

# Package ‘restfulSE’

March 30, 2021

**Title** Access matrix-like HDF5 server content or BigQuery content through a SummarizedExperiment interface

**Description** This package provides functions and classes to interface with remote data stores by operating on SummarizedExperiment-like objects.

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**Suggests** knitr, testthat, Rtsne, org.Mm.eg.db, org.Hs.eg.db, BiocStyle, restfulSEData

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**Depends** R (>= 3.6), SummarizedExperiment, DelayedArray

**License** Artistic-2.0

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---

assay,BQSummarizedExperiment,missing-method  
*extract assay data*

---

### Description

extract assay data

### Usage

```
## S4 method for signature 'BQSummarizedExperiment,missing'
assay(x, i, withDimnames = TRUE, ...)
```

**Arguments**

x	BQSummarizedExperiment instance
i	index for retrieval, ignored at present
...	not used

**Value**

matrix

**Note**

Very experimental approach to retrieving numerical data given a SummarizedExperiment 'shell'. We need more checking of consistency between assay and clinical data before creating the shell. We use dcast to transform query result to a matrix, and some 'individuals' may have multiple contributions ... we use fun.aggregate = max and will see warnings until this is cleared up.

---

assayNames,BQSummarizedExperiment-method

*Placeholder for assay name extractor for a BQSummarizedExperiment instance.*

---

**Description**

Placeholder for assay name extractor for a BQSummarizedExperiment instance.

**Usage**

```
## S4 method for signature 'BQSummarizedExperiment'  
assayNames(x, ...)
```

**Arguments**

x	instance of BQSummarizedExperiment
...	not used

**Value**

string indicating that assay is served by BigQuery, nameless

**Note**

This function supplies a placeholder for this early version of a SummarizedExperiment instance to BigQuery. At present there is only one assay supported; future work will help to reduce special coding for BigQuery back end.

---

assays, RESTfulSummarizedExperiment-method  
*Assays access for RESTfulSummarizedExperiment*

---

### Description

Assays access for RESTfulSummarizedExperiment

### Usage

```
## S4 method for signature 'RESTfulSummarizedExperiment'
assays(x, withDimnames = TRUE, ...)
```

### Arguments

x	instance of RESTfulSummarizedExperiment
withDimnames	logical defaults to TRUE
...	not used

### Value

at present a SimpleList is returned as a dummy placeholder

---

basic_clinvars	<i>provide a collection of basic clinical variables to limit size of clinical data return</i>
----------------	---

---

### Description

provide a collection of basic clinical variables to limit size of clinical data return

### Usage

```
basic_clinvars()
```

### Value

character(20) vector of variable names

### Note

Use `pancan_app()` to determine other variables available

---

BQ3_Array	<i>create BQ3_Array instance given url (filepath) and entity (host) name</i>
-----------	--

---

**Description**

create BQ3\_Array instance given url (filepath) and entity (host) name

**Usage**

```
BQ3_Array(filepath)
```

**Arguments**

filepath            a BQ3\_Source instance

**Value**

an instance of [DelayedArray-class](#)

**Examples**

```
# authentication issues may arise.  if you are authorized
# to use bigquery with GPC project isb-cgc, a token may
# be generated through the following
# options(httr_oob_default=TRUE)
# example(BQ3_Source)
# a browser authentication event may occur, or if you are in
# a browserless session, a URL will be emitted, possibly in
# the context of warnings ... browse to this URL and an
# authentication event will occur, and a token will be provided
# this can be provided back to the R session to allow the
# query to proceed
#
if (interactive()) {
  con = cgcConn("TCGA_hg38_data_v0")
  ss = BQ3_Source(con, filterval="TCGA-LUAD")
  BQ3_Array(ss)
}
```

---

BQ3_Array-class	<i>extension of DelayedArray for BigQuery content</i>
-----------------	---

---

**Description**

extension of DelayedArray for BigQuery content

---

BQ3\_ArraySeed-class     *BQ3\_Array for BigQuery matrix content*

---

### Description

BQ3\_Array for BigQuery matrix content

---

BQ3\_Matrix-class     *extension of DelayedMatrix for HDF Server content*

---

### Description

extension of DelayedMatrix for HDF Server content

---

BQ3\_Source     *construct a BigQuery resource interface*

---

### Description

construct a BigQuery resource interface

### Usage

```
BQ3_Source(
  bqconn,
  tblnm = "RNAseq_Gene_Expression",
  rowkeyfield = "Ensembl_gene_id",
  colkeyfield = "case_barcode",
  filtervbl = "project_short_name",
  filterval = "TCGA-GBM",
  assayvbl = "HTSeq__Counts",
  assaysampletype = "TP",
  maxnrec = Inf
)
```

### Arguments

bqconn	instance of BigQueryConnection from bigrquery
tblnm	character(1) table name known to bqconn
rowkeyfield	character(1) field in the table that will generate rownames for matrices derived from table
colkeyfield	character(1) field in the table that will generate colnames for matrices derived from table
filtervbl	character(1) field in the table that will be used to filter out a group of records, for example, all records pertaining to a given tumor in TCGA
filterval	character(1) value in the range of filtervbl to identify records to retain –

assayvbl	character(1) field with assay quantifications
assaysampletype	character(1) value for filtering pancancer-atlas assays, which include normals and other sample types, defaulting to "TP"; ignored if project element of bqconn is not 'pancancer-atlas'
maxnrec	numeric(1) defaults to Inf: number of records to convert with as.data.frame

**Value**

instance of BQ3\_Source

**Note**

Tailored to ISB-CGC projects 'isb-cgc' and 'pancancer-atlas'.

**Examples**

```
if (interactive()) {
  con = cgcConn("TCGA_hg38_data_v0")
  lungConn = BQ3_Source(con, filtervbl="TCGA-LUAD")
  lungConn
}
```

---

BQ3_Source-class	<i>Represent information about a BigQuery resource with a 'triple' database schema. This is targeting the isb-cgc TCGA layout. BigQuery Records are regarded as triples, within major groups defined by filtervbl. Triples have content subject - gene - value, to be pivoted to genes(rows) x subjects(columns) with values as entries.</i>
------------------	--

---

**Description**

Represent information about a BigQuery resource with a 'triple' database schema. This is targeting the isb-cgc TCGA layout. BigQuery Records are regarded as triples, within major groups defined by filtervbl. Triples have content subject - gene - value, to be pivoted to genes(rows) x subjects(columns) with values as entries.

---

bqConn	<i>generate a connection to BigQuery for specific dataset</i>
--------	---

---

**Description**

generate a connection to BigQuery for specific dataset

**Usage**

```
bqConn(dataset, project, billing)
```

**Arguments**

dataset	character(1) name of dataset in project
project	character(1) name of project
billing	character(1) billing code for project

**Value**

an instance of `BigQueryConnection`

**Note**

You will need to authenticate with Google.

**Examples**

```
bqConn
```

---

BQM_Array	<i>create BQM_Array instance given url (filepath) and entity (host) name</i>
-----------	--

---

**Description**

create BQM\_Array instance given url (filepath) and entity (host) name

**Usage**

```
BQM_Array(filepath)
```

**Arguments**

filepath	a BQM_Source instance
----------	-----------------------

**Value**

an instance of [DelayedArray-class](#)

**Examples**

```
# authentication issues may arise. if you are authorized
# to use bigquery with GPC project isb-cgc, a token may
# be generated through the following
# options(httr_oob_default=TRUE)
# example(BQM_Source)
# a browser authentication event may occur, or if you are in
# a browserless session, a URL will be emitted, possibly in
# the context of warnings ... browse to this URL and an
# authentication event will occur, and a token will be provided
# this can be provided back to the R session to allow the
# query to proceed
#
if (interactive()) {
```



```

con = bqConn(dataset="yriMulti", project=Sys.getenv("CGC_BILLING"),
             billing=Sys.getenv("CGC_BILLING"))
ss = BQM_Source(con, "banovichSE_methylationData", "cg_Methyl450")
#BQM_Array(ss)
BQM_Array(ss)["cg00000029",c("NA18498", "NA18499", "NA18501"),drop=FALSE]
}

```

---

BQM_Array-class	<i>extension of DelayedArray for BigQuery content</i>
-----------------	---

---

### Description

extension of DelayedArray for BigQuery content

---

BQM_ArraySeed-class	<i>BQM_Array for BigQuery matrix content</i>
---------------------	--

---

### Description

BQM\_Array for BigQuery matrix content

---

BQM_Matrix-class	<i>extension of DelayedMatrix for HDF Server content</i>
------------------	--

---

### Description

extension of DelayedMatrix for HDF Server content

---

BQM_Source	<i>construct a BigQuery resource interface, for a matrix-like table with one column devoted to row identification (rowkeyfield) and all other columns assumed numeric</i>
------------	---

---

### Description

construct a BigQuery resource interface, for a matrix-like table with one column devoted to row identification (rowkeyfield) and all other columns assumed numeric

### Usage

```
BQM_Source(bqconn, tblnm, rowkeyfield, maxdfsize = 5e+05)
```

**Arguments**

bqconn	instance of BigQueryConnection from bigrquery
tblnm	character(1) table name known to bqconn
rowkeyfield	character(1) field in the table that will
maxdfsize	numeric(1) field in the table that will constrain as.data.frame for determining rownames generate rownames for matrices derived from table

**Value**

instance of BQM\_Source

**Examples**

```
if (interactive()) {
  con = bqConn(dataset="yriMulti", project=Sys.getenv("CGC_BILLING"),
    billing=Sys.getenv("CGC_BILLING"))
  banoMeth = BQM_Source(con, tblnm="banovichSE_MethylationData",
    rowkeyfield="cg_methyl450")
  banoMeth
}
```

---

BQM_Source-class	<i>Represent information about a BigQuery resource with a 'triple' database schema. This is targeting the isb-cgc TCGA layout. Big-Query Records are regarded as triples, within major groups defined by filtervbl. Triples have content subject - gene - value, to be pivoted to genes(rows) x subjects(columns) with values as entries.</i>
------------------	---

---

**Description**

Represent information about a BigQuery resource with a 'triple' database schema. This is targeting the isb-cgc TCGA layout. BigQuery Records are regarded as triples, within major groups defined by filtervbl. Triples have content subject - gene - value, to be pivoted to genes(rows) x subjects(columns) with values as entries.

---

BQSummarizedExperiment-class	<i>Define a class to use BigQuery data through SummarizedExperiment interface</i>
------------------------------	---

---

**Description**

Define a class to use BigQuery data through SummarizedExperiment interface

**Slots**

rowQref a `BigQueryConnection` wrapped in `tbl_dbi` that holds rowData for the `SummarizedExperiment` instance

colQref a `BigQueryConnection` wrapped in `tbl_dbi` that holds colData for the `SummarizedExperiment` instance

rowkey `character(1)` name of a field in the table referenced by rowQref to be used as key for features

colkey `character(1)` name of a field in the table referenced by colQref to use as key for samples

assayvbl `character(1)` name to be used to select table providing assay content

**Note**

This is an experimental structure to probe the concept that one can use a `SummarizedExperiment` object to interact with BigQuery data, particularly TCGA data. The slots rowQref and colQref are expected to be `BigQuery` connections which supply information on features and samples respectively, in a way that is consistent with the assay representation. See [seByTumor](#) for illustration.

---

cgcConn

*Simplify connection to a BigQuery dataset for the project "isb-cgc"*


---

**Description**

Simplify connection to a BigQuery dataset for the project "isb-cgc"

**Usage**

```
cgcConn(
  dataset = "TCGA_bioclin_v0",
  project = "isb-cgc",
  billing = Sys.getenv("CGC_BILLING")
)
```

**Arguments**

dataset	character string with dataset name
project	character string with project name
billing	character(1) with billing code

**Value**

instance of [BigQueryConnection-class](#)

**Note**

This function operates on a BigQuery project to select a dataset and return a connection. If the google billing code is assigned to environment variable CGC\_BILLING, that will be used to authenticate the user and collect charges. Alternately the billing code can be given as a parameter.

**Examples**

```

if (interactive()) {
  cgcConn
  require(bigrquery)
  # defaults concern new GDC-compliant format
  if (nchar(Sys.getenv("CGC_BILLING"))>0) {
    clin = cgcConn()
    dbListTables(clin)
  }
}

```

---

dim,BQ3\_ArraySeed-method

*dim derived from saved dimnames*

---

**Description**

dim derived from saved dimnames

**Usage**

```

## S4 method for signature 'BQ3_ArraySeed'
dim(x)

```

**Arguments**

x                   instance of BQ3\_ArraySeed

**Value**

integer(2) vector of dimensions corresponding to R's layout, assuming 2-d data

---

dim,BQM\_ArraySeed-method

*dim derived from saved dimnames*

---

**Description**

dim derived from saved dimnames

**Usage**

```

## S4 method for signature 'BQM_ArraySeed'
dim(x)

```

**Arguments**

x                   instance of BQM\_ArraySeed

**Value**

integer(2) vector of dimensions corresponding to R's layout, assuming 2-d data

---

dim,RESTfulSummarizedExperiment-method

*Dimension access for RESTfulSummarizedExperiment*

---

### **Description**

Dimension access for RESTfulSummarizedExperiment

### **Usage**

```
## S4 method for signature 'RESTfulSummarizedExperiment'  
dim(x)
```

### **Arguments**

x                    instance of RESTfulSummarizedExperiment

### **Value**

vector of nrows, ncols

---

dimnames,BQ3\_ArraySeed-method

*dimnames are saved in the BQ3\_ArraySeed*

---

### **Description**

dimnames are saved in the BQ3\_ArraySeed

### **Usage**

```
## S4 method for signature 'BQ3_ArraySeed'  
dimnames(x)
```

### **Arguments**

x                    instance of BQ3\_ArraySeed

### **Value**

currently returns list(NULL, NULL) as we do not store dimnames in HDF5

---

dimnames, BQM\_ArraySeed-method  
*dimnames are saved in the BQM\_ArraySeed*

---

### Description

dimnames are saved in the BQM\_ArraySeed

### Usage

```
## S4 method for signature 'BQM_ArraySeed'
dimnames(x)
```

### Arguments

x                    instance of BQM\_ArraySeed

### Value

currently returns list(NULL, NULL) as we do not store dimnames in HDF5

---

goPatt                    *Create a data.frame with ENSEMBL and SYMBOL identifiers associated with a GO TERM specified by a regular expression in termPattern*

---

### Description

Create a data.frame with ENSEMBL and SYMBOL identifiers associated with a GO TERM specified by a regular expression in termPattern

### Usage

```
goPatt(
  termPattern = "neurotro",
  targets = c("ENSEMBL", "SYMBOL"),
  organism = "Hs",
  inst = "eg"
)
```

### Arguments

termPattern            a character string encoding a regular expression to be matched to keys of type TERM in GO.db

targets                columns to be returned from org.[organism].[inst].db

organism               two-letter code for organism in the OrgDb family of packages

inst                    two- or three-letter code (e.g., eg for ENTREZ GENE or sgd for yeastgenome.org) identifying institute responsible for annotation

**Value**

data.frame

**Examples**

```
gp = goPatt()
dim(gp)
head(gp)
```

---

gtexTiss	<i>Convenience function for access to gene-level GTEx tissues, as quantified in recount</i>
----------	---

---

**Description**

Convenience function for access to gene-level GTEx tissues, as quantified in recount

**Usage**

```
gtexTiss(endpoint = URL_hsdS(), svrtype = "hsds", dsetname = "/assay001")
```

**Arguments**

endpoint	endpoint URL of remote server
svrtype	type of server, must be either 'hsds' or 'h5serv'
dsetname	complete internal path to dataset in H5 file

**Value**

SummarizedExperiment instance

**Examples**

```
gtexTiss()
```

---

isbCgcDatasets	<i>Access the dataset names in the "isb-cgc" project</i>
----------------	--

---

**Description**

Access the dataset names in the "isb-cgc" project

**Usage**

```
isbCgcDatasets()
```

**Value**

character vector

**Examples**

```
isbCgcDatasets() # might be out of date ... can use list_datasets in bigquery
```

---

isbCgcTables                      *List the tables in a selected dataset*

---

**Description**

List the tables in a selected dataset

**Usage**

```
isbCgcTables(  
  dataset = "TCGA_hg19_data_v0",  
  billing = Sys.getenv("CGC_BILLING")  
)
```

**Arguments**

dataset	character string identifying a table in "isb-cgc"
billing	Google BigQuery billing code, which can be set in an environment variable CGC_BILLING

**Value**

character vector

**Examples**

```
if (interactive()) {  
  # be sure that .cgcBilling is set  
  code = Sys.getenv("CGC_BILLING")  
  if (!(nchar(code)==0)) {  
    isbCgcTables()  
  }  
}
```

---

newDA                              *DelayedArray bridge*

---

**Description**

DelayedArray bridge

**Usage**

```
newDA(seed = new("array"), Class = "DelayedArray")
```



---

pancan_SE	<i>illustrate DelayedArray assay from BigQuery backend in Summarized-Experiment</i>
-----------	---

---

## Description

illustrate DelayedArray assay from BigQuery backend in SummarizedExperiment

## Usage

```
pancan_SE(
  bqcon,
  colDataTableName = "clinical_PANCAN_patient_with_followup",
  clinVars = basic_clinvars(),
  colDSubjectIdName = "bcr_patient_barcode",
  colDFilterField = "acronym",
  colDFilterValue = "BRCA",

  assayDataTableName = "pancanMiRs_EBadjOnProtocolPlatformWithoutRepsWithUnCorrectMiRs_08_04_16",
  assayFeatureName = "ID",
  assaySampleTypeCode = "TP",
  subjectIDName = "ParticipantBarcode",
  tumorFieldName = "Study",
  tumorFieldValue = "BRCA",
  assayValueFieldName = "miRNAexpr"
)
```

## Arguments

bqcon	a BigQueryConnection instance
colDataTableName	character(1) defaulting to "clinical_PANCAN_patient_with_followup"
clinVars	character() vector of variables to be retained from the table named by 'colDataTableName', defaults to vector returned by clinVars()
colDSubjectIdName	character(1) defaulting to "bcr_patient_barcode"
colDFilterField	character(1) defaulting to "acronym"
colDFilterValue	character(1) defaulting to "BRCA"; a vector may be used, in which case multiple tumor types will be represented – must agree with tumorFieldValue, as clinical and assay data are collected separately
assayDataTableName	character(1) defaulting to "pancanMiRs_EBadjOnProtocolPlatformWithoutRepsWithUnCorrectMiR"
assayFeatureName	character(1) defaulting to "ID"
assaySampleTypeCode	character(1) defaulting to "TP"
subjectIDName	character(1) defaulting to "ParticipantBarcode"

```
tumorFieldName character(1) defaulting to "Study"
tumorFieldValue
    character() defaulting to "BRCA"; a vector may be used in which case multiple
    tumor types will be represented – must agree with colDFilterValue
assayValueFieldName
    character(1) defaulting to "miRNAexpr"
```

**Value**

an instance of SummarizedExperiment

**Note**

The parameters need different assignments for different tables. Field names are not standardized across tables as of August 2018. AUTHENTICATION CONCERNS: You must have a valid BigQuery project identifier in the environment variable CGC\_BILLING, or pass such as 'billing' when using DBI::dbConnect(bigquery::bigquery(), ...). To get such a project identifier, you need to have a Google identity and you must have created a BigQuery project with that identity. Notes at <https://isb-cancer-genomics-cloud.readthedocs.io/en/latest/sections/progapi/bigqueryGUI/WalkthroughOfGoogleBigQuery.html> provide details. Another approach that can be used involves the Google Cloud SDK. Assuming you have a Google identity and have installed a recent SDK instance, you can use (in the shell) gcloud auth login to pick the identity that has a project with id PROJECT\_ID. Use that project id as the billing code for bigrquery dbConnect, or set CGC\_BILLING in the environment to evaluate to that project id.

**Examples**

```
if (interactive() & requireNamespace("DBI") &
    requireNamespace("bigrquery")) {
  billco = Sys.getenv("CGC_BILLING")
  if (nchar(billco)==0)
    stop("need CGC_BILLING set to your BigQuery project ID, see note in ?pancan_SE")
  bqcon = DBI::dbConnect(bigrquery::bigquery(), project = "pancancer-atlas",
    dataset = "Annotated", billing = billco)
  brca_mirSE = pancan_SE(bqcon)
  brca_mirSE
}
```

---

RESTfulSummarizedExperiment

*Construct RESTfulSummarizedExperiment*

---

**Description**

Construct RESTfulSummarizedExperiment

hidden constructor

**Usage**

```

RESTfulSummarizedExperiment(se, source)

.RESTfulSummarizedExperiment(se, source)

## S4 method for signature 'RESTfulSummarizedExperiment,missing'
assay(x, i, withDimnames = TRUE, ...)

```

**Arguments**

se	SummarizedExperiment instance, assay component can be empty SimpleList
source	instance of H5S_dataset
x	instance of RESTfulSummarizedExperiment
i	not used
...	not used

**Value**

instance of RESTfulSummarizedExperiment  
matrix

**Note**

RESTfulSummarizedExperiment contains a global dimnames list generated at creation. It is possible that standard operations on a SummarizedExperiment will engender dimnames components that differ from the initial global dimnames, principally through unification (adding suffixes when dimname elements are repeated). When this is detected, assay() will fail with a complaint about length(setdiff(\*names(x), x@globalDimnames[...])).

**Examples**

```

require("rhdf5client")
hsds = H5S_source(serverURL=URL_hsds())
hsdsCon = setPath(hsds, "/home/reshg/bano_meQTLex.h5")
fetchDatasets(hsdsCon)
banoh5 = H5S_dataset2(hsdsCon, "d-435d7ad4-9f13-11e8-92c2-0242ac120021")
ehub = ExperimentHub::ExperimentHub()
myfiles <- AnnotationHub::query(ehub, "restfulSEData")
myfiles[["EH551"]] -> banoSEMeta
rr = RESTfulSummarizedExperiment(banoSEMeta, banoh5)
rr
rr2 = rr[1:4, 1:5] # just modify metadata
rr2
assay(rr2) # extract data

```

---

RESTfulSummarizedExperiment-class

*HDF5Server-based assay for SummarizedExperiment*

---

### Description

HDF5Server-based assay for SummarizedExperiment

### Usage

```
## S4 method for signature 'RESTfulSummarizedExperiment'
assayNames(x, ...)
```

```
## S4 method for signature 'RESTfulSummarizedExperiment,numeric,numeric,ANY'
x[i, j, ..., drop = FALSE]
```

### Arguments

x	instance of RESTfulSummarizedExperiment
...	not used
i	numeric selection vector
j	numeric selection vector
drop	not used

### Value

instance of RESTfulSummarizedExperiment

---

se100k

*Convenience functions using HSDS server to extract tenx neurons full or subset data*

---

### Description

Convenience functions using HSDS server to extract tenx neurons full or subset data

### Usage

```
se100k(endpoint = URL_hsdS(), svrtype = "hsds", dsetname = "/assay001")
```

```
se1.3M(endpoint = URL_hsdS(), svrtype = "hsds", dsetname = "/newassay001")
```

### Arguments

endpoint	endpoint URL of remote server
svrtype	type of server, must be either 'hsds' or 'h5serv'
dsetname	complete internal path to dataset in H5 file

**Value**

RESTfulSummarizedExperiment  
SummarizedExperiment instance

**Note**

se1.3M provides access to the full 1.3 million neurons with features in their order as given in the original HDF5 while se100k provides access to only 100k neurons with expression features sorted by genomic location

**Examples**

```
ss = se100k()
# get a set of genes from Tasic et al. 2016 Nature Neuroscience
tc = tasicCortex()
adultCort = tc$GENEID
# subset
csums = apply(assay(ss[adultCort,1:500]),1,sum)
names(csums) = tc$SYMBOL
csums
```

---

seByTumor

*Given a BigQueryConnection to the 2017 GDC-oriented ISB TCGA bigtables, obtain a SummarizedExperiment 'shell' rowData and colData*

---

**Description**

Given a BigQueryConnection to the 2017 GDC-oriented ISB TCGA bigtables, obtain a SummarizedExperiment 'shell' rowData and colData

**Usage**

```
seByTumor(
  tumorCode = "LUAD",
  assayTblName = "RNAseq_Gene_Expression",
  rdColsToKeep = c("gene_name", "Ensembl_gene_id", "gene_type"),
  bqConnClinical,
  bqConnAssay,
  rowkey = "Ensembl_gene_id",
  colkey = "case_barcode",
  assayvbl = "HTSeq__Counts"
)
```

**Arguments**

tumorCode	one of the concise TCGA codes in a character string – not checked, defaults to "LUAD", lung adenocarcinoma
assayTblName	the name of the assay whose annotation will be used as rowData
rdColsToKeep	columns of assay table to use in rowData component

bqConnClinical	instance of BigQueryConnection from bigrquery, for access to clinical metadata – current expectation is that the BigQuery dataset is named "TCGA_bioclin_v0" and has a table called "Clinical"
bqConnAssay	instance of BigQueryConnection from bigrquery – current expectation is that the BigQuery dataset is named "TCGA_hg19_data_v0"
rowkey	name of a field to be used as key for rows
colkey	name of a field to use as key for samples
assayvbl	name of field to use for numerical values

## Value

SummarizedExperiment

## Note

This function demonstrates the use of external resources for rowData, colData and assay components of a SummarizedExperiment instance. The intention is that the full complement of activities supported by [SummarizedExperiment-class](#) are likewise supported through this class, with assay data and sample and feature metadata all external and in BigQuery projects. The seByTumor function is provided to generate an example of this approach with minimal user configuration.

## Examples

```
if (interactive()) {
  require(bigrquery)
  # be sure that .cgcBilling is set
  code = Sys.getenv("CGC_BILLING")
  if (!(nchar(code)==0)) {
    clinQ = cgcConn(billing=code)
    assayQ = cgcConn( dataset = "TCGA_hg38_data_v0", billing=code )
    myexpShell = seByTumor( bqConnClinical=clinQ,
                          bqConnAssay=assayQ)
    print(myexpShell)
    print(nrow(myexpShell) == 60483)
    print(ncol(myexpShell) == 515) # 7/18/2018
    assay(myexpShell[11:15,1:4]) # some case_barcodes repeat
  }
}
```

---

seByTumor\_2016

*Given a BigQueryConnection to the 2016 ISB TCGA bigtables, obtain a SummarizedExperiment 'shell' rowData and colData*

---

## Description

Given a BigQueryConnection to the 2016 ISB TCGA bigtables, obtain a SummarizedExperiment 'shell' rowData and colData

**Usage**

```
seByTumor_2016(
  tumorCode = "LUAD",
  assayTblName = "mRNA_UNC_HiSeq_RSEM",
  rdColsToKeep = c("original_gene_symbol", "HGNC_gene_symbol", "gene_id", "Study"),
  bqConn
)
```

**Arguments**

tumorCode	one of the concise TCGA codes in a character string – not checked, defaults to "LUAD", lung adenocarcinoma
assayTblName	the name of the assay whose annotation will be used as rowData
rdColsToKeep	columns of assay table to use in rowData component
bqConn	instance of BigQueryConnection from bigrquery

**Value**

SummarizedExperiment instance, with BigQuery reference as assay

---

tasicCortex	<i>A set of mouse cortex marker genes.</i>
-------------	--

---

**Description**

A set of mouse cortex marker genes.

**Usage**

```
tasicCortex()
```

**Value**

data.frame with columns SYMBOL, GENEID

**Note**

<http://www.nature.com/doifinder/10.1038/nn.4216>, Fig 1C

**Examples**

```
head(tasicCortex())
```

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