

restfulSE – experiments with HDF5 server content wrapped in SummarizedExperiment

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1 restfulSE

This R package includes proof-of-concept code illustrating several approaches to SummarizedExperiment design with assays stored out-of-memory.

1.1 HDF5 server backed SummarizedExperiment

HDF Server “extends the HDF5 data model to efficiently store large data objects (e.g. up to multi-TB data arrays) and access them over the web using a RESTful API.” In this `restfulSE` package, several data structures are introduced

- to model the server data architecture and
- to perform targeted extraction of numerical data from HDF5 arrays stored on the server.

We work with HDF Object store (<https://www.hdfgroup.org/solutions/hdf-cloud/>).

1.1.1 Illustration with 10x genomics 1.3 million neurons

We used Martin Morgan's `TENxGenomics` package to transform the sparse-formatted HDF5 supplied by 10x into a dense HDF5 matrix to support natural slicing. Thanks to native compression in HDF5, the data volume expansion is modest.

A helper function in the `restfulSE` package creates a `RESTfulSummarizedExperiment` instance that points to the full numerical dataset.

```
library(restfulSE)
my10x = sel.3M()
## snapshotDate(): 2019-04-29
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
## downloading 0 resources
## loading from cache
##      'EH1656 : 1656'
my10x
## class: SummarizedExperiment
## dim: 27998 1306127
## metadata(0):
## assays(1): counts
## rownames(27998): ENSMUSG000000051951 ENSMUSG000000089699 ...
##      ENSMUSG000000096730 ENSMUSG000000095742
## rowData names(12): ensid seqnames ... symbol entrezid
## colnames(1306127): AACCTGAGATAGGAG-1 AACCTGAGCGGCTTC-1 ...
##      TTTGTCAGTTAAAGTG-133 TTTGTCATCTGAAAGA-133
## colData names(4): Barcode Sequence Library Mouse
```

As an exercise, we acquire the ENSEMBL identifiers for mouse genes annotated to hippocampus development, which has GO ID `GO:0021766`, and check counts for 10 genes on 6 samples:

```
library(org.Mm.eg.db)
##
hippdev = select(org.Mm.eg.db,
  keys="GO:0021766", keytype="GO", column="ENSEMBL")$ENSEMBL
```

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```
## 'select()' returned 1:many mapping between keys and columns
hippdev = intersect(hippdev, rownames(my10x))
#unnname(assay(my10x[ hippdev[1:10], 10001:10006]))
```

The result:

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
[1,]	0	0	0	0	0	0
[2,]	0	0	0	0	0	0
[3,]	0	0	0	1	0	0
[4,]	0	1	2	6	5	0
[5,]	0	0	0	0	0	0
[6,]	1	2	4	8	7	3
[7,]	0	0	0	0	0	0
[8,]	0	0	0	0	0	2
[9,]	0	0	0	0	0	0
[10,]	3	0	3	0	1	9

1.1.2 Illustration with GTEx tissue expression

We exported the content of the [recount2 GTEx gene-level quantifications](#) to our HDF5 server. A convenience function is available:

```
tiss = gtexTiss()
## snapshotDate(): 2019-04-29
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
## downloading 0 resources
## loading from cache
## 'EH556 : 556'
tiss
## class: RangedSummarizedExperiment
## dim: 58037 9662
## metadata(0):
## assays(1): recount
## rownames(58037): ENSG000000000003.14 ENSG000000000005.5 ...
## ENSG00000283698.1 ENSG00000283699.1
## rowData names(3): gene_id bp_length symbol
## colnames(9662): SRR660824 SRR2166176 ... SRR612239 SRR615898
## colData names(82): project sample ... title characteristics
```

We'll use this remote data as a tool for investigating transcriptional patterns in brain anatomy. We can identify the samples from brain using the 'smtsd' colData element:

```
binds = grep("Brain", tiss$smtsd)
table(tiss$smtsd[binds][1:100]) # check diversity in 100 samples
##
## Brain - Amygdala
## 4
## Brain - Anterior cingulate cortex (BA24)
## 5
## Brain - Caudate (basal ganglia)
```

```
##                                10
##      Brain - Cerebellar Hemisphere
##                                9
##      Brain - Cerebellum
##                                13
##      Brain - Cortex
##                                13
##      Brain - Frontal Cortex (BA9)
##                                10
##      Brain - Hippocampus
##                                8
##      Brain - Hypothalamus
##                                5
## Brain - Nucleus accumbens (basal ganglia)
##                                7
##      Brain - Putamen (basal ganglia)
##                                4
##      Brain - Spinal cord (cervical c-1)
##                                3
##      Brain - Substantia nigra
##                                9
```

We'll identify genes annotated to neurotrophic functions using another convenience function in this package:

```
ntgenes = goPatt(termPattern="neurotroph")
## 'select()' returned 1:1 mapping between keys and columns
## 'select()' returned 1:many mapping between keys and columns
head(ntgenes)
```

	GO	EVIDENCE	ONTOLOGY	ENSEMBL	SYMBOL
## 1	G0:0004897	IDA	MF	ENSG00000122756	CNTFR
## 2	G0:0004897	IMP	MF	ENSG00000160712	IL6R
## 3	G0:0004897	IDA	MF	ENSG00000134352	IL6ST
## 4	G0:0004897	IDA	MF	ENSG00000113594	LIFR
## 5	G0:0043121	ISS	MF	ENSG00000064300	NGFR
## 6	G0:0043121	IDA	MF	ENSG00000148053	NTRK2

2 Some details

2.1 Motivation

Extensive human and computational effort is expended on downloading and managing large genomic data at site of analysis. Interoperable formats that are accessible via generic operations like those in RESTful APIs may help to improve cost-effectiveness of genome-scale analyses.

In this report we examine the use of HDF5 server as a back end for assay data, mediated through the RangedSummarizedExperiment API for interactive use.

A modest server configured to deliver HDF5 content via a RESTful API has been prepared and is used in this vignette.

2.2 Executive summary

We want to provide rapid access to array-like data. We'll work with the Banovich 450k data as there is a simple check against an in-memory representation.

We build a SummarizedExperiment by combining an assay-free RangedSummarizedExperiment with this reference.

```
ehub = ExperimentHub::ExperimentHub()
## snapshotDate(): 2019-04-29
tag = names(AnnotationHub::query(ehub, "banoSEMeta"))
banoSE = ehub[[tag[1]]]
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
## downloading 0 resources
## loading from cache
## 'EH551 : 551'
ds = HSDSArray(endpoint=URL_hsd(),svrtype="hsds",
               domain="/shared/bioconductor/bano_meQTLex.h5",dsetname="/assay001")
assays(banoSE) = SimpleList(betas=ds)
```

We can update the SummarizedExperiment metadata through subsetting operations, and then extract the relevant assay data. The data are retrieved from the remote server with the `assay` method.

```
rbanoSub = banoSE[5:8, c(3:9, 40:50)]
## Loading required package: Biostrings
## Loading required package: XVector
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:DelayedArray':
##
##     type
## The following object is masked from 'package:base':
##
##     strsplit
#assay(rbanoSub)
```

2.3 10xGenomics examples

2.3.1 t-SNE for a set of genes annotated to hippocampus

We have used Martin Morgan's TENxGenomics package to create a dense HDF5 representation of the assay data, and placed it on the `bigec2` server. The metadata are available as `se100k` in this package; we have used `EnsDb.Mmusculus.v79` to supply gene ranges where available; genes reported but without addresses are addressed at chr1:2 with width 0. The rows are sorted by genomic address within chromosomes.

```
tenx100k = se100k()
## snapshotDate(): 2019-04-29
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
```

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```
## downloading 0 resources
## loading from cache
##      'EH552 : 552'
tenx100k
## class: RangedSummarizedExperiment
## dim: 27998 100000
## metadata(1): source
## assays(1): counts
## rownames(27998): ENSMUSG000000109048 ENSMUSG000000109510 ...
##      ENSMUSG000000096768 ENSMUSG000000096850
## rowData names(6): gene_id gene_name ... seq_coord_system symbol
## colnames(100000): AACCTGAGATAGGAG-1 AACCTGAGCGGCTTC-1 ...
##      GACGTTAGTCATACTG-11 GACGTTAGTCCGTGAC-11
## colData names(4): Barcode Sequence Library Mouse
```

We will subset genes annotated to hippocampus development. Here are some related categories:

```
12092 G0:0021766      hippocampus development
12096 G0:0021770      parahippocampal gyrus development
34609 G0:0097410      hippocampal interneuron differentiation
34631 G0:0097432      hippocampal pyramidal neuron differentiation
34656 G0:0097457      hippocampal mossy fiber
35169 G0:0098686      hippocampal mossy fiber to CA3 synapse
42398 G0:1990026      hippocampal mossy fiber expansion
```

```
library(org.Mm.eg.db)
atab = select(org.Mm.eg.db, keys="G0:0021766", keytype="G0", columns="ENSEMBL")
## 'select()' returned 1:many mapping between keys and columns
hg = atab[, "ENSEMBL"]
length(hgok <- intersect(hg, rownames(tenx100k)))
## [1] 61
```

This is a very scattered collection of rows in the matrix. We acquire expression measures for genes annotated to hippocampus on 4000 samples. t-SNE is then used to project the log-transformed measures to the plane.

```
hipn = assay(tenx100k[hgok, 1:4000]) # slow
#d = dist(t(log(1+hipn)), method="manhattan")
#proj = Rtsne(d)
```

```
#plot(proj$Y)
```

2.3.2 A set of genes related to the visual cortex

Tasic et al. (Nature neuro 2016, DOI 10.1038/nn.4216) describe single cell analysis of the adult murine brain, identify clusters of cells with distinct transcriptional profiles and anatomic location, and enumerate lists of genes that discriminate these clusters. The tasicST6 DataFrame provides details.

```
#data("tasicST6", package = "restfulSEData")
ehub = ExperimentHub::ExperimentHub()
## snapshotDate(): 2019-04-29
tag = names(AnnotationHub::query(ehub, "tasicST6"))
tasicST6 = ehub[[tag[1]]]
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
## downloading 0 resources
## loading from cache
## 'EH557 : 557'
tasicST6
## DataFrame with 49 rows and 4 columns
##      clid      txtype1      txtype2
##      <character> <character> <character>
## 1      f01      Vip      Mybpc1
## 2      f02      Vip      Parm1
## 3      f03      Vip      Sncg
## 4      f04      Vip      Chat
## 5      f05      Vip      Gpc3
## ...      ...      ...      ...
## 45     f45      Oligo 9630013A20Rik
## 46     f46      Oligo      Opalin
## 47     f47      Micro      Ctss
## 48     f48      Endo      Xdh
## 49     f49      SMC      Myl9
##
##
## 1
## 2
## 3
## 4
## 5
## ...
## 45      c("Brca1", "Rnf122", "Mbp", "Zcchc12", "E
## 46
## 47      c("Cx3cr1", "Clqb", "Cd53", "Csflr", "Itgam", "Abi3", "Clqa", "
## 48      c("Tbc1d4", "AI467606", "Exosc7", "Eltd1", "Fas", "Hmgcs2", "No
## 49      c("Bgn", "Nupr1", "Casq2", "Mylk", "Gprc5c", "Slc38a11", "Slc6a20a", "Pcolce", "Vtn", "Cnn2", "Nid1",
```

Key high-level discrimination concerns cells regarded as GABAergic vs. glutamatergic (inhibitory vs excitatory neurotransmission).

2.4 Background

Banovich et al. published a subset of DNA methylation measures assembled on 64 samples of immortalized B-cells from the YRI HapMap cohort.

```
library(restfulSE)
#data("banoSEMeta", package = "restfulSEData")
ehub = ExperimentHub::ExperimentHub()
## snapshotDate(): 2019-04-29
```

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```
tag = names(AnnotationHub::query(ehub, "banoSEMeta"))
banoSEMeta = ehub[[tag[1]]]
## see ?restfulSEData and browseVignettes('restfulSEData') for documentation
## downloading 0 resources
## loading from cache
##      'EH551 : 551'
#banoSEMeta
```

The numerical data have been exported using H. Pages' `saveHDF5SummarizedExperiment` applied to the `banovichSE` `SummarizedExperiment` in the `yriMulti` package. The HDF5 component is simply copied into the server data space on the remote server.