

Summary of available functionality in TCGAutils

Category and Function	Description
MultiAssayExperiment helpers	
generateMap	Automatically generate a sampleMap structure from assays
imputeAssay	Impute values in numerical assays based on KNN
mergeColData	Add additional data to the colData slot of MAE
qreduceTCGA	Convert RaggedExperiment assays to RSE based on heuristics
symbolsToRanges	Convert gene symbols to genomic ranges using org.db
mirToRanges	Convert microRNA sequences to genomic ranges from mirbase.org file
simplifyTCGA	Use qreduceTCGA, symbolsToRanges, and mirToRanges in succession
curatedTCGAData helpers	
getSubtypeMap	Obtain the available subtype information
getClinicalNames	Get a list of clinical variable names for all cancer types
splitAssays	Separate assays based on sample data found in barcodes
sampleTables	Get a list of samples in each assay in a MAE
TCGAPrimaryTumors	Select only primary tumors from TCGA data barcodes
oncoPrintTCGA	Produce an oncoPrint plot from TCGA mutation data
TCGA Identifiers	
TCGAbarcode	Chop TCGA barcode into sections
TCGAbiospec	Get a table of information extracted from a vector of barcodes
TCGAsampleSelect	Indicate which barcodes belong to a specific sample type
UUIDtoBarcode	Translate universal identifiers to TCGA barcodes
UUIDtoUUID	Translate between case and file universal identifiers
barcodeToUUID	Translate TCGA barcodes to universal identifiers
filenameToBarcode	Obtain TCGA barcodes from a vector of TCGA file names
Flat to Bioconductor classes	
makeGRangesListFromCopyNumber	Create a GRangesList from a copy number data.frame
makeGRangesListFromExonFiles	Obtain a GRangesList object from a list of individual exon files
makeSummarizedExperimentFromGISTIC	Create a SummarizedExperiment object from a Firehose GISTIC RTCGAToolbox object
Genome Builds	
translateBuild	Translate build version name between UCSC and NCBI
extractBuild	Find build in string pattern such as a file name
uniformBuilds	Homogenize a vector of builds based on a threshold for the alternative build name
Reference data	
diseaseCodes	Get a table of TCGA cancer codes and subtype availability
sampleTypes	Get a table of sample type codes and their definition
clinicalNames	Obtain a CharacterList of common variable names for each TCGA disease code
getFilename	Obtain a file name string for the relevant data query
Miscellaneous	
findGRangesCols	Find the minimum necessary variable names for conversion to GRanges