R/Bioconductor 201

Physalia course 2023

Instructor: Jacques Serizay

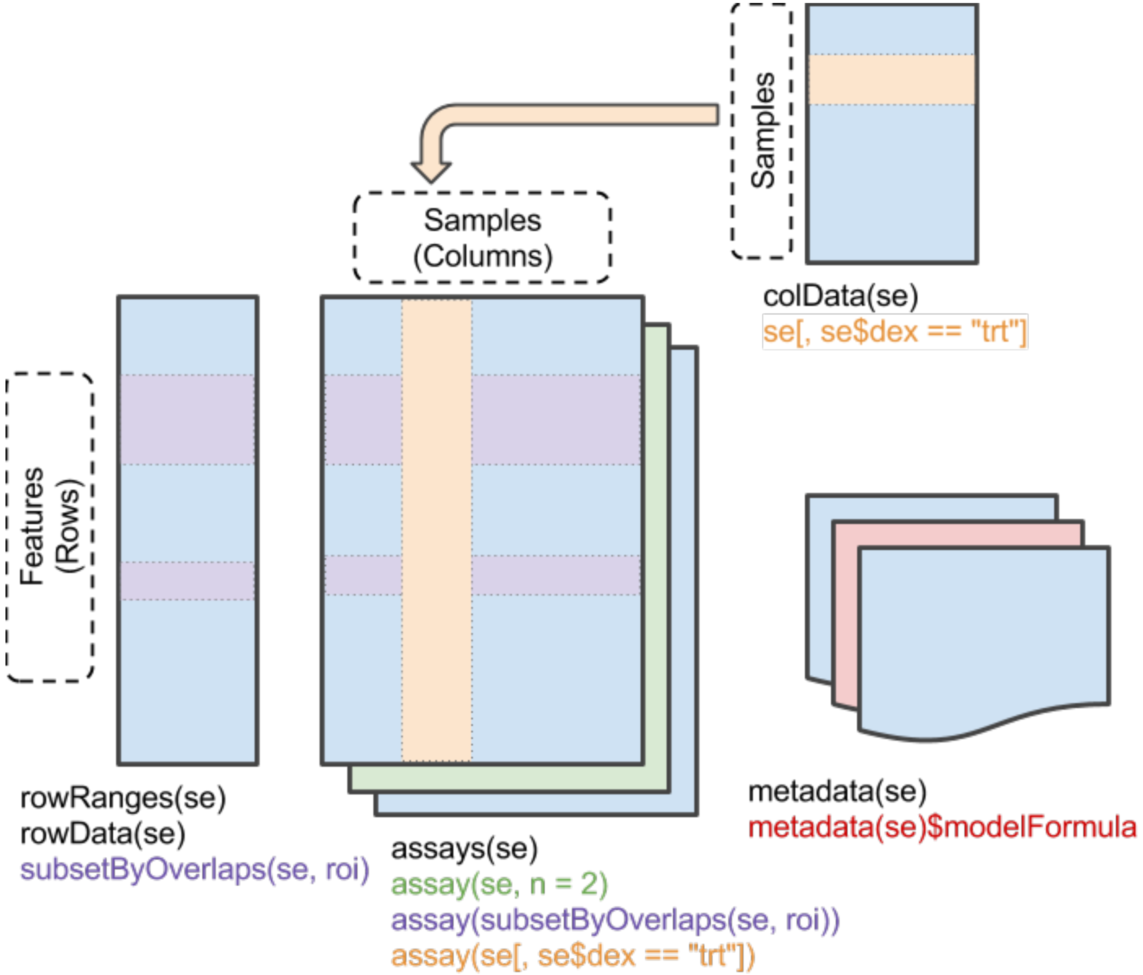
SummarizedExperiment

Published: 29 January 2015

Orchestrating high-throughput genomic analysis with Bioconductor

Wolfgang Huber ✉, Vincent J Carey, Robert Gentleman, Simon Anders, Marc Carlson, Benilton S Carvalho, Hector Corrada Bravo, Sean Davis, Laurent Gatto, Thomas Girke, Raphael Gottardo, Florian Hahne, Kasper D Hansen, Rafael A Irizarry, Michael Lawrence, Michael I Love, James MacDonald, Valerie Obenchain, Andrzej K Oleś, Hervé Pagès, Alejandro Reyes, Paul Shannon, Gordon K Smyth, Dan Tenenbaum, Levi Waldron & Martin Morgan -Show fewer authors

Nature Methods **12**, 115–121(2015) | Cite this article

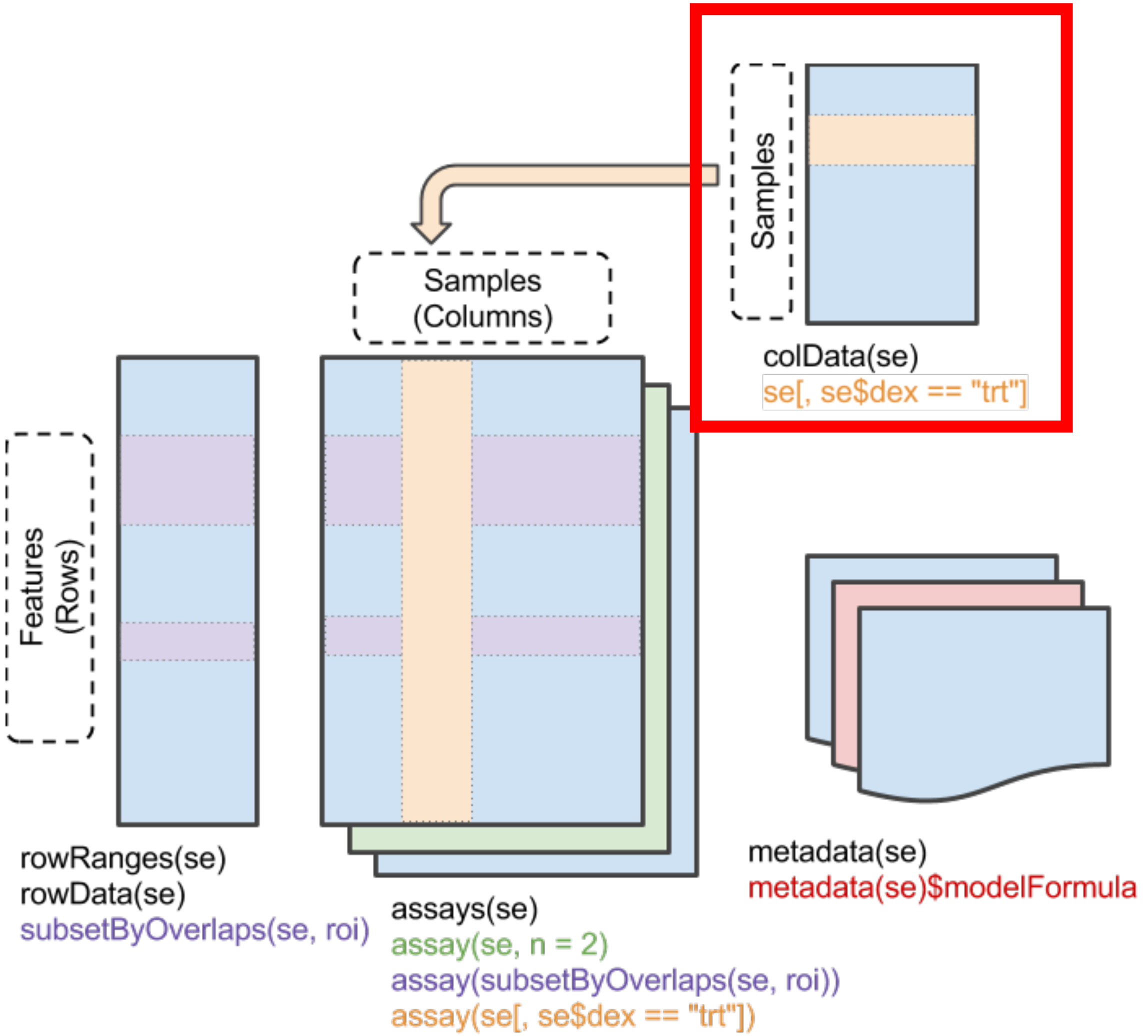


```
colData(se)
se[, se$dex == "trt"]
rowRanges(se)
rowData(se)
subsetByOverlaps(se, roi)
assays(se)
assay(se, n = 2)
assay(subsetByOverlaps(se, roi))
assay(se[, se$dex == "trt"])
metadata(se)
metadata(se)$modelFormula
```

SummarizedExperiment

- colData(): Annotations on each column, as a DataFrame.

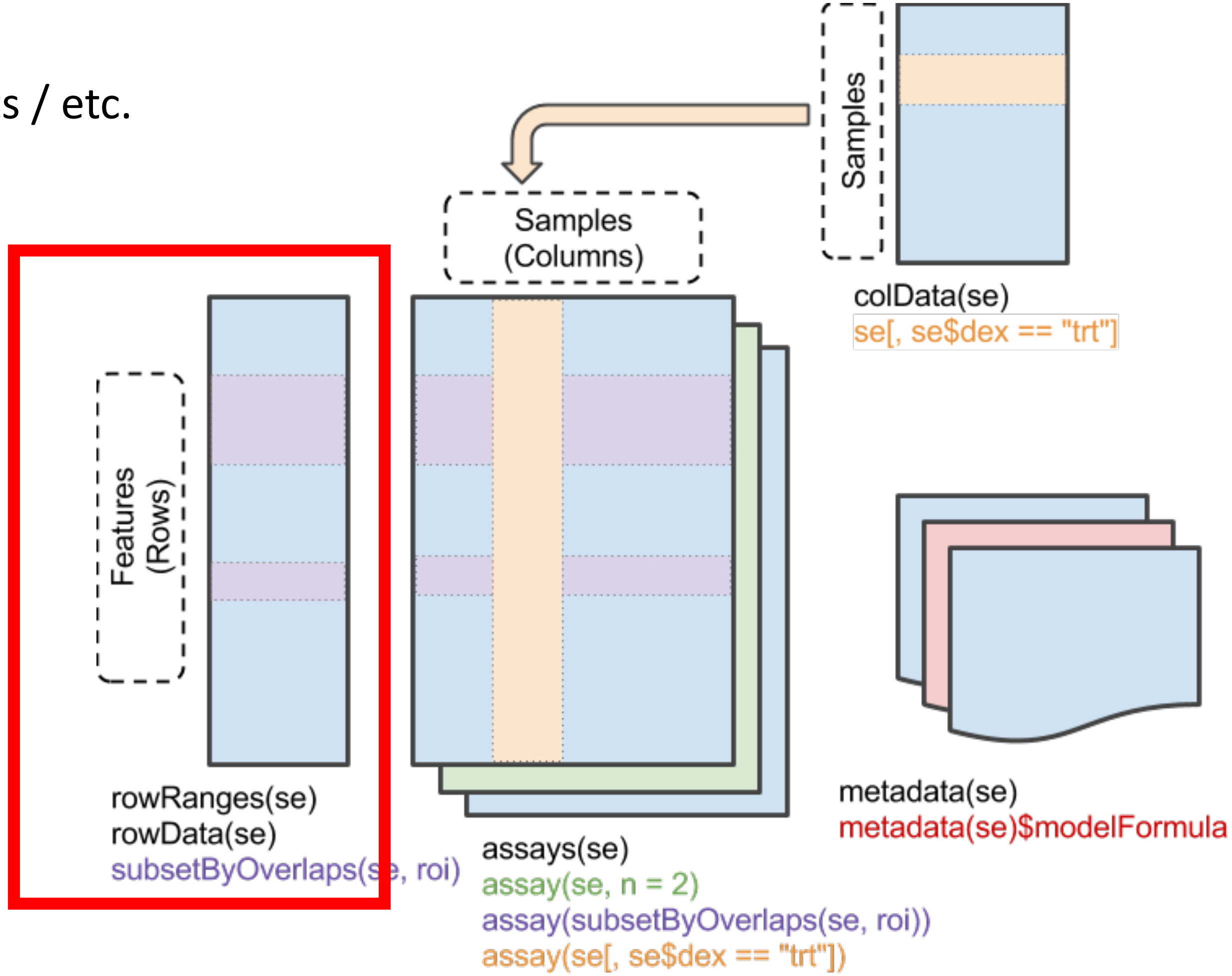
  E.g., description of each sample



SummarizedExperiment

- rowData/rowRanges(): Annotations on each row.

  E.g., coordinates of gene / exons /peaks in transcripts / etc.



SummarizedExperiment

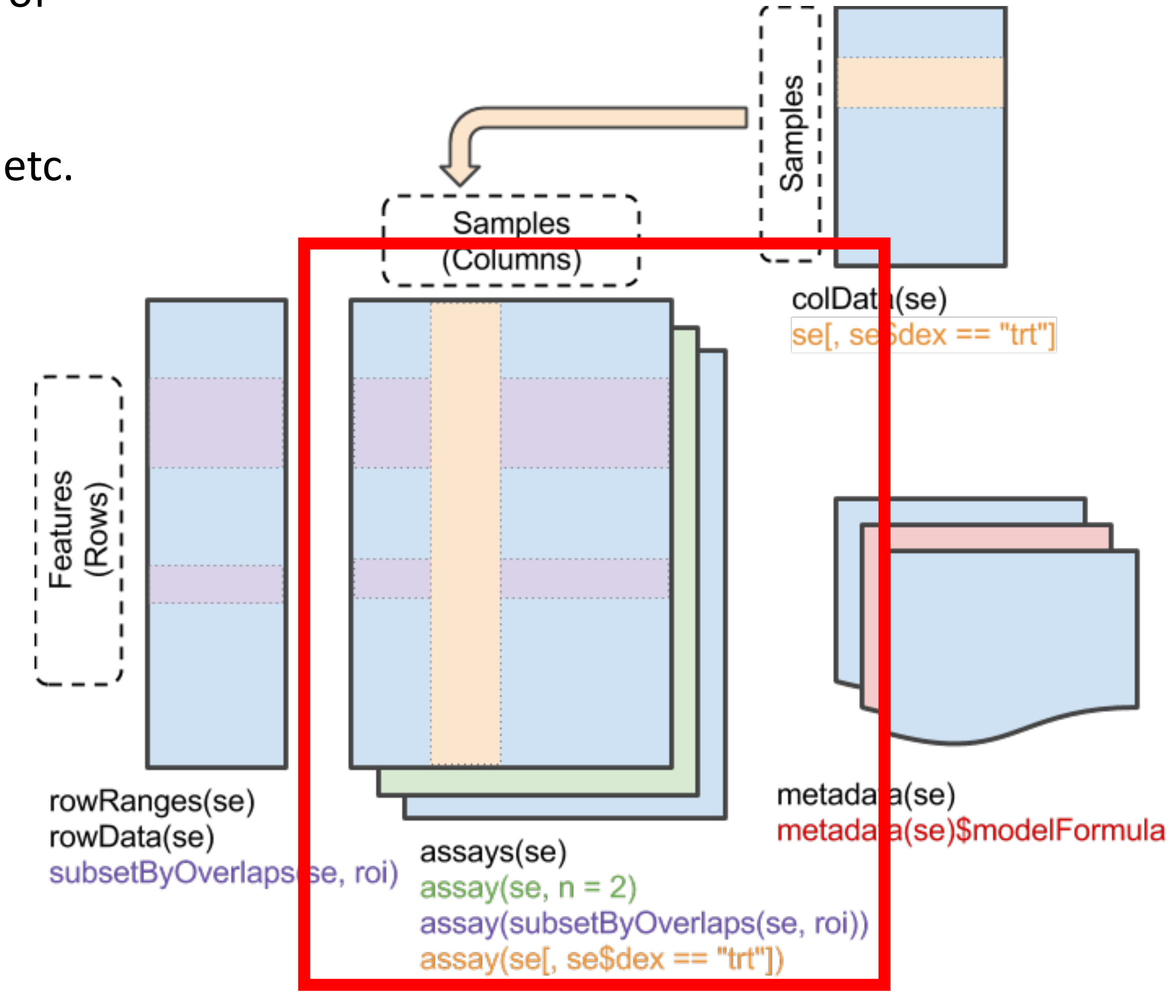
- assay(), assays(): A matrix-like or list of matrix-like objects of identical dimension

  rows: refer to **rowRanges**: genes, genomic coordinates, etc.

  columns: refer to **colData**: samples, cells, etc.

  Implements dim(), dimnames() and 2-dimensional [,]

  Can be several assays!!!



colDat (se)
se[, se dex == "trt"]

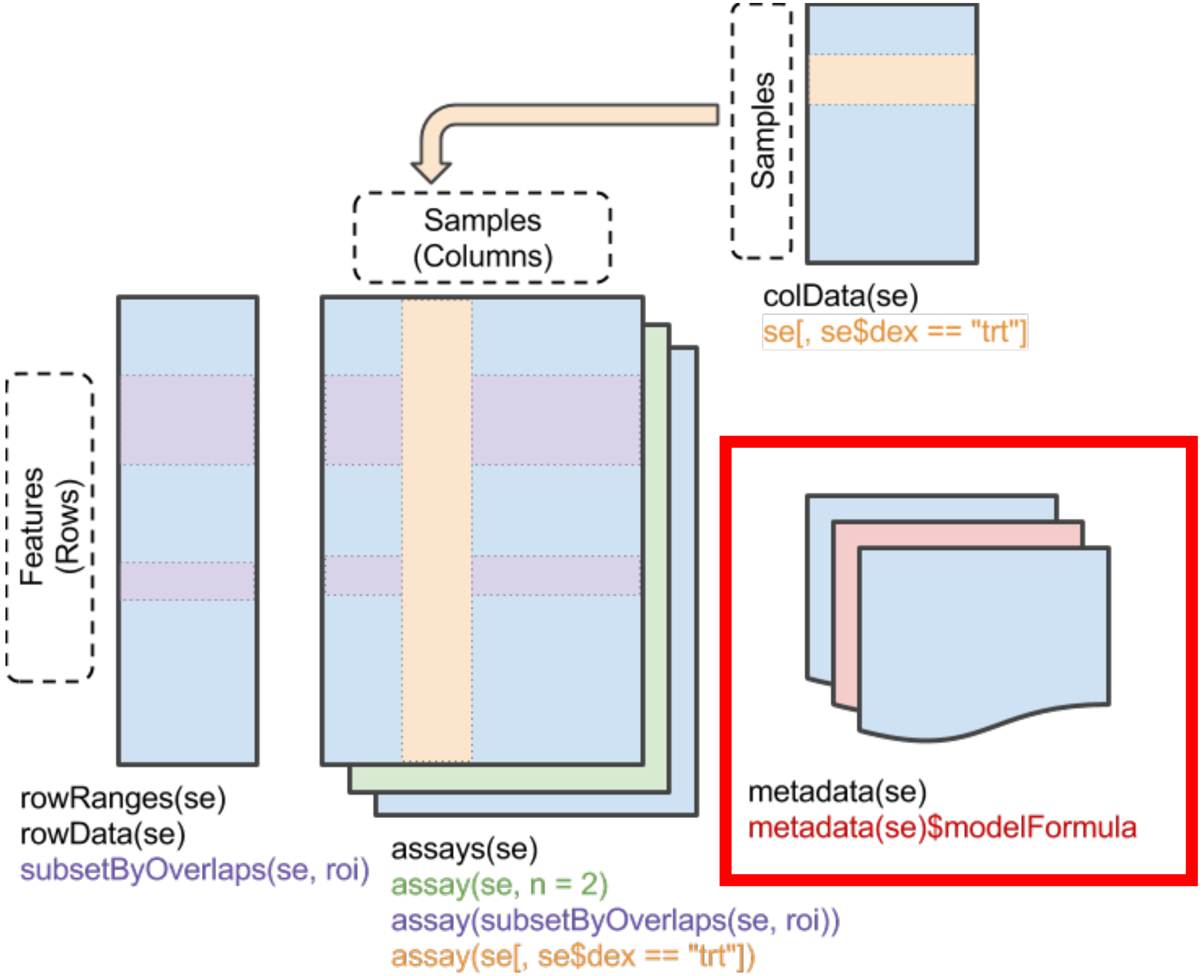
rowRanges(se)
rowData(se)
subsetByOverlaps se, roi)

assays(se)
assay(se, n = 2)
assay(subsetByOverlaps(se, roi))
assay(se[, se$dex == "trt"])

metada a(se)
metada a(se)$modelFormula

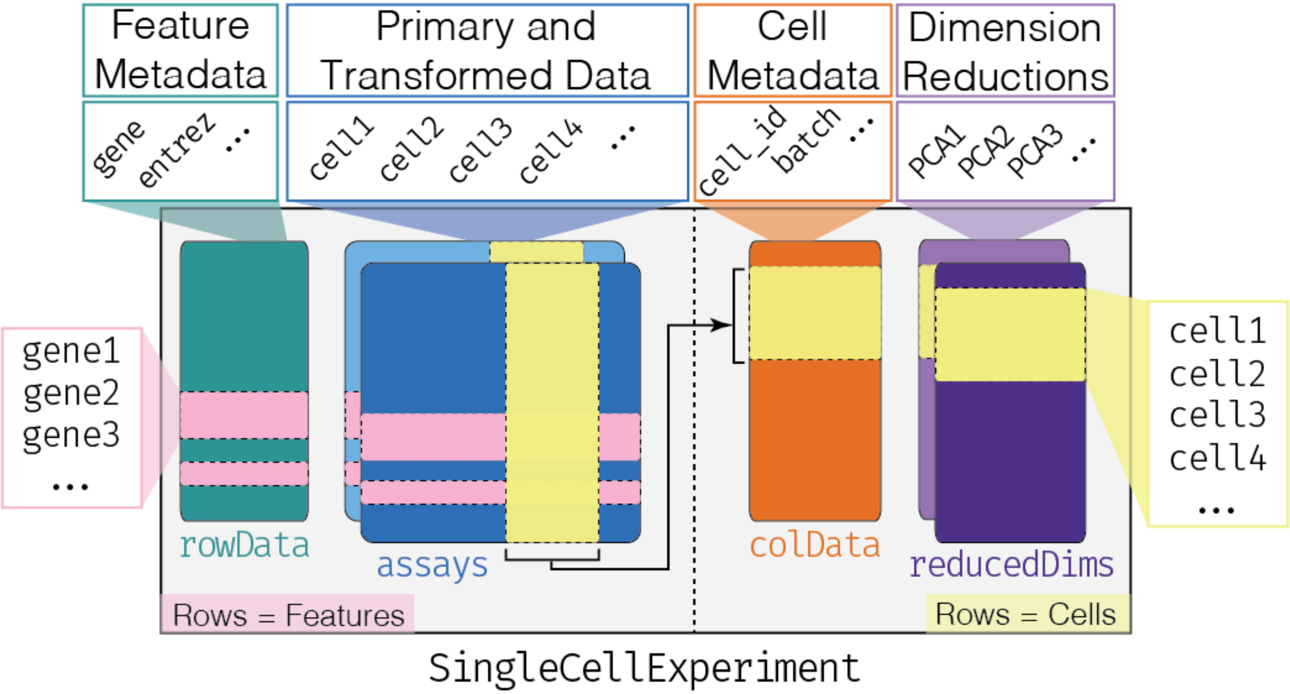
SummarizedExperiment

- metadata(): List of unstructured metadata describing the overall content of the object.



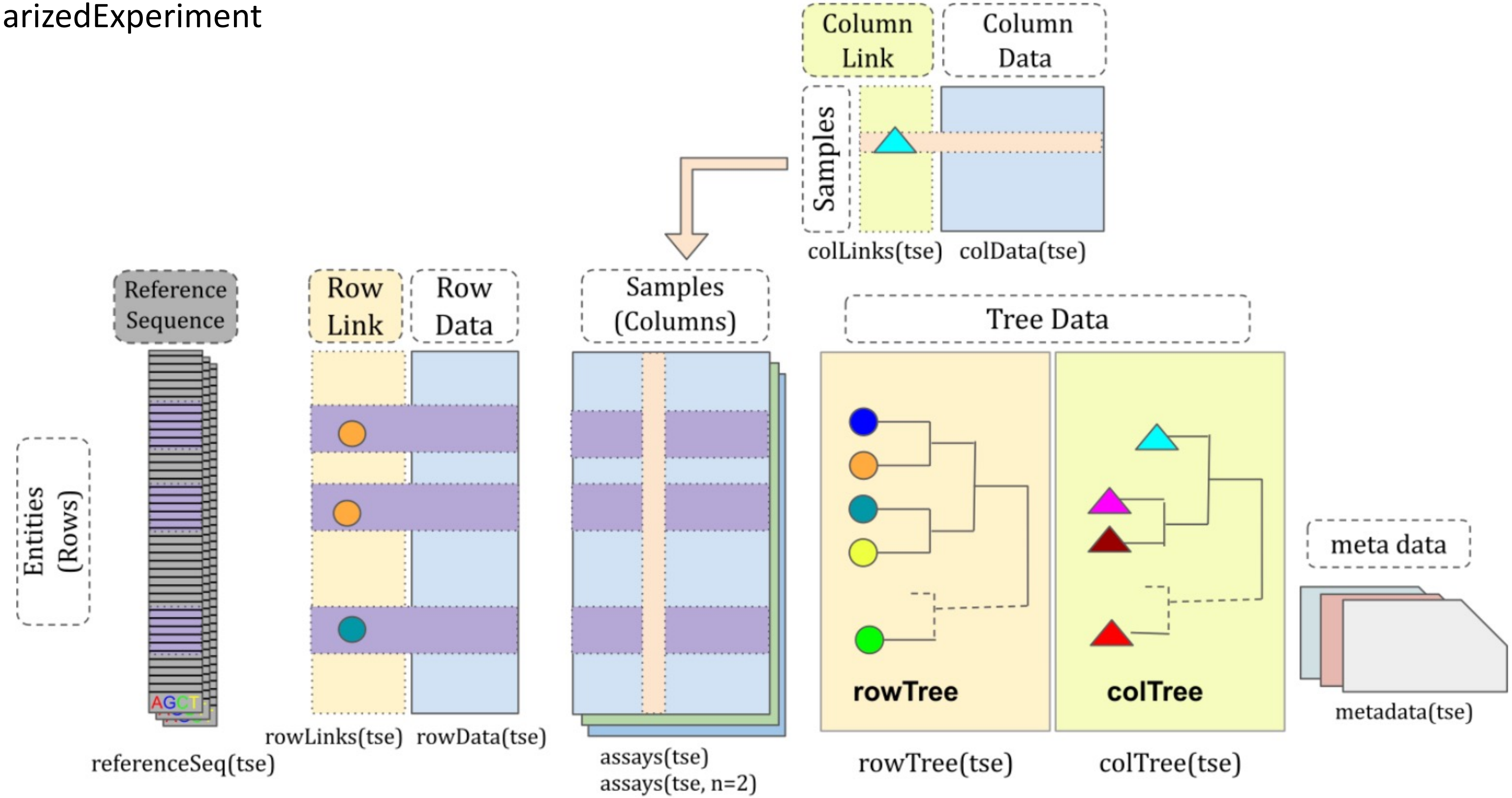
Classes derived from SummarizedExperiment

- SingleCellExperiment



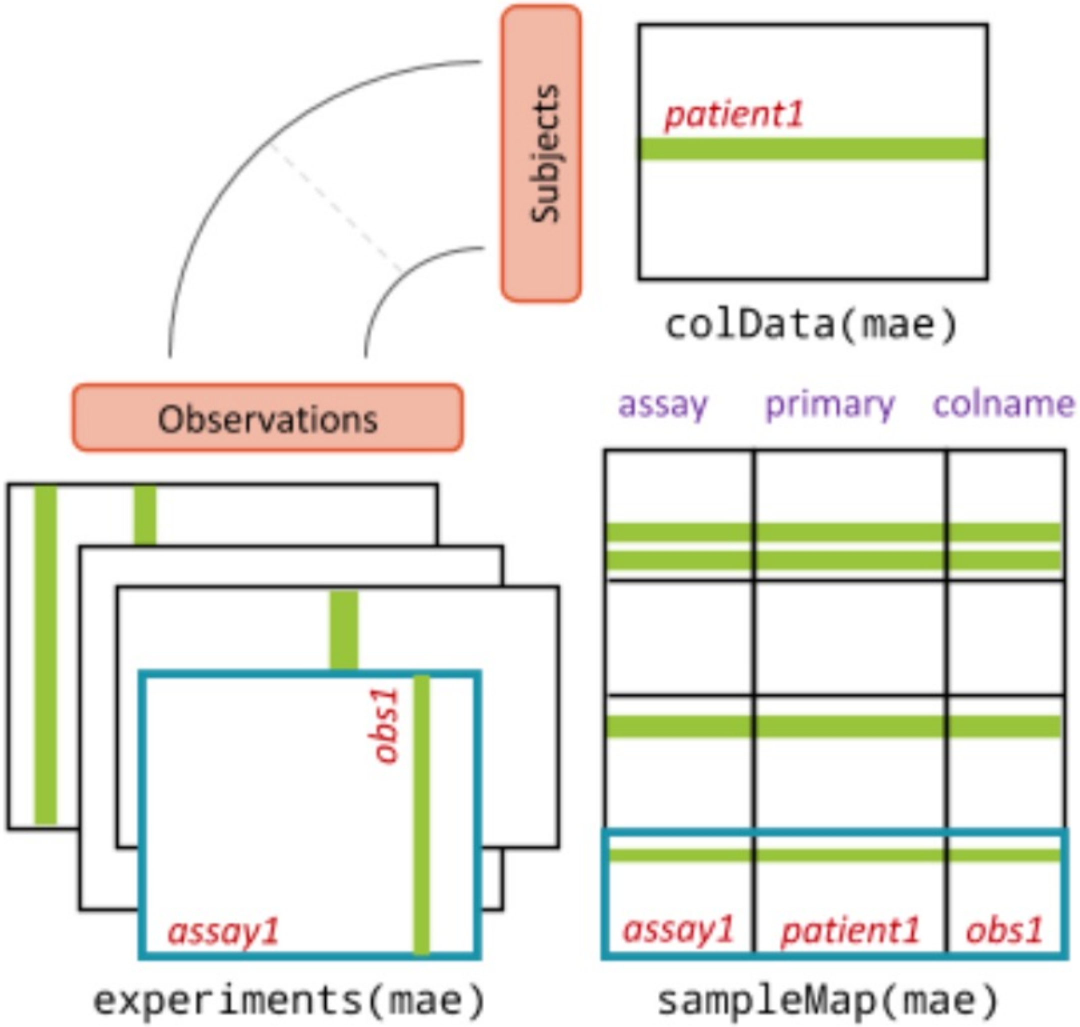
Classes derived from SummarizedExperiment

- TreeSummarizedExperiment



Classes derived from SummarizedExperiment

- MultiAssayExperiment



BPPARAM

Genomic analyses require heavy resources

Generally, benefits from parallelization

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Genomic analyses require heavy resources

Generally, benefits from parallelization

BiocParallel is a Bioconductor package designed to reduce the complexity faced when developing and using software that performs parallel computations

BiocParallel aims to provide a unified interface to existing parallel infrastructures where code can be easily executed in different environments

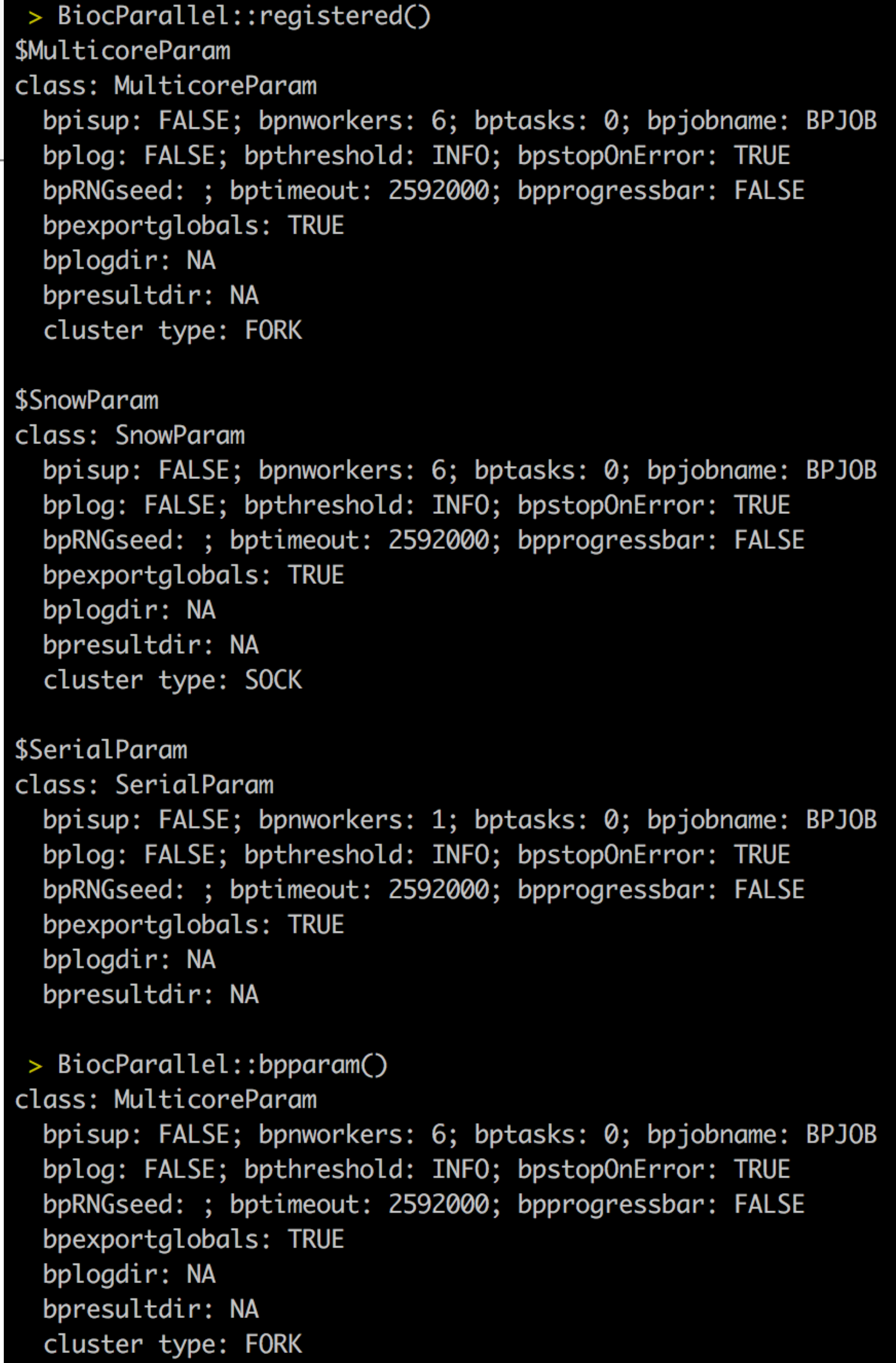
BPPARAM

Declaring configurations:

registered()

bpparam()

register(…, default = TRUE)



```
> BiocParallel::registered()
$MulticoreParam
class: MulticoreParam
  bpisup: FALSE; bpnworkers: 6; bptasks: 0; bpjobname: BPJOB
  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: FORK

$SnowParam
class: SnowParam
  bpisup: FALSE; bpnworkers: 6; bptasks: 0; bpjobname: BPJOB
  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: SOCK

$SerialParam
class: SerialParam
  bpisup: FALSE; bpnworkers: 1; bptasks: 0; bpjobname: BPJOB
  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA

> BiocParallel::bpparam()
class: MulticoreParam
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  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: FORK
```

BPPARAM

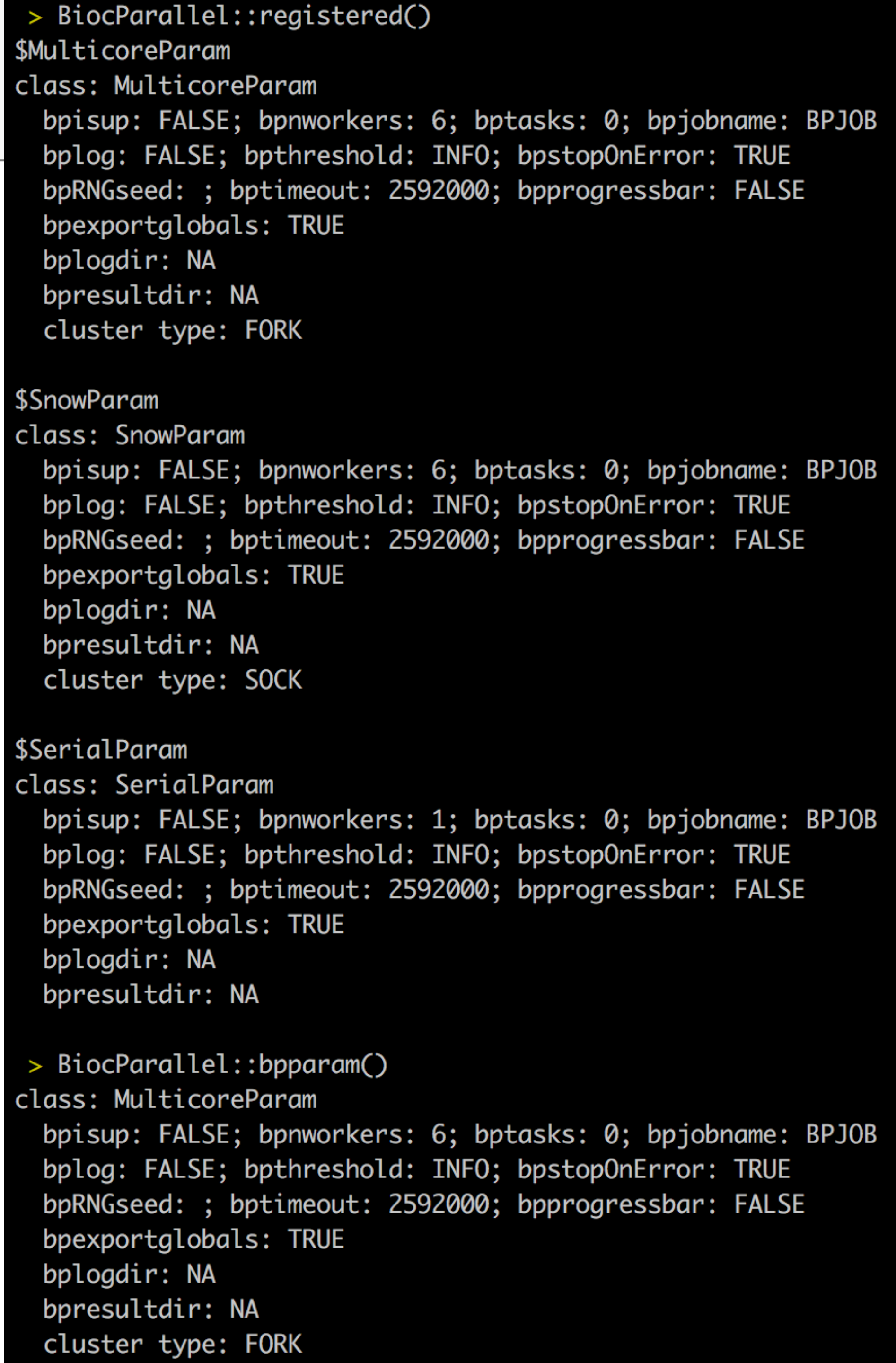
Declaring configurations:

registered()

bpparam()

register(…, default = TRUE)

- MulticoreParam()
- SerialParam()
- SnowParam()



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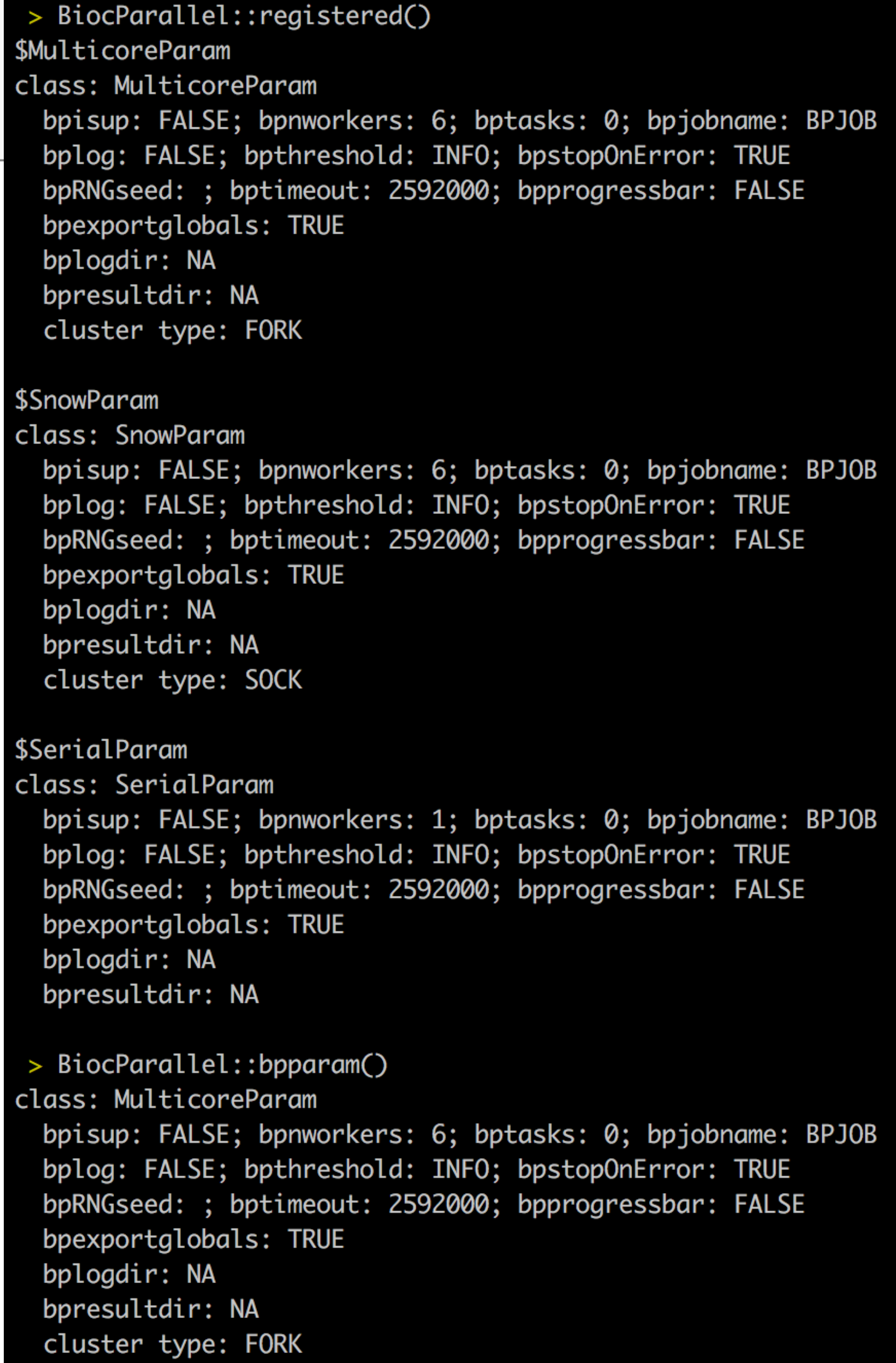
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: FORK
```

BPPARAM

Execute in parallel:

bplapply()   e.g., bplapply(1:4, FUN)



```
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  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
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  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: SOCK

$SerialParam
class: SerialParam
  bpisup: FALSE; bpnworkers: 1; bptasks: 0; bpjobname: BPJOB
  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA

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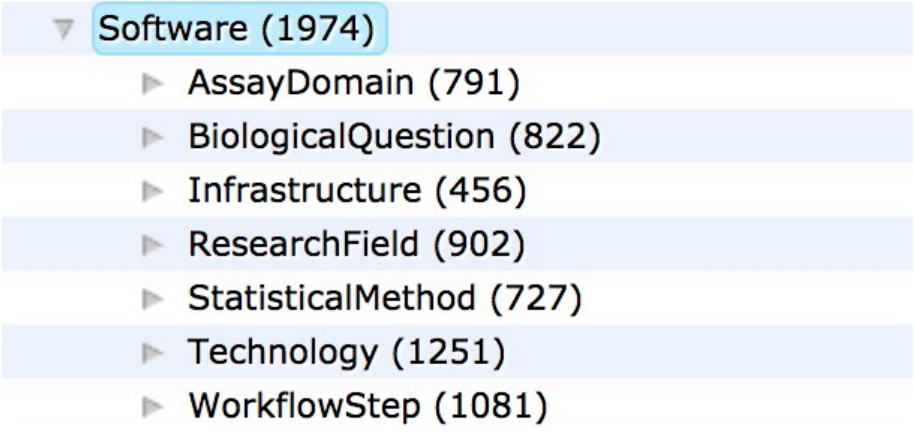
class: MulticoreParam
  bpisup: FALSE; bpnworkers: 6; bptasks: 0; bpjobname: BPJOB
  bplog: FALSE; bpthreshold: INFO; bpstopOnError: TRUE
  bpRNGseed: ; bptimeout: 2592000; bpprogressbar: FALSE
  bpexportglobals: TRUE
  bplogdir: NA
  bpresultdir: NA
  cluster type: FORK
```

Bioconductor is not only for analysis packages

https://www.bioconductor.org/packages/release/BiocViews.html



- Software (1974)
  - AssayDomain (791)
  - BiologicalQuestion (822)
  - Infrastructure (456)
  - ResearchField (902)
  - StatisticalMethod (727)
  - Technology (1251)
  - WorkflowStep (1081)

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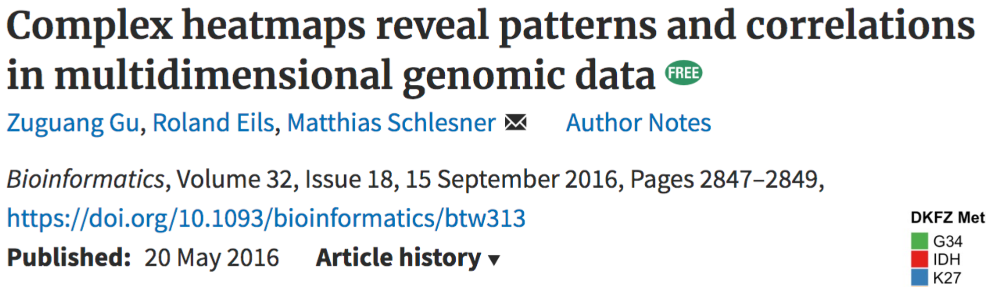
  - WorkflowStep (1081)

- AnnotationData (971)
  - ChipManufacturer (388)
  - ChipName (196)
  - CustomArray (2)
  - CustomDBSchema (6)
  - FunctionalAnnotation (31)
  - Organism (634)
  - PackageType (682)
  - SequenceAnnotation (1)

- Workflow (28)
  - AnnotationWorkflow (3)
  - BasicWorkflow (5)
  - EpigeneticsWorkflow (4)
  - GeneExpressionWorkflow (11)
  - GenomicVariantsWorkflow (2)
  - ImmunoOncologyWorkflow (14)
  - ProteomicsWorkflow (2)
  - ResourceQueryingWorkflow (2)
  - SingleCellWorkflow (2)

- ExperimentData (398)
  - AssayDomainData (81)
  - DiseaseModel (90)
  - OrganismData (139)
  - PackageTypeData (41)
  - RepositoryData (94)
  - ReproducibleResearch (22)
  - SpecimenSource (103)
  - TechnologyData (266)

Visualization tools

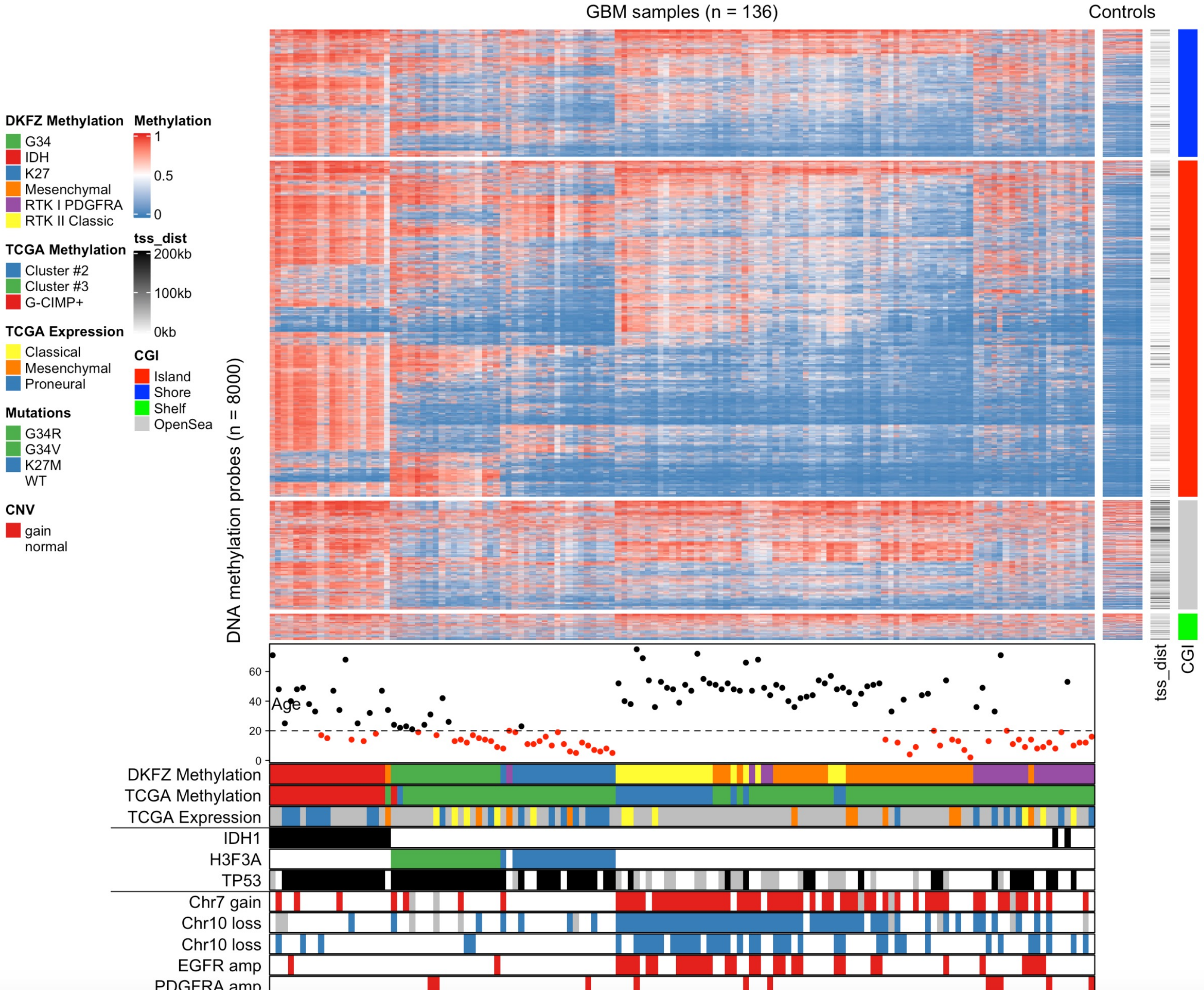


Complex heatmaps reveal patterns and correlations in multidimensional genomic data FREE

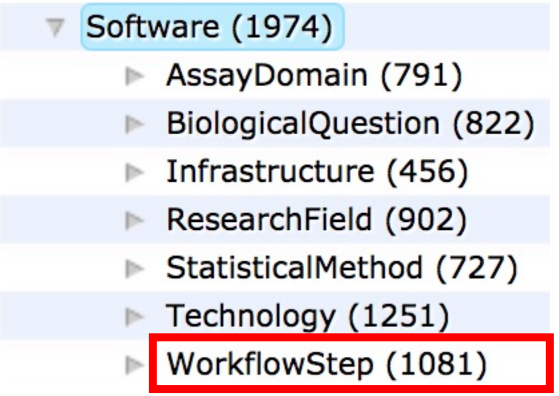
Zuguang Gu, Roland Eils, Matthias Schlesner ✉ Author Notes

Bioinformatics, Volume 32, Issue 18, 15 September 2016, Pages 2847–2849, https://doi.org/10.1093/bioinformatics/btw313

Published: 20 May 2016 **Article history** ▾



NGS workflow management tools



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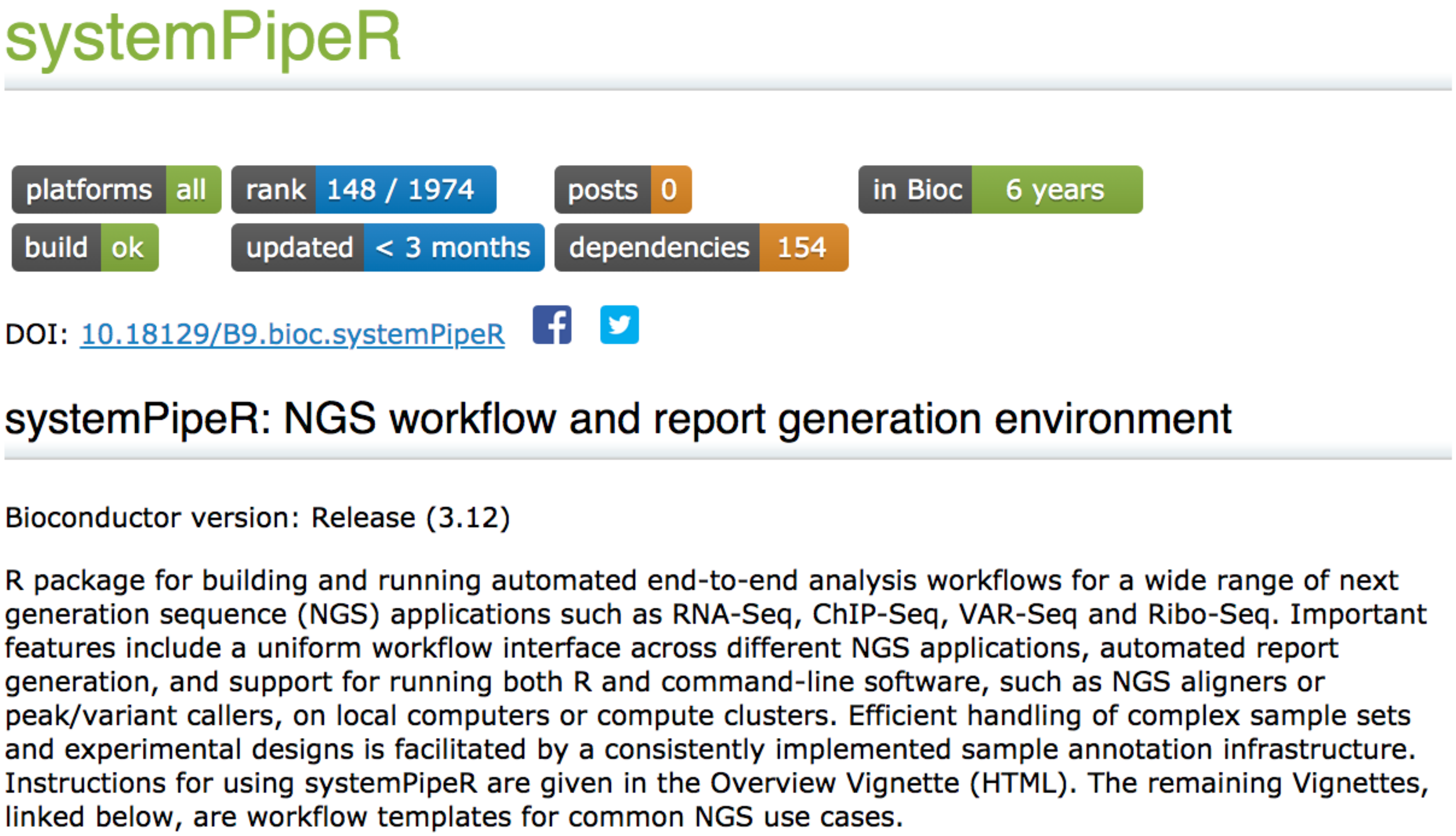


systemPipeR

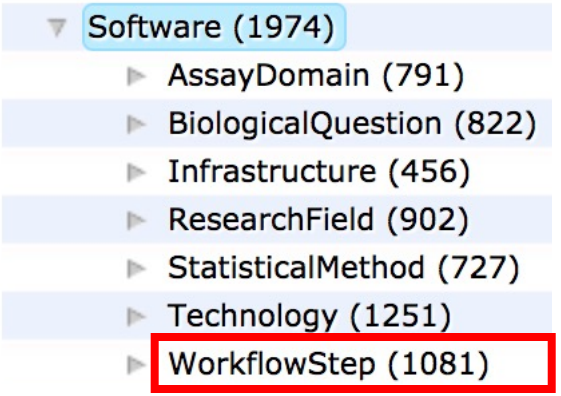
DOI: 10.18129/B9.bioc.systemPipeR

systemPipeR: NGS workflow and report generation environment

Bioconductor version: Release (3.12)

R package for building and running automated end-to-end analysis workflows for a wide range of next generation sequence (NGS) applications such as RNA-Seq, ChIP-Seq, VAR-Seq and Ribo-Seq. Important features include a uniform workflow interface across different NGS applications, automated report generation, and support for running both R and command-line software, such as NGS aligners or peak/variant callers, on local computers or compute clusters. Efficient handling of complex sample sets and experimental designs is facilitated by a consistently implemented sample annotation infrastructure. Instructions for using systemPipeR are given in the Overview Vignette (HTML). The remaining Vignettes, linked below, are workflow templates for common NGS use cases.

Reporting tools



- Software (1974)
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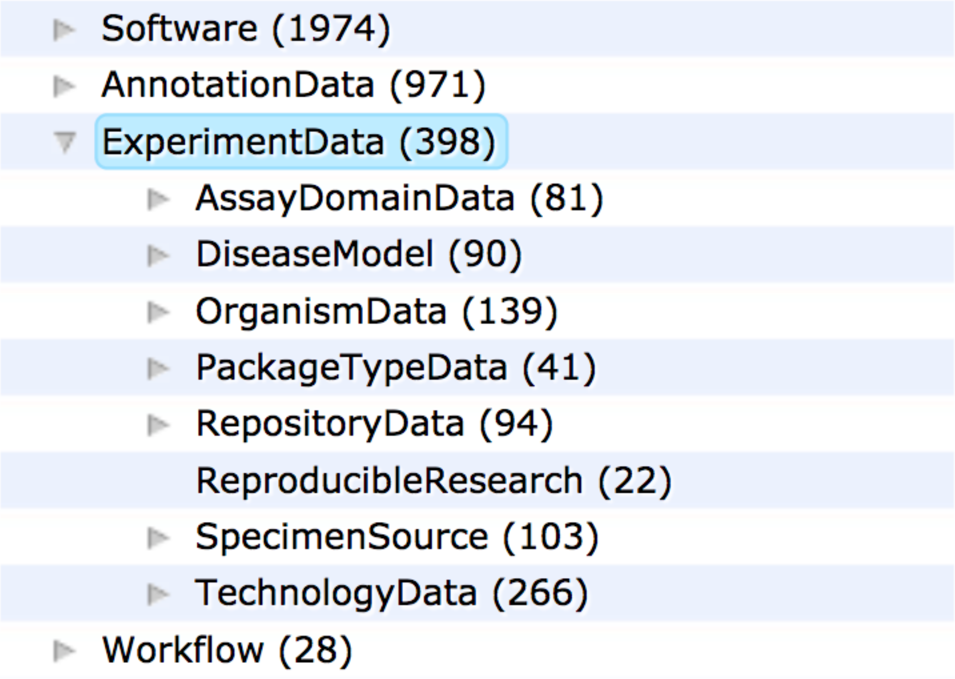
  - BiologicalQuestion (822)
  - Infrastructure (456)
  - ResearchField (902)
  - StatisticalMethod (727)
  - Technology (1251)
  - WorkflowStep (1081)

```
DESeq2Report::DESeq2Report(
      dds = dds,
      project = "OsmoResponse",
      intgroup = "timepoint”
)
```

Bioconductor is not only for analysis packages

https://www.bioconductor.org/packages/release/BiocViews.html



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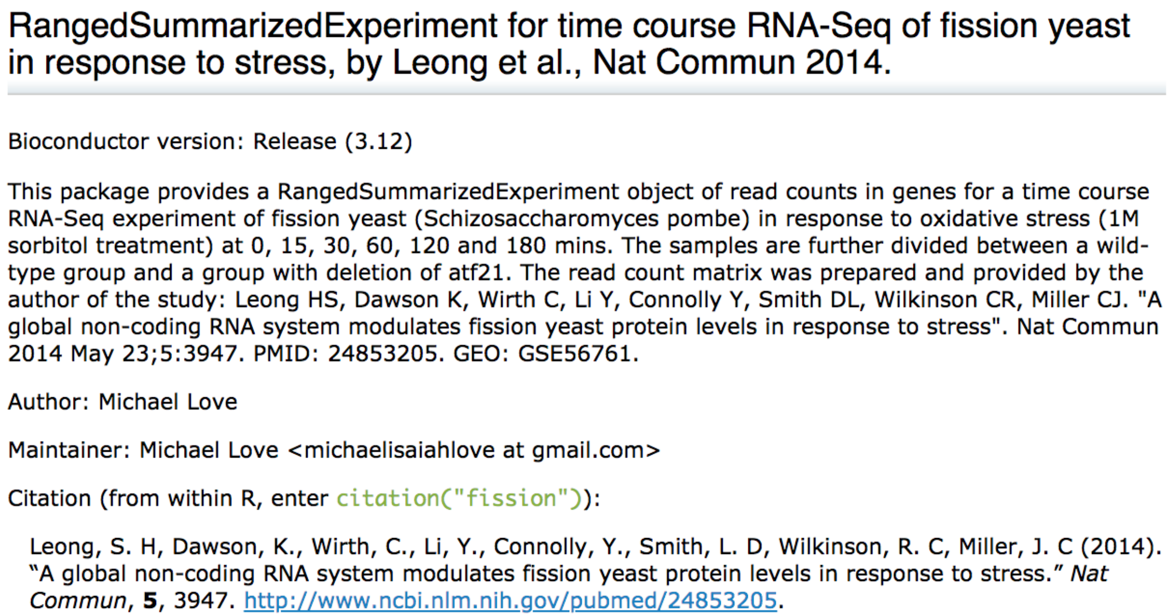
  - ▸ SpecimenSource (103)
  - ▸ TechnologyData (266)
- ▸ Workflow (28)

Retrieving specific experiments



RangedSummarizedExperiment for time course RNA-Seq of fission yeast in response to stress, by Leong et al., Nat Commun 2014.

Bioconductor version: Release (3.12)

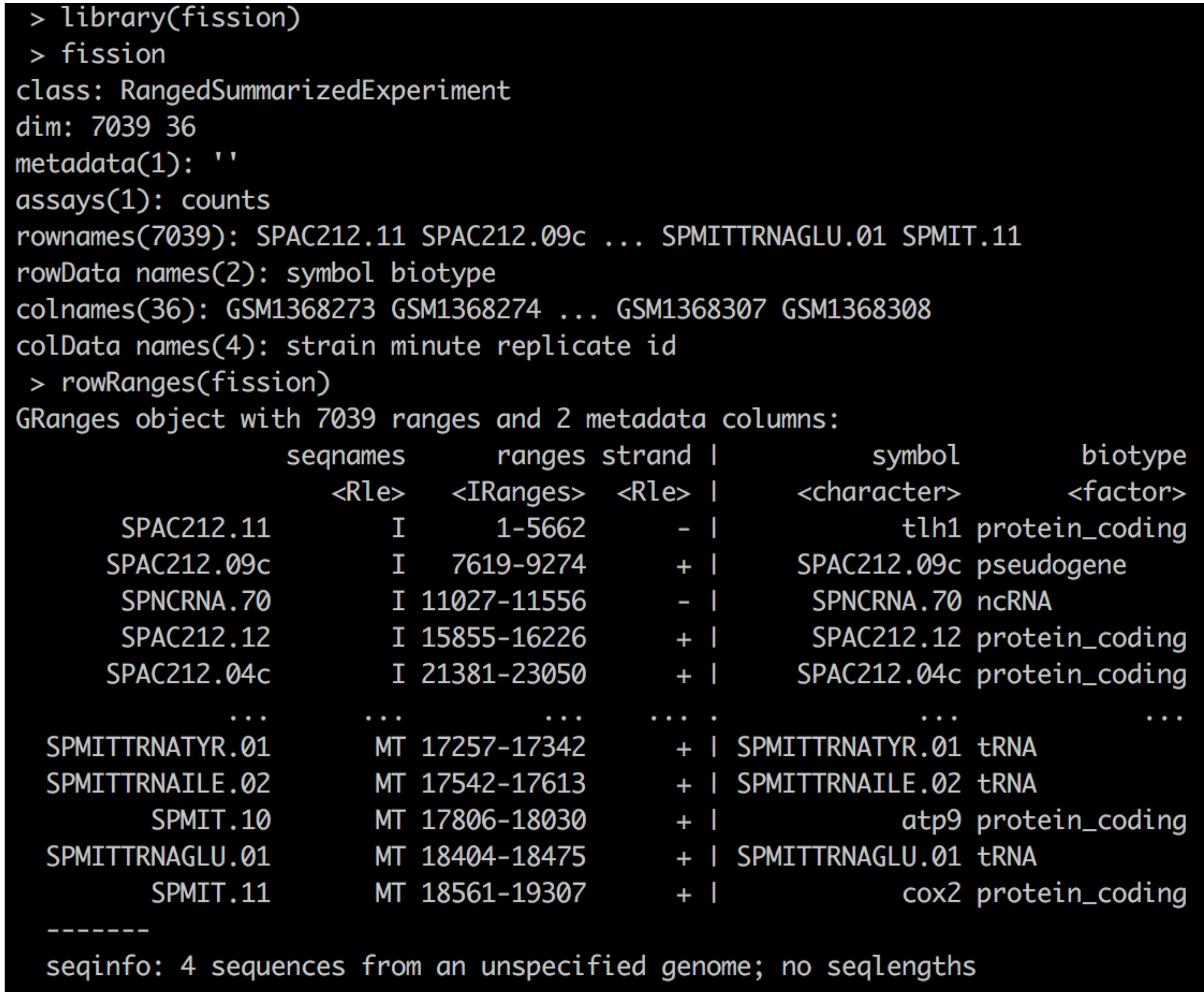
This package provides a RangedSummarizedExperiment object of read counts in genes for a time course RNA-Seq experiment of fission yeast (Schizosaccharomyces pombe) in response to oxidative stress (1M sorbitol treatment) at 0, 15, 30, 60, 120 and 180 mins. The samples are further divided between a wild-type group and a group with deletion of atf21. The read count matrix was prepared and provided by the author of the study: Leong HS, Dawson K, Wirth C, Li Y, Connolly Y, Smith DL, Wilkinson CR, Miller CJ. "A global non-coding RNA system modulates fission yeast protein levels in response to stress". Nat Commun 2014 May 23;5:3947. PMID: 24853205. GEO: GSE56761.

Author: Michael Love

Maintainer: Michael Love <michaelisaiahlove at gmail.com>

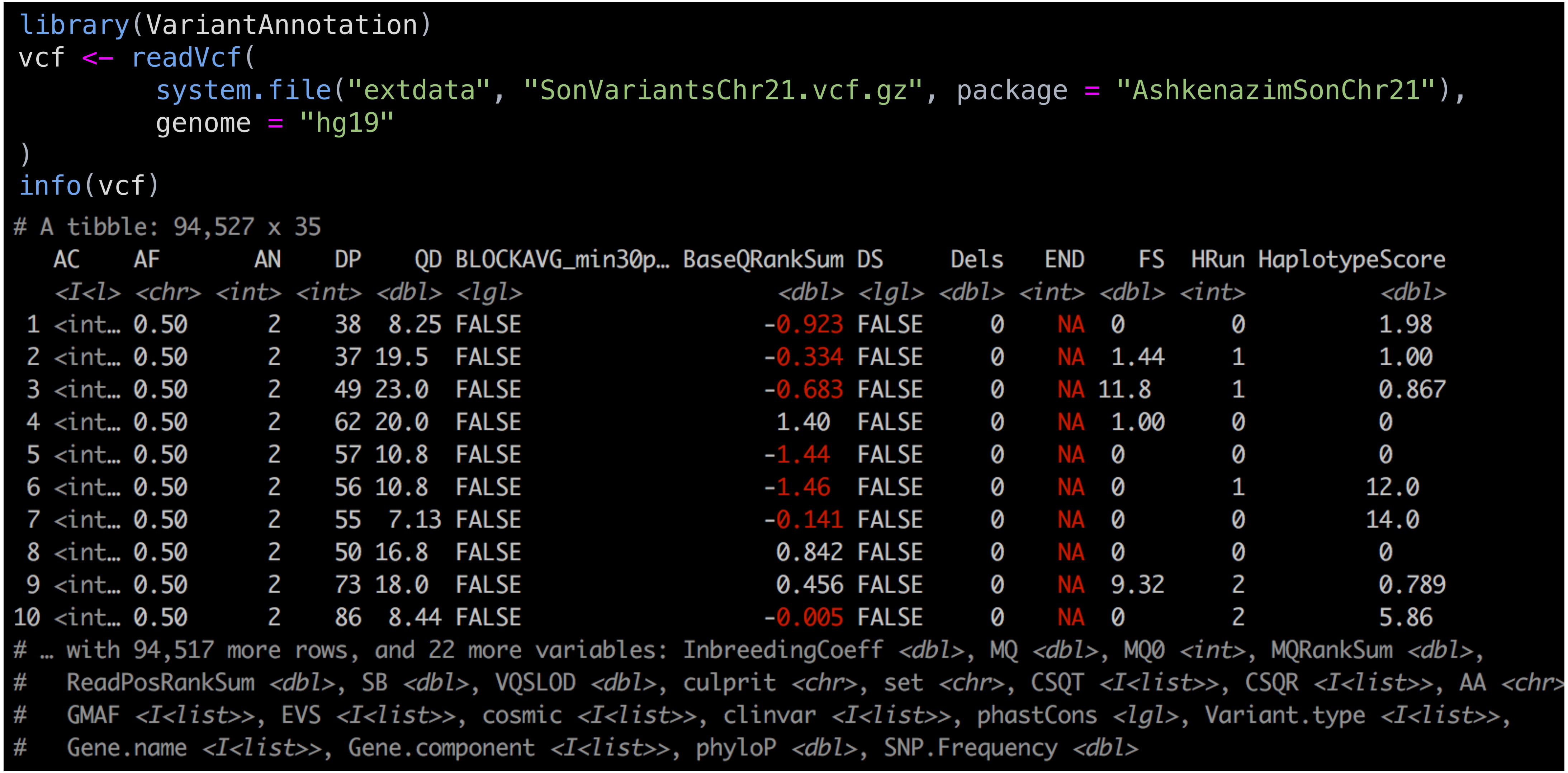
Citation (from within R, enter `citation("fission")`):

> Leong, S. H, Dawson, K., Wirth, C., Li, Y., Connolly, Y., Smith, L. D, Wilkinson, R. C, Miller, J. C (2014). "A global non-coding RNA system modulates fission yeast protein levels in response to stress." *Nat Commun*, **5**, 3947. http://www.ncbi.nlm.nih.gov/pubmed/24853205.



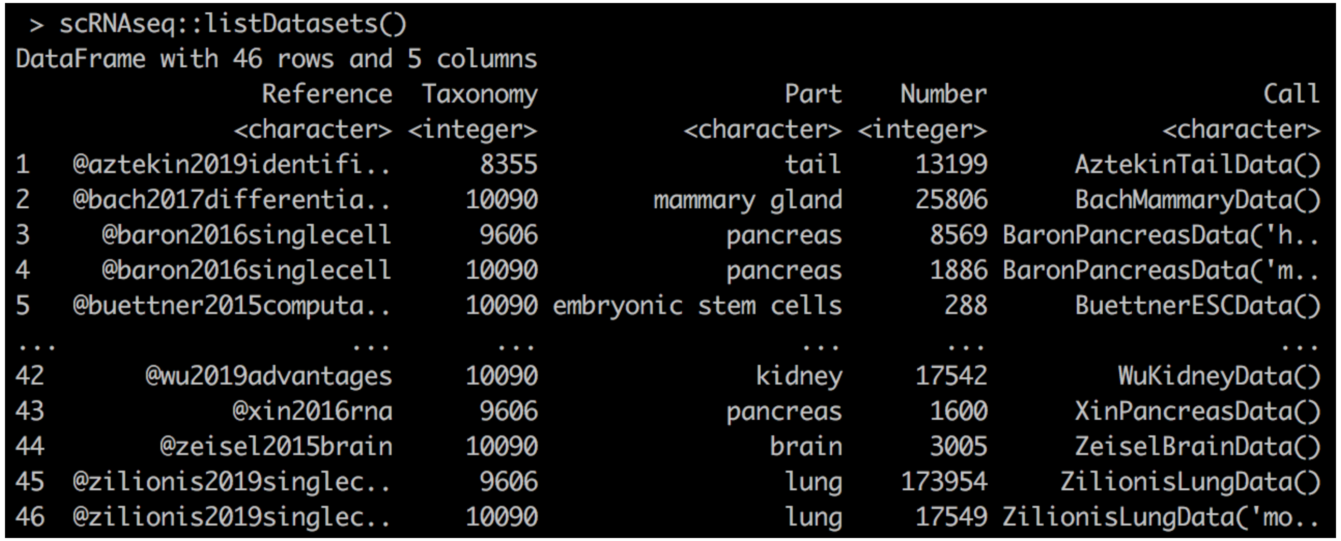
```
 > library(fission)
 > fission
class: RangedSummarizedExperiment
dim: 7039 36
metadata(1): ''
assays(1): counts
rownames(7039): SPAC212.11 SPAC212.09c ... SPMITTRNAGLU.01 SPMIT.11
rowData names(2): symbol biotype
colnames(36): GSM1368273 GSM1368274 ... GSM1368307 GSM1368308
colData names(4): strain minute replicate id
 > rowRanges(fission)
GRanges object with 7039 ranges and 2 metadata columns:
                seqnames        ranges strand |          symbol       biotype
                   <Rle>     <IRanges>  <Rle> |     <character>      <factor>
       SPAC212.11        I        1-5662      - |            tlh1 protein_coding
      SPAC212.09c        I     7619-9274      + |     SPAC212.09c pseudogene
       SPNCRNA.70        I   11027-11556      - |      SPNCRNA.70 ncRNA
       SPAC212.12        I   15855-16226      + |      SPAC212.12 protein_coding
      SPAC212.04c        I   21381-23050      + |     SPAC212.04c protein_coding
              ...      ...           ...    ... .             ...            ...
  SPMITTRNATYR.01       MT   17257-17342      + | SPMITTRNATYR.01 tRNA
  SPMITTRNAILE.02       MT   17542-17613      + | SPMITTRNAILE.02 tRNA
         SPMIT.10       MT   17806-18030      + |            atp9 protein_coding
  SPMITTRNAGLU.01       MT   18404-18475      + | SPMITTRNAGLU.01 tRNA
         SPMIT.11       MT   18561-19307      + |            cox2 protein_coding
  -------
  seqinfo: 4 sequences from an unspecified genome; no seqlengths
```

Retrieving specific experiments

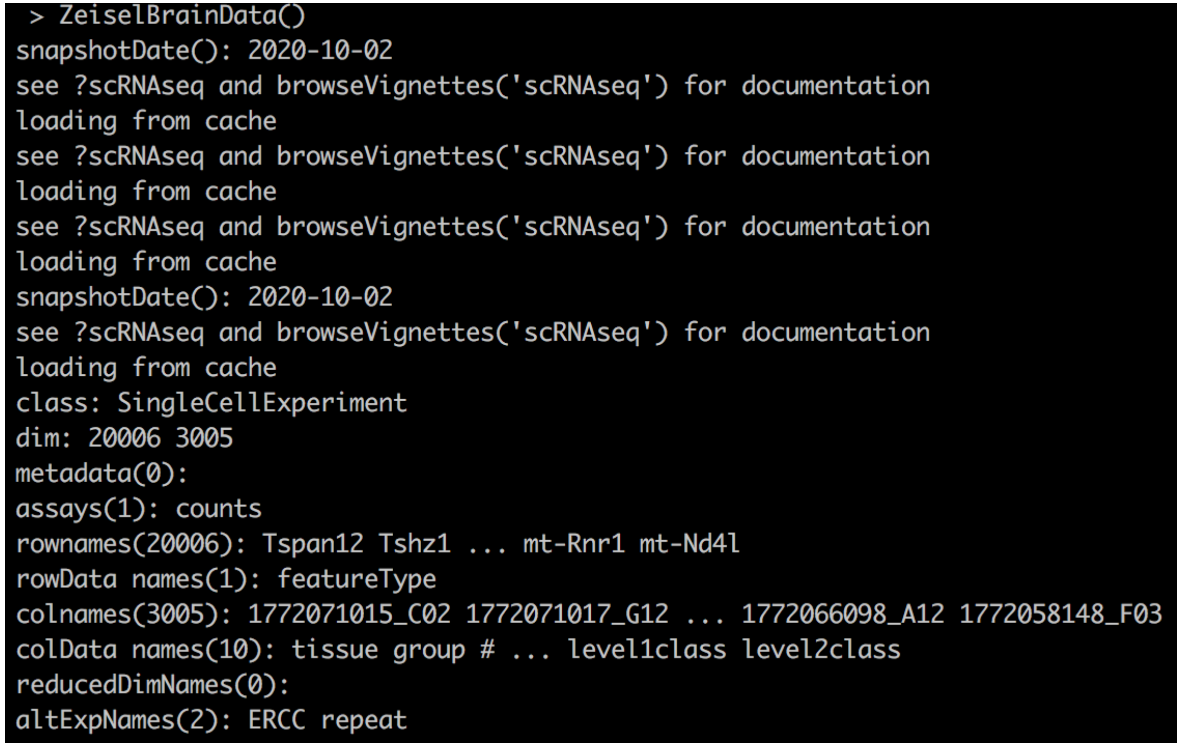


```
library(VariantAnnotation)
vcf <- readVcf(
        system.file("extdata", "SonVariantsChr21.vcf.gz", package = "AshkenazimSonChr21"),
        genome = "hg19"
)
info(vcf)
# A tibble: 94,527 x 35
   AC     AF        AN    DP    QD BLOCKAVG_min30p… BaseQRankSum DS     Dels   END    FS  HRun HaplotypeScore
   <I<l> <chr> <int> <int> <dbl> <lgl>                    <dbl> <lgl> <dbl> <int> <dbl> <int>          <dbl>
 1 <int… 0.50       2    38  8.25 FALSE                  -0.923 FALSE     0    NA  0        0          1.98
 2 <int… 0.50       2    37 19.5  FALSE                  -0.334 FALSE     0    NA  1.44     1          1.00
 3 <int… 0.50       2    49 23.0  FALSE                  -0.683 FALSE     0    NA 11.8      1          0.867
 4 <int… 0.50       2    62 20.0  FALSE                   1.40  FALSE     0    NA  1.00     0          0
 5 <int… 0.50       2    57 10.8  FALSE                  -1.44  FALSE     0    NA  0        0          0
 6 <int… 0.50       2    56 10.8  FALSE                  -1.46  FALSE     0    NA  0        1         12.0
 7 <int… 0.50       2    55  7.13 FALSE                  -0.141 FALSE     0    NA  0        0         14.0
 8 <int… 0.50       2    50 16.8  FALSE                   0.842 FALSE     0    NA  0        0          0
 9 <int… 0.50       2    73 18.0  FALSE                   0.456 FALSE     0    NA  9.32     2          0.789
10 <int… 0.50       2    86  8.44 FALSE                  -0.005 FALSE     0    NA  0        2          5.86
# … with 94,517 more rows, and 22 more variables: InbreedingCoeff <dbl>, MQ <dbl>, MQ0 <int>, MQRankSum <dbl>,
#   ReadPosRankSum <dbl>, SB <dbl>, VQSLOD <dbl>, culprit <chr>, set <chr>, CSQT <I<list>>, CSQR <I<list>>, AA <chr>
#   GMAF <I<list>>, EVS <I<list>>, cosmic <I<list>>, clinvar <I<list>>, phastCons <lgl>, Variant.type <I<list>>,
#   Gene.name <I<list>>, Gene.component <I<list>>, phyloP <dbl>, SNP.Frequency <dbl>
```

Retrieving specific experiments

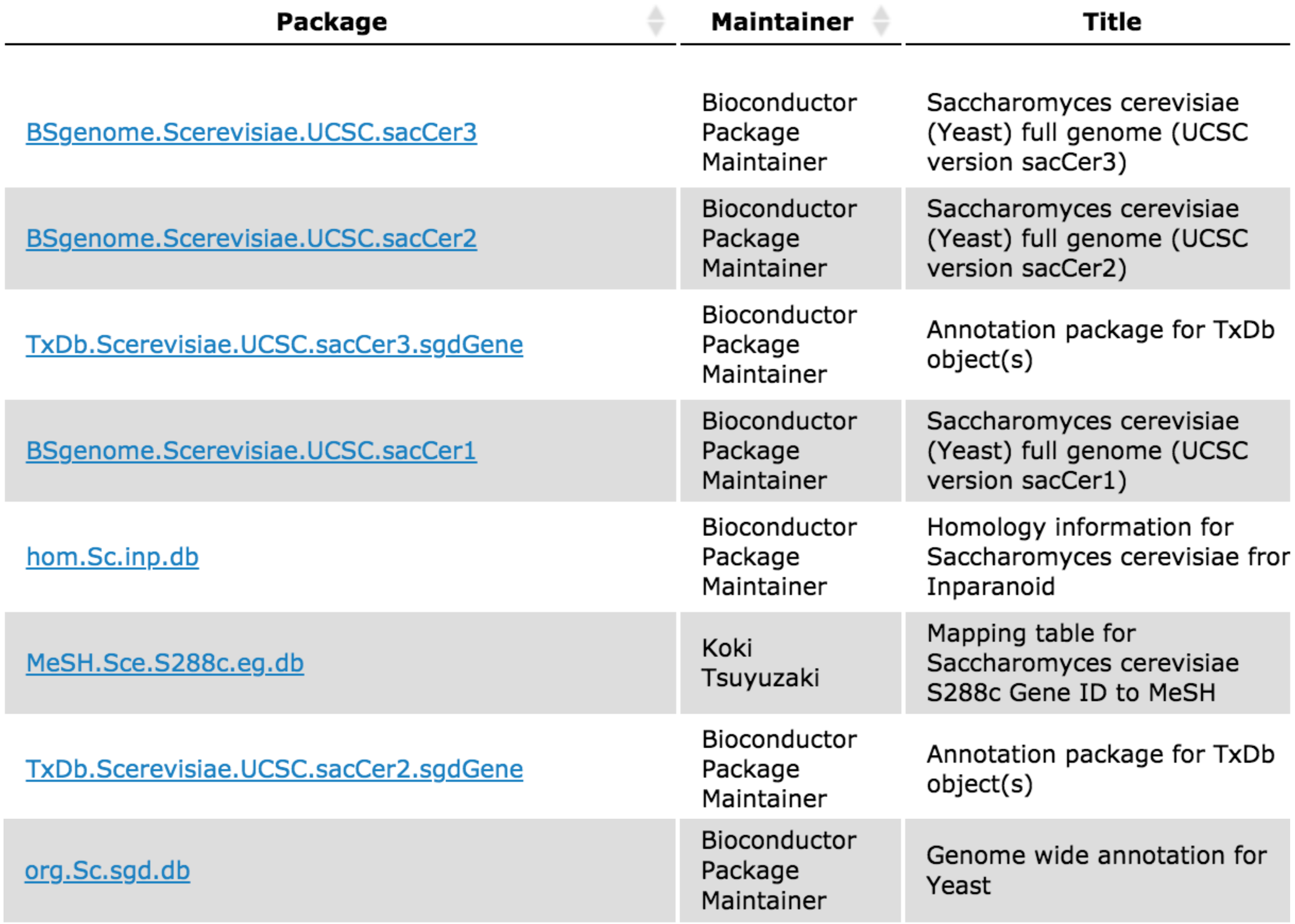


```
 > scRNAseq::listDatasets()
DataFrame with 46 rows and 5 columns
                 Reference  Taxonomy                 Part    Number                Call
               <character> <integer>          <character> <integer>         <character>
1   @aztekin2019identifi..      8355                 tail     13199     AztekinTailData()
2   @bach2017differentia..     10090        mammary gland     25806     BachMammaryData()
3     @baron2016singlecell      9606             pancreas      8569 BaronPancreasData('h..
4     @baron2016singlecell     10090             pancreas      1886 BaronPancreasData('m..
5   @buettner2015computa..     10090 embryonic stem cells       288     BuettnerESCData()
...                    ...       ...                  ...       ...                   ...
42       @wu2019advantages     10090               kidney     17542        WuKidneyData()
43             @xin2016rna      9606             pancreas      1600      XinPancreasData()
44         @zeisel2015brain     10090                brain      3005      ZeiselBrainData()
45  @zilionis2019singlec..      9606                 lung    173954     ZilionisLungData()
46  @zilionis2019singlec..     10090                 lung     17549 ZilionisLungData('mo..
```



```
 > ZeiselBrainData()
snapshotDate(): 2020-10-02
see ?scRNAseq and browseVignettes('scRNAseq') for documentation
loading from cache
see ?scRNAseq and browseVignettes('scRNAseq') for documentation
loading from cache
see ?scRNAseq and browseVignettes('scRNAseq') for documentation
loading from cache
snapshotDate(): 2020-10-02
see ?scRNAseq and browseVignettes('scRNAseq') for documentation
loading from cache
class: SingleCellExperiment
dim: 20006 3005
metadata(0):
assays(1): counts
rownames(20006): Tspan12 Tshz1 ... mt-Rnr1 mt-Nd4l
rowData names(1): featureType
colnames(3005): 1772071015_C02 1772071017_G12 ... 1772066098_A12 1772058148_F03
colData names(10): tissue group # ... level1class level2class
reducedDimNames(0):
altExpNames(2): ERCC repeat
```

Bioconductor Annotation packages



	Package	Maintainer	Title
BS	BSgenome.Scerevisiae.UCSC.sacCer3	Bioconductor Package Maintainer	Saccharomyces cerevisiae (Yeast) full genome (UCSC version sacCer3)
BS	BSgenome.Scerevisiae.UCSC.sacCer2	Bioconductor Package Maintainer	Saccharomyces cerevisiae (Yeast) full genome (UCSC version sacCer2)
TxDb	TxDb.Scerevisiae.UCSC.sacCer3.sgdGene	Bioconductor Package Maintainer	Annotation package for TxDb object(s)
BS	BSgenome.Scerevisiae.UCSC.sacCer1	Bioconductor Package Maintainer	Saccharomyces cerevisiae (Yeast) full genome (UCSC version sacCer1)
	hom.Sc.inp.db	Bioconductor Package Maintainer	Homology information for Saccharomyces cerevisiae fror Inparanoid
	MeSH.Sce.S288c.eg.db	Koki Tsuyuzaki	Mapping table for Saccharomyces cerevisiae S288c Gene ID to MeSH
TxDb	TxDb.Scerevisiae.UCSC.sacCer2.sgdGene	Bioconductor Package Maintainer	Annotation package for TxDb object(s)
org	org.Sc.sgd.db	Bioconductor Package Maintainer	Genome wide annotation for Yeast

org packages

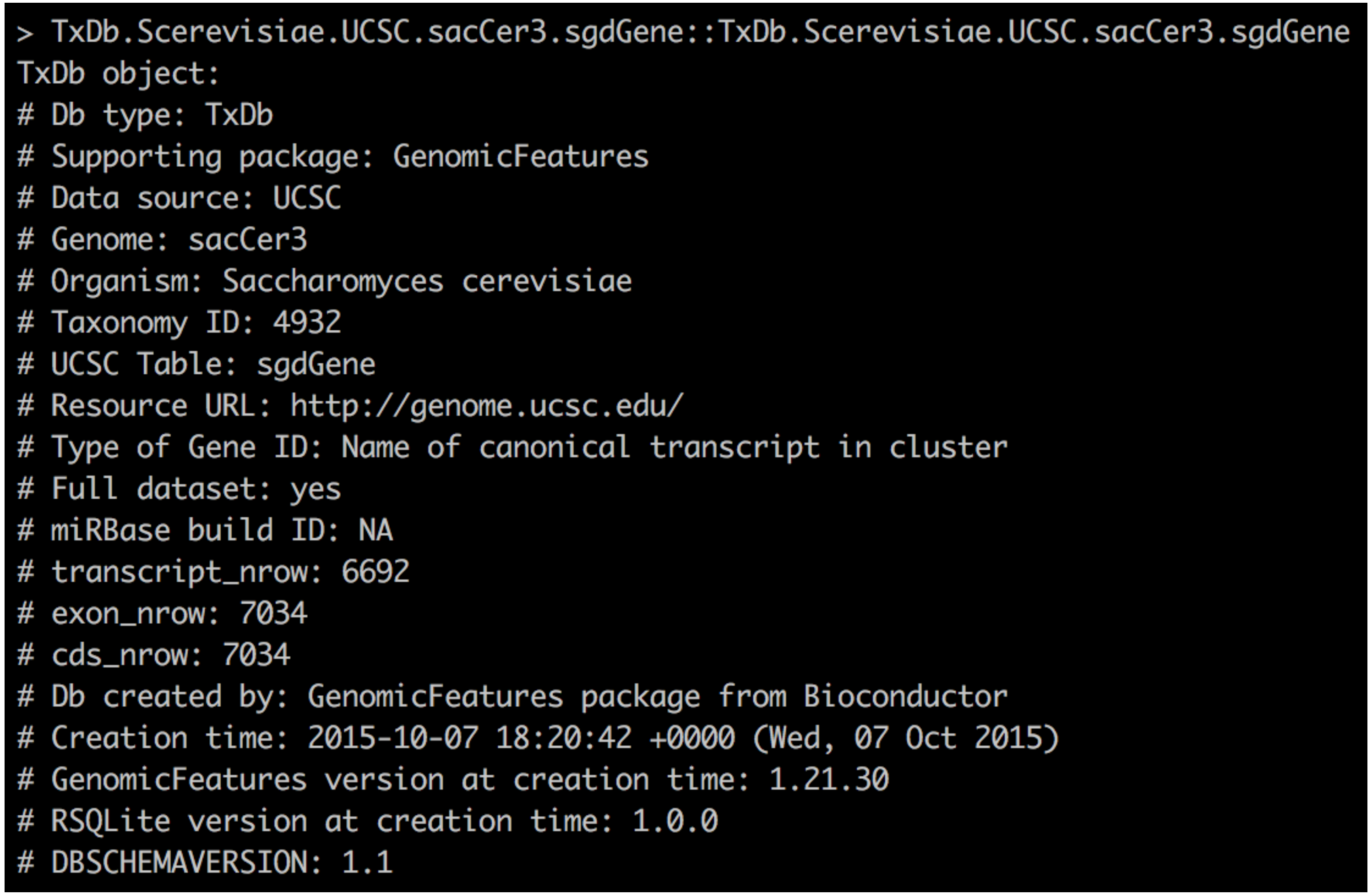
```
> library(org.Sc.sgd.db)
> org.Sc.sgd.db
OrgDb object:
| DBSCHEMAVERSION: 2.1
| Db type: OrgDb
| Supporting package: AnnotationDbi
| DBSCHEMA: YEAST_DB
| ORGANISM: Saccharomyces cerevisiae
| SPECIES: Yeast
| YGSOURCENAME: Yeast Genome
| YGSOURCEURL: http://sgd-archive.yeastgenome.org
| YGSOURCEDATE: 2019-Oct25
| CENTRALID: ORF
| TAXID: 559292
| KEGGSOURCENAME: KEGG GENOME
| KEGGSOURCEURL: ftp://ftp.genome.jp/pub/kegg/genomes
| KEGGSOURCEDATE: 2011-Mar15
| GOSOURCENAME: Gene Ontology
| GOSOURCEURL: http://current.geneontology.org/ontology/go-basic.obo
| GOSOURCEDATE: 2020-09-10
| EGSOURCEDATE: 2020-Sep23
| EGSOURCENAME: Entrez Gene
| EGSOURCEURL: ftp://ftp.ncbi.nlm.nih.gov/gene/DATA
| ENSOURCEDATE: 2020-Aug18
| ENSOURCENAME: Ensembl
| ENSOURCEURL: ftp://ftp.ensembl.org/pub/current_fasta
| UPSOURCENAME: Uniprot
| UPSOURCEURL: http://www.UniProt.org/
| UPSOURCEDATE: Mon Oct  5 00:25:28 2020
```

TxDb packages

A TxDb package connects a set of genomic coordinates to various transcript oriented features.

In other words, TxDb packages provide **gene annotation models**

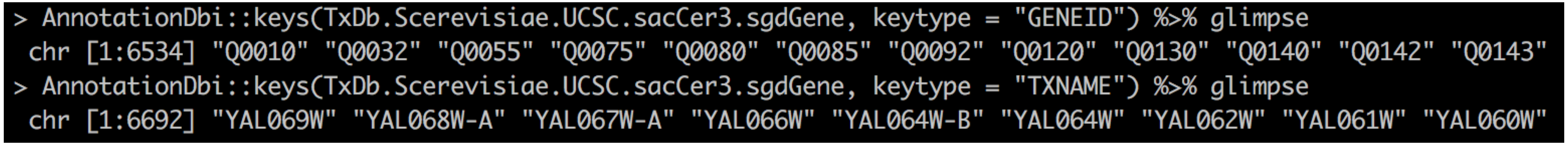
TxDb packages



```
> TxDb.Scerevisiae.UCSC.sacCer3.sgdGene::TxDb.Scerevisiae.UCSC.sacCer3.sgdGene
TxDb object:
# Db type: TxDb
# Supporting package: GenomicFeatures
# Data source: UCSC
# Genome: sacCer3
# Organism: Saccharomyces cerevisiae
# Taxonomy ID: 4932
# UCSC Table: sgdGene
# Resource URL: http://genome.ucsc.edu/
# Type of Gene ID: Name of canonical transcript in cluster
# Full dataset: yes
# miRBase build ID: NA
# transcript_nrow: 6692
# exon_nrow: 7034
# cds_nrow: 7034
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2015-10-07 18:20:42 +0000 (Wed, 07 Oct 2015)
# GenomicFeatures version at creation time: 1.21.30
# RSQLite version at creation time: 1.0.0
# DBSCHEMAVERSION: 1.1
```

TxDb packages

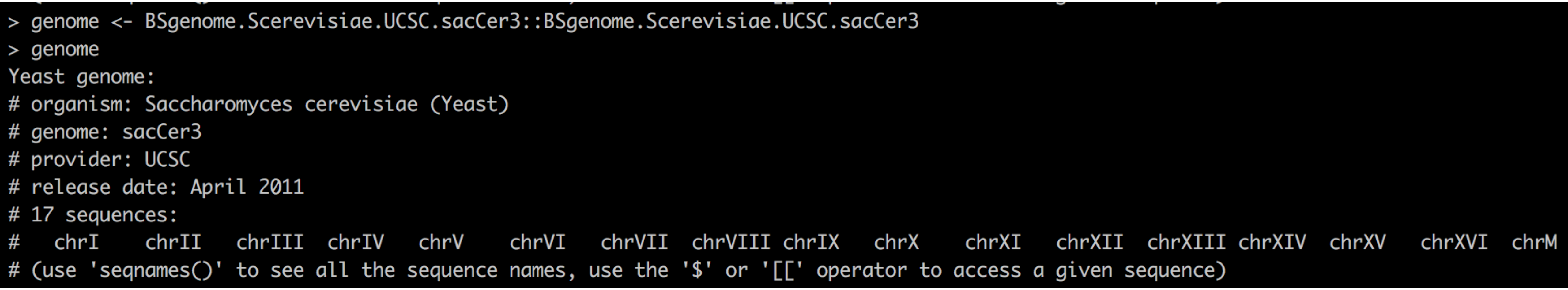
TxDb databases can be explored with AnnotationDbi functions



```
> AnnotationDbi::keys(TxDb.Scerevisiae.UCSC.sacCer3.sgdGene, keytype = "GENEID") %>% glimpse
 chr [1:6534] "Q0010" "Q0032" "Q0055" "Q0075" "Q0080" "Q0085" "Q0092" "Q0120" "Q0130" "Q0140" "Q0142" "Q0143"
> AnnotationDbi::keys(TxDb.Scerevisiae.UCSC.sacCer3.sgdGene, keytype = "TXNAME") %>% glimpse
 chr [1:6692] "YAL069W" "YAL068W-A" "YAL067W-A" "YAL066W" "YAL064W-B" "YAL064W" "YAL062W" "YAL061W" "YAL060W"
```

BSgenome packages

Data packages that contain the full genome sequences of a given organism



```
> genome <- BSgenome.Scerevisiae.UCSC.sacCer3::BSgenome.Scerevisiae.UCSC.sacCer3
> genome
Yeast genome:
# organism: Saccharomyces cerevisiae (Yeast)
# genome: sacCer3
# provider: UCSC
# release date: April 2011
# 17 sequences:
#   chrI    chrII   chrIII  chrIV   chrV    chrVI   chrVII  chrVIII chrIX   chrX    chrXI   chrXII  chrXIII chrXIV  chrXV   chrXVI  chrM
# (use 'seqnames()' to see all the sequence names, use the '$' or '[[' operator to access a given sequence)
```

BSgenome packages

Biostrings package is used to interact with BSgenome databases

```
> genome <- BSgenome.Scerevisiae.UCSC.sacCer3::BSgenome.Scerevisiae.UCSC.sacCer3
> genome
Yeast genome:
# organism: Saccharomyces cerevisiae (Yeast)
# genome: sacCer3
# provider: UCSC
# release date: April 2011
# 17 sequences:
#   chrI     chrII    chrIII   chrIV    chrV     chrVI    chrVII   chrVIII chrIX    chrX     chrXI    chrXII   chrXIII chrXIV   chrXV    chrXVI   chrM
# (use 'seqnames()' to see all the sequence names, use the '$' or '[[' operator to access a given sequence)
> Biostrings::getSeq(genome)
DNAStringSet object of length 17:
       width seq                                                    names
 [1]  230218 CCACACCACACCCACACACCCACACACCACACCACACACCACACCACACCCA...GTGTGGGTGTGGTGTGGTGTGTGGGTGTGGTGTGGGTGTGGTGTGTGTGGG chrI
 [2]  813184 AAATAGCCCTCATGTACGTCTCCTCCAAGCCCTGTTGTCTCTTACCCGGATG...AGGGTGTGTGGGTGTGGGTGTGGTGTGTGTGGGTGTGGTGTGTGGGTGTGT chrII
 [3]  316620 CCCACACACCACACCCACACCACACCCACACACCACACACACCACACCCACA...GGTGTGGTGTGTGGGTGTGGGTGTGTGGGTGTGGTGGGTGTGGTGTGTGTG chrIII
 [4] 1531933 ACACCACACCCACACCACACCCACACACACCACACCCACACACCACACCCAC...AGACAATCTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGG chrIV
 [5]  576874 CGTCTCCTCCAAGCCCTGTTGTCTCTTACCCGGATGTTCAACCAAAAGCTAC...TAGAAGTGCTGTAGGGCTAAAGAACAGGGTTTCATTTTCATTTTTTTTTTT chrV
 ...     ... ...
[13]  924431 CCACACACACACCACACCCACACCACACCCACACCCACACCCACACCCACAC...TGGGTGTGGTGTGGTGTGTGGGTGTGGTGTGGGTGTGGTGTGTGTGTGGGG chrXIII
[14]  784333 CCGGCTTTCTGACCGAAATTAAAAAAAAAAAATGAAAATGAAACCCTGTTCT...GGGTGTGGTGTGTGGGTGTGGTGTGTGGGTGTGTGTGGGTGTGGTGTGGGT chrXIV
[15] 1091291 ACACCACACCCACACCACACCCACACCCACACACCACACCCACACACACACA...ATGACAGCGAGAGTAGAGGTAGATGTGAGAGAGTGTGTGGGTGTGGTGTGT chrXV
[16]  948066 AAATAGCCCTCATGTACGTCTCCTCCAAGCCCTGTTGTCTCTTACCCGGATG...CTAAAGAACAGGGTTTCATTTTCATTTTTTTTTTTTAATTTCGGTCAGAAA chrXVI
[17]   85779 TTCATAATTAATTTTTTATATATATATTATATTATAATATTAATTTATATTA...ATAGTTATATTATTATACAGAAATATGCTTAATTATAATATAATATCCATA chrM
```

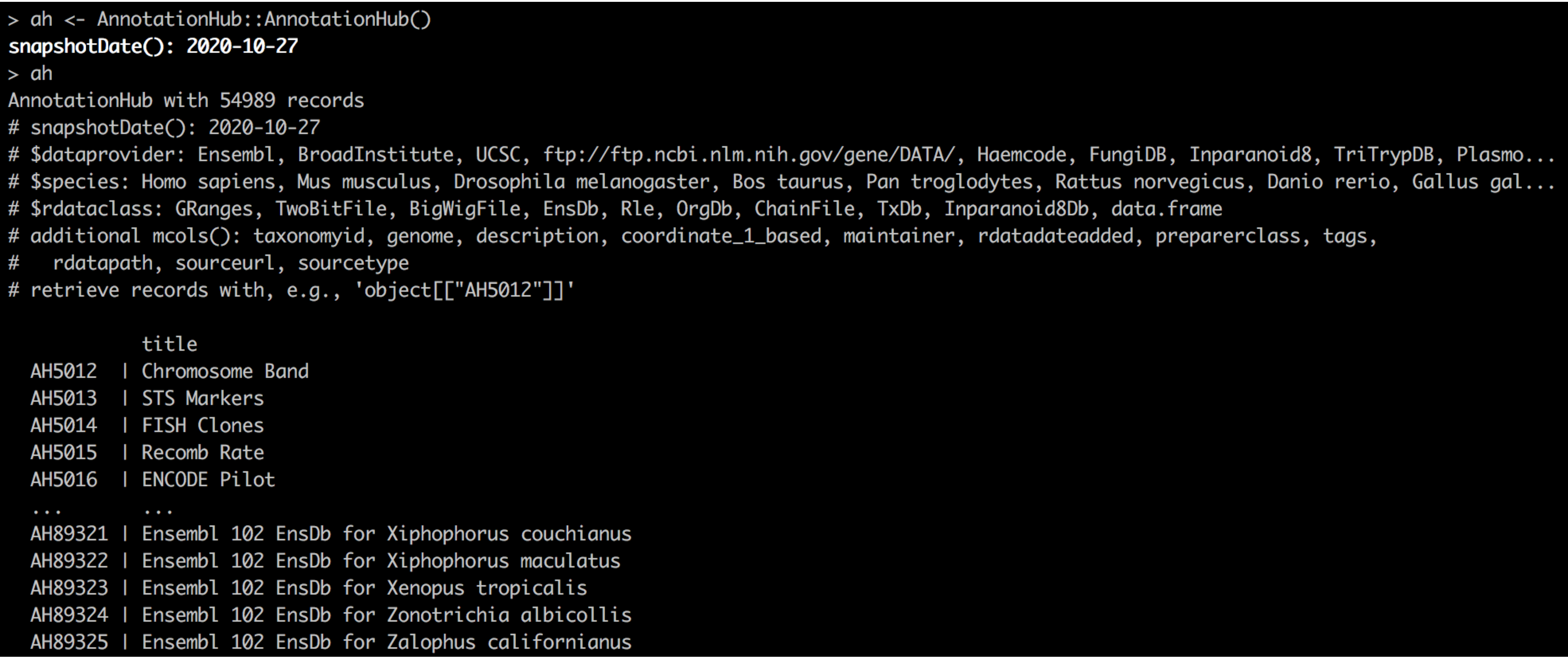
AnnotationHub: retrieving release-specific files

The AnnotationHub package provides a client interface to resources stored at the AnnotationHub web service

It is different from AnnotationDbi-supported packages (e.g. orgDb or TxDb packages), since it allows access to files **on top of** databases

AnnotationHub: retrieving release-specific files

The AnnotationHub package provides a client interface to resources stored at the AnnotationHub web service.



```
> ah <- AnnotationHub::AnnotationHub()
snapshotDate(): 2020-10-27
> ah
AnnotationHub with 54989 records
# snapshotDate(): 2020-10-27
# $dataprovider: Ensembl, BroadInstitute, UCSC, ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/, Haemcode, FungiDB, Inparanoid8, TriTrypDB, Plasmo...
# $species: Homo sapiens, Mus musculus, Drosophila melanogaster, Bos taurus, Pan troglodytes, Rattus norvegicus, Danio rerio, Gallus gal...
# $rdataclass: GRanges, TwoBitFile, BigWigFile, EnsDb, Rle, OrgDb, ChainFile, TxDb, Inparanoid8Db, data.frame
# additional mcols(): taxonomyid, genome, description, coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
#   rdatapath, sourceurl, sourcetype
# retrieve records with, e.g., 'object[["AH5012"]]'

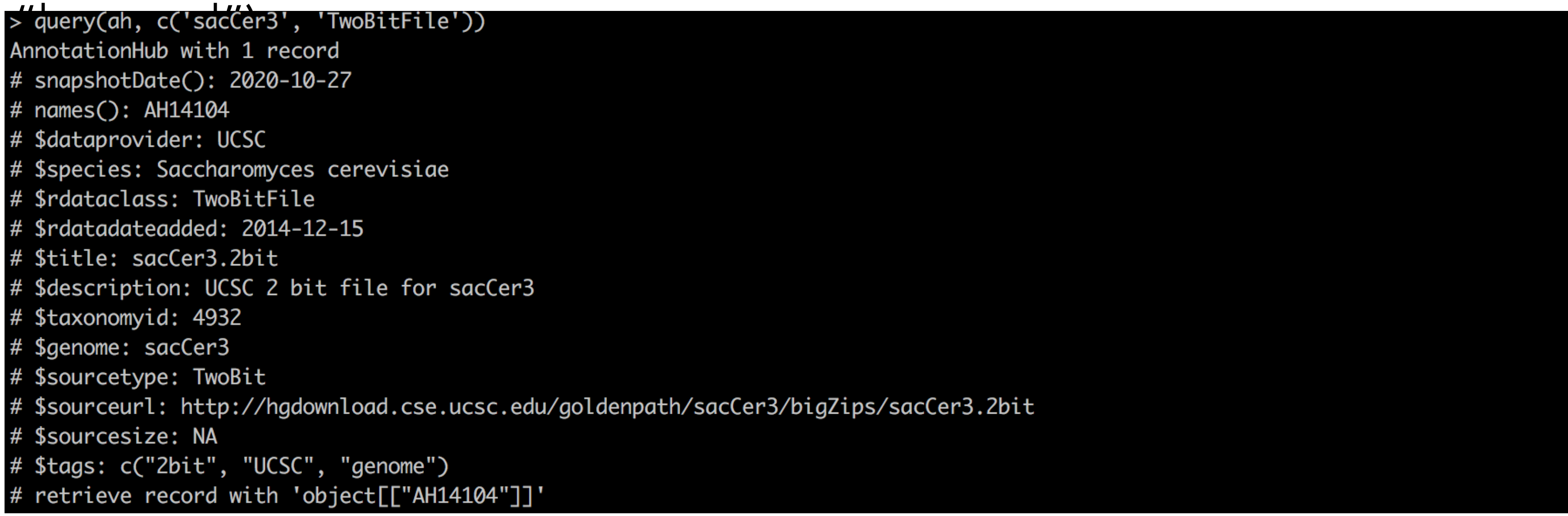
            title
  AH5012  | Chromosome Band
  AH5013  | STS Markers
  AH5014  | FISH Clones
  AH5015  | Recomb Rate
  AH5016  | ENCODE Pilot
  ...       ...
  AH89321 | Ensembl 102 EnsDb for Xiphophorus couchianus
  AH89322 | Ensembl 102 EnsDb for Xiphophorus maculatus
  AH89323 | Ensembl 102 EnsDb for Xenopus tropicalis
  AH89324 | Ensembl 102 EnsDb for Zonotrichia albicollis
  AH89325 | Ensembl 102 EnsDb for Zalophus californianus
```

AnnotationHub: retrieving release-specific files

- Queries are done using query(ah, “keyword”)

AnnotationHub: retrieving release-specific files

Queries are done using query(ah,



```
> query(ah, c('sacCer3', 'TwoBitFile'))
AnnotationHub with 1 record
# snapshotDate(): 2020-10-27
# names(): AH14104
# $dataprovider: UCSC
# $species: Saccharomyces cerevisiae
# $rdataclass: TwoBitFile
# $rdatadateadded: 2014-12-15
# $title: sacCer3.2bit
# $description: UCSC 2 bit file for sacCer3
# $taxonomyid: 4932
# $genome: sacCer3
# $sourcetype: TwoBit
# $sourceurl: http://hgdownload.cse.ucsc.edu/goldenpath/sacCer3/bigZips/sacCer3.2bit
# $sourcesize: NA
# $tags: c("2bit", "UCSC", "genome")
# retrieve record with 'object[["AH14104"]]'
```

AnnotationHub: retrieving release-specific files

Queries are done using query(ah,

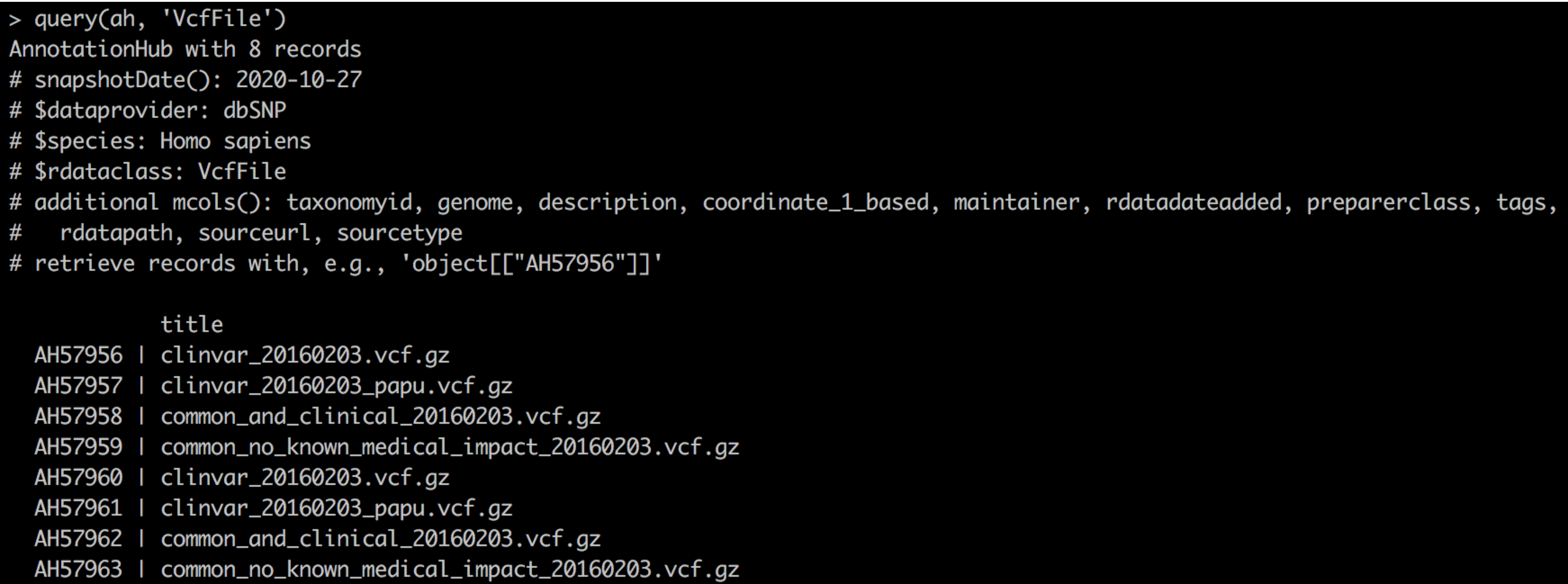
Objects are retrieved using ah[[“…

```
> query(ah, c('sacCer3', 'TwoBitFile'))
AnnotationHub with 1 record
# snapshotDate(): 2020-10-27
# names(): AH14104
# $dataprovider: UCSC
# $species: Saccharomyces cerevisiae
# $rdataclass: TwoBitFile
# $rdatadateadded: 2014-12-15
# $title: sacCer3.2bit
# $description: UCSC 2 bit file for sacCer3
# $taxonomyid: 4932
# $genome: sacCer3
# $sourcetype: TwoBit
# $sourceurl: http://hgdownload.cse.ucsc.edu/goldenpath/sacCer3/bigZips/sacCer3.2bit
# $sourcesize: NA
# $tags: c("2bit", "UCSC", "genome")
# retrieve record with 'object[["AH14104"]]'
> twobit <- ah[['AH14104']]
loading from cache
> twobit
TwoBitFile object
resource: /Users/jacquesserizay/Library/Caches/AnnotationHub/a6c5475f3d0f_18199
> seqs <- getSeq(twobit)
> seqs
DNAStringSet object of length 17:
       width seq                                                                                    names
 [1]  230218 CCACACCACACCCACACACCCACACACCACACCACACACCACACCACACCCA...GTGTGGGTGTGGTGTGGTGTGTGGGTGTGGTGTGGGTGTGGTGTGTGGG chrI
 [2]  813184 AAATAGCCCTCATGTACGTCTCCTCCAAGCCCTGTTGTCTCTTACCCGGATG...AGGGTGTGTGGGTGTGGGTGTGGTGTGTGTGGGTGTGGTGTGTGGGTGTGT chrII
 [3]  316620 CCCACACACCACACCCACACCACACCCACACACCACACACACCACACCCACA...GGTGTGGTGTGTGGGTGTGGGTGTGTGGGTGTGGTGGGTGTGGTGTGTGTG chrIII
 [4] 1531933 ACACCACACCCACACCACACCCACACACACCACACCCACACACCACACCCAC...AGACAATCTATAAAAAGTAAACATAAAATAAAGGTAGTAAGTAGCTTTTGG chrIV
 [5]  439888 CACACACACCACACCCACACCACACCACACCACACCCACACCCACACACACC...GGATGTGGTGTGGATGTGGTGTGGGTGTGGATGTGGGTGTGGTGTGTGTGT chrIX
 ...     ... ...
[13]  924431 CCACACACACACCACACCCACACCACACCCACACCCACACCCACACCCACAC...TGGGTGTGGTGTGGTGTGTGGGTGTGGTGTGGGTGTGGTGTGTGTGTGGGG chrXIII
[14]  784333 CCGGCTTTCTGACCGAAATTAAAAAAAAAAAAATGAAAATGAAACCCTGTTCT...GGGTGTGGTGTGTGGGTGTGGTGTGTGGGTGTGTGTGGGTGTGGTGTGGGT chrXIV
[15] 1091291 ACACCACACCCACACCACACCCACACCCACACACCACACCCACACACACACA...ATGACAGCGAGAGTAGAGGTAGATGTGAGAGAGTGTGTGGGTGTGGTGTGT chrXV
[16]  948066 AAATAGCCCTCATGTACGTCTCCTCCAAGCCCTGTTGTCTCTTACCCGGATG...CTAAAGAACAGGGTTTCATTTTCATTTTTTTTTTTTTAATTTCGGTCAGAAA chrXVI
[17]   85779 TTCATAATTAATTTTTTATATATATATTATATTATAATATTAATTTATATTA...ATAGTTATATTATTATACAGAAATATGCTTAATTATAATATAATATCCATA chrM
```

AnnotationHub: retrieving release-specific files

Many **many** resources available on AnnotationHub

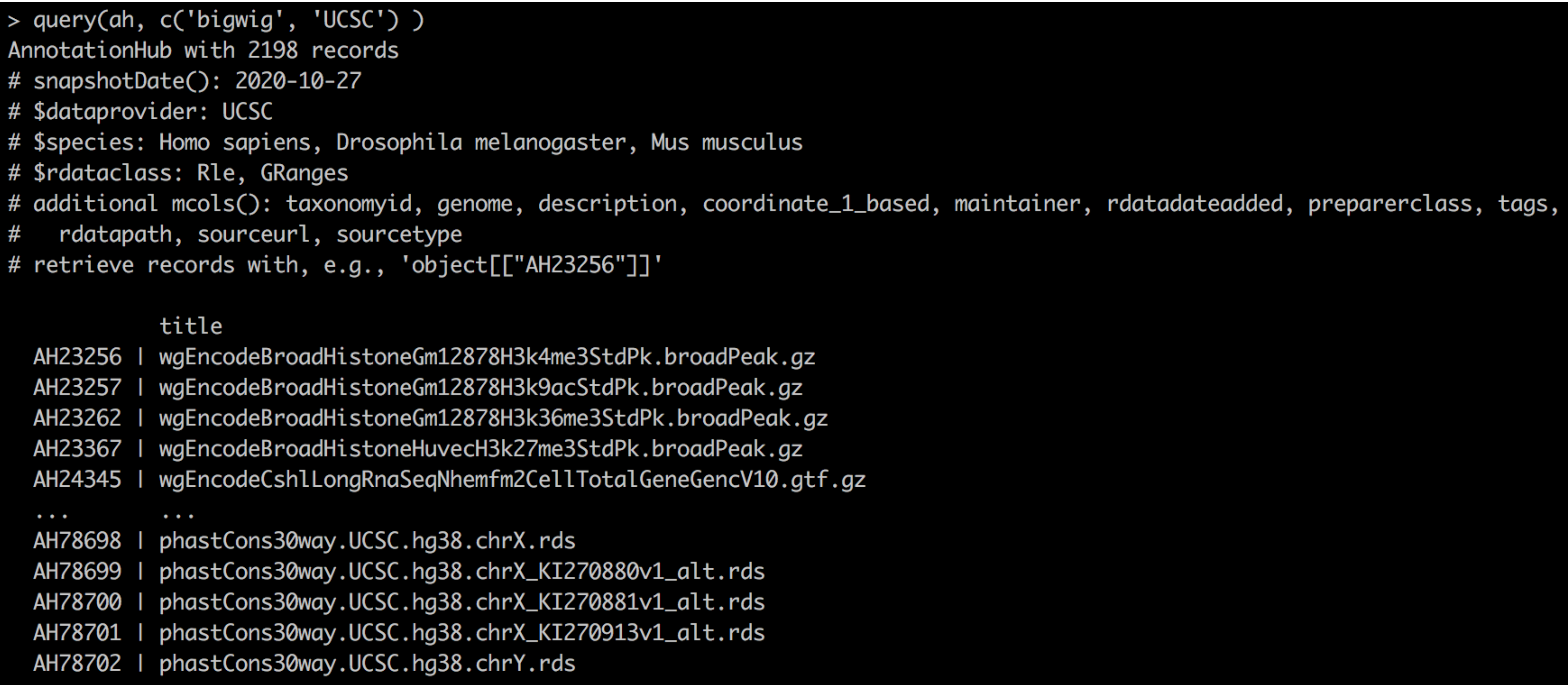
AnnotationHub: retrieving release-specific files



```
> query(ah, 'VcfFile')
AnnotationHub with 8 records
# snapshotDate(): 2020-10-27
# $dataprovider: dbSNP
# $species: Homo sapiens
# $rdataclass: VcfFile
# additional mcols(): taxonomyid, genome, description, coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
#   rdatapath, sourceurl, sourcetype
# retrieve records with, e.g., 'object[["AH57956"]]'

            title
  AH57956 | clinvar_20160203.vcf.gz
  AH57957 | clinvar_20160203_papu.vcf.gz
  AH57958 | common_and_clinical_20160203.vcf.gz
  AH57959 | common_no_known_medical_impact_20160203.vcf.gz
  AH57960 | clinvar_20160203.vcf.gz
  AH57961 | clinvar_20160203_papu.vcf.gz
  AH57962 | common_and_clinical_20160203.vcf.gz
  AH57963 | common_no_known_medical_impact_20160203.vcf.gz
```

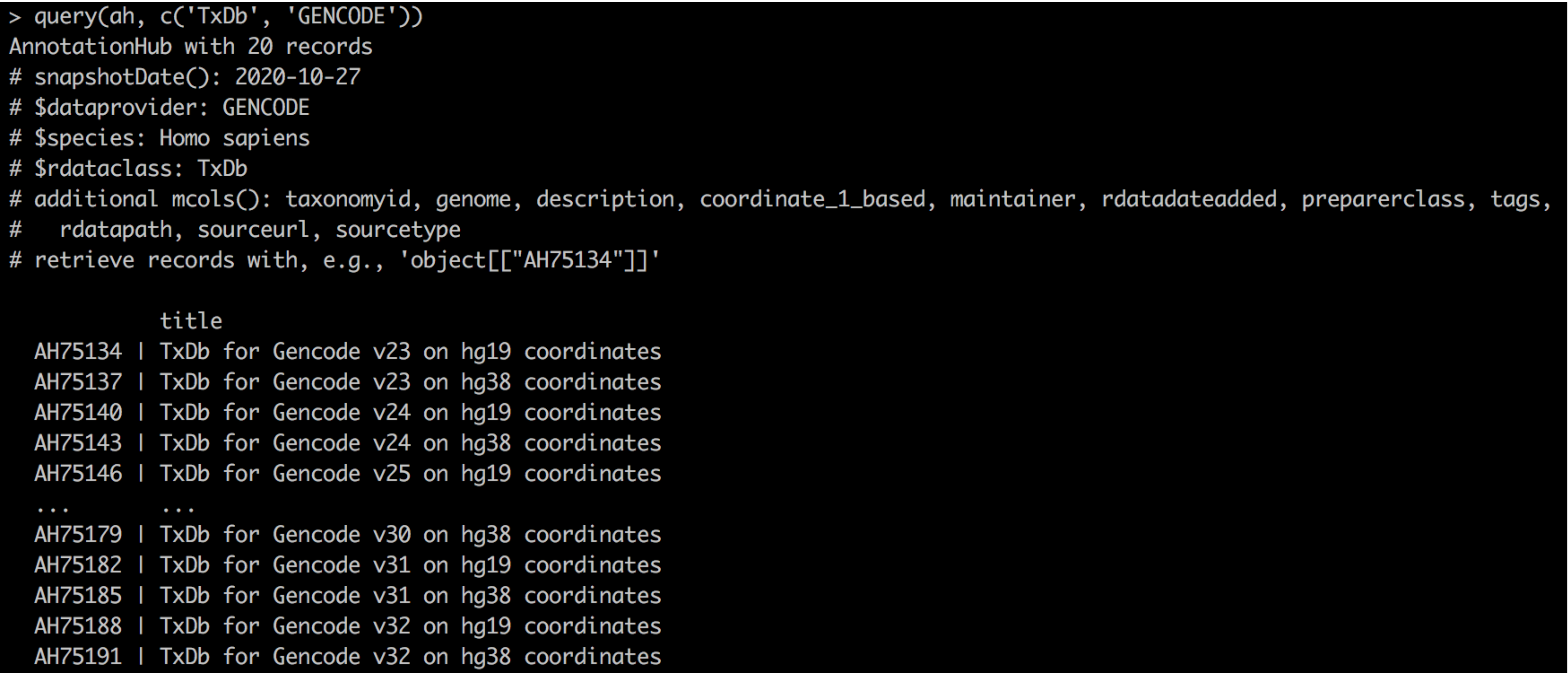
AnnotationHub: retrieving release-specific files



```
> query(ah, c('bigwig', 'UCSC') )
AnnotationHub with 2198 records
# snapshotDate(): 2020-10-27
# $dataprovider: UCSC
# $species: Homo sapiens, Drosophila melanogaster, Mus musculus
# $rdataclass: Rle, GRanges
# additional mcols(): taxonomyid, genome, description, coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
#   rdatapath, sourceurl, sourcetype
# retrieve records with, e.g., 'object[["AH23256"]]'

            title
  AH23256 | wgEncodeBroadHistoneGm12878H3k4me3StdPk.broadPeak.gz
  AH23257 | wgEncodeBroadHistoneGm12878H3k9acStdPk.broadPeak.gz
  AH23262 | wgEncodeBroadHistoneGm12878H3k36me3StdPk.broadPeak.gz
  AH23367 | wgEncodeBroadHistoneHuvecH3k27me3StdPk.broadPeak.gz
  AH24345 | wgEncodeCshlLongRnaSeqNhemfm2CellTotalGeneGencV10.gtf.gz
  ...       ...
  AH78698 | phastCons30way.UCSC.hg38.chrX.rds
  AH78699 | phastCons30way.UCSC.hg38.chrX_KI270880v1_alt.rds
  AH78700 | phastCons30way.UCSC.hg38.chrX_KI270881v1_alt.rds
  AH78701 | phastCons30way.UCSC.hg38.chrX_KI270913v1_alt.rds
  AH78702 | phastCons30way.UCSC.hg38.chrY.rds
```

AnnotationHub: retrieving release-specific files



```
> query(ah, c('TxDb', 'GENCODE'))
AnnotationHub with 20 records
# snapshotDate(): 2020-10-27
# $dataprovider: GENCODE
# $species: Homo sapiens
# $rdataclass: TxDb
# additional mcols(): taxonomyid, genome, description, coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
#   rdatapath, sourceurl, sourcetype
# retrieve records with, e.g., 'object[["AH75134"]]'

            title
  AH75134 | TxDb for Gencode v23 on hg19 coordinates
  AH75137 | TxDb for Gencode v23 on hg38 coordinates
  AH75140 | TxDb for Gencode v24 on hg19 coordinates
  AH75143 | TxDb for Gencode v24 on hg38 coordinates
  AH75146 | TxDb for Gencode v25 on hg19 coordinates
  ...       ...
  AH75179 | TxDb for Gencode v30 on hg38 coordinates
  AH75182 | TxDb for Gencode v31 on hg19 coordinates
  AH75185 | TxDb for Gencode v31 on hg38 coordinates
  AH75188 | TxDb for Gencode v32 on hg19 coordinates
  AH75191 | TxDb for Gencode v32 on hg38 coordinates
```