

Package ‘curatedTCGAData’

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Type Package

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

Version 1.2.0

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

License Artistic-2.0

Depends R (>= 3.4.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, S4Vectors, utils

Suggests BiocStyle, knitr, readr, rmarkdown, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData

LazyData true

RoxygenNote 6.0.1

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curatedTCGAData-package

curatedTCGAData-package

Description

The following are the TCGA cancer codes and full names.

| 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 |

Examples

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

ACC

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
```

```
[3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
[4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
[5] Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
[6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
[7] Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
[8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
[9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
```

```
> rownames( ACC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
```

```
> colnames( ACC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["Methylation-20160128"]] TCGA-OR-A5J1-01A-11D-A29J-05 ...
[["miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
[["Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 2.2 Mb |
| 2 | CNVSNP-20160128 | 0.6 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 12.6 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RPPAArray-20160128 | 0 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                78
              NA's
                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 11:
 [1] CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
 [2] CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
 [3] CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
 [8] Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 427 columns
[10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns
[11] RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns

```

```
> rownames( BLCA )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 TAKR
...
<1 more element>
```

```
> colnames( BLCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["CNASNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["CNVSNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["Methylation-20160128"]] TCGA-2F-A9KO-01A-11D-A38H-05 ...
[["miRNASeqGene-20160128"]] TCGA-2F-A9KO-01A-11R-A38M-13 ...
[["Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
[["RNASeqGene-20160128"]] TCGA-BL-A0C8-01A-11R-A10U-07 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 1 Mb |
| 2 | CNASNP-20160128 | 13.1 Mb |
| 3 | CNVSNP-20160128 | 3 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 56.1 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RNASeqGene-20160128 | 1.3 Mb |
| 11 | RPPAArray-20160128 | 0 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                327
                NA's
                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 13:
 [1] CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [10] Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
```

```
[11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
[13] RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
```

```
> rownames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg000002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>
```

```
> colnames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A1-A0SD-01A-11D-A112-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3C-AAAU-01A-11D-A41Q-05 ...
[["miRNASeqGene-20160128"]] TCGA-3C-AAAU-01A-11R-A41G-13 ...
[["mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
...
<3 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.2 Mb |
| 2 | CNASNP-20160128 | 30.9 Mb |
| 3 | CNVSNP-20160128 | 8.2 Mb |
| 4 | GISTIC_AllByGene-20160128 | 5 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 5 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75.1 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray-20160128 | 1.2 Mb |
| 10 | Mutation-20160128 | 67.4 Mb |
| 11 | RNASeq2GeneNorm-20160128 | 1.4 Mb |
| 12 | RNASeqGene-20160128 | 1.4 Mb |
| 13 | RPPAArray-20160128 | 0.1 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 |
|-----|------|------|
| 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      asian
                                   1      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 10:
 [1] CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [8] Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns

> rownames( CESC )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
```

```

[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( CESC )
```

```
CharacterList of length 10
```

```

[["CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["Methylation-20160128"]] TCGA-2W-A8YY-01A-11D-A37Q-05 ...
[["miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
[["Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2W-A8YY-01A-11R-A37O-07 ...
[["RPPAArray-20160128"]] TCGA-2W-A8YY-01A-21-A40H-20 ...

```

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

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.3 Mb |
| 2 | CNASNP-20160128 | 7.3 Mb |
| 3 | CNVSNP-20160128 | 1.8 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 29.8 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RPPAArray-20160128 | 0 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 | | | | |
| | 29 | 3 | NA's | | | |
| | | | 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
307

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 9:
 [1] CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
 [7] Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns

```

```
> rownames( CHOL )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
```

```
> colnames( CHOL )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["Methylation-20160128"]] TCGA-3X-AAV9-01A-72D-A418-05 ...
[["miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 1.1 Mb |
| 2 | CNVSNP-20160128 | 0.2 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 4.6 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RPPAArray-20160128 | 0 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

Colon adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( COAD )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
 [10] Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 191 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns

> rownames( COAD )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
```

```

[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( COAD )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A6-2672-11A-01D-1551-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3L-AA1B-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-A6-2675-01A-02T-1722-13 ...
[["mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 1.1 Mb |
| 2 | CNASNP-20160128 | 12.5 Mb |
| 3 | CNVSNP-20160128 | 2.7 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray-20160128 | 1.1 Mb |
| 10 | Mutation-20160128 | 23.6 Mb |
| 11 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 12 | RNASeqGene-20160128 | 1.3 Mb |
| 13 | RPPAArray-20160128 | 0 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

Create a MultiAssayExperiment from specific assays and cohorts

Usage

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

Arguments

| | |
|-------------|---|
| diseaseCode | a character vector containing the name(s) of TCGA cohorts |
| assays | a character vector containing the name(s) of TCGA assays |
| dry.run | logical (default TRUE) whether to return the dataset names before actual download |

Details

This function will check against available resources in ExperimentHub. Currently, only the latest runDate ("2016-01-28") is supported. Use the `dry.run = FALSE` to download remote datasets and build an integrative [MultiAssayExperiment](#) object.

Value

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

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 9:
 [1] CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
 [7] Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns

> rownames( DLBC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( DLBC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["Methylation-20160128"]] TCGA-FA-8693-01A-11D-2399-05 ...
[["miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
```

```
[[ "RPPAArray-20160128" ]] TCGA-FA-8693-01A-21-A45K-20 ...
```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|---|-----------------------------------|-------|---------|
| 1 | CNASNP-20160128 | | 1.2 Mb |
| 2 | CNVSNP-20160128 | | 0.3 Mb |
| 3 | GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 5 | Methylation-20160128 | | 75 Mb |
| 6 | miRNASeqGene-20160128 | | 0.1 Mb |
| 7 | Mutation-20160128 | | 12.6 Mb |
| 8 | RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 9 | RPPAArray-20160128 | | 0 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                                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 11:
 [1] CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
 [8] Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 196 columns
[10] RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
[11] RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns

> rownames( ESCA )
CharacterList of length 11

```

```

[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 AB074166 ... VCY XKRY ZFY
...
<1 more element>

```

```

> colnames( ESCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["Methylation-20160128"]] TCGA-2H-A9GF-01A-11D-A37D-05 ...
[["miRNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[["Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["RNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.5 Mb |
| 2 | CNASNP-20160128 | 5.5 Mb |
| 3 | CNVSNP-20160128 | 1.7 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 41.2 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RNASeqGene-20160128 | 1.7 Mb |
| 11 | RPPAArray-20160128 | 0 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 16:
 [1] CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
 [2] CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
 [3] CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
 [4] CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
 [5] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [6] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [7] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
 [8] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns
 [9] miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
[10] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
[11] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
[12] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 502 columns
[13] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
[14] Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
```

[15] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
 [16] RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns

```
> rownames( GBM )
CharacterList of length 16
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg000002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] ebv-miR-BART1-3p ebv-miR-BART1-5p ... kshv-miR-K12-9*
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<6 more elements>
```

```
> colnames( GBM )
CharacterList of length 16
[["CNACGH_CGH_hg_244a-20160128"]] TCGA-02-0001-01C-01D-0185-02 ...
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-02-2466-01A-01D-0787-02 ...
[["CNASNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["CNVSNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["Methylation_methyl27-20160128"]] TCGA-02-0001-01C-01D-0186-05 ...
[["Methylation_methyl450-20160128"]] TCGA-06-0125-01A-01D-A45W-05 ...
[["miRNAArray-20160128"]] TCGA-02-0001-01C-01T-0179-07 ...
[["miRNASeqGene-20160128"]] character(0)
...
<6 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|------------------------------------|---------------|
| 1 | CNACGH_CGH_hg_244a-20160128 | 2.3 Mb |
| 2 | CNACGH_CGH_hg_415k_g4124a-20160128 | 1.7 Mb |
| 3 | CNASNP-20160128 | 16.4 Mb |
| 4 | CNVSNP-20160128 | 4.2 Mb |
| 5 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 6 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | Methylation_methyl27-20160128 | 4.9 Mb |
| 8 | Methylation_methyl450-20160128 | 75 Mb |
| 9 | miRNAArray-20160128 | 0.1 Mb |
| 10 | miRNASeqGene-20160128 | 0.1 Mb |
| 11 | mRNAArray_huex-20160128 | 1.2 Mb |
| 12 | mRNAArray_TX_g4502a-20160128 | 1.2 Mb |
| 13 | mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 14 | Mutation-20160128 | 31 Mb |
| 15 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 16 | RPPAArray-20160128 | 0 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 11:
 [1] CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [8] Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
[10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
[11] RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns

> rownames( HNSC )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b

```

```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZ33 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZ33 psiTPTE22 tAKR
...
<1 more element>

```

```

> colnames( HNSC )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["Methylation-20160128"]] TCGA-4P-AA8J-01A-11D-A392-05 ...
[["miRNASeqGene-20160128"]] TCGA-4P-AA8J-01A-11R-A39B-13 ...
[["Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["RNASeqGene-20160128"]] TCGA-BA-4074-01A-01R-1436-07 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 1 Mb |
| 2 | CNASNP-20160128 | 13.6 Mb |
| 3 | CNVSNP-20160128 | 3.3 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 68.9 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RNASeqGene-20160128 | 1.3 Mb |
| 11 | RPPAArray-20160128 | 0 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 | | | | | | | asian |
| | | | 2 | | | | 11 |
| black or african american | | | | | | | white |
| | | | 48 | | | | 452 |
| | | | NA's | | | | |
| | | | 15 | | | | |
| ethnicity: | | | | | | | |
| hispanic or latino not hispanic or latino | | | | | | | NA's |
| | | | 26 | | | 465 | 37 |

Including an additional 1426 columns

KICH

Kidney Chromophobe

Description

A document describing the TCGA cancer code

Details

```
> experiments( KICH )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns
 [2] CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
 [7] Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns

> rownames( KICH )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
```

```

[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( KICH )
```

```
CharacterList of length 9
```

```

[["CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["Methylation-20160128"]] TCGA-KL-8323-01A-21D-2312-05 ...
[["miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...

```

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

| | | assay | size.Mb |
|---|-----------------------------------|-------|---------|
| 1 | CNASNP-20160128 | | 1.6 Mb |
| 2 | CNVSNP-20160128 | | 0.3 Mb |
| 3 | GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 5 | Methylation-20160128 | | 75 Mb |
| 6 | miRNASeqGene-20160128 | | 0.1 Mb |
| 7 | Mutation-20160128 | | 2.6 Mb |
| 8 | RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 9 | RPPAArray-20160128 | | 0 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
  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

Details

```

> experiments( KIRC )
ExperimentList class object of length 12:
 [1] CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
 [2] CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
 [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [9] Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 606 columns
[11] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
[12] RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns

> rownames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC

```

```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A3-3306-11A-01D-0859-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3Z-A93Z-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-3Z-A93Z-01A-11R-A37P-13 ...
[["mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 13.4 Mb |
| 2 | CNVSNP-20160128 | 2.6 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation_methyl27-20160128 | 4.9 Mb |
| 6 | Methylation_methyl450-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | mRNAArray-20160128 | 1.1 Mb |
| 9 | Mutation-20160128 | 8.2 Mb |
| 10 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | RNASeqGene-20160128 | 1.3 Mb |
| 12 | RPPAArray-20160128 | 0.1 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                                56          466
                    NA's
                    7

ethnicity:
  hispanic or latino not hispanic or latino          NA's
                    26                                359          152

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 12:
 [1] CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
 [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
 [9] Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 323 columns
[11] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
[12] RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns

> rownames( KIRP )
CharacterList of length 12

```



```

[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( KIRP )
CharacterList of length 12
[["CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["Methylation_methyl27-20160128"]] TCGA-AL-3466-01A-01D-1191-05 ...
[["Methylation_methyl450-20160128"]] TCGA-2K-A9WE-01A-11D-A383-05 ...
[["miRNASeqGene-20160128"]] TCGA-2K-A9WE-01A-11R-A38N-13 ...
[["mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 8.2 Mb |
| 2 | CNVSNP-20160128 | 1.4 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation_methyl27-20160128 | 4.9 Mb |
| 6 | Methylation_methyl450-20160128 | 75 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | mRNAArray-20160128 | 1.1 Mb |
| 9 | Mutation-20160128 | 10.6 Mb |
| 10 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | RNASeqGene-20160128 | 1.3 Mb |
| 12 | RPPAArray-20160128 | 0 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:

| | |
|----|------|
| 34 | NA's |
| 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 | 2 | asian | 6 |
| black or african american | 61 | white | 207 |
| NA's | 15 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|----|
| hispanic or latino | 12 | not hispanic or latino | 243 | NA's | 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 7:

- [1] CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
- [2] CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
- [3] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
- [4] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns
- [5] Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns

```
[6] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
[7] RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
```

```
> rownames( LAML )
CharacterList of length 7
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ABCB10 ... VCY XGPY2 XKRY2 ZFY
```

```
> colnames( LAML )
CharacterList of length 7
[["CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["Methylation_methyl450-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|--------------------------------|---------|
| 1 | CNASNP-20160128 | 23.5 Mb |
| 2 | CNVSNP-20160128 | 0.9 Mb |
| 3 | Methylation_methyl27-20160128 | 4.9 Mb |
| 4 | Methylation_methyl450-20160128 | 75 Mb |
| 5 | Mutation-20160128 | 2.6 Mb |
| 6 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 7 | RNASeqGene-20160128 | 1.3 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 11:
 [1] CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns

```

```
[3] CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
[6] Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
[7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
[8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
[9] Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
[11] RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns
```

```
> rownames( LGG )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<1 more element>
```

```
> colnames( LGG )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["Methylation-20160128"]] TCGA-CS-4938-01B-11D-1894-05 ...
[["miRNASeqGene-20160128"]] TCGA-CS-4938-01B-11R-1895-13 ...
[["mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.2 Mb |
| 2 | CNASNP-20160128 | 11.3 Mb |
| 3 | CNVSNP-20160128 | 2.4 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | mRNAArray-20160128 | 1.1 Mb |
| 9 | Mutation-20160128 | 4.2 Mb |

10 RNASeq2GeneNorm-20160128 1.3 Mb
 11 RPPAArray-20160128 0.1 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 | 1 |
| | | 191 | |

race:

| | | | |
|----------------------------------|----|-------|-----|
| american indian or alaska native | 1 | asian | 8 |
| black or african american | 21 | white | 475 |
| NA's | 11 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|----|
| hispanic or latino | 32 | not hispanic or latino | 449 | NA's | 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 10:
 [1] CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
 [9] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns

> rownames( LIHC )
CharacterList of length 10
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
```



```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( LIHC )
```

```
CharacterList of length 10
```

```

[["CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["Methylation-20160128"]] TCGA-2V-A95S-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
[["Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
[["RPPAArray-20160128"]] TCGA-BC-4072-01B-21-A40L-20 ...

```

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

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 9.9 Mb |
| 2 | CNVSNP-20160128 | 2.7 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75.1 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 16.8 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RNASeqGene-20160128 | 1.3 Mb |
| 10 | RPPAArray-20160128 | 0 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 | | white | |

```

              17
            NA's
              10

```

```

ethnicity:
  hispanic or latino not hispanic or latino      NA's
              18                      340              19

```

Including an additional 1218 columns

LUAD *Lung adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```

> experiments( LUAD )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
[10] Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
[11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 576 columns
[12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
[13] RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns

> rownames( LUAD )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( LUAD )

```

CharacterList of length 13

```

[["CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["Methylation_methyl27-20160128"]] TCGA-05-4244-01A-01D-1104-05 ...
[["Methylation_methyl450-20160128"]] TCGA-05-4384-01A-01D-1756-05 ...
[["miRNASeqGene-20160128"]] TCGA-05-4384-01A-01T-1754-13 ...
[["mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|-----------------------------------|---------|
| 1 | CNASeq-20160128 | 10.8 Mb |
| 2 | CNASNP-20160128 | 13.7 Mb |
| 3 | CNVSNP-20160128 | 3.4 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75.1 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray-20160128 | 1.1 Mb |
| 10 | Mutation-20160128 | 92.9 Mb |
| 11 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 12 | RNASeqGene-20160128 | 1.3 Mb |
| 13 | RPPAArray-20160128 | 0.1 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          asian
                1                          8
        black or african american          white
                53                         392
                NA's
                66

```

```

ethnicity:
  hispanic or latino not hispanic or latino  NA's
                7                          388          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 15:
 [1] CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [9] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
[10] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
[11] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
[12] Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
[13] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
[14] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
[15] RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns

> rownames( LUSC )
CharacterList of length 15
[["CNACGH-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b

```

```

[["mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
[["mRNAArray_TX_g4502a-20160128"]] ELM02 CREB3L1 RPS11 ... SNRPD2 AQP7 CTSC
...
<5 more elements>

```

```

> colnames( LUSC )
CharacterList of length 15
[["CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["Methylation_methyl27-20160128"]] TCGA-18-3406-11A-01D-0979-05 ...
[["Methylation_methyl450-20160128"]] TCGA-18-3417-11A-01D-1440-05 ...
[["miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
...
<5 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNACGH-20160128 | 2.5 Mb |
| 2 | CNASNP-20160128 | 14.8 Mb |
| 3 | CNVSNP-20160128 | 3.9 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray_huex-20160128 | 1.2 Mb |
| 10 | mRNAArray_TX_g4502a-20160128 | 1.1 Mb |
| 11 | mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 12 | Mutation-20160128 | 81 Mb |
| 13 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 14 | RNASeqGene-20160128 | 1.3 Mb |
| 15 | RPPAArray-20160128 | 0 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 8:
[1] CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
[2] CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
[3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
[4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
[5] Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
[6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
[7] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns
[8] RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns

```

```
> rownames( MESO )
CharacterList of length 8
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
```

```
> colnames( MESO )
CharacterList of length 8
[["CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
[["miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 2.5 Mb |
| 2 | CNVSNP-20160128 | 0.6 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 8 | RPPAArray-20160128 | 0 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 17:
 [1] CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [7] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [8] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns
 [9] miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
[10] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
[11] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
[12] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
[13] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
[14] Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
[15] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
[16] RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
[17] RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns

> rownames( OV )
CharacterList of length 17
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659

```

```

[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] DarkCorner dmr_285 dmr_3 ... NegativeControl SCorner3
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<7 more elements>

```

```

> colnames( OV )
CharacterList of length 17
[["CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["Methylation_methyl27-20160128"]] TCGA-04-1331-01A-01D-0432-05 ...
[["Methylation_methyl450-20160128"]] TCGA-13-A5FT-01A-11D-A409-05 ...
[["miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
...
<7 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|------------------------------------|---------|
| 1 | CNACGH_CGH_hg_244a-20160128 | 3.6 Mb |
| 2 | CNACGH_CGH_hg_415k_g4124a-20160128 | 6.8 Mb |
| 3 | CNASNP-20160128 | 24.6 Mb |
| 4 | CNVSNP-20160128 | 7.3 Mb |
| 5 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 6 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | Methylation_methyl27-20160128 | 4.9 Mb |
| 8 | Methylation_methyl450-20160128 | 75 Mb |
| 9 | miRNAArray-20160128 | 0.1 Mb |
| 10 | miRNASeqGene-20160128 | 0.1 Mb |
| 11 | mRNAArray_huex-20160128 | 1.2 Mb |
| 12 | mRNAArray_TX_g4502a-20160128 | 1.2 Mb |
| 13 | mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 14 | Mutation-20160128 | 7.6 Mb |
| 15 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 16 | RNASeqGene-20160128 | 1.3 Mb |
| 17 | RPPAArray-20160128 | 0.1 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

Pancreatic adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( PAAD )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns

> rownames( PAAD )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( PAAD )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 5.6 Mb |
| 2 | CNVSNP-20160128 | 1 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 111 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RPPAArray-20160128 | 0 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 9:
 [1] CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns

> rownames( PCPG )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( PCPG )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["Methylation-20160128"]] TCGA-P7-A5NX-01A-11D-A35E-05 ...
[["miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|---|-----------------------------------|-------|---------|
| 1 | CNASNP-20160128 | | 8.1 Mb |
| 2 | CNVSNP-20160128 | | 0.9 Mb |
| 3 | GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 5 | Methylation-20160128 | | 75 Mb |
| 6 | miRNASeqGene-20160128 | | 0.1 Mb |
| 7 | Mutation-20160128 | | 8.4 Mb |
| 8 | RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 9 | RPPAArray-20160128 | | 0 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
                                18
paraganglioma; extra-adrenal pheochromocytoma
                                13
                                pheochromocytoma
                                148
```

```
number_of_lymph_nodes:
  0 1 2 13 NA's
  16 3 1 1 158
```

```
race:
american indian or alaska native          asian
                                1                                6
                                black or african american
                                20                                white
                                NA's                                148
                                4
```

```
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 10:
 [1] CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
```

```

[3] CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
[6] Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns
[7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[8] Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
[9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
[10] RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns

```

```

> rownames( PRAD )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```

> colnames( PRAD )
CharacterList of length 10
[["CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["Methylation-20160128"]] TCGA-2A-A8VL-01A-21D-A378-05 ...
[["miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.7 Mb |
| 2 | CNASNP-20160128 | 15.6 Mb |
| 3 | CNVSNP-20160128 | 3.4 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 21.5 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RPPAArray-20160128 | 0 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

Rectum adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( READ )
```

```
ExperimentList class object of length 13:
```

- [1] CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
- [2] CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
- [3] CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
- [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
- [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
- [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns

```
[7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns
[8] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
[10] Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
[12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
```

```
> rownames( READ )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>
```

```
> colnames( READ )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["Methylation_methyl27-20160128"]] TCGA-AF-2689-11A-01D-1552-05 ...
[["Methylation_methyl450-20160128"]] TCGA-AF-2687-01A-02D-1734-05 ...
[["miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
...
<3 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 1.5 Mb |
| 2 | CNASNP-20160128 | 4.3 Mb |
| 3 | CNVSNP-20160128 | 1.1 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray-20160128 | 1.1 Mb |
| 10 | Mutation-20160128 | 9.6 Mb |
| 11 | RNASeq2GeneNorm-20160128 | 1.3 Mb |


```

12          RNASeqGene-20160128  1.3 Mb
13          RPPAArray-20160128   0 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

Sarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( SARC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns

```

```
[7] Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
[8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
[9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
```

```
> rownames( SARC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
```

```
> colnames( SARC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["Methylation-20160128"]] TCGA-3B-A9HI-01A-11D-A388-05 ...
[["miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 9.2 Mb |
| 2 | CNVSNP-20160128 | 3 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 18.1 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RPPAArray-20160128 | 0 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 8:
 [1] CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns
 [5] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [6] Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [7] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [8] RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns

> rownames( SKCM )
CharacterList of length 8
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( SKCM )
CharacterList of length 8
[["CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["Methylation-20160128"]] TCGA-3N-A9WB-06A-11D-A38H-05 ...
[["miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|-----------------------|----------|
| 1 | CNASeq-20160128 | 0.9 Mb |
| 2 | CNASNP-20160128 | 12.3 Mb |
| 3 | CNVSNP-20160128 | 3.2 Mb |
| 4 | Methylation-20160128 | 75.1 Mb |
| 5 | miRNASeqGene-20160128 | 0.1 Mb |
| 6 | Mutation-20160128 | 299.6 Mb |

7 RNASeq2GeneNorm-20160128 1.3 Mb
 8 RPPAArray-20160128 0 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 12:
[1] CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
[2] CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
[3] CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
[6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns
[8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
[9] Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
[11] RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
[12] RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
```

```
> rownames( STAD )
CharacterList of length 12
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<2 more elements>
```

```
> colnames( STAD )
CharacterList of length 12
[["CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["Methylation_methyl27-20160128"]] TCGA-BR-4183-11A-01D-1129-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3M-AB46-01A-11D-A411-05 ...
[["miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
...
<2 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|-----------------------------------|----------|
| 1 | CNASeq-20160128 | 0.9 Mb |
| 2 | CNASNP-20160128 | 12.1 Mb |
| 3 | CNVSNP-20160128 | 3.4 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | Mutation-20160128 | 161.5 Mb |
| 10 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | RNASeqGene-20160128 | 1.7 Mb |
| 12 | RPPAArray-20160128 | 0 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 9:
 [1] CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns

> rownames( TGCT )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
```

```

[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( TGCT )
```

```
CharacterList of length 9
```

```

[["CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["Methylation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Z-05 ...
[["miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...

```

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

| | | assay | size.Mb |
|---|-----------------------------------|-------|---------|
| 1 | CNASNP-20160128 | | 3.8 Mb |
| 2 | CNVSNP-20160128 | | 0.8 Mb |
| 3 | GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 5 | Methylation-20160128 | | 75 Mb |
| 6 | miRNASeqGene-20160128 | | 0.1 Mb |
| 7 | Mutation-20160128 | | 10 Mb |
| 8 | RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 9 | RPPAArray-20160128 | | 0 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 11:
 [1] CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
 [2] CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
 [3] CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
 [8] Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
 [10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns

> rownames( THCA )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( THCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["Methylation-20160128"]] TCGA-4C-A93U-01A-11D-A398-05 ...
[["miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...

```

```

[["Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|-----------------------------------|---------|
| 1 | CNASeq-20160128 | 0.2 Mb |
| 2 | CNASNP-20160128 | 10.7 Mb |
| 3 | CNVSNP-20160128 | 1.8 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation-20160128 | 75.1 Mb |
| 7 | miRNASeqGene-20160128 | 0.1 Mb |
| 8 | Mutation-20160128 | 14 Mb |
| 9 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | RNASeqGene-20160128 | 1.3 Mb |
| 11 | RPPAArray-20160128 | 0 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
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

THYM

*Thymoma***Description**

A document describing the TCGA cancer code

Details

```
> experiments( THYM )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns

> rownames( THYM )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( THYM )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["Methylation-20160128"]] TCGA-3G-AB00-01A-22D-A424-05 ...
[["miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|---------------------------|---------------|
| 1 | CNASNP-20160128 | 2.9 Mb |
| 2 | CNVSNP-20160128 | 0.5 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |


```

4 GISTIC_ThresholdedByGene-20160128 4.9 Mb
5           Methylation-20160128 75 Mb
6           miRNASeqGene-20160128 0.1 Mb
7           Mutation-20160128 3.1 Mb
8           RNASeq2GeneNorm-20160128 1.3 Mb
9           RPPAArray-20160128 0 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 | 6 |
| | NA's | 103 |
| | 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 13:
 [1] CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [10] Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 380 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns

> rownames( UCEC )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
```

```

[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

```

```

> colnames( UCEC )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A5-A0G2-01A-11D-A039-05 ...
[["Methylation_methyl450-20160128"]] TCGA-2E-A9G8-01A-11D-A409-05 ...
[["miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 1 Mb |
| 2 | CNASNP-20160128 | 16.9 Mb |
| 3 | CNVSNP-20160128 | 3.7 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | Methylation_methyl27-20160128 | 4.9 Mb |
| 7 | Methylation_methyl450-20160128 | 75.1 Mb |
| 8 | miRNASeqGene-20160128 | 0.1 Mb |
| 9 | mRNAArray-20160128 | 1.1 Mb |
| 10 | Mutation-20160128 | 73.1 Mb |
| 11 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 12 | RNASeqGene-20160128 | 1.3 Mb |
| 13 | RPPAArray-20160128 | 0.1 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          mixed serous and endometrioid
                                     411                                     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 9:
 [1] CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns

> rownames( UCS )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)

```

```

[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( UCS )
```

```
CharacterList of length 9
```

```

[["CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["Methylation-20160128"]] TCGA-N5-A4R8-01A-11D-A28S-05 ...
[["miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...

```

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

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASNP-20160128 | 1.5 Mb |
| 2 | CNVSNP-20160128 | 0.6 Mb |
| 3 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 5 | Methylation-20160128 | 75 Mb |
| 6 | miRNASeqGene-20160128 | 0.1 Mb |
| 7 | Mutation-20160128 | 19.7 Mb |
| 8 | RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | RPPAArray-20160128 | 0 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 (mmtt): nos | 24 |
| uterine carcinosarcoma/ mmtt: heterologous type | 20 |
| uterine carcinosarcoma/mmtt: 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

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 10:
 [1] CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns

> rownames( UVM )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( UVM )
CharacterList of length 10
[["CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["Methylation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39X-05 ...
[["miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
[["Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|-----------------------------------|---------------|
| 1 | CNASeq-20160128 | 0.2 Mb |
| 2 | CNASNP-20160128 | 1.9 Mb |
| 3 | CNVSNP-20160128 | 0.4 Mb |
| 4 | GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

```

6           Methylation-20160128  75 Mb
7           miRNASeqGene-20160128 0.1 Mb
8           Mutation-20160128 12.3 Mb
9           RNASeq2GeneNorm-20160128 1.3 Mb
10          RPPAArray-20160128   0 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 |

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