]] chr1:26963410-27155421 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["BLCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BLCA_Mutation-20160128"]] character(0)
[["BLCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["BLCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<2 more elements>

> colnames( BLCA )
```

CharacterList of length 12

```

[["BLCA_CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["BLCA_CNASNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_CNVSNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_AllByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_Peaks-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_miRNASeqGene-20160128"]] TCGA-2F-A9KO-01A-11R-A38M-13 ...
[["BLCA_Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["BLCA_RNASeq2GeneNorm-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
[["BLCA_RNASeqGene-20160128"]] TCGA-BL-A0C8-01A-11R-A10U-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | BLCA_CNASeq-20160128 | 1 Mb |
| 2 | BLCA_CNASNP-20160128 | 13.1 Mb |
| 3 | BLCA_CNVSNP-20160128 | 3 Mb |
| 4 | BLCA_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | BLCA_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | BLCA_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | BLCA_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | BLCA_Mutation-20160128 | 56.1 Mb |
| 9 | BLCA_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | BLCA_RNASeqGene-20160128 | 1.3 Mb |
| 11 | BLCA_RPPAArray-20160128 | 0 Mb |
| 12 | BLCA_Methylation-20160128 | 75.1 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

232 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
180.000 180.000  1.125  0.992  1.332

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 34.00  60.00   69.00   68.08  76.00   90.00    1

```

```

vital_status:
 0  1

```


230 182

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 19.0 | 235.8 | 410.5 | 552.8 | 654.5 | 3183.0 | 232 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|--------|---------|--------|------|
| -64.0 | 398.2 | 639.0 | 1016.7 | 1458.8 | 5050.0 | 182 |

tumor_tissue_site:

bladder

412

pathologic_stage:

| stage i | stage ii | stage iii | stage iv | NA's |
|---------|----------|-----------|----------|------|
| 2 | 131 | 141 | 136 | 2 |

pathology_M_stage:

| m0 | m1 | mx | NA's |
|-----|----|-----|------|
| 196 | 11 | 202 | 3 |

gender:

female male

108 304

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1999 | 2009 | 2011 | 2010 | 2012 | 2013 | 18 |

radiation_therapy:

no yes NA's

366 20 26

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 30.00 | 80.00 | 90.00 | 83.09 | 90.00 | 100.00 | 276 |

histological_type:

muscle invasive urothelial carcinoma (pt2 or above)

409

NA's

3

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.15 | 20.00 | 30.00 | 39.04 | 50.00 | 730.00 | 188 |

number_of_lymph_nodes:

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

0.000 0.000 0.000 2.088 2.000 97.000 115

race:

| | | |
|--|---------------------------------|-------|
| | asian black or african american | white |
| | 44 | 23 |
| | NA's | 327 |
| | 18 | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 9 | 371 | 32 |

Including an additional 1695 columns

BRCA

Breast invasive carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( BRCA )
ExperimentList class object of length 14:
 [1] BRCA_CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] BRCA_CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] BRCA_CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] BRCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] BRCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 1080 columns
 [6] BRCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [7] BRCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [8] BRCA_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [9] BRCA_Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
[10] BRCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[11] BRCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
[12] BRCA_RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
[13] BRCA_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
[14] BRCA_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns

> rownames( BRCA )
CharacterList of length 14
[["BRCA_CNASeq-20160128"]] character(0)
[["BRCA_CNASNP-20160128"]] character(0)
[["BRCA_CNVSNP-20160128"]] character(0)
[["BRCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["BRCA_GISTIC_Peaks-20160128"]] chr1:12675879-21133098 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["BRCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BRCA_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["BRCA_Mutation-20160128"]] character(0)
```

```

[["BRCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<4 more elements>

> colnames( BRCA )
CharacterList of length 14
[["BRCA_CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["BRCA_CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_Peaks-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_miRNASeqGene-20160128"]] TCGA-3C-AAAU-01A-11R-A41G-13 ...
[["BRCA_mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["BRCA_Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
[["BRCA_RNASeq2GeneNorm-20160128"]] TCGA-3C-AAAU-01A-11R-A41B-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | BRCA_CNASeq-20160128 | 0.2 Mb |
| 2 | BRCA_CNASNP-20160128 | 30.9 Mb |
| 3 | BRCA_CNVSNP-20160128 | 8.2 Mb |
| 4 | BRCA_GISTIC_AllByGene-20160128 | 5 Mb |
| 5 | BRCA_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | BRCA_GISTIC_ThresholdedByGene-20160128 | 5 Mb |
| 7 | BRCA_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | BRCA_mRNAArray-20160128 | 1.2 Mb |
| 9 | BRCA_Mutation-20160128 | 67.4 Mb |
| 10 | BRCA_RNASeq2GeneNorm-20160128 | 1.4 Mb |
| 11 | BRCA_RNASeqGene-20160128 | 1.4 Mb |
| 12 | BRCA_RPPAArray-20160128 | 0.1 Mb |
| 13 | BRCA_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | BRCA_Methylation_methyl450-20160128 | 75.1 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

    947 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
151.00 151.00   3.48   2.83   4.50

```

Available sample meta-data:

years_to_birth:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 26.0 49.0 59.0 58.6 68.0 90.0 16

vital_status:
 0 1 NA's
 945 152 1

days_to_death:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 116.0 700.5 1272.0 1644.7 2367.0 7455.0 947

days_to_last_followup:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 -7 440 761 1183 1572 8605 153

tumor_tissue_site:
 breast NA's
 1097 1

pathology_M_stage:
 cm0 (i+) m0 m1 mx NA's
 6 906 22 163 1

gender:
 female male NA's
 1085 12 1

date_of_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 1988 2007 2009 2008 2010 2013 3

days_to_last_known_alive:
 735 2576 NA's
 1 1 1096

radiation_therapy:
 no yes NA's
 446 556 96

number_of_lymph_nodes:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.000 0.000 1.000 2.363 2.000 35.000 169

race:
 american indian or alaska native 1
 asian 61

| | |
|---|-------|
| black or african american | white |
| 183 | 757 |
| NA's | |
| 96 | |
| ethnicity: | |
| hispanic or latino not hispanic or latino | NA's |
| 39 | 884 |
| | 175 |

Including an additional 2667 columns

CESC *Cervical squamous cell carcinoma and endocervical adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( CESC )
ExperimentList class object of length 11:
 [1] CESC_CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CESC_CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CESC_CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] CESC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] CESC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 60 rows and 295 columns
 [6] CESC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [7] CESC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [8] CESC_Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [9] CESC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
[10] CESC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns
[11] CESC_Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns

> rownames( CESC )
CharacterList of length 11
[["CESC_CNASeq-20160128"]] character(0)
[["CESC_CNASNP-20160128"]] character(0)
[["CESC_CNVSNP-20160128"]] character(0)
[["CESC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["CESC_GISTIC_Peaks-20160128"]] chr1:1-28840301 ... chr22:48668582-51304566
[["CESC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["CESC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CESC_Mutation-20160128"]] character(0)
[["CESC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["CESC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( CESC )
CharacterList of length 11
```

```

[["CESC_CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CESC_CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_Peaks-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
[["CESC_Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["CESC_RNASeq2GeneNorm-20160128"]] TCGA-2W-A8YY-01A-11R-A37O-07 ...
[["CESC_RPPAArray-20160128"]] TCGA-2W-A8YY-01A-21-A40H-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | CESC_CNASeq-20160128 | 0.3 Mb |
| 2 | CESC_CNASNP-20160128 | 7.3 Mb |
| 3 | CESC_CNVSNP-20160128 | 1.8 Mb |
| 4 | CESC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | CESC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | CESC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | CESC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | CESC_Mutation-20160128 | 32.9 Mb |
| 9 | CESC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | CESC_RPPAArray-20160128 | 0 Mb |
| 11 | CESC_Methylation-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

235 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
72.00  72.00   1.70   1.39   2.29

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  20.0   38.0   46.0   48.2   56.0   88.0    2

```

```

vital_status:
  0  1
235 72

```

days_to_death:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 14.0 349.5 620.0 881.3 1069.5 4086.0 235

days_to_last_followup:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0 374 688 1071 1362 6408 72

tumor_tissue_site:
 cervical
 307

pathology_N_stage:
 n0 n1 nx NA's
 135 60 67 45

pathology_M_stage:
 m0 m1 mx NA's
 116 10 131 50

gender:
 female
 307

date_of_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 1994 2006 2010 2008 2012 2013 2

radiation_therapy:
 no yes NA's
 55 129 123

number_pack_years_smoked:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.20 6.50 15.00 17.38 25.00 57.00 214

number_of_lymph_nodes:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.000 0.000 0.000 1.044 1.000 16.000 148

ethnicity:
 hispanic or latino not hispanic or latino NA's
 24 171 112

weight_kg_at_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 31.00 58.25 70.50 73.04 83.75 210.00 29

tumor_status:

| | | | | | | | |
|-----------------------|----|--|------|--|--|--|--|
| tumor free with tumor | | | NA's | | | | |
| 201 | 80 | | 26 | | | | |

tobacco_smoking_year_stopped:

| | | | | | | |
|------|---------|--------|------|---------|------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 1949 | 1995 | 2003 | 2000 | 2010 | 2013 | 264 |

tobacco_smoking_pack_years_smoked:

| | | | | | | |
|------|---------|--------|-------|---------|-------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.20 | 6.50 | 15.00 | 17.38 | 25.00 | 57.00 | 214 |

tobacco_smoking_history:

| | | | | | | |
|-------|---------|--------|-------|---------|-------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 1.000 | 1.000 | 1.000 | 1.829 | 2.000 | 5.000 | 44 |

agebeganmokinginyears:

| | | | | | | |
|-------|---------|--------|-------|---------|-------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 11.00 | 16.00 | 18.00 | 21.14 | 24.00 | 44.00 | 222 |

radiation_therapy_status:

| | | |
|----------------------|-------------------------|------|
| completed as planned | treatment not completed | NA's |
| 29 | 3 | 275 |

pregnancies_count_total:

| | | | | | | |
|------|---------|--------|------|---------|-------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.00 | 2.00 | 3.00 | 3.61 | 5.00 | 15.00 | 40 |

pregnancies_count_stillbirth:

| | | | |
|-----|---|---|------|
| 0 | 1 | 3 | NA's |
| 106 | 5 | 1 | 195 |

pregnancy_spontaneous_abortion_count:

| | | | | | | |
|--------|---------|--------|--------|---------|--------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.0000 | 0.0000 | 0.0000 | 0.5442 | 1.0000 | 6.0000 | 160 |

pregnancies_count_live_birth:

| | | | | | | |
|-------|---------|--------|-------|---------|--------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.000 | 1.250 | 2.000 | 2.844 | 4.000 | 11.000 | 45 |

pregnancy_therapeutic_abortion_count:

| | | | | | | |
|--------|---------|--------|--------|---------|---------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.0000 | 0.0000 | 0.0000 | 0.8525 | 1.0000 | 13.0000 | 185 |

pregnancies_count_ectopic:

| | | | |
|-----|----|---|------|
| 0 | 1 | 2 | NA's |
| 104 | 11 | 1 | 191 |

lymph_node_location:

lymph_node_location_positive_pathology_name|lymph_node_location_positive_pathology_text

menopause_status:

| | |
|--|-----|
| indeterminate (neither pre or postmenopausal) | 3 |
| peri (6-12 months since last menstrual period) | 25 |
| post (prior bilateral ovariectomy or >12 mo since lmp with no prior hysterectomy) | 84 |
| pre (<6 months since lmp and no prior bilateral ovariectomy and not on estrogen replacement) | 125 |
| NA's | 70 |

lymphovascular_involvement:

| | | |
|--------|---------|------|
| absent | present | NA's |
| 72 | 80 | 155 |

lymph_nodes_examined_he_count:

| | | | | | | |
|-------|---------|--------|-------|---------|--------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 0.000 | 0.000 | 0.000 | 1.044 | 1.000 | 16.000 | 148 |

lymph_nodes_examined:

| | | | | | | |
|------|---------|--------|-------|---------|-------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 2.00 | 13.00 | 21.00 | 22.28 | 29.00 | 63.00 | 127 |

keratinization_squamous_cell:

| | |
|--|-----|
| keratinizing squamous cell carcinoma | 55 |
| non-keratinizing squamous cell carcinoma | 120 |
| NA's | 132 |

initial_pathologic_dx_year:

| | | | | | | |
|------|---------|--------|------|---------|------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 1994 | 2006 | 2010 | 2008 | 2012 | 2013 | 2 |

hysterectomy_type:

| | |
|---|-----|
| hysterectomy_performed_type hysterectomy_performed_text | 307 |
|---|-----|

history_hormonal_contraceptives_use:

| | | | |
|--------------|-------------|------------|------|
| current user | former user | never used | NA's |
| 15 | 54 | 90 | 148 |

height_cm_at_diagnosis:

| | | | | | | |
|------|---------|--------|------|---------|------|------|
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
| 132 | 157 | 160 | 161 | 165 | 183 | 43 |

corpus_involvement:

| | | |
|--------|---------|------|
| absent | present | NA's |
|--------|---------|------|

```

          99      19      189

chemo_concurrent_type:
carboplatin  cisplatin      other      NA's
              7           104           2          194

cervix_suv_results:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.00   8.70   12.00   13.22  16.92   28.80   290

cause_of_death:
cardiopulmonary arrest      lung cancer      renal failure
              1                      1                      1
              NA's
              304

age_at_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  20.00  38.00  46.00  48.27  56.50  88.00

```

Including an additional 1330 columns

CHOL

Cholangiocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( CHOL )
ExperimentList class object of length 10:
 [1] CHOL_CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CHOL_CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] CHOL_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] CHOL_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 19 rows and 36 columns
 [5] CHOL_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [6] CHOL_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
 [7] CHOL_Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [8] CHOL_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [9] CHOL_RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns
[10] CHOL_Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns

> rownames( CHOL )
CharacterList of length 10
[["CHOL_CNASNP-20160128"]] character(0)
[["CHOL_CNVSNP-20160128"]] character(0)
[["CHOL_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["CHOL_GISTIC_Peaks-20160128"]] chr1:7829287-29140747 ... chr16:1-90354753

```

```

[["CHOL_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["CHOL_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CHOL_Mutation-20160128"]] character(0)
[["CHOL_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["CHOL_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["CHOL_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```
> colnames( CHOL )
```

```
CharacterList of length 10
```

```

[["CHOL_CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_Peaks-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["CHOL_Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["CHOL_RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["CHOL_RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...
[["CHOL_Methylation-20160128"]] TCGA-3X-AAV9-01A-72D-A418-05 ...

```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|----|--|---------------|
| 1 | CHOL_CNASNP-20160128 | 1.1 Mb |
| 2 | CHOL_CNVSNP-20160128 | 0.2 Mb |
| 3 | CHOL_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | CHOL_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | CHOL_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | CHOL_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | CHOL_Mutation-20160128 | 4.6 Mb |
| 8 | CHOL_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | CHOL_RPPAArray-20160128 | 0 Mb |
| 10 | CHOL_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```

18 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
18.000 18.000  1.370  0.742  2.532

```

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

```
years_to_birth:
```

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

29.00 56.50 66.50 63.03 72.00 82.00

vital_status:

0 1
18 18

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 21.0 | 195.2 | 500.0 | 592.9 | 731.0 | 1939.0 | 18 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 10.0 | 539.8 | 942.5 | 936.6 | 1394.0 | 1976.0 | 18 |

tumor_tissue_site:

bile duct
36

pathology_T_stage:

| t1 | t2 | t2a | t2b | t3 |
|----|----|-----|-----|----|
| 19 | 6 | 2 | 4 | 5 |

pathology_N_stage:

| n0 | n1 | nx |
|----|----|----|
| 26 | 5 | 5 |

pathology_M_stage:

| m0 | m1 | mx |
|----|----|----|
| 28 | 5 | 3 |

gender:

| female | male |
|--------|------|
| 20 | 16 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 2005 | 2010 | 2011 | 2010 | 2012 | 2013 |

radiation_therapy:

| no NA's |
|---------|
| 35 1 |

histological_type:

| | |
|----------------------------------|-------------------------------------|
| cholangiocarcinoma; distal | cholangiocarcinoma; hilar/perihilar |
| | 2 4 |
| cholangiocarcinoma; intrahepatic | |
| | 30 |

residual_tumor:

| r0 | r1 | rx |
|----|----|----|
| 28 | 5 | 3 |

```

race:
      asian black or african american      white
      3                                 2      31

ethnicity:
      hispanic or latino not hispanic or latino      NA's
      2                                 33      1

```

Including an additional 622 columns

| | |
|------|-----------------------------|
| COAD | <i>Colon adenocarcinoma</i> |
|------|-----------------------------|

Description

A document describing the TCGA cancer code

Details

```

> experiments( COAD )
ExperimentList class object of length 14:
 [1] COAD_CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] COAD_CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] COAD_CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] COAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [5] COAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 66 rows and 449 columns
 [6] COAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [7] COAD_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
 [8] COAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
 [9] COAD_Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
[10] COAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 191 columns
[11] COAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
[12] COAD_RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns
[13] COAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
[14] COAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns

> rownames( COAD )
CharacterList of length 14
[["COAD_CNASeq-20160128"]] character(0)
[["COAD_CNASNP-20160128"]] character(0)
[["COAD_CNVSNP-20160128"]] character(0)
[["COAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["COAD_GISTIC_Peaks-20160128"]] chr1:26527443-27650365 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["COAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["COAD_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["COAD_Mutation-20160128"]] character(0)
[["COAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<4 more elements>

```

```
> colnames( COAD )
CharacterList of length 14
[["COAD_CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["COAD_CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_Peaks-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_miRNASeqGene-20160128"]] TCGA-A6-2675-01A-02T-1722-13 ...
[["COAD_mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["COAD_Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
[["COAD_RNASeq2GeneNorm-20160128"]] TCGA-A6-2671-01A-01R-1410-07 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | COAD_CNASeq-20160128 | 1.1 Mb |
| 2 | COAD_CNASNP-20160128 | 12.5 Mb |
| 3 | COAD_CNVSNP-20160128 | 2.7 Mb |
| 4 | COAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | COAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | COAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | COAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | COAD_mRNAArray-20160128 | 1.1 Mb |
| 9 | COAD_Mutation-20160128 | 23.6 Mb |
| 10 | COAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | COAD_RNASeqGene-20160128 | 1.3 Mb |
| 12 | COAD_RPPAArray-20160128 | 0 Mb |
| 13 | COAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | COAD_Methylation_methyl450-20160128 | 75 Mb |

Available sample meta-data:

```
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  31.00  58.00  68.00  66.95  77.00  90.00    2
```

```
tumor_tissue_site:
```

```
colon NA's
  456    1
```

```
date_of_initial_pathologic_diagnosis:
```

```

      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
1998    2007    2009    2008    2010    2013

radiation_therapy:
  no  yes NA's
378   9   70

number_of_lymph_nodes:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
0.000  0.000  0.000  2.058  2.000  50.000    25

race:
american indian or alaska native          asian
                                1              11
      black or african american          white
                                59             213
                                NA's
                                173

ethnicity:
  hispanic or latino not hispanic or latino   NA's
                                4              270
                                183

```

Including an additional 2604 columns

curatedTCGAData *Create a MultiAssayExperiment from specific assays and cohorts*

Description

curatedTCGAData assembles data on-the-fly from ExperimentHub to provide cohesive [MultiAssayExperiment](#) container objects. All the user has to do is to provide TCGA disease code(s) and assay types. It is highly recommended to use the companion package 'TCGAutils', developed to work with TCGA data specifically from 'curatedTCGAData' and some flat files.

Usage

```
curatedTCGAData(diseaseCode = "*", assays = "*", dry.run = TRUE, ...)
```

Arguments

| | |
|-------------|---|
| diseaseCode | a character vector containing the name(s) of TCGA cohorts |
| assays | a character vector of TCGA assays, glob matches allowed; see below for more details |
| dry.run | logical (default TRUE) whether to return the dataset names before actual download |
| ... | Additional arguments passed on to the ExperimentHub constructor |

Details

This function will check against available resources in ExperimentHub. Only the latest runDate ("2016-01-28") is supported. Use the `dry.run = FALSE` to download remote datasets and build an integrative [MultiAssayExperiment](#) object. For a list of 'diseaseCodes', see the [curatedTCGAData-package](#) help page.

Value

a [MultiAssayExperiment](#) of the specified assays and cancer codes

Available Assays

Below is a list of partial ExperimentList assay names and their respective description. These assays can be entered as part of the assays argument in the main function. Partial glob matches are allowed such as: 'CN*' for "CNASeq", "CNASNP", "CNVSNP" assays. Credit: Ludwig G.

| ExperimentList data types | Description |
|---|--|
| SummarizedExperiment* | |
| RNASeqGene | RSEM TPM gene expression values |
| RNASeq2GeneNorm | Upper quartile normalized RSEM TPM gene expression values |
| miRNAArray | Probe-level miRNA expression values |
| miRNASeqGene | Gene-level log2 RPM miRNA expression values |
| mRNAArray | Unified gene-level mRNA expression values |
| mRNAArray_huex | Gene-level mRNA expression values from Affymetrix Human Exon Array |
| mRNAArray_TX_g4502a | Gene-level mRNA expression values from Agilent 244K Array |
| mRNAArray_TX_ht_hg_u133a | Gene-level mRNA expression values from Affymetrix Human Genome U133 Array |
| GISTIC_AllByGene | Gene-level GISTIC2 copy number values |
| GISTIC_ThresholdedByGene | Gene-level GISTIC2 thresholded discrete copy number values |
| RPPAArray | Reverse Phase Protein Array normalized protein expression values |
| RangedSummarizedExperiment | |
| GISTIC_Peaks | GISTIC2 thresholded discrete copy number values in recurrent peak regions |
| SummarizedExperiment with HDF5Array DelayedMatrix | |
| Methylation_methyl27 | Probe-level methylation beta values from Illumina HumanMethylation 27K BeadChip |
| Methylation_methyl450 | Probe-level methylation beta values from Infinium HumanMethylation 450K BeadChip |
| RaggedExperiment | |
| CNASNP | Segmented somatic Copy Number Alteration calls from SNP array |
| CNVSNP | Segmented germline Copy Number Variant calls from SNP Array |
| CNASeq | Segmented somatic Copy Number Alteration calls from low pass DNA Sequencing |


```

Mutation*           Somatic mutations calls
CNACGH_CGH_hg_244a Segmented somatic Copy Number Alteration calls
                    from CGH Agilent Microarray 244A
CNACGH_CGH_hg_415k_g4124a Segmented somatic Copy Number Alteration calls
                    from CGH Agilent Microarray 415K
* All can be converted to RangedSummarizedExperiment (except RPPAArray) with
TCGAutils

```

See Also

curatedTCGAData-package

Examples

```
curatedTCGAData(diseaseCode = c("GBM", "ACC"), assays = "CNASNP")
```

DLBC

Lymphoid Neoplasm Diffuse Large B-cell Lymphoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( DLBC )
ExperimentList class object of length 10:
 [1] DLBC_CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] DLBC_CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] DLBC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] DLBC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 39 rows and 48 columns
 [5] DLBC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [6] DLBC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
 [7] DLBC_Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [8] DLBC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [9] DLBC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns
[10] DLBC_Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns

> rownames( DLBC )
CharacterList of length 10
[["DLBC_CNASNP-20160128"]] character(0)
[["DLBC_CNVSNP-20160128"]] character(0)
[["DLBC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["DLBC_GISTIC_Peaks-20160128"]] chr1:1-48649489 ... chr22:41635693-51304566
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["DLBC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["DLBC_Mutation-20160128"]] character(0)
[["DLBC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["DLBC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363

```

```
[[ "DLBC_Methylation-20160128" ]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( DLBC )
```

```
CharacterList of length 10
```

```
[[ "DLBC_CNASNP-20160128" ]] TCGA-FA-8693-01A-11D-2389-01 ...
[[ "DLBC_CNVSNP-20160128" ]] TCGA-FA-8693-01A-11D-2389-01 ...
[[ "DLBC_GISTIC_AllByGene-20160128" ]] TCGA-FA-8693-01A-11D-2389-01 ...
[[ "DLBC_GISTIC_Peaks-20160128" ]] TCGA-FA-8693-01A-11D-2389-01 ...
[[ "DLBC_GISTIC_ThresholdedByGene-20160128" ]] TCGA-FA-8693-01A-11D-2389-01 ...
[[ "DLBC_miRNASeqGene-20160128" ]] TCGA-FA-8693-01A-11R-2401-13 ...
[[ "DLBC_Mutation-20160128" ]] TCGA-FA-8693-01A-11D-2397-10 ...
[[ "DLBC_RNASeq2GeneNorm-20160128" ]] TCGA-FA-8693-01A-11R-2404-07 ...
[[ "DLBC_RPPAArray-20160128" ]] TCGA-FA-8693-01A-21-A45K-20 ...
[[ "DLBC_Methylation-20160128" ]] TCGA-FA-8693-01A-11D-2399-05 ...
```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|----|--|---------------|
| 1 | DLBC_CNASNP-20160128 | 1.2 Mb |
| 2 | DLBC_CNVSNP-20160128 | 0.3 Mb |
| 3 | DLBC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | DLBC_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | DLBC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | DLBC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | DLBC_Mutation-20160128 | 12.6 Mb |
| 8 | DLBC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | DLBC_RPPAArray-20160128 | 0 Mb |
| 10 | DLBC_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
39 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
9.000 9.000 1.630 0.858 NA
```

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

```
years_to_birth:
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 23.00 | 46.00 | 57.50 | 56.27 | 67.00 | 82.00 |

```
vital_status:
```

```
0 1
39 9
```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
    58   313    595   1505  1252   6425   39

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
    0   616    946   1328  1581   5980    9

gender:
female  male
   26   22

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
 1987   2009   2011   2009  2012   2013

radiation_therapy:
no  yes  NA's
40  7    1

histological_type:
diffuse large b-cell lymphoma (dlbcl) nos (any anatomic site nodal or extranodal)
                                                                                     41
                                                                 primary dlbcl of the cns
                                                                                                     3
                                                                 primary mediastinal (thymic) dlbcl
                                                                                                     4

race:
                                asian black or african american                white
                                18                                           1
                                1                                           29

ethnicity:
  hispanic or latino not hispanic or latino
                                12                                           36

Including an additional 607 columns

```

ESCA

Esophageal carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( ESCA )
ExperimentList class object of length 12:

```

```

[1] ESCA_CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
[2] ESCA_CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
[3] ESCA_CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
[4] ESCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
[5] ESCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 77 rows and 184 columns
[6] ESCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
[7] ESCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
[8] ESCA_Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
[9] ESCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 196 columns
[10] ESCA_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
[11] ESCA_RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns
[12] ESCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns

```

```

> rownames( ESCA )
CharacterList of length 12
[["ESCA_CNASeq-20160128"]] character(0)
[["ESCA_CNASNP-20160128"]] character(0)
[["ESCA_CNVSNP-20160128"]] character(0)
[["ESCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["ESCA_GISTIC_Peaks-20160128"]] chr1:23960869-31653987 ... chr22:1-18218209
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["ESCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ESCA_Mutation-20160128"]] character(0)
[["ESCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["ESCA_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
...
<2 more elements>

```

```

> colnames( ESCA )
CharacterList of length 12
[["ESCA_CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["ESCA_CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_Peaks-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_miRNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[["ESCA_Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["ESCA_RNASeq2GeneNorm-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["ESCA_RNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | ESCA_CNASeq-20160128 | 0.5 Mb |
| 2 | ESCA_CNASNP-20160128 | 5.5 Mb |
| 3 | ESCA_CNVSNP-20160128 | 1.7 Mb |
| 4 | ESCA_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | ESCA_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | ESCA_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

| | | |
|----|-------------------------------|--------|
| 7 | ESCA_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | ESCA_Mutation-20160128 | 45 Mb |
| 9 | ESCA_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | ESCA_RNASeqGene-20160128 | 1.7 Mb |
| 11 | ESCA_RPPAArray-20160128 | 0 Mb |
| 12 | ESCA_Methylation-20160128 | 75 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

108 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
77.000 77.000 0.962 0.677 1.353

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 27.00 | 54.00 | 61.00 | 62.46 | 72.00 | 90.00 |

vital_status:

| 0 | 1 |
|-----|----|
| 108 | 77 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 9.0 | 180.0 | 351.0 | 495.2 | 650.0 | 2532.0 | 108 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 4.0 | 336.5 | 402.5 | 570.1 | 696.8 | 3714.0 | 77 |

tumor_tissue_site:

| esophagus |
|-----------|
| 185 |

pathology_M_stage:

| m0 | m1 | m1a | mx | NA's |
|-----|----|-----|----|------|
| 136 | 4 | 5 | 18 | 22 |

gender:

| female | male |
|--------|------|
|--------|------|

27 158

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1998 | 2007 | 2011 | 2009 | 2012 | 2013 | 7 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 124 | 43 | 18 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 20.00 | 60.00 | 80.00 | 73.82 | 90.00 | 100.00 | 117 |

histological_type:

| | |
|-------------------------------|-----------------------------------|
| esophagus adenocarcinoma, nos | esophagus squamous cell carcinoma |
| 89 | 96 |

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 1.00 | 17.62 | 30.00 | 34.48 | 47.25 | 102.00 | 87 |

residual_tumor:

| r0 | r1 | r2 | rx | NA's |
|-----|----|----|----|------|
| 137 | 13 | 2 | 7 | 26 |

number_of_lymph_nodes:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 0.000 | 0.000 | 1.000 | 2.526 | 4.000 | 21.000 | 50 |

race:

| | | |
|-------|---------------------------|-------|
| asian | black or african american | white |
| 46 | 5 | 114 |
| NA's | | |
| 20 | | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 6 | 88 | 91 |

Including an additional 940 columns

GBM

*Glioblastoma multiforme***Description**

A document describing the TCGA cancer code

Details

```

> experiments( GBM )
ExperimentList class object of length 18:
 [1] GBM_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
 [2] GBM_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
 [3] GBM_CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
 [4] GBM_CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
 [5] GBM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [6] GBM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 68 rows and 577 columns
 [7] GBM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [8] GBM_miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
 [9] GBM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
[10] GBM_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
[11] GBM_mRNAArray_TX_g4502a_1-20160128: SummarizedExperiment with 17814 rows and 401 columns
[12] GBM_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 101 columns
[13] GBM_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
[14] GBM_Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
[15] GBM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
[16] GBM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns
[17] GBM_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
[18] GBM_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns

> rownames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["GBM_CNASNP-20160128"]] character(0)
[["GBM_CNVSNP-20160128"]] character(0)
[["GBM_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GBM_GISTIC_Peaks-20160128"]] chr1:3394251-6475685 ...
[["GBM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["GBM_miRNAArray-20160128"]] ebv-miR-BART1-3p ... kshv-miR-K12-9*
[["GBM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["GBM_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<8 more elements>

> colnames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] TCGA-02-0001-01C-01D-0185-02 ...
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-02-2466-01A-01D-0787-02 ...
[["GBM_CNASNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_CNVSNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_AllByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_Peaks-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_ThresholdedByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_miRNAArray-20160128"]] TCGA-02-0001-01C-01T-0179-07 ...
[["GBM_miRNASeqGene-20160128"]] character(0)
[["GBM_mRNAArray_huex-20160128"]] TCGA-02-0001-01C-01R-0178-03 ...
...
<8 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------|---------|
| 1 | GBM_CNACGH_CGH_hg_244a-20160128 | | 2.3 Mb |
| 2 | GBM_CNACGH_CGH_hg_415k_g4124a-20160128 | | 1.7 Mb |
| 3 | GBM_CNASNP-20160128 | | 16.4 Mb |
| 4 | GBM_CNVSNP-20160128 | | 4.2 Mb |
| 5 | GBM_GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 6 | GBM_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 7 | GBM_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 8 | GBM_miRNAArray-20160128 | | 0.1 Mb |
| 9 | GBM_miRNASeqGene-20160128 | | 0.1 Mb |
| 10 | GBM_mRNAArray_huex-20160128 | | 1.2 Mb |
| 11 | GBM_mRNAArray_TX_g4502a_1-20160128 | | 1.1 Mb |
| 12 | GBM_mRNAArray_TX_g4502a-20160128 | | 1.1 Mb |
| 13 | GBM_mRNAArray_TX_ht_hg_u133a-20160128 | | 0.8 Mb |
| 14 | GBM_Mutation-20160128 | | 31 Mb |
| 15 | GBM_RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 16 | GBM_RPPAArray-20160128 | | 0 Mb |
| 17 | GBM_Methylation_methyl27-20160128 | | 4.9 Mb |
| 18 | GBM_Methylation_methyl450-20160128 | | 75 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

109 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
490.000 490.000 1.047 0.981 1.156

Available sample meta-data:

years_to_birth:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
10.00 50.00 59.00 57.82 68.00 89.00 4

vital_status:
0 1 NA's
104 491 4

days_to_death:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
3.0 170.5 382.0 504.5 609.2 3881.0 109

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


```

0.0  156.2  261.0  479.4  628.0  2818.0  497

tumor_tissue_site:
brain NA's
 595   4

gender:
female  male  NA's
 230   365   4

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
 1989  2002   2006   2005  2009  2013   4

radiation_therapy:
no  yes NA's
78 489 32

karnofsky_performance_score:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
 0.00  70.00  80.00  77.04  80.00 100.00 157

histological_type:
  glioblastoma multiforme (gbm)          treated primary gbm
                                   31                               20
untreated primary (de novo) gbm          NA's
                                   544                               4

race:
                                   asian black or african american          white
                                   13                               51                               506
                                   NA's
                                   29

ethnicity:
  hispanic or latino not hispanic or latino          NA's
                                   13                               489                               97

```

Including an additional 4368 columns

HNSC

Head and Neck squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( HNSC )
ExperimentList class object of length 12:

```

```

[1] HNSC_CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
[2] HNSC_CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
[3] HNSC_CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
[4] HNSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
[5] HNSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 72 rows and 522 columns
[6] HNSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
[7] HNSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
[8] HNSC_Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
[9] HNSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
[10] HNSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
[11] HNSC_RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns
[12] HNSC_Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns

```

```

> rownames( HNSC )
CharacterList of length 12
[["HNSC_CNASeq-20160128"]] character(0)
[["HNSC_CNASNP-20160128"]] character(0)
[["HNSC_CNVSNP-20160128"]] character(0)
[["HNSC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["HNSC_GISTIC_Peaks-20160128"]] chr1:1-27864255 ... chr21:41298805-43485528
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["HNSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["HNSC_Mutation-20160128"]] character(0)
[["HNSC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["HNSC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( HNSC )
CharacterList of length 12
[["HNSC_CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["HNSC_CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_Peaks-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_miRNASeqGene-20160128"]] TCGA-4P-AA8J-01A-11R-A39B-13 ...
[["HNSC_Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["HNSC_RNASeq2GeneNorm-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["HNSC_RNASeqGene-20160128"]] TCGA-BA-4074-01A-01R-1436-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | HNSC_CNASeq-20160128 | 1 Mb |
| 2 | HNSC_CNASNP-20160128 | 13.6 Mb |
| 3 | HNSC_CNVSNP-20160128 | 3.3 Mb |
| 4 | HNSC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | HNSC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | HNSC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

```

7          HNSC_miRNASeqGene-20160128  0.1 Mb
8          HNSC_Mutation-20160128    68.9 Mb
9          HNSC_RNASeq2GeneNorm-20160128  1.3 Mb
10         HNSC_RNASeqGene-20160128    1.3 Mb
11         HNSC_RPPAArray-20160128      0 Mb
12         HNSC_Methylation-20160128   75.1 Mb

```

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```

305 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
223.00 223.00   1.18   1.06   1.35

```

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

```
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 19.00  53.00   61.00   60.91  69.00   89.00     1

```

```
vital_status:
  0  1
304 224

```

```
days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  2.0  260.0   430.0   740.0  814.5  6417.0   305

```

```
days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 11.0  529.5   851.0  1042.9  1404.0  5480.0   225

```

```
tumor_tissue_site:
head and neck
      528

```

```
pathology_M_stage:
  m0  m1  mx NA's
 191   1  65  271

```

```
gender:
female  male

```

142 386

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1992 | 2007 | 2010 | 2008 | 2011 | 2013 | 1 |

days_to_last_known_alive:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 98.0 | 483.0 | 848.5 | 1226.9 | 1647.5 | 3930.0 | 506 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 163 | 303 | 62 |

histological_type:

| | |
|---|-----|
| head & neck squamous cell carcinoma | 517 |
| head & neck squamous cell carcinoma basaloid type | 10 |
| head & neck squamous cell carcinoma, spindle cell variant | 1 |

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|---------|----------|----------|----------|----------|-----------|------|
| 0.01685 | 25.00000 | 40.00000 | 45.75496 | 60.00000 | 300.00000 | 230 |

year_of_tobacco_smoking_onset:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1936 | 1959 | 1968 | 1967 | 1975 | 2001 | 246 |

number_of_lymph_nodes:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 0.000 | 0.000 | 1.000 | 2.186 | 3.000 | 44.000 | 115 |

race:

| | | | |
|----------------------------------|----|-------|-----|
| american indian or alaska native | 2 | asian | 11 |
| black or african american | 48 | white | 452 |
| NA's | 15 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|----|
| hispanic or latino | 26 | not hispanic or latino | 465 | NA's | 37 |
|--------------------|----|------------------------|-----|------|----|

Including an additional 1426 columns

Description

A document describing the TCGA cancer code

Details

```
> experiments( KICH )
ExperimentList class object of length 10:
 [1] KICH_CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns
 [2] KICH_CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
 [3] KICH_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [4] KICH_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 2 rows and 66 columns
 [5] KICH_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [6] KICH_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
 [7] KICH_Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
 [8] KICH_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [9] KICH_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
 [10] KICH_Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns

> rownames( KICH )
CharacterList of length 10
[["KICH_CNASNP-20160128"]] character(0)
[["KICH_CNVSNP-20160128"]] character(0)
[["KICH_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["KICH_GISTIC_Peaks-20160128"]] chr8:116272008-117149163 chr15:1-66482794
[["KICH_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["KICH_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KICH_Mutation-20160128"]] character(0)
[["KICH_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KICH_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["KICH_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( KICH )
CharacterList of length 10
[["KICH_CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_Peaks-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["KICH_Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["KICH_RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...
[["KICH_Methylation-20160128"]] TCGA-KL-8323-01A-21D-2312-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | KICH_CNASNP-20160128 | 1.6 Mb |
| 2 | KICH_CNVSNP-20160128 | 0.3 Mb |
| 3 | KICH_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | KICH_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | KICH_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

| | | |
|----|-------------------------------|--------|
| 6 | KICH_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | KICH_Mutation-20160128 | 2.6 Mb |
| 8 | KICH_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | KICH_RPPAArray-20160128 | 0 Mb |
| 10 | KICH_Methylation-20160128 | 75 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

57 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
9.00 9.00 2.34 1.99 NA

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 17.00 | 42.00 | 50.00 | 51.52 | 61.75 | 86.00 |

vital_status:

| | |
|----|----|
| 0 | 1 |
| 56 | 10 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 325 | 725 | 855 | 1001 | 1158 | 2172 | 57 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 30 | 1366 | 2713 | 2320 | 3138 | 4676 | 10 |

tumor_tissue_site:

| |
|--------|
| kidney |
| 66 |

pathologic_stage:

| stage i | stage ii | stage iii | stage iv |
|---------|----------|-----------|----------|
| 21 | 25 | 14 | 6 |

pathology_N_stage:

| | | | |
|----|----|----|----|
| n0 | n1 | n2 | nx |
| 40 | 3 | 2 | 21 |

pathology_M_stage:

```

m0  m1  mx NA's
34  2   9  21

gender:
female  male
  27    39

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.
  2000  2004   2005  2005  2007  2011

radiation_therapy:
no
66

karnofsky_performance_score:
  90 100 NA's
  3  10  53

histological_type:
kidney chromophobe
  66

number_pack_years_smoked:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
  1.00  8.00  24.00  25.09  31.00  75.00  55

year_of_tobacco_smoking_onset:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.  NA's
  1949  1964   1974   1974   1984   1997   58

race:
                asian black or african american                white
                2                                4                    58
                NA's
                2

ethnicity:
  hispanic or latino not hispanic or latino                NA's
                4                                32                    30

Including an additional 718 columns

```

KIRC

Kidney renal clear cell carcinoma

Description

A document describing the TCGA cancer code

| | | |
|----|--|---------|
| 3 | KIRC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | KIRC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | KIRC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | KIRC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | KIRC_mRNAArray-20160128 | 1.1 Mb |
| 8 | KIRC_Mutation-20160128 | 8.2 Mb |
| 9 | KIRC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | KIRC_RNASeqGene-20160128 | 1.3 Mb |
| 11 | KIRC_RPPAArray-20160128 | 0.1 Mb |
| 12 | KIRC_Methylation_methyl27-20160128 | 4.9 Mb |
| 13 | KIRC_Methylation_methyl450-20160128 | 75.1 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

360 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
177.00 177.00 2.24 1.77 2.61

Available sample meta-data:

years_to_birth:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
26.00 52.00 61.00 60.57 70.00 90.00 1

vital_status:
0 1
360 177

days_to_death:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
2.0 333.0 819.0 961.2 1432.0 3615.0 360

days_to_last_followup:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.0 710.5 1454.5 1536.9 2172.0 4537.0 177

tumor_tissue_site:
kidney
537

pathologic_stage:
stage i stage ii stage iii stage iv NA's
269 57 125 84 2

pathology_N_stage:

n0 n1 nx
240 17 280

pathology_M_stage:

m0 m1 mx NA's
426 79 30 2

gender:

female male
191 346

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1998 | 2004 | 2006 | 2006 | 2007 | 2013 |

days_to_last_known_alive:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 0 | 191 | 1172 | 1117 | 1887 | 2799 | 510 |

radiation_therapy:

no yes NA's
142 2 393

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.00 | 90.00 | 90.00 | 85.56 | 100.00 | 100.00 | 483 |

histological_type:

kidney clear cell renal carcinoma
537

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|-------|------|
| 7.00 | 14.00 | 30.00 | 28.33 | 40.00 | 65.00 | 516 |

year_of_tobacco_smoking_onset:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1946 | 1966 | 1978 | 1979 | 1996 | 2001 | 525 |

race:

| | |
|---------------------------------|-------|
| asian black or african american | white |
| 8 | 466 |
| NA's | |
| 7 | |

ethnicity:

| | |
|---|------|
| hispanic or latino not hispanic or latino | NA's |
| 26 | 152 |
| 359 | |

Including an additional 2250 columns

KIRP

*Kidney renal papillary cell carcinoma***Description**

A document describing the TCGA cancer code

Details

```
> experiments( KIRP )
ExperimentList class object of length 13:
 [1] KIRP_CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] KIRP_CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns
 [3] KIRP_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [4] KIRP_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 28 rows and 288 columns
 [5] KIRP_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [6] KIRP_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [7] KIRP_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
 [8] KIRP_Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
 [9] KIRP_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 323 columns
 [10] KIRP_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
 [11] KIRP_RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns
 [12] KIRP_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
 [13] KIRP_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns

> rownames( KIRP )
CharacterList of length 13
[["KIRP_CNASNP-20160128"]] character(0)
[["KIRP_CNVSNP-20160128"]] character(0)
[["KIRP_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["KIRP_GISTIC_Peaks-20160128"]] chr1:1-29472434 ... chr22:29969457-30128393
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["KIRP_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KIRP_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRP_Mutation-20160128"]] character(0)
[["KIRP_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KIRP_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

> colnames( KIRP )
CharacterList of length 13
[["KIRP_CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_Peaks-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_miRNASeqGene-20160128"]] TCGA-2K-A9WE-01A-11R-A38N-13 ...
[["KIRP_mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["KIRP_Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["KIRP_RNASeq2GeneNorm-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
```

```

[["KIRP_RNASeqGene-20160128"]] TCGA-AL-3466-01A-02R-1351-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | KIRP_CNASNP-20160128 | 8.2 Mb |
| 2 | | KIRP_CNVSNP-20160128 | 1.4 Mb |
| 3 | | KIRP_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | | KIRP_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | | KIRP_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | | KIRP_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | | KIRP_mRNAArray-20160128 | 1.1 Mb |
| 8 | | KIRP_Mutation-20160128 | 10.6 Mb |
| 9 | | KIRP_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | | KIRP_RNASeqGene-20160128 | 1.3 Mb |
| 11 | | KIRP_RPPAArray-20160128 | 0 Mb |
| 12 | | KIRP_Methylation_methyl27-20160128 | 4.9 Mb |
| 13 | | KIRP_Methylation_methyl450-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

247 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
44.00  44.00   1.76   1.35   3.60

```

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|-------|------|
| 28.00 | 53.25 | 61.50 | 61.52 | 71.00 | 88.00 | 5 |

vital_status:

| 0 | 1 |
|-----|----|
| 247 | 44 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 122.0 | 341.2 | 641.0 | 989.8 | 1498.5 | 2941.0 | 247 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 0.0 | 438.2 | 774.5 | 1070.2 | 1513.0 | 5925.0 | 45 |

tumor_tissue_site:

kidney
291

pathologic_stage:

| stage i | stage ii | stage iii | stage iv | NA's |
|---------|----------|-----------|----------|------|
| 173 | 21 | 52 | 15 | 30 |

pathology_N_stage:

| n0 | n1 | n2 | nx | NA's |
|----|----|----|-----|------|
| 50 | 24 | 4 | 212 | 1 |

pathology_M_stage:

| m0 | m1 | mx | NA's |
|----|----|-----|------|
| 95 | 9 | 172 | 15 |

gender:

| female | male |
|--------|------|
| 77 | 214 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1996 | 2008 | 2011 | 2010 | 2012 | 2013 | 25 |

days_to_last_known_alive:

| NA's |
|-------|
| 34 |
| 1 290 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 209 | 1 | 81 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.00 | 90.00 | 90.00 | 87.66 | 100.00 | 100.00 | 214 |

histological_type:

kidney papillary renal cell carcinoma
291

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 3.00 | 15.00 | 24.50 | 31.73 | 41.25 | 185.00 | 215 |

year_of_tobacco_smoking_onset:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1941 | 1961 | 1970 | 1972 | 1984 | 2010 | 235 |

race:

american indian or alaska native

asian

| | | |
|---|------|-------|
| | 2 | 6 |
| black or african american | | white |
| | 61 | 207 |
| | NA's | |
| | 15 | |
| ethnicity: | | |
| hispanic or latino not hispanic or latino | | NA's |
| | 12 | 243 |
| | | 36 |

Including an additional 1686 columns

LAML

Acute Myeloid Leukemia

Description

A document describing the TCGA cancer code

Details

```
> experiments( LAML )
ExperimentList class object of length 10:
 [1] LAML_CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
 [2] LAML_CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
 [3] LAML_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [4] LAML_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 191 columns
 [5] LAML_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [6] LAML_Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns
 [7] LAML_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [8] LAML_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
 [9] LAML_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
 [10] LAML_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns

> rownames( LAML )
CharacterList of length 10
[["LAML_CNASNP-20160128"]] character(0)
[["LAML_CNVSNP-20160128"]] character(0)
[["LAML_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LAML_GISTIC_Peaks-20160128"]] chr1:47516423-47533836 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LAML_Mutation-20160128"]] character(0)
[["LAML_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["LAML_RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ... XGPY2 XKRY2 ZFY
[["LAML_Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["LAML_Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873

> colnames( LAML )
CharacterList of length 10
[["LAML_CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["LAML_CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
```

```

[["LAML_GISTIC_AllByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_Peaks-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["LAML_RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["LAML_Methylation_methyl450-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LAML_CNASNP-20160128 | 23.5 Mb |
| 2 | LAML_CNVSNP-20160128 | 0.9 Mb |
| 3 | LAML_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | LAML_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | LAML_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | LAML_Mutation-20160128 | 2.8 Mb |
| 7 | LAML_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 8 | LAML_RNASeqGene-20160128 | 1.3 Mb |
| 9 | LAML_Methylation_methyl27-20160128 | 4.9 Mb |
| 10 | LAML_Methylation_methyl450-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

      80 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
120.000 120.000  0.748  0.586  0.918

```

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 18.00 | 44.75 | 57.00 | 55.02 | 67.00 | 88.00 |

vital_status:

| | |
|----|-----|
| 0 | 1 |
| 67 | 133 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 91.5 | 273.0 | 355.7 | 489.0 | 1706.0 | 80 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 296.2 | 699.0 | 913.5 | 1506.8 | 2861.0 | 132 |

tumor_tissue_site:

| | |
|-------------|------|
| bone marrow | NA's |
| 199 | 1 |

gender:

| | |
|--------|------|
| female | male |
| 91 | 109 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 2001 | 2004 | 2006 | 2006 | 2008 | 2010 |

race:

| | | |
|-------|---------------------------|-------|
| asian | black or african american | white |
| 2 | 15 | 181 |
| NA's | | |
| 2 | | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 3 | 194 | 3 |

Including an additional 478 columns

LGG

*Brain Lower Grade Glioma***Description**

A document describing the TCGA cancer code

Details

```
> experiments( LGG )
ExperimentList class object of length 12:
 [1] LGG_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] LGG_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
 [3] LGG_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
 [4] LGG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [5] LGG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
 [6] LGG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [7] LGG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
 [8] LGG_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
 [9] LGG_Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[10] LGG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
[11] LGG_RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns
[12] LGG_Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
```



```
> rownames( LGG )
CharacterList of length 12
[["LGG_CNASeq-20160128"]] character(0)
[["LGG_CNASNP-20160128"]] character(0)
[["LGG_CNVSNP-20160128"]] character(0)
[["LGG_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["LGG_GISTIC_Peaks-20160128"]] chr1:3814904-5625565 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LGG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LGG_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LGG_Mutation-20160128"]] character(0)
[["LGG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<2 more elements>
```

```
> colnames( LGG )
CharacterList of length 12
[["LGG_CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["LGG_CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_Peaks-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_miRNASeqGene-20160128"]] TCGA-CS-4938-01B-11R-1895-13 ...
[["LGG_mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["LGG_Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["LGG_RNASeq2GeneNorm-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<2 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | LGG_CNASeq-20160128 | 0.2 Mb |
| 2 | LGG_CNASNP-20160128 | 11.3 Mb |
| 3 | LGG_CNVSNP-20160128 | 2.4 Mb |
| 4 | LGG_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LGG_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LGG_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LGG_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LGG_mRNAArray-20160128 | 1.1 Mb |
| 9 | LGG_Mutation-20160128 | 4.2 Mb |
| 10 | LGG_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | LGG_RPPAArray-20160128 | 0.1 Mb |
| 12 | LGG_Methylation-20160128 | 75.1 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

391 observations deleted due to missingness
 n events median 0.95LCL 0.95UCL
 125.00 125.00 2.23 1.87 2.83

 Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|-------|------|
| 14.00 | 32.00 | 41.00 | 42.93 | 53.00 | 86.00 | 2 |

vital_status:

| 0 | 1 | NA's |
|-----|-----|------|
| 389 | 126 | 1 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 7 | 438 | 814 | 1219 | 1547 | 5166 | 391 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| -1.0 | 384.0 | 629.0 | 880.1 | 1147.0 | 6423.0 | 127 |

tumor_tissue_site:

| central nervous system | NA's |
|------------------------|------|
| 515 | 1 |

gender:

| female | male | NA's |
|--------|------|------|
| 230 | 285 | 1 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1992 | 2008 | 2011 | 2009 | 2012 | 2013 | 1 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 186 | 296 | 34 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 40.00 | 80.00 | 90.00 | 86.64 | 100.00 | 100.00 | 209 |

histological_type:

| astrocytoma | oligoastrocytoma | oligodendroglioma | NA's |
|-------------|------------------|-------------------|------|
| 194 | 130 | 191 | 1 |

race:

| american indian or alaska native | asian |
|----------------------------------|-------|
| | |

| | | |
|---|------|-------|
| | 1 | 8 |
| black or african american | | white |
| | 21 | 475 |
| | NA's | |
| | 11 | |
| ethnicity: | | |
| hispanic or latino not hispanic or latino | | NA's |
| | 32 | 449 |
| | | 35 |

Including an additional 1764 columns

LIHC *Liver hepatocellular carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LIHC )
ExperimentList class object of length 11:
 [1] LIHC_CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] LIHC_CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] LIHC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] LIHC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 59 rows and 370 columns
 [5] LIHC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [6] LIHC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] LIHC_Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] LIHC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
 [9] LIHC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
 [10] LIHC_RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns
 [11] LIHC_Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns

> rownames( LIHC )
CharacterList of length 11
[["LIHC_CNASNP-20160128"]] character(0)
[["LIHC_CNVSNP-20160128"]] character(0)
[["LIHC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LIHC_GISTIC_Peaks-20160128"]] chr1:1-6847369 ... chr22:44205320-51304566
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LIHC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LIHC_Mutation-20160128"]] character(0)
[["LIHC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pt359_S363
...
<1 more element>

> colnames( LIHC )
```

```

CharacterList of length 11
[["LIHC_CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_Peaks-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
[["LIHC_Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...
[["LIHC_RNASeq2GeneNorm-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["LIHC_RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
[["LIHC_RPPAArray-20160128"]] TCGA-BC-4072-01B-21-A40L-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LIHC_CNASNP-20160128 | 9.9 Mb |
| 2 | LIHC_CNVSNP-20160128 | 2.7 Mb |
| 3 | LIHC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | LIHC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | LIHC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | LIHC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | LIHC_Mutation-20160128 | 16.8 Mb |
| 8 | LIHC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | LIHC_RNASeqGene-20160128 | 1.3 Mb |
| 10 | LIHC_RPPAArray-20160128 | 0 Mb |
| 11 | LIHC_Methylation-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

245 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
132.000 132.000  1.144  0.956  1.633

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 16.00  51.00   61.00   59.27  69.00   87.00    4

vital_status:
 0  1
245 132

```

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 9.0 | 194.8 | 417.5 | 672.1 | 837.0 | 3258.0 | 245 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 395.8 | 649.5 | 885.8 | 1222.0 | 3675.0 | 133 |

tumor_tissue_site:
liver
377

pathology_N_stage:

| n0 | n1 | nx | NA's |
|-----|----|-----|------|
| 257 | 4 | 115 | 1 |

pathology_M_stage:

| m0 | m1 | mx |
|-----|----|-----|
| 272 | 4 | 101 |

gender:
female male
122 255

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1995 | 2008 | 2011 | 2010 | 2012 | 2013 | 3 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 345 | 9 | 23 |

histological_type:

| | | | |
|----------------------------------|---|--------------------------|-----|
| fibrolamellar carcinoma | 3 | hepatocellular carcinoma | 367 |
| hepatocholangiocarcinoma (mixed) | 7 | | |

residual_tumor:

| r0 | r1 | r2 | rx | NA's |
|-----|----|----|----|------|
| 330 | 17 | 1 | 22 | 7 |

race:

| | | | |
|----------------------------------|----|-------|-----|
| american indian or alaska native | 2 | asian | 161 |
| black or african american | 17 | white | 187 |
| NA's | 10 | | |


```

[["LUAD_CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_Peaks-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_miRNASeqGene-20160128"]] TCGA-05-4384-01A-01T-1754-13 ...
[["LUAD_mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
[["LUAD_RNASeq2GeneNorm-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|---------|
| 1 | LUAD_CNASeq-20160128 | 10.8 Mb |
| 2 | LUAD_CNASNP-20160128 | 13.7 Mb |
| 3 | LUAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | LUAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LUAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LUAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LUAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LUAD_mRNAArray-20160128 | 1.1 Mb |
| 9 | LUAD_Mutation-20160128 | 92.9 Mb |
| 10 | LUAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | LUAD_RNASeqGene-20160128 | 1.3 Mb |
| 12 | LUAD_RPPAArray-20160128 | 0.1 Mb |
| 13 | LUAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | LUAD_Methylation_methyl450-20160128 | 75.1 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

336 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
184.00 184.00   1.70   1.37   2.00

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 33.00  59.00   66.00   65.22  72.00   88.00    31

```

```

vital_status:
 0  1

```

332 188

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 297.8 | 619.0 | 791.4 | 1120.0 | 4961.0 | 336 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 459.5 | 670.0 | 968.7 | 1139.0 | 7248.0 | 193 |

tumor_tissue_site:

lung

520

gender:

female male

279 241

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1991 | 2007 | 2010 | 2008 | 2011 | 2013 | 19 |

days_to_last_known_alive:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 9.0 | 96.5 | 141.0 | 327.6 | 386.0 | 1178.0 | 513 |

radiation_therapy:

no yes NA's

413 61 46

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.00 | 80.00 | 90.00 | 78.55 | 100.00 | 100.00 | 382 |

number_pack_years_smoked:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.15 | 20.50 | 40.00 | 41.79 | 50.00 | 154.00 | 165 |

year_of_tobacco_smoking_onset:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1930 | 1956 | 1965 | 1965 | 1972 | 1999 | 241 |

residual_tumor:

r0 r1 r2 rx NA's

347 13 4 26 130

race:

| | | | |
|---|----|-------|-------------|
| american indian or alaska native | 1 | asian | 8 |
| black or african american | 53 | white | 392 |
| NA's | 66 | | |
| ethnicity: | | | |
| hispanic or latino not hispanic or latino | 7 | 388 | NA's 125 |

Including an additional 2607 columns

LUSC *Lung squamous cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LUSC )
ExperimentList class object of length 16:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [8] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [9] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [10] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [11] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [12] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [13] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [14] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
 [15] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [16] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns

> rownames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LUSC_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:45736500-51304566
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LUSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
```

```

[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
...
<6 more elements>

```

```

> colnames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
...
<6 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LUSC_CNACGH-20160128 | 2.5 Mb |
| 2 | LUSC_CNASNP-20160128 | 14.8 Mb |
| 3 | LUSC_CNVSNP-20160128 | 3.9 Mb |
| 4 | LUSC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LUSC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LUSC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LUSC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LUSC_mRNAArray_huex-20160128 | 1.2 Mb |
| 9 | LUSC_mRNAArray_TX_g4502a-20160128 | 1.1 Mb |
| 10 | LUSC_mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 11 | LUSC_Mutation-20160128 | 81 Mb |
| 12 | LUSC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 13 | LUSC_RNASeqGene-20160128 | 1.3 Mb |
| 14 | LUSC_RPPAArray-20160128 | 0 Mb |
| 15 | LUSC_Methylation_methyl27-20160128 | 4.9 Mb |
| 16 | LUSC_Methylation_methyl450-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

289 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
215.00 215.00 1.51 1.25 1.88

```

 Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|-------|------|
| 39.00 | 62.00 | 68.00 | 67.26 | 73.00 | 90.00 | 10 |

vital_status:

| 0 | 1 |
|-----|-----|
| 284 | 220 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 1.0 | 280.0 | 550.0 | 872.3 | 1110.5 | 5287.0 | 289 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 0 | 394 | 757 | 1049 | 1374 | 4765 | 221 |

tumor_tissue_site:

| |
|------|
| lung |
| 504 |

pathology_N_stage:

| n0 | n1 | n2 | n3 | nx |
|-----|-----|----|----|----|
| 320 | 133 | 40 | 5 | 6 |

gender:

| female | male |
|--------|------|
| 131 | 373 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1992 | 2005 | 2009 | 2008 | 2011 | 2013 | 25 |

days_to_last_known_alive:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 4.0 | 298.8 | 706.0 | 904.8 | 1051.8 | 3724.0 | 436 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 387 | 53 | 64 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|-------|------|
| 0.0 | 0.0 | 80.0 | 60.3 | 90.0 | 100.0 | 338 |

histological_type:

```

lung basaloid squamous cell carcinoma
15
lung papillary squamous cell carcinoma
6
lung small cell squamous cell carcinoma
1
lung squamous cell carcinoma- not otherwise specified (nos)
482

```

```

number_pack_years_smoked:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  1.00  31.12  50.00  52.91  64.50  240.00    77

```

```

year_of_tobacco_smoking_onset:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  1933  1952  1960  1960  1968  1997    183

```

```

residual_tumor:
  r0  r1  r2  rx NA's
  401  12  4  23  64

```

```

race:
      asian black or african american      white
      9          31          351
      NA's
      113

```

```

ethnicity:
  hispanic or latino not hispanic or latino      NA's
      8          319          177

```

Including an additional 2238 columns

MESO

Mesothelioma

Description

A document describing the TCGA cancer code

Details

```

> experiments( MESO )
ExperimentList class object of length 9:
 [1] MESO_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
 [2] MESO_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
 [3] MESO_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [4] MESO_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
 [5] MESO_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [6] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
 [7] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns

```

```
[8] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[9] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
```

```
> rownames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["MESO_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:29969457-30128393
[["MESO_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | MESO_CNASNP-20160128 | 2.5 Mb |
| 2 | MESO_CNVSNP-20160128 | 0.6 Mb |
| 3 | MESO_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | MESO_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | MESO_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | MESO_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | MESO_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 8 | MESO_RPPAArray-20160128 | 0 Mb |
| 9 | MESO_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
14 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
73.00 73.00 1.25 1.11 1.67
```

 Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 28.00 | 57.00 | 64.00 | 62.99 | 69.00 | 81.00 |

vital_status:

| | |
|----|----|
| 0 | 1 |
| 13 | 74 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 20.0 | 253.0 | 457.0 | 584.1 | 789.0 | 2790.0 | 14 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| -8 | 499 | 1168 | 1091 | 1490 | 2359 | 74 |

tumor_tissue_site:

| |
|--------|
| pleura |
| 87 |

pathology_N_stage:

| | | | | |
|----|----|----|----|----|
| n0 | n1 | n2 | n3 | nx |
| 44 | 10 | 26 | 3 | 4 |

pathology_M_stage:

| | | |
|----|----|----|
| m0 | m1 | mx |
| 57 | 3 | 27 |

gender:

| | |
|--------|------|
| female | male |
| 16 | 71 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1999 | 2008 | 2010 | 2009 | 2012 | 2013 |

radiation_therapy:

| | | |
|----|-----|------|
| no | yes | NA's |
| 62 | 24 | 1 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.00 | 80.00 | 90.00 | 77.65 | 90.00 | 100.00 | 70 |

histological_type:

| | | |
|-----------------------|--------------------------------|-------|
| biphasic mesothelioma | diffuse malignant mesothelioma | - nos |
|-----------------------|--------------------------------|-------|

| | | | |
|--------------------------|----|--------------------------|---|
| | 23 | | 5 |
| epithelioid mesothelioma | | sarcomatoid mesothelioma | |
| | 57 | | 2 |

residual_tumor:

| | | | | |
|----|----|----|----|------|
| r0 | r1 | r2 | rx | NA's |
| 17 | 3 | 15 | 11 | 41 |

race:

| | | | |
|--|-------|---------------------------|-------|
| | asian | black or african american | white |
| | 1 | 1 | 85 |

ethnicity:

| | |
|------------------------|------|
| not hispanic or latino | NA's |
| 73 | 14 |

Including an additional 636 columns

OV

Ovarian serous cystadenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( OV )
ExperimentList class object of length 19:
 [1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
 [7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [9] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [10] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [11] OV_mRNAArray_TX_g4502a_1-20160128: SummarizedExperiment with 17814 rows and 546 columns
 [12] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 31 columns
 [13] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [14] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [15] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [16] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [17] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
 [18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

> rownames( OV )
CharacterList of length 19
```

```

[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["OV_GISTIC_Peaks-20160128"]] chr1:26963410-27570286 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
...
<9 more elements>

```

```

> colnames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
...
<9 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | OV_CNACGH_CGH_hg_244a-20160128 | 3.6 Mb |
| 2 | OV_CNACGH_CGH_hg_415k_g4124a-20160128 | 6.8 Mb |
| 3 | OV_CNASNP-20160128 | 24.6 Mb |
| 4 | OV_CNVSNP-20160128 | 7.3 Mb |
| 5 | OV_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 6 | OV_GISTIC_Peaks-20160128 | 0.1 Mb |
| 7 | OV_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 8 | OV_miRNAArray-20160128 | 0.1 Mb |
| 9 | OV_miRNASeqGene-20160128 | 0.1 Mb |
| 10 | OV_mRNAArray_huex-20160128 | 1.2 Mb |
| 11 | OV_mRNAArray_TX_g4502a_1-20160128 | 1.2 Mb |
| 12 | OV_mRNAArray_TX_g4502a-20160128 | 1.1 Mb |
| 13 | OV_mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 14 | OV_Mutation-20160128 | 10.3 Mb |
| 15 | OV_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 16 | OV_RNASeqGene-20160128 | 1.3 Mb |
| 17 | OV_RPPAArray-20160128 | 0.1 Mb |
| 18 | OV_Methylation_methyl27-20160128 | 4.9 Mb |
| 19 | OV_Methylation_methyl450-20160128 | 75 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

247 observations deleted due to missingness

| n | events | median | 0.95LCL | 0.95UCL |
|--------|--------|--------|---------|---------|
| 343.00 | 343.00 | 2.94 | 2.76 | 3.17 |

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|-------|------|
| 26.00 | 51.00 | 59.00 | 59.78 | 69.00 | 89.00 | 21 |

vital_status:

| 0 | 1 |
|-----|-----|
| 246 | 344 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 8.0 | 567.5 | 1073.0 | 1147.4 | 1557.0 | 4624.0 | 247 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 16 | 266 | 842 | 1216 | 1931 | 5481 | 358 |

tumor_tissue_site:

| omentum | ovary | peritoneum | ovary | NA's |
|---------|-------|------------|-------|------|
| 3 | 575 | | 2 | 10 |

gender:

| female | NA's |
|--------|------|
| 580 | 10 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 1992 | 2001 | 2004 | 2004 | 2007 | 2013 | 10 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 556 | 5 | 29 |

karnofsky_performance_score:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 40.00 | 60.00 | 80.00 | 75.83 | 80.00 | 100.00 | 506 |

histological_type:

```
serous cystadenocarcinoma          NA's
                        580          10
```

```
residual_tumor:
  r0  r1  r2  rx NA's
  15  31  5   3  536
```

```
ethnicity:
  hispanic or latino not hispanic or latino  NA's
                        11                    338          241
```

Including an additional 2869 columns

| | |
|------|----------------------------------|
| PAAD | <i>Pancreatic adenocarcinoma</i> |
|------|----------------------------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( PAAD )
ExperimentList class object of length 10:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [10] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

> rownames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PAAD_GISTIC_Peaks-20160128"]] chr1:26795113-27650365 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PAAD_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
```

```

[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
[["PAAD_Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...
    
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PAAD_CNASNP-20160128 | 5.6 Mb |
| 2 | PAAD_CNVSNP-20160128 | 1 Mb |
| 3 | PAAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | PAAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | PAAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | PAAD_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | PAAD_Mutation-20160128 | 111 Mb |
| 8 | PAAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | PAAD_RPPAArray-20160128 | 0 Mb |
| 10 | PAAD_Methylation-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
    
```

```

      85 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
100.000 100.000  1.079  0.967  1.315
    
```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 35.00  57.00   65.00   64.86  73.00   88.00
    
```

```

vital_status:
  0  1
 85 100
    
```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 12.0  228.5   394.0   459.5  596.5  2182.0     85
    
```

days_to_last_followup:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.0 338.0 517.0 692.4 951.0 2741.0 100

tumor_tissue_site:
 pancreas
 185

pathology_N_stage:
 n0 n1 n1b nx NA's
 50 126 4 4 1

pathology_M_stage:
 m0 m1 mx
 85 5 95

gender:
 female male
 83 102

date_of_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 2001 2010 2012 2011 2012 2013 1

radiation_therapy:
 no yes NA's
 125 45 15

histological_type:
 pancreas-adenocarcinoma ductal type
 154
 pancreas-adenocarcinoma-other subtype
 25
 pancreas-colloid (mucinous non-cystic) carcinoma
 4
 pancreas-undifferentiated carcinoma
 1
 NA's
 1

number_pack_years_smoked:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.30 15.00 25.00 26.84 40.00 75.00 128

year_of_tobacco_smoking_onset:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 1948 1960 1971 1971 1982 1993 138

residual_tumor:
 r0 r1 r2 rx NA's

```
111 53 5 4 12
```

```
number_of_lymph_nodes:
```

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.000  0.000  2.000  2.989  4.000 16.000    4
```

```
race:
```

```
      asian black or african american      white
      11              7              162
      NA's
      5
```

```
ethnicity:
```

```
  hispanic or latino not hispanic or latino      NA's
      5              137              43
```

```
Including an additional 960 columns
```

```
PCPG
```

```
Pheochromocytoma and Paraganglioma
```

Description

A document describing the TCGA cancer code

Details

```
> experiments( PCPG )
ExperimentList class object of length 10:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
[10] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns

> rownames( PCPG )
CharacterList of length 10
[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PCPG_GISTIC_Peaks-20160128"]] chr1:117751737-118152240 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pt359_S363
```

```
[[ "PCPG_Methylation-20160128" ]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( PCPG )
```

```
CharacterList of length 10
```

```
[[ "PCPG_CNASNP-20160128" ]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[[ "PCPG_CNVSNP-20160128" ]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[[ "PCPG_GISTIC_AllByGene-20160128" ]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[[ "PCPG_GISTIC_Peaks-20160128" ]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[[ "PCPG_GISTIC_ThresholdedByGene-20160128" ]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[[ "PCPG_miRNASeqGene-20160128" ]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[[ "PCPG_Mutation-20160128" ]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[[ "PCPG_RNASeq2GeneNorm-20160128" ]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[[ "PCPG_RPPAArray-20160128" ]] TCGA-P7-A5NX-01A-21-A43B-20 ...
[[ "PCPG_Methylation-20160128" ]] TCGA-P7-A5NX-01A-11D-A35E-05 ...
```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|----|--|---------------|
| 1 | PCPG_CNASNP-20160128 | 8.1 Mb |
| 2 | PCPG_CNVSNP-20160128 | 0.9 Mb |
| 3 | PCPG_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | PCPG_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | PCPG_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | PCPG_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | PCPG_Mutation-20160128 | 8.4 Mb |
| 8 | PCPG_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | PCPG_RPPAArray-20160128 | 0 Mb |
| 10 | PCPG_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
173 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
6.00  6.00  1.24  0.26    NA
```

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

```
years_to_birth:
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 19.00 | 35.00 | 46.00 | 47.33 | 58.50 | 83.00 |

```
vital_status:
```

| 0 | 1 |
|-----|---|
| 173 | 6 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 88.0 | 148.5 | 452.5 | 901.0 | 715.2 | 3563.0 | 173 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 2 | 352 | 766 | 1071 | 1301 | 9634 | 6 |

tumor_tissue_site:

| adrenal gland | extra-adrenal site |
|---------------|--------------------|
| 147 | 32 |

gender:

| female | male |
|--------|------|
| 101 | 78 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1988 | 2009 | 2011 | 2010 | 2012 | 2013 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 172 | 5 | 2 |

karnofsky_performance_score:

| 70 | 80 | 90 | 100 | NA's |
|----|----|----|-----|------|
| 1 | 2 | 13 | 46 | 117 |

histological_type:

| paraganglioma | paraganglioma; extra-adrenal pheochromocytoma | pheochromocytoma |
|---------------|---|------------------|
| 18 | 13 | 148 |

number_of_lymph_nodes:

| 0 | 1 | 2 | 13 | NA's |
|----|---|---|----|------|
| 16 | 3 | 1 | 1 | 158 |

race:

| american indian or alaska native | black or african american | NA's | asian | white |
|----------------------------------|---------------------------|------|-------|-------|
| 1 | 20 | 4 | 6 | 148 |

ethnicity:

| hispanic or latino | not hispanic or latino | NA's |
|--------------------|------------------------|------|
| 5 | 138 | 36 |

Including an additional 894 columns

PRAD

Prostate adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( PRAD )
ExperimentList class object of length 11:
 [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
 [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [7] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
 [8] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [9] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
[10] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
[11] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns

> rownames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PRAD_GISTIC_Peaks-20160128"]] chr1:63901623-66226788 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PRAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
```



```

[["PRAD_RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PRAD_CNASeq-20160128 | 0.7 Mb |
| 2 | PRAD_CNASNP-20160128 | 15.6 Mb |
| 3 | PRAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | PRAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | PRAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | PRAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | PRAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | PRAD_Mutation-20160128 | 21.5 Mb |
| 9 | PRAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | PRAD_RPPAArray-20160128 | 0 Mb |
| 11 | PRAD_Methylation-20160128 | 75.1 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

488 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
10.00  10.00   3.02   1.99     NA

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  41.00  56.00   61.00   61.02  66.00   78.00    11

```

```

vital_status:
  0  1
488 10

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  146.0  743.8  1102.0  1579.0  2315.5  3502.0   488

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  23.0  523.5  926.0  1076.5  1458.0  5024.0   10

```

tumor_tissue_site:
 prostate
 498

pathology_N_stage:
 n0 n1 NA's
 346 79 73

gender:
 male
 498

date_of_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 2000 2009 2011 2010 2012 2013 31

radiation_therapy:
 no yes NA's
 395 59 44

histological_type:
 prostate adenocarcinoma acinar type prostate adenocarcinoma, other subtype
 483 15

residual_tumor:
 r0 r1 r2 rx NA's
 316 147 5 15 15

number_of_lymph_nodes:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.0000 0.0000 0.0000 0.4447 0.0000 15.0000 91

gleason_score:
 6 7 8 9 10
 45 248 64 137 4

psa_value:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.000 0.030 0.100 1.742 0.110 323.000 57

days_to_psa:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 -164.0 191.0 512.0 685.6 926.0 3447.0 53

race:
 asian black or african american white
 2 7 147
 NA's
 342

ethnicity:

| | |
|------------------------|------|
| not hispanic or latino | NA's |
| 152 | 346 |

Including an additional 1126 columns

| | |
|------|------------------------------|
| READ | <i>Rectum adenocarcinoma</i> |
|------|------------------------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( READ )
ExperimentList class object of length 14:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
 [6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [7] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
 [8] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [9] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[10] READ_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
[11] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[12] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[13] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns

> rownames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["READ_GISTIC_Peaks-20160128"]] chr1:3814904-31841618 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["READ_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["READ_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<4 more elements>

> colnames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
```

```

[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2GeneNorm-20160128"]] TCGA-AF-2691-01A-01R-0821-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | READ_CNASeq-20160128 | 1.5 Mb |
| 2 | READ_CNASNP-20160128 | 4.3 Mb |
| 3 | READ_CNVSNP-20160128 | 1.1 Mb |
| 4 | READ_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | READ_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | READ_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | READ_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | READ_mRNAArray-20160128 | 1.1 Mb |
| 9 | READ_Mutation-20160128 | 9.6 Mb |
| 10 | READ_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | READ_RNASeqGene-20160128 | 1.3 Mb |
| 12 | READ_RPPAArray-20160128 | 0 Mb |
| 13 | READ_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | READ_Methylation_methyl450-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

142 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
27.00  27.00   2.00   1.44   3.25

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 31.00  57.00   66.00   64.37  72.00   90.00

```

vital_status:

```

 0  1
141 28

```

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 59.0 | 347.5 | 730.0 | 786.1 | 1193.0 | 1741.0 | 142 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 0.0 | 366.0 | 625.0 | 779.5 | 1096.0 | 3932.0 | 28 |

tumor_tissue_site:

| rectum | NA's |
|--------|------|
| 166 | 3 |

pathology_M_stage:

| m0 | m1 | m1a | mx | NA's |
|-----|----|-----|----|------|
| 128 | 22 | 2 | 14 | 3 |

gender:

| female | male |
|--------|------|
| 77 | 92 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1999 | 2007 | 2009 | 2008 | 2010 | 2012 |

days_to_last_known_alive:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 31.0 | 292.2 | 863.0 | 1420.1 | 2214.5 | 3667.0 | 161 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 114 | 22 | 33 |

histological_type:

| rectal adenocarcinoma | rectal mucinous adenocarcinoma |
|-----------------------|--------------------------------|
| 150 | 13 |
| NA's | |
| 6 | |

tumor_stage:

| stage iia | NA's |
|-----------|------|
| 1 | 168 |

residual_tumor:

| r0 | r1 | r2 | rx | NA's |
|-----|----|----|----|------|
| 126 | 2 | 12 | 5 | 24 |

number_of_lymph_nodes:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|-------|---------|--------|-------|---------|--------|------|
| 0.000 | 0.000 | 0.000 | 2.692 | 3.000 | 31.000 | 10 |

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
           1                                 84      84
```

Including an additional 2242 columns

| | |
|------|----------------|
| SARC | <i>Sarcoma</i> |
|------|----------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( SARC )
ExperimentList class object of length 10:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
 [10] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

> rownames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SARC_GISTIC_Peaks-20160128"]] chr1:1-5923787 ... chr22:45095899-51304566
[["SARC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SARC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
```

```

[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
[["SARC_Methylation-20160128"]] TCGA-3B-A9HI-01A-11D-A388-05 ...

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------|---------|
| 1 | SARC_CNASNP-20160128 | | 9.2 Mb |
| 2 | SARC_CNVSNP-20160128 | | 3 Mb |
| 3 | SARC_GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 4 | SARC_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 5 | SARC_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 6 | SARC_miRNASeqGene-20160128 | | 0.1 Mb |
| 7 | SARC_Mutation-20160128 | | 19.5 Mb |
| 8 | SARC_RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 9 | SARC_RPPAArray-20160128 | | 0 Mb |
| 10 | SARC_Methylation-20160128 | | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

162 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
99.00 99.00 1.78 1.51 2.46

```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 20.00  53.00  61.00  60.88  71.00  90.00    1

```

```

vital_status:
 0  1
162 99

```

```

days_to_death:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 17.0  322.5  648.0  863.6 1169.5 2694.0 162

```

```

days_to_last_followup:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 15.0  585.8 1092.0 1391.1 1891.8 5723.0 99

```

```

gender:

```

```
female  male
  142    119
```

```
date_of_initial_pathologic_diagnosis:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
  1994  2007   2010   2009  2012   2013     4
```

```
radiation_therapy:
  no  yes NA's
  181 74  6
```

```
residual_tumor:
  r0  r1  r2  rx NA's
  155 70  9  26  1
```

```
race:
      asian black or african american      white
      6              18              228
      NA's
      9
```

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
      5              223              33
```

Including an additional 1413 columns

SKCM

Skin Cutaneous Melanoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( SKCM )
ExperimentList class object of length 11:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [8] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [9] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
[10] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
[11] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns
```



```

> rownames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SKCM_GISTIC_Peaks-20160128"]] chr1:1-6847369 ... chr22:41468899-41849552
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["SKCM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | SKCM_CNASeq-20160128 | 0.9 Mb |
| 2 | SKCM_CNASNP-20160128 | 12.3 Mb |
| 3 | SKCM_CNVSNP-20160128 | 3.2 Mb |
| 4 | SKCM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | SKCM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | SKCM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | SKCM_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | SKCM_Mutation-20160128 | 299.6 Mb |
| 9 | SKCM_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | SKCM_RPPAArray-20160128 | 0 Mb |
| 11 | SKCM_Methylation-20160128 | 75.1 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

249 observations deleted due to missingness
 n events median 0.95LCL 0.95UCL
 221.00 221.00 2.99 2.40 3.90

 Available sample meta-data:

years_to_birth:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 15.00 48.00 58.00 58.24 71.00 90.00 8

vital_status:
 0 1
 247 223

days_to_death:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 79 518 1093 1789 2073 10870 249

days_to_last_followup:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 -2.0 477.5 1146.0 1885.3 2658.8 11252.0 230

days_to_submitted_specimen_dx:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 -2 0 344 1017 1372 10847 14

melanoma_ulceration:
 no yes NA's
 146 167 157

melanoma_primary_known:
 no yes
 47 423

Breslow_thickness:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.000 1.300 3.000 5.585 6.950 75.000 111

gender:
 female male
 180 290

date_of_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 1978 2003 2008 2006 2011 2013 11

radiation_therapy:

| | | |
|-----|-----|------|
| no | yes | NA's |
| 420 | 49 | 1 |

race:

| | | | |
|--|-------|---------------------------|-------|
| | asian | black or african american | white |
| | 12 | 1 | 447 |
| | NA's | | |
| | 10 | | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 11 | 446 | 13 |

Including an additional 1517 columns

STAD

Stomach adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( STAD )
ExperimentList class object of length 13:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [8] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [9] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
[10] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
[11] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
[12] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[13] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns

> rownames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["STAD_GISTIC_Peaks-20160128"]] chr1:10686864-11068052 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["STAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
```

```

[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["STAD_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
...
<3 more elements>

> colnames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeqGene-20160128"]] TCGA-BR-4191-01A-02R-1131-13 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | STAD_CNASeq-20160128 | 0.9 Mb |
| 2 | STAD_CNASNP-20160128 | 12.1 Mb |
| 3 | STAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | STAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | STAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | STAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | STAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | STAD_Mutation-20160128 | 161.5 Mb |
| 9 | STAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | STAD_RNASeqGene-20160128 | 1.7 Mb |
| 11 | STAD_RPPAArray-20160128 | 0 Mb |
| 12 | STAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 13 | STAD_Methylation_methyl450-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

273 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
170.000 170.000 0.948 0.792 1.085

```

Available sample meta-data:

```

-----
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  30.00  58.00   67.00   65.73  73.00   90.00    9

vital_status:
  0  1
268 175

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  0.0   194.0   346.0   423.7  553.5  2197.0  273

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  0.0   335.5   547.5   673.7  912.0  3720.0  177

tumor_tissue_site:
stomach
  443

pathology_M_stage:
  m0  m1  mx
391  30  22

gender:
female  male
  158   285

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  1996   2010   2011   2010   2012   2013    6

radiation_therapy:
  no  yes NA's
323  77  43

residual_tumor:
  r0  r1  r2  rx NA's
350  18  19  25  31

number_of_lymph_nodes:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  0.000  0.000  3.000   5.635  8.000  57.000   51

race:
                                asian

```

```

89
black or african american
13
native hawaiian or other pacific islander
1
white
278
NA's
62

ethnicity:
hispanic or latino not hispanic or latino      NA's
5                                             318      120

Including an additional 1390 columns

```

```

TGCT          Testicular Germ Cell Tumors

```

Description

A document describing the TCGA cancer code

Details

```

> experiments( TGCT )
ExperimentList class object of length 10:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
[10] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["TGCT_GISTIC_Peaks-20160128"]] chr1:1-48649489 ... chr22:18613558-22141824
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["TGCT_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```
> colnames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
[["TGCT_Methylation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Z-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | TGCT_CNASNP-20160128 | 3.8 Mb |
| 2 | TGCT_CNVSNP-20160128 | 0.8 Mb |
| 3 | TGCT_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | TGCT_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | TGCT_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | TGCT_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | TGCT_Mutation-20160128 | 10 Mb |
| 8 | TGCT_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | TGCT_RPPAArray-20160128 | 0 Mb |
| 10 | TGCT_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
130 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
4.0000 4.0000 1.5493 0.0466 NA
```

Available sample meta-data:

```
years_to_birth:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
 14.00 26.00 31.00 31.99 37.00 67.00
```

```
vital_status:
 0 1
130 4
```

```
days_to_death:
```

17 513 618 6972 NA's
 1 1 1 1 130

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 3.0 | 688.2 | 1265.5 | 2092.7 | 2826.2 | 7437.0 | 4 |

tumor_tissue_site:

testes
 134

pathology_T_stage:

t1 t2 t3 tx
 76 51 6 1

pathology_N_stage:

| n0 | n1 | n2 | nx | NA's |
|----|----|----|----|------|
| 46 | 11 | 2 | 65 | 10 |

pathology_M_stage:

| m0 | m1 | m1a | m1b | NA's |
|-----|----|-----|-----|------|
| 115 | 2 | 1 | 1 | 15 |

gender:

male
 134

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 1992 | 2006 | 2009 | 2008 | 2012 | 2013 |

radiation_therapy:

| no | yes | NA's |
|-----|-----|------|
| 111 | 21 | 2 |

karnofsky_performance_score:

| 80 | 90 | 100 | NA's |
|----|----|-----|------|
| 5 | 41 | 56 | 32 |

race:

| asian | black or african american | white |
|-------|---------------------------|-------|
| 4 | 6 | 119 |
| NA's | | |
| 5 | | |

ethnicity:

| hispanic or latino | not hispanic or latino | NA's |
|--------------------|------------------------|------|
| 12 | 111 | 11 |

Including an additional 762 columns

THCA

*Thyroid carcinoma***Description**

A document describing the TCGA cancer code

Details

```
> experiments( THCA )
ExperimentList class object of length 12:
 [1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
 [2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
 [3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
 [4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns
 [6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [7] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
 [8] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
 [9] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
[10] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
[11] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
[12] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns

> rownames( THCA )
CharacterList of length 12
[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THCA_GISTIC_Peaks-20160128"]] chr1:158681167-215338621 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( THCA )
CharacterList of length 12
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
```

...
<2 more elements>

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------|---------|
| 1 | THCA_CNASeq-20160128 | | 0.2 Mb |
| 2 | THCA_CNASNP-20160128 | | 10.7 Mb |
| 3 | THCA_CNVSNP-20160128 | | 1.8 Mb |
| 4 | THCA_GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 5 | THCA_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 6 | THCA_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 7 | THCA_miRNASeqGene-20160128 | | 0.1 Mb |
| 8 | THCA_Mutation-20160128 | | 14 Mb |
| 9 | THCA_RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 10 | THCA_RNASeqGene-20160128 | | 1.3 Mb |
| 11 | THCA_RPPAArray-20160128 | | 0 Mb |
| 12 | THCA_Methylation-20160128 | | 75.1 Mb |

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

487 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
16.00 16.00 2.80 2.23 4.80

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 15.00 | 35.00 | 46.00 | 47.26 | 58.00 | 89.00 |

vital_status:

| 0 | 1 |
|-----|----|
| 487 | 16 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 174 | 743 | 1021 | 1176 | 1631 | 2973 | 487 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|------|---------|------|------|
| 0 | 535 | 943 | 1220 | 1513 | 5423 | 16 |

tumor_tissue_site:

thyroid
503

pathology_N_stage:
n0 n1 n1a n1b nx
227 58 93 75 50

pathology_M_stage:
m0 m1 mx NA's
280 9 213 1

date_of_initial_pathologic_diagnosis:
Min. 1st Qu. Median Mean 3rd Qu. Max.
1993 2008 2010 2009 2011 2013

radiation_therapy:
no yes NA's
181 306 16

radiation_exposure:
no yes NA's
423 17 63

extrathyroidal_extension:
minimal (t3) moderate/advanced (t4a) none
133 18 333
very advanced (t4b) NA's
1 18

residual_tumor:
r0 r1 r2 rx NA's
385 52 4 30 32

number_of_lymph_nodes:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.000 0.000 1.000 3.658 5.000 41.000 114

multifocality:
multifocal unifocal NA's
227 266 10

tumor_size:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.300 1.700 2.600 2.975 4.000 8.200 100

Including an additional 1481 columns

Description

A document describing the TCGA cancer code

Details

```
> experiments( THYM )
ExperimentList class object of length 10:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
 [10] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THYM_GISTIC_Peaks-20160128"]] chr1:208606110-249250621 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["THYM_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
[["THYM_Methylation-20160128"]] TCGA-3G-AB00-01A-22D-A424-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | THYM_CNASNP-20160128 | 2.9 Mb |
| 2 | THYM_CNVSNP-20160128 | 0.5 Mb |
| 3 | THYM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | THYM_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | THYM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

```

6          THYM_miRNASeqGene-20160128  0.1 Mb
7          THYM_Mutation-20160128    3.3 Mb
8          THYM_RNASeq2GeneNorm-20160128  1.3 Mb
9          THYM_RPPAArray-20160128     0 Mb
10         THYM_Methylation-20160128   75 Mb
    
```

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

Call: survfit(formula = survival::Surv(colDat\$days_to_death/365, colDat\$vital_status) ~
-1)

```

115 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
9.00  9.00  2.34  1.04  NA
    
```

Available sample meta-data:

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 17.00  49.50   60.00   58.15  68.50   84.00    1
    
```

```

vital_status:
 0  1
115 9
    
```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  124   379    853   1423  2488   3488   115
    
```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  14.0   725.2 1267.5 1486.3 1947.0 4575.0    10
    
```

```

tumor_tissue_site:
anterior mediastinum          thymus
                        27                97
    
```

```

gender:
female  male
  60    64
    
```

```

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 2000   2008   2010   2010   2012   2013    1
    
```

```

radiation_therapy:
no yes
    
```

81 43

race:

| | |
|---------------------------------|-------|
| asian black or african american | white |
| 13 | 103 |
| NA's | |
| 2 | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 10 | 100 | 14 |

Including an additional 685 columns

UCEC

*Uterine Corpus Endometrial Carcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( UCEC )
ExperimentList class object of length 14:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [8] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [9] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
[10] UCEC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 380 columns
[11] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
[12] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
[13] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
[14] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

> rownames( UCEC )
CharacterList of length 14
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["UCEC_GISTIC_Peaks-20160128"]] chr1:13949775-15575840 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCEC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCEC_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC

```

```

[[ "UCEC_Mutation-20160128" ]] character(0)
[[ "UCEC_RNASeq2GeneNorm-20160128" ]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<4 more elements>

> colnames( UCEC )
CharacterList of length 14
[[ "UCEC_CNASeq-20160128" ]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[[ "UCEC_CNASNP-20160128" ]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[[ "UCEC_CNVSNP-20160128" ]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[[ "UCEC_GISTIC_AllByGene-20160128" ]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[[ "UCEC_GISTIC_Peaks-20160128" ]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[[ "UCEC_GISTIC_ThresholdedByGene-20160128" ]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[[ "UCEC_miRNASeqGene-20160128" ]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[[ "UCEC_mRNAArray-20160128" ]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[[ "UCEC_Mutation-20160128" ]] TCGA-A5-A0G3-01A-11W-A062-09 ...
[[ "UCEC_RNASeq2GeneNorm-20160128" ]] TCGA-A5-A0G1-01A-11R-A118-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | UCEC_CNASeq-20160128 | 1 Mb |
| 2 | UCEC_CNASNP-20160128 | 16.9 Mb |
| 3 | UCEC_CNVSNP-20160128 | 3.7 Mb |
| 4 | UCEC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | UCEC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | UCEC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | UCEC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | UCEC_mRNAArray-20160128 | 1.1 Mb |
| 9 | UCEC_Mutation-20160128 | 73.1 Mb |
| 10 | UCEC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | UCEC_RNASeqGene-20160128 | 1.3 Mb |
| 12 | UCEC_RPPAArray-20160128 | 0.1 Mb |
| 13 | UCEC_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | UCEC_Methylation_methyl450-20160128 | 75.1 Mb |

Available sample meta-data:

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 50.0 | 367.0 | 709.0 | 881.8 | 1063.0 | 3423.0 | 457 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| -6.0 | 543.0 | 948.5 | 1195.1 | 1753.2 | 6859.0 | 92 |

tumor_tissue_site:

```

endometrial other specify
      547          1

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  1995  2007  2009  2009  2010  2013    9

days_to_last_known_alive:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  145   404   729  1405  2096  4144  535

radiation_therapy:
  no yes NA's
  295 228  25

histological_type:
endometrioid endometrial adenocarcinoma
              411
  mixed serous and endometrioid
              22
  serous endometrial adenocarcinoma
              115

residual_tumor:
  r0 r1 r2 rx NA's
  376 22 16 41 93

```

Including an additional 1779 columns

UCS

Uterine Carcinosarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( UCS )
ExperimentList class object of length 10:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
[10] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns

```



```
> rownames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["UCS_GISTIC_Peaks-20160128"]] chr1:1-19401404 ... chr22:41958863-51304566
[["UCS_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UCS_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
[["UCS_Methylation-20160128"]] TCGA-N5-A4R8-01A-11D-A28S-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | UCS_CNASNP-20160128 | 1.5 Mb |
| 2 | UCS_CNVSNP-20160128 | 0.6 Mb |
| 3 | UCS_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | UCS_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | UCS_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | UCS_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | UCS_Mutation-20160128 | 19.7 Mb |
| 8 | UCS_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | UCS_RPPAArray-20160128 | 0 Mb |
| 10 | UCS_Methylation-20160128 | 75 Mb |

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

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
22 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
35.00 35.00 1.43 1.04 1.96
```

 Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 51.00 | 62.00 | 68.00 | 69.72 | 76.00 | 90.00 |

vital_status:

| | |
|----|----|
| 0 | 1 |
| 22 | 35 |

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 8.0 | 304.0 | 522.0 | 705.4 | 790.5 | 3115.0 | 22 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|--------|---------|--------|------|
| 0.0 | 591.2 | 828.0 | 1183.4 | 1647.5 | 4269.0 | 35 |

tumor_tissue_site:

| |
|--------|
| uterus |
| 57 |

gender:

| |
|--------|
| female |
| 57 |

date_of_initial_pathologic_diagnosis:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 2002 | 2007 | 2009 | 2009 | 2011 | 2012 |

radiation_therapy:

| no | yes | NA's |
|----|-----|------|
| 29 | 25 | 3 |

histological_type:

| | |
|--|----|
| uterine carcinosarcoma/ malignant mixed mullerian tumor (mmt): nos | 24 |
| uterine carcinosarcoma/ mmt: heterologous type | 20 |
| uterine carcinosarcoma/mmt: homologous type | 13 |

race:

| | |
|---------------------------------|-------|
| asian black or african american | white |
| 3 | 9 |
| NA's | 44 |
| 1 | |

ethnicity:

| | |
|---|------|
| hispanic or latino not hispanic or latino | NA's |
|---|------|

1

43

13

Including an additional 632 columns

UVM

Uveal Melanoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 11:
 [1] UVM_CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] UVM_CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] UVM_CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] UVM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] UVM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 80 columns
 [6] UVM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [7] UVM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] UVM_Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] UVM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns
 [11] UVM_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( UVM )
CharacterList of length 11
[["UVM_CNASeq-20160128"]] character(0)
[["UVM_CNASNP-20160128"]] character(0)
[["UVM_CNVSNP-20160128"]] character(0)
[["UVM_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["UVM_GISTIC_Peaks-20160128"]] chr1:19073360-24108626 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UVM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UVM_Mutation-20160128"]] character(0)
[["UVM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UVM_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<1 more element>

> colnames( UVM )
CharacterList of length 11
[["UVM_CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["UVM_CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_Peaks-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
```

```

[["UVM_Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["UVM_RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|---------------------------------------|---------|
| 1 | | UVM_CNASeq-20160128 | 0.2 Mb |
| 2 | | UVM_CNASNP-20160128 | 1.9 Mb |
| 3 | | UVM_CNVSNP-20160128 | 0.4 Mb |
| 4 | | UVM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | | UVM_GISTIC_Peaks-20160128 | 0 Mb |
| 6 | | UVM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | | UVM_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | | UVM_Mutation-20160128 | 12.3 Mb |
| 9 | | UVM_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | | UVM_RPPAArray-20160128 | 0 Mb |
| 11 | | UVM_Methylation-20160128 | 75 Mb |

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

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

57 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
23.00  23.00   1.66   1.14   3.05

```

Available sample meta-data:

years_to_birth:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 22.00 | 51.00 | 61.50 | 61.65 | 74.25 | 86.00 |

vital_status:

```

0 1
57 23

```

days_to_death:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 40.0 | 393.5 | 606.0 | 693.9 | 1029.0 | 1581.0 | 57 |

days_to_last_followup:

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA's |
|------|---------|--------|-------|---------|--------|------|
| 4.0 | 495.0 | 821.0 | 861.9 | 1184.0 | 2600.0 | 23 |

```
tumor_tissue_site:
choroid
    80
```

```
pathology_N_stage:
n0  nx  NA's
52  27  1
```

```
pathology_M_stage:
m0  m1  m1b  mx  NA's
51  2   2   23  2
```

```
gender:
female  male
    35   45
```

```
date_of_initial_pathologic_diagnosis:
    Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
    2007   2011   2012   2012   2013   2013
```

```
radiation_therapy:
no  yes  NA's
76  3    1
```

```
race:
white  NA's
    55   25
```

```
ethnicity:
    hispanic or latino  not hispanic or latino  NA's
            1                    52            27
```

Including an additional 448 columns

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