

tcgaR

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1 Introduction

Clinical data

```
library(tcgaR)
clinical.kirc <- getClinicalData("kirc")
names(clinical.kirc)[1:10]

## [1] "bcr_patient_barcode"      "bcr_patient_uuid"      "form_completion_date"
## [4] "histologic_diagnosis"    "tumor_grade"           "laterality"
## [7] "prospective_collection"  "retrospective_collection" "gender"
## [10] "birth_days_to"
```

Session info

Here is the output of `sessionInfo` on the system on which this document was compiled:

- R version 3.1.0 (2014-04-10), x86_64-apple-darwin10.8.0
- Locale: en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, utils
- Other packages: Biobase 2.25.0, BiocGenerics 0.11.3, Biostrings 2.33.13, bitops 1.0-6, bumphunter 1.5.3, downloader 0.3, foreach 1.4.2, GenomInfoDb 1.1.6, GenomicRanges 1.17.28, illuminaio 0.7.0, IRanges 1.99.23, iterators 1.0.7, lattice 0.20-29, locfit 1.5-9.1, minfi 1.11.5, RCurl 1.95-4.1, S4Vectors 0.1.2, tcgaR 0.99.0, XVector 0.5.7
- Loaded via a namespace (and not attached): annotate 1.43.4, AnnotationDbi 1.27.9, base64 1.1, beanplot 1.1, BiocStyle 1.3.1, codetools 0.2-8, DBI 0.2-7, digest 0.6.4, doRNG 1.6, evaluate 0.5.5, formatR 0.10, genefilter 1.47.6, grid 3.1.0, highr 0.3, knitr 1.6, limma 3.21.4, MASS 7.3-33, matrixStats 0.8.14, mclust 4.3, multtest 2.21.0, nlme 3.1-117, nor1mix 1.1-4, pkgmaker 0.22, plyr 1.8.1, preprocessCore 1.27.0, R.methodsS3 1.6.1, RColorBrewer 1.0-5, Rcpp 0.11.1, registry 0.2, reshape 0.8.5, rngtools 1.2.4, RSQLite 0.11.4, siggenes 1.39.0,

splines 3.1.0, stats4 3.1.0, stringr 0.6.2, survival 2.37-7, tools 3.1.0, XML 3.98-1.1, xtable 1.7-3, zlibbioc 1.11.1