Using TileDB with R

An Introductory Tutorial

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Overview

Outline

Brief Introduction

Key Topics

- Dense Arrays
- Sparse Arrays
- Full TileDB API
- S3 Access
- Arrow Format
- Time Travel
- Encryption

Applications

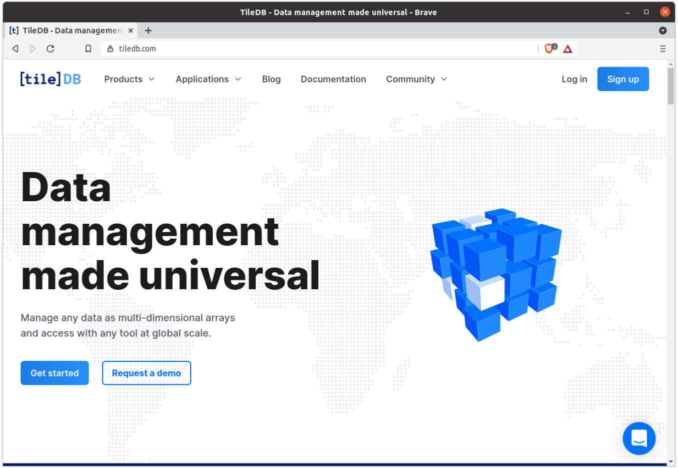
- SQL Access Example
- Data Science with Flights
- LiDAR / Geospatial
- Finance / Time Series
- Genomics: GWAS

Wrap-Up

Further References

Introduction

TileDB



Data management made universal

Manage any data as multi-dimensional arrays and access with any tool at global scale.

Universal Data Management

Any Data in Multi-Dimensional Arrays

Serverless, and at scale

In this tutorial with an R focus

Tutorial Resources

To install the package with code examples and the slides, use

```r
remotes::install_github('eddelbuettel/tiledb-user2021')
```

or

```r
repos <- c(”https://eddelbuettel.github.io/tiledb-user2021/”,
           ”https://cloud.r-project.org”)
install.packages(”tiledb.user2021”, repos=repos)
```

Loading the package will show where the example files are located.

The conference slack channel for the tutorial is `#tut_tiledb`.

Introductory Example

```r
# if needed: install.packages(”tiledb”)     # installation from CRAN
library(tiledb)                             # load the package
library(palmerpenguins)                     # example data
setwd(”/tmp”)                               # or other scratch space

# create array from data frame with default settings
fromDataFrame(penguins, ”penguins”)

# read array as data.frame and without (default, added) row index
arr <- tiledb_array(”penguins”, as.data.frame=TRUE, extended=FALSE)
show(arr)                                   # some array information
```

Introductory Example (cont.)

```
> df <- arr[]
> str(df)
'data.frame':	344 obs. of  8 variables:
 $ species          : chr  ”Adelie” ”Adelie” ”Adelie” ”Adelie” ...
 $ island           : chr  ”Torgersen” ”Torgersen” ”Torgersen” ”Torgersen” ...
 $ bill_length_mm   : num  39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
 $ bill_depth_mm    : num  18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
 $ flipper_length_mm: int  181 186 195 NA 193 190 181 195 193 190 ...
 $ body_mass_g      : int  3750 3800 3250 NA 3450 3650 3625 4675 3475 4250 ...
 $ sex              : chr  ”male” ”female” ”female” NA ...
 $ year             : int  2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
>
```

Introductory Example (cont.)

Key Features

- We will discuss available options to create arrays
  - dense arrays versus sparse arrays
  - one or multiple indices (on sparse arrays)
  - options for creating and accessing arrays
  - but we mention tuning (tile extent, tile layout, ...) only in passing
- We will show different ways to read arrays back into R

Dense Arrays

Dense Data

The introductory example `quickstart_dense.R` creates an array with two integer domains and a single integer attribute:

```r
# The array will be 4x4 with dims ”rows” and ”cols” and domain [1,4]
dom <- tiledb_domain(dims = c(tiledb_dim(”rows”, c(1L, 4L), 4L, ”INT32”),
                              tiledb_dim(”cols”, c(1L, 4L), 4L, ”INT32”)))
# The array will be dense with a single attribute ”a” so
# each cell (i,j) cell can store an integer.
schema <- tiledb_array_schema(dom, attrs=c(tiledb_attr(”a”, type=”INT32”)))
# Create the (empty) array on disk.
uri <- ”quickstart_dense”
tiledb_array_create(uri, schema)
```

Dense Data (cont.)

Having created the array we can now open it for writing and add data.

```r
# equivalent to matrix(1:16, 4, 4, byrow=TRUE)
data <- array(c(c(1L, 5L, 9L, 13L),
                c(2L, 6L, 10L, 14L),
                c(3L, 7L, 11L, 15L),
                c(4L, 8L, 12L, 16L)), dim = c(4,4))
# Open the array and write to it.
A <- tiledb_array(uri = uri)
A[] <- data
```

Dense Data (cont.)

Data can be read back with different convenience wrappers:

```
arr <- tiledb_array(uri); arr[]                     # list of columns
arr <- tiledb_array(uri, as.data.frame=TRUE); arr[] # a data.frame
arr <- tiledb_array(uri, as.matrix=TRUE); arr[]     # a matrix
arr <- tiledb_array(uri, as.array=TRUE); arr[]      # an array
```

Dense Data (cont.)

A data.frame example for dense arrays:

```
library(tiledb)          # load our package
uri <- tempfile()        # any local directory, more later on cloud access

## any data.frame, data.table, tibble ...; here we use penguins_raw
fromDataFrame(palmerpenguins::penguins_raw,  uri)

# we want a data.frame, and we skip the implicit row numbers added as index
x <- tiledb_array(uri, as.data.frame = TRUE, extended = FALSE)

newdf <- x[]             # full array (we can index rows and/or cols too)
```

Dense Data (cont.)

```
> str(newdf[, 1:14])   # omitting last three cols for brevity
'data.frame':   344 obs. of  17 variables:
 $ studyName          : chr  ”PAL0708” ”PAL0708” ”PAL0708” ”PAL0708” ...
 $ Sample Number      : num  1 2 3 4 5 6 7 8 9 10 ...
 $ Species            : chr  ”Adelie Penguin (Pygoscelis adeliae)”  ...
 $ Region             : chr  ”Anvers” ”Anvers” ”Anvers” ”Anvers” ...
 $ Island             : chr  ”Torgersen” ”Torgersen” ”Torgersen” ”Torgersen” ...
 $ Stage              : chr  ”Adult, 1 Egg Stage” ”Adult, 1 Egg Stage” ...
 $ Individual ID      : chr  ”N1A1” ”N1A2” ”N2A1” ”N2A2” ...
 $ Clutch Completion  : chr  ”Yes” ”Yes” ”Yes” ”Yes” ...
 $ Date Egg           : Date, format: ”2007-11-11” ...
 $ Culmen Length (mm) : num  39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
 $ Culmen Depth (mm)  : num  18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
 $ Flipper Length (mm): num  181 186 195 NA 193 190 181 195 193 190 ...
 $ Body Mass (g)      : num  3750 3800 3250 NA 3450 ...
 $ Sex                : chr  ”MALE” ”FEMALE” ”FEMALE” NA ...
```

Sparse Arrays

Sparse Array: Numeric

```
library(tiledb)                      # TileDB package
library(Matrix)                      # for sparse matrix functionality
uri <- tempfile()                    # array location
set.seed(123)                        # fix RNG seed

mat <- matrix(0, nrow=8, ncol=20)
mat[sample(seq_len(8*20), 15)] <- seq(1, 15)
spmat <- as(mat, ”dgTMatrix”)        # new sparse 'dgTMatrix'

fromSparseMatrix(spmat, uri)         # store the sparse matrix in TileDB
chk <- toSparseMatrix(uri)           # and retrieve it to check
```

Sparse Array: Numeric (cont.)

```
> chk      # to check retrieved sparse matrix
8 x 20 sparse Matrix of class ”dgTMatrix”

[1,] . . . . . . . .  . . .  .  . . . . . 13  . 8
[2,] . . . . . . 3 .  . . .  9  . . . . .  .  . .
[3,] . . . . . 5 . .  . . . 10 14 . . . .  .  . .
[4,] . . . . . . . .  . . . 12  . . . . .  .  . .
[5,] . . . . . . . .  . . .  .  . . . . .  .  . 7
[6,] . 2 . . . . . .  . . .  .  . . 4 . .  .  . .
[7,] . . . . . . . .  . . .  .  . . . . .  . 11 1
[8,] . . . . . . . . 15 . .  .  . . . . .  .  . 6
>
```

[tile]DB

Sparse Array: Data Frame

```r
library(tiledb)          # load our package
uri <- tempfile()        # any local directory, more later on cloud access
## now sparse with a character and integer ('year') index colum
## with wider range than seen in the data for year we allow appending
fromDataFrame(palmerpenguins::penguins,  uri, sparse = TRUE,
              col_index = c(”species”, ”year”),
              tile_domain=list(year=c(2000L, 2021L)))

x <- tiledb_array(uri, as.data.frame = TRUE, extended = FALSE)
newdf <- x[]             # full array (we can index rows and/or cols too)
```

Sparse Array: Data Frame (cont.)

```
x <- tiledb_array(uri, as.data.frame = TRUE, extended = FALSE)
selected_ranges(x) <- list(year=cbind(2007L, 2008L),
                           species=cbind(”Gentoo”, ”Gentoo”))
newdf <- x[]
```

Now we retrieve with two constraints: ‘years’ from 2007 to 2008 (both included), and ‘species’ equal to “Gentoo” (given as lower and upper range which implies equality). Note that both are *dimension* columns.

Sparse Array: Data Frame (cont.)

```
qc <- tiledb_query_condition_init(”body_mass_g”, 6000, ”INT32”, ”GE”)
query_condition(x) <- qc
newdf <- x[]
```

This selects rows based on the given attribute value, here `body_mass_g` which is required to be greater or equal to 6000 (grams).

Query conditions on attributes can also be combined (via standard Boolean operators).

Also (but not on CRAN yet): `qc <- parse_query_condition(body_mass_g >= 6000)`

Sparse Array: Select Attribute Columns

```r
x <- tiledb_array(uri, as.data.frame = TRUE, extended = FALSE)
attrs(x) <- c(”island”, ”sex”)
```

This results in just the two selected attribute columns being returned (along with the two dimension columns).

Column selections can be combined with row selections.

Sparse Array: Incremental Writes

Setting the initial *domain* of the dimension columns (to ranges that accomodate future writes) allows incremental writes in batches.

As TileDB is serverless and inherently parallel, multiple writes can be made at the same time.

fromDataFrame & tiledb_array

fromDataFrame

High-level Array Writer

- Helper function to *create* arrays from existing data.frame data in R
- Can write dense arrays as well as sparse arrays
  - can add ad-hoc row-indices (dense and sparse)
  - or can use multiple index colums (sparse)
  - these can use int, numeric, or char data
- Defaults to using a ZStd compression filter
- Can set different TileDB array attributes and parameters
- Can support *append* mode via explicit dimension domain values
- We will see some examples later

tiledb_array

High-level Array Reader

- General array accessor for both dense and sparse arrays
- Supports multiple options to return as
    - data.frame
    - matrix
    - array
- Supports selection of row ranges (via dimension constraint)
- Supports selection of returned columns

Full TileDB API

Full API

```r
dims <- c(tiledb_dim(”rows”, c(1L, 4L), 4L, ”INT32”),
          tiledb_dim(”cols”, c(1L, 4L), 4L, ”INT32”))
attrs <- tiledb_attr(”a”, type = ”INT32”)
schema <- tiledb_array_schema(tiledb_domain(dims), attrs)
tiledb_array_create(uri, schema)
data <- 1:16
arr <- tiledb_array(uri = uri)
qry <- tiledb_query(arr, ”WRITE”)
qry <- tiledb_query_set_layout(qry, ”ROW_MAJOR”)
qry <- tiledb_query_set_buffer(qry, ”a”, data)
qry <- tiledb_query_submit(qry)
qry <- tiledb_query_finalize(qry)
stopifnot(tiledb_query_status(qry)==”COMPLETE”)
```

This example shows “quickstart_dense”

Each key function in the underlying TileDB Embedded (C++) API has been wrapped and is accessible directly.

This is useful when the higher-level functions need to be tweaked or customized.

Full API (using R 4.1.0 pipe)

```r
dims <- c(tiledb_dim(”rows”, c(1L, 4L), 4L, ”INT32”),
          tiledb_dim(”cols”, c(1L, 4L), 4L, ”INT32”))
attrs <- tiledb_attr(”a”, type = ”INT32”)
schema <- tiledb_array_schema(tiledb_domain(dims), attrs)
tiledb_array_create(uri, schema)
data <- 1:16
tiledb_array(uri = uri) |>
    tiledb_query(”WRITE”) |>
    tiledb_query_set_layout(”ROW_MAJOR”) |>
    tiledb_query_set_buffer(”a”, data) |>
    tiledb_query_submit() |>
    tiledb_query_finalize()
stopifnot(tiledb_query_status(qry)==”COMPLETE”)
```

This example shows “quickstart_dense” with the native pipe.

As many of the TileDB APi functions operate on the query type argument and return it, this style is easily supported.

Full API

Another example: retrieve the default configuration, overriden number of threads and asking for fragment meta-data consolitation (useful after many chunks have been written):

```
cfg <- tiledb_config()
cfg[”sm.num_reader_threads”] <- 8
cfg[”sm.num_writer_threads”] <- 8
cfg[”vfs.num_threads”] <- 8
cfg[”sm.consolidation.mode”] <- ”fragment_meta”
ctx <- tiledb_ctx(cfg)
array_consolidate(uri=uri, cfg=cfg)
```

S3

S3

```
uri <- ”s3://namespace/bucket”          # change URI as needed

## you need either these two environment variables
##   AWS_SECRET_ACCESS_KEY
##   AWS_ACCESS_KEY_ID
## or set this in the TileDB config object

fromSparseMatrix(spmat, uri)     # stored
chk <- toSparseMatrix(uri)       # retrieved

## lazy eval: e.g. for subsets only requested data transferred to client
```

S3 (cont.)

```
> pp <- tiledb_array(”s3://tiledb-conferences/useR-2021/palmer_penguins”, as.data.frame=TRUE)
> dat <- pp[]
> head(dat)
  species year    island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g    sex
1  Adelie 2007     Dream           36.0          17.9               190        3450 female
2  Adelie 2007     Dream           42.3          21.2               191        4150   male
3  Adelie 2007 Torgersen           40.3          18.0               195        3250 female
4  Adelie 2007 Torgersen           34.6          21.1               198        4400   male
5  Adelie 2007 Torgersen           36.6          17.8               185        3700 female
6  Adelie 2007 Torgersen           36.7          19.3               193        3450 female
>
```

Arrow

Arrow

```r
suppressMessages( { library(tiledb); library(arrow) } )
val <- 1:3     # arbitrary, could be rnorm() too
typ <- int8()  # any Arrow type
vec <- Array$create(val, typ)           # Arrow vector

aa <- tiledb_arrow_array_ptr()
as <- tiledb_arrow_schema_ptr()
on.exit( { tiledb_arrow_array_del(aa); tiledb_arrow_schema_del(as) } )
arrow::ExportArray(vec, aa, as)  # export Arrow to TileDB

newvec <- arrow::Array$create(arrow::ImportArray(aa, as))
stopifnot(all.equal(vec, newvec))
print(newvec)   # show round-turn
```

Arrow (cont.)

```
> print(newvec)   # show round-turn
Array
<int8>
[
  1,
  2,
  3
]
>
```

Additional examples demonstrate zero-copy transfer from Arrow into TileDB Arrays, and the inverse from TileDB to Arrow.

Additional higher-level functions will likely get added soon.

Time Travel

Time Travel

```r
uri <- ”... some uri, either local or on s3 or ...”

arr <- tiledb_array(uri,
                    as.data.frame = TRUE,   # convenient format
                    timestamp = as.POSIXct(”2021-01-02 03:04:05”))
## standard access to 'arr' as before
```

TileDB Arrays add content in immutable “layers” (or fragments).

We can access their content at points in time!

Time Travel (cont.)

```r
D <- data.frame(key=1:10, value=1:10)
uri <- tempfile()

fromDataFrame(D, uri, col_index=”key”,
              sparse=TRUE, allows_dups=FALSE)
now <- Sys.time()

Sys.sleep(60)                           # one minute
arr <- tiledb_array(uri)
D$value <- 100 + D$value
arr[] <- D
then <- Sys.time()
```

Time Travel (cont.)

```
## we have written twice
show(arr[])

arrEarlier <- tiledb_array(uri, timestamp=now)
show(arrEarlier[])

arrLater <- tiledb_array(uri, timestamp=then)
show(arrLater[])
```

Encryption

Encryption

```
uri <- ”... some uri, either local or on s3 or ...”

arr <- tiledb_array(uri,
                    as.data.frame = TRUE,   # convenient format
                    encryption_key = ”...an AES-256 key here...”)
## standard access to 'arr' as before
```

TileDB Arrays support encryption. The underlying files are controlled by standard filesystem access control layers, and additionally the content can be encrypted using standard AES-256 technology.

Encryption (cont.)

```
dom <- tiledb_domain(dims = tiledb_dim(”rows”, c(1L, 4L), 4L, ”INT32”))
schema <- tiledb_array_schema(dom, attrs=tiledb_attr(”a”, type = ”INT32”),
                              sparse = TRUE)
uri <- tempfile()
enckey <- ”0123456789abcdef0123456789ABCDEF”
invisible( tiledb_array_create(uri, schema, enckey) ) # schema with key

arr <- tiledb_array(uri, encryption_key = enckey)     # open with key to
arr[] <- data.frame(rows=1:4, a=101:104)              # write and read

chk <- tiledb_array(uri, encryption_key = enckey, as.data.frame=TRUE)
chk[]
```

Applications

SQL

SQL

Setup

- TileDB integrates with different frontends as well as languages
- One example: MariaDB with TileDB accessed via a ‘storage plugin’
- Due to architectural choices at MariaDB, plugins
  - have to be compiled with the exact configuration as the server itself
  - we need to consistently build MariaDB, TileDB plugin … and TileDB
- One easy way to do this is via Docker container `tiledb-mariadb-r`
- See `https://hub.docker.com/r/tiledb/tiledb-mariadb-r/`

SQL (cont.)

Setup (cont.)

We launch the container as a daemon, allow MariaDB to accept empty password, and name the running image ‘tiledb-mariadb-r’:

```
## line break for display here
docker run --name tiledb-mariadb-r -it -d --rm \
   -e MYSQL_ALLOW_EMPTY_PASSWORD=1 tiledb/tiledb-mariadb-r
```

If desired, we can mount local directories via the standard Docker option `-v local:container` to access host data in container.

SQL (cont.)

We then start R via Docker connecting to this session:

```
docker exec -it -u root tiledb-mariadb-r R
```

and in R write

```
library(tiledb)
fromDataFrame(palmerpenguins::penguins_raw, ”/tmp/penguinsraw”)
```

to create a TileDB Array in the context of the container.

SQL (cont.)

We then start R again via the same command for another R shell but now access the data.

Note that per standard semantics this query did *not* yet materialize.

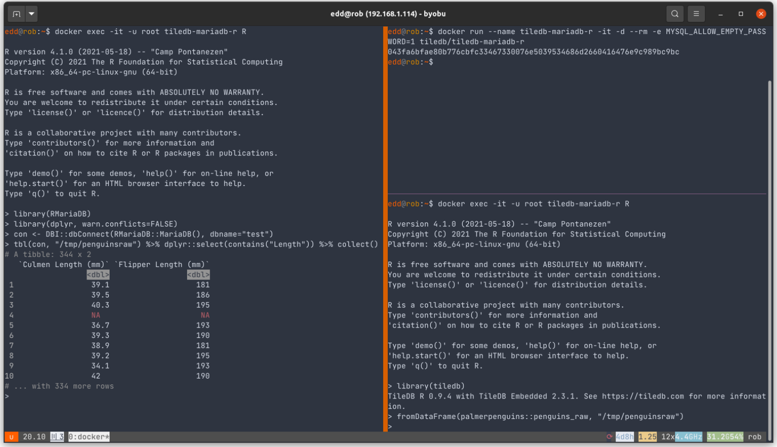
```
> library(RMariaDB)
> library(dplyr, warn.conflicts=FALSE)
> con <- DBI::dbConnect(RMariaDB::MariaDB(), dbname=”test”)
> tbl(con, ”/tmp/penguinsraw”) |> dplyr::select(contains(”Length”))
# Source:   lazy query [?? x 2]
# Database: mysql [@localhost:NA/test]
   `Culmen Length (mm)` `Flipper Length (mm)`
                  <dbl>                 <dbl>
 1                 39.1                   181
 2                 39.5                   186
 3                 40.3                   195
 4                 NA                      NA
 5                 36.7                   193
 6                 39.3                   190
 7                 38.9                   181
 8                 39.2                   195
 9                 34.1                   193
10                 42                     190
# ... with more rows
>
```

SQL (cont.)

By adding `collect()` to the pipeline we ensure an actual retrieval of the data.

```
> tbl(con, ”/tmp/penguinsraw”) |>
+     dplyr::select(contains(”Length”)) |>
+     collect()
# A tibble: 344 x 2
   `Culmen Length (mm)` `Flipper Length (mm)`
                  <dbl>                 <dbl>
 1                 39.1                   181
 2                 39.5                   186
 3                 40.3                   195
 4                 NA                      NA
 5                 36.7                   193
 6                 39.3                   190
 7                 38.9                   181
 8                 39.2                   195
 9                 34.1                   193
10                 42                     190
# ... with 334 more rows
>
```

SQL (cont.)



```
edd@rob:~$ docker exec -it -u root tiledb-mariadb-r R

R version 4.1.0 (2021-05-18) -- "Camp Pontanezen"
Copyright (C) 2021 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> library(RMariaDB)
> library(dplyr, warn.conflicts=FALSE)
> con <- DBI::dbConnect(RMariaDB::MariaDB(), dbname="test")
> tbl(con, "/tmp/penguinsraw") %>% dplyr::select(contains("Length")) %>% collect()
# A tibble: 344 x 2
   `Culmen Length (mm)` `Flipper Length (mm)`
                  <dbl>                 <dbl>
 1                 39.1                   181
 2                 39.5                   186
 3                 40.3                   195
 4                 NA                      NA
 5                 36.7                   193
 6                 39.3                   190
 7                 38.9                   181
 8                 39.2                   195
 9                 34.1                   193
10                 42                     190
# ... with 334 more rows
>
```

```
edd@rob:~$ docker run --name tiledb-mariadb-r -it -d --rm -e MYSQL_ALLOW_EMPTY_PASS
WORD=1 tiledb/tiledb-mariadb-r
043fa6bfae80b776cbfc33467330076e5039534686d2660416476e9c989bc9bc
edd@rob:~$
```

```
edd@rob:~$ docker exec -it -u root tiledb-mariadb-r R

R version 4.1.0 (2021-05-18) -- "Camp Pontanezen"
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Platform: x86_64-pc-linux-gnu (64-bit)

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> library(tiledb)
TileDB R 0.9.4 with TileDB Embedded 2.3.1. See https://tiledb.com for more informat
ion.
> fromDataFrame(palmerpenguins::penguins_raw, "/tmp/penguinsraw")
>
```

Start with top right to launch container ad daemon.

Next bottom right to create an array.

Finally left pane to access it.

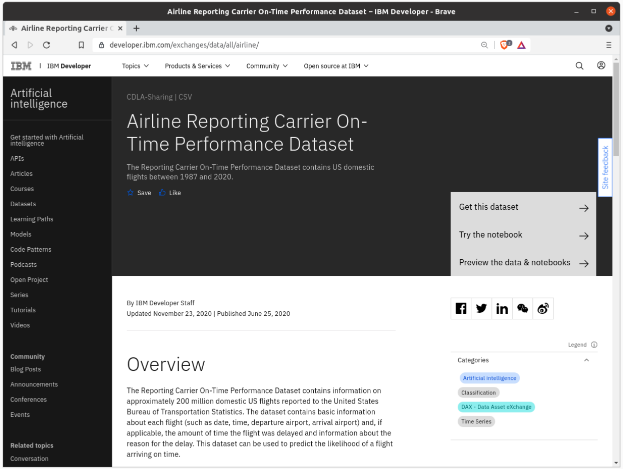
Data Science with Flights Data

Data Science Example: Large Data Frame

We have already seen several examples for data.frames. The ability to index on different column types maps well with data.frame objects.

This example uses the well known flights data set.

Data Science Example: Large Data Frame



CDLA-Sharing | CSV

Airline Reporting Carrier On-Time Performance Dataset

The Reporting Carrier On-Time Performance Dataset contains US domestic flights between 1987 and 2020.

By IBM Developer Staff
Updated November 23, 2020 | Published June 25, 2020

Overview

The Reporting Carrier On-Time Performance Dataset contains information on approximately 200 million domestic US flights reported to the United States Bureau of Transportation Statistics. The dataset contains basic information about each flight (such as date, time, departure airport, arrival airport) and, if applicable, the amount of time the flight was delayed and information about the reason for the delay. This dataset can be used to predict the likelihood of a flight arriving on time.

We use the full ‘flights’ data set (available under a permissible data license at the IBM site shown on the left.

It is available as both the full data set with 194 million rows, as well as in a 2 million row subset.

[tile]DB

Large Data Frame (cont.)

Creating the TileDB Array

The data comes as `tar.gz` containing a compressed csv file.

We cannot efficiently read all of the csv so we wrap a loop around, extracting chunks (via `sed`) which `data.table::fread()` can ingest. (We also skip a number of uninformative extra columns.)

We select four index columns. Three of these are character based and automatically obtain a `<null,null>` domain which we can append to.

For the fourth, we explicitly set an earlier start data and later (current) end date.

Large Data Frame (cont.)

```
createIteratively <- function(csvxzfile, uri, n=100000, N=2000000) {
    stopifnot(`no csv.xz`=file.exists(csvxzfile))

    cmd <- paste0(”xz -c -d ”, csvxzfile, ”| sed -n -e'1,”, format(n+1, scientific=FALSE), ”'p”)
    cat(cmd, ”\n”)
    D <- fread(cmd=cmd, drop=c(48,57:109))
    cn <- colnames(D)   # used below
    D <- filterData(D)  # helper converting a few columns: utf8 char, bool to int, factor to char
    if (tiledb_vfs_is_dir(uri)) tiledb_vfs_remove_dir(uri)
    fromDataFrame(D, uri, sparse=TRUE,
                  col_index = c(”FlightDate”, ”Reporting_Airline”, ”Origin”, ”Dest”),
                  tile_domain=list(FlightDate=c(as.Date(”1970-01-01”), Sys.Date())))
    written <- n        # keep track of data written

    ## remainder on next slide
```

Large Data Frame (cont.)

```
    ## continued from previous slide

    arr <- tiledb_array(uri)
    while (written < N) {
        cmd <- paste0(”xz -c -d ”, csvxzfile, ”| sed -n -e'1d' -e'”,
                      format(written+1+1, scientific=FALSE), ”,”,
                      format(min(written+n+1, N+1), scientific=FALSE), ”'p”)
        cat(cmd, ”\n”)
        D <- fread(cmd=cmd, drop=c(48,57:109))
        colnames(D) <- cn                       # assign colnames from first chunk
        D <- filterData(D)
        arr[] <- D                              # append chunk to TileDB array
        written <- written + n
    }
    invisible(NULL)
}
```

Large Data Frame (cont.)

Operating on the full dataset–but selecting *by dimensions* ‘FlightDate’ and ‘Reporting_Airline’:

```
arr <- tiledb_array(uri, as.data.frame=TRUE)
fromD <- as.Date(”2000-01-01”)
toD <- as.Date(”2000-12-31”)
selected_ranges(arr) <- list(FlightDate=cbind(fromD, toD),
                             Reporting_Airline=cbind(”UA”, ”UA”))
res <- arr[]
print(dim(res)) ## 776559 x 55
```

Large Data Frame (cont.)

We we add additional conditions on attributes:

```
## as before
qc1 <- tiledb_query_condition_init(”ArrDelay”, 120, ”FLOAT64”, ”GE”)
qc2 <- tiledb_query_condition_init(”DepDelay”, 120, ”FLOAT64”, ”GE”)
query_condition(arr) <- tiledb_query_condition_combine(qc1, qc2, ”AND”)
res <- arr[]
print(dim(res))  ## now 21893 x 55
```

Large Data Frame (cont.)

With not-yet-on-CRAN-but-at-GitHub current version can use a more direct approach:

```r
qc <- parse_query_condition(ArrDelay >= 120.001 && DepDelay >= 120.001)
query_condition(arr) <- qc
res <- arr[]
print(dim(res))  ## now 21893 x 55
```

(The query condition parsing is independent of the array and does not know the underlying types which is why we used 120.001 to provide a hint that the delay columns are FLOAT64.)

Large Data Frame (cont.)

Not that this is fully remote evaluation: we transmit the request including the selection constraints, and only the requested data is returned: here 22k rows out of 194 million.

Large Data Frame and SQL

We combine the two previous applications! Launching first in the directory above the ‘flights’ array:

```
docker run --name tiledb-mariadb-r -it -d --rm \
       -e MYSQL_ALLOW_EMPTY_PASSWORD=1 \
       -v $PWD:/mnt tiledb/tiledb-mariadb-r
```

to make the current (“outer”) directory (accessed via shell variable `$PWD`) in the container a path `/mnt`. Then we launch `R` in the container via

```
docker exec -it -u root tiledb-mariadb-r R
```

Large Data Frame and SQL

```
> library(RMariaDB); library(dplyr, warn.conflicts=FALSE)
> con <- DBI::dbConnect(RMariaDB::MariaDB(), dbname=”test”)
> tbl(con, ”/mnt/airline”) |> dplyr::select(contains(”Dep”))
# Source:   lazy query [?? x 7]
# Database: mysql [@localhost:NA/test]
   DepartureDelayGroups DepDel15 DepTime DepTimeBlk DepDelay DepDelayMinutes
                  <int>    <dbl>   <int> <chr>         <dbl>           <dbl>
 1                    0        0    1402 1400-1459         1               1
 2                    0        0    1750 1700-1759         0               0
 3                    0        0    1108 1100-1159         0               0
 4                    0        0     511 0001-0559         0               0
 5                    0        0     928 0900-0959         1               1
 6                    0        0    1631 1600-1659         1               1
 7           2147483647        0    2111 2100-2159        -3               0
 8           2147483647        0    1305 1300-1359        -1               0
 9                    0        0     858 0800-0859         3               3
10                    0        0     648 0600-0659         2               2
# ... with more rows, and 1 more variable: CRSDepTime <int>
>
```

LiDAR

LiDAR

- LiDAR stands for Light Detection and Ranging
- It is a method for determining ranges (often using lasers)
- Used in spatial analysis, forestry, or even autonomous driving
- Many (public) data sets via LAS or LAZ (compressed) files
- As these are multidimensional arrays use maps well to TileDB

Lidar Ingest

The PDAL (Point Data Abstraction Library) is central, and the `pdal` binary can be built with TileDB support.

We use a Docker container tiledb-geospatial to read LAS (or LAZ) files and create an array as described on the TileDB docs website.

Command:

```
pdal pipeline -i pipeline.json
```

where `pdal` may come from the tiledb-geospatial container, and the JSON control file shown to the right might control *reading* and *writing* steps.

```
[
    {
    ”type”: ”readers.las”,
    ”filename”: ”autzen.laz”
    },
    {
    ”type”: ”writers.tiledb”,
    ”array_name”: ”autzen_tiledb”,
    ”chunk_size”: 10000000
    }
]
```

LiDAR

```
lasfile <- ”LAS_17258975.las”
if (!file.exists(lasfile)) {
    ## note: the file is 451 mb
    op <- options()                     # store
    options(timeout=3600)               # (much) more patience downloading
    lasfileurl <- file.path(”https://clearinghouse.isgs.illinois.edu/las-east/cook/las/”, lasfile)
    download.file(lasfileurl,lasfile)
    options(op)                         # reset
}

if (!dir.exists(”las_array”)) {
    wd <- getwd()
    cmd <- paste0(”docker run --rm -ti -u 1000:1000 -v ”, wd, ”:/data ”,
                  ”-w /data tiledb/tiledb-geospatial pdal pipeline -i pipeline.json”)
    system(cmd)                         # fancier return code check possible
}
```

LiDAR (cont.)

Note that we can loop similarly over many LAS or LAZ files, and can also inject them in parallel. The JSON file needs `”append”: true` to append; this way we can store *many* LAS or LAZ files in a single TileDB Array, locally or in the cloud.

Being able to store many such files in a single (cloud-hosted or local) array shows one of the strengths of TileDB. And data requests will transfer only the requested subset.

LiDAR (cont)

We can then read from the LiDAR array. The following extracts just 100k rows of points from a well-known building:

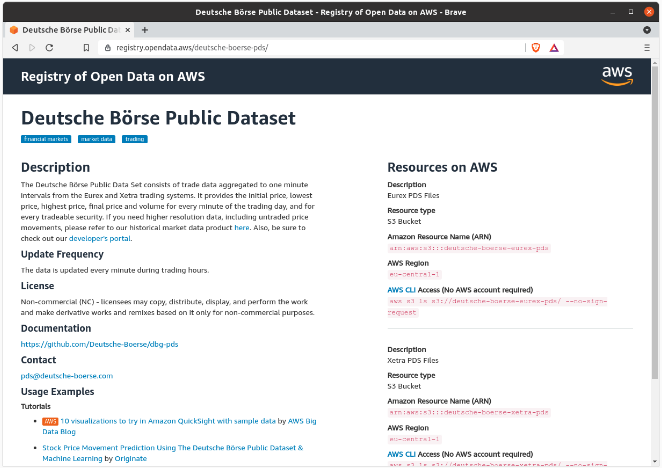
```r
library(tiledb)
arr <- tiledb_array(”las_array”, as.data.frame=TRUE)
selected_ranges(arr) <- list(X = cbind(1174100, 1174400),  Y = cbind(1899125, 1899250))
L <- arr[]
## print(dim(L))    # 108655 x 15

library(lidR)
L$ScanAngleRank <- as.integer(L$ScanAngleRank)
LL <- LAS(L)
plot(LL)                                # open rgl device
## plot(LL, backend=”lidRviewer”)       # if lidRviewer is installed
```

Finance / Time Series

Time Series

TileDB can also be used for financial data such as transactions data from an exchange, times and sales data from trades, or aggregates. In this example we will look at a data set provided (and regularly updated) by Deutsche Boerse covering one-minute bars of each stock and etf (for the stock exchanges) and each future (for the Eurex sister exchange focussing on derivatives).

Time Series


Deutsche Börse Public Dataset - Registry of Open Data on AWS - Brave
Deutsche Börse Public Dat
registry.opendata.aws/deutsche-boerse-pds/
Registry of Open Data on AWS
aws

Deutsche Börse Public Dataset

financial markets · market data · trading

Description

The Deutsche Börse Public Data Set consists of trade data aggregated to one minute intervals from the Eurex and Xetra trading systems. It provides the initial price, lowest price, highest price, final price and volume for every minute of the trading day, and for every tradeable security. If you need higher resolution data, including untraded price movements, please refer to our historical market data product here. Also, be sure to check out our developer's portal.

Update Frequency

The data is updated every minute during trading hours.

License

Non-commercial (NC) - licensees may copy, distribute, display, and perform the work and make derivative works and remixes based on it only for non-commercial purposes.

Documentation

https://github.com/Deutsche-Boerse/dbg-pds

Contact

pds@deutsche-boerse.com

Usage Examples

Tutorials

- AWS 10 visualizations to try in Amazon QuickSight with sample data by AWS Big Data Blog
- Stock Price Movement Prediction Using The Deutsche Börse Public Dataset & Machine Learning by Originate

Resources on AWS

Description
Eurex PDS Files

Resource type
S3 Bucket

Amazon Resource Name (ARN)
`arn:aws:s3:::deutsche-boerse-eurex-pds`

AWS Region
`eu-central-1`

AWS CLI Access (No AWS account required)

```
aws s3 ls s3://deutsche-boerse-eurex-pds/ --no-sign-request
```

Description
Xetra PDS Files

Resource type
S3 Bucket

Amazon Resource Name (ARN)
`arn:aws:s3:::deutsche-boerse-xetra-pds`

AWS Region
`eu-central-1`

AWS CLI Access (No AWS account required)

```
aws s3 ls s3://deutsche-boerse-xetra-pds/ --no-sign-
```

Provided by the exchange via AWS

“[...] provides the initial price, lowest price, highest price, final price and volume for every minute of the trading day, and for every tradeable security.”

“If you need higher resolution data, including untraded price movements, please refer to our historical market data product here.”

Time Series

List the files (here a small demo sample).

Helper function to construct datetime column, and remove date and time columns.

Simple injection loop. First file creates the array and defines the schema. We set minimum amd maximum time values.

Injection could run in parallel, or an automated script appending new data.

```r
uri <- ”dboerse”
files <- list.files(pattern=”2020-.*\\.csv”) # files retrieved Fall of 2020

readAndAddDatetime <- function(file) {  # simple helper
    D <- fread(file)
    setDT(D)
    D[, Datetime := as.POSIXct(paste(Date, Time))]
    D[, `:=`(Date = NULL, Time = NULL)]
    invisible(D)
}

n <- length(files)
for (i in seq_len(n)) {
    D <- readAndAddDatetime(files[i])
    if (i == 1) {
        fromDataFrame(D, uri, sparse = TRUE,
                      col_index=c(”Mnemonic”,”Datetime”),
                      tile_domain=list(Datetime=c(as.POSIXct(”1970-01-01 00:00:00”), Sys.time())))
    } else {
        arr <- tiledb_array(uri, as.data.frame = TRUE)
        arr[] <- D
        tiledb_array_close(arr)
    }
}
```

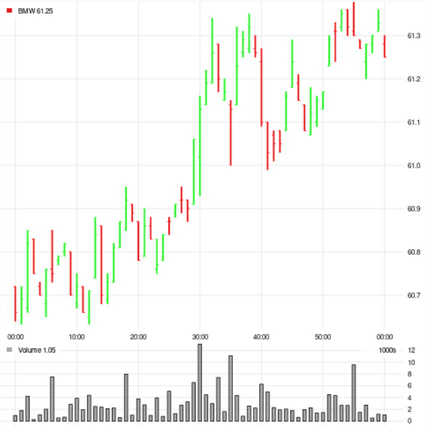
Time Series

Simple usage example: one hour of BMW trades in one-minute bars

```r
arr <- tiledb_array(uri, as.data.frame = TRUE)
selected_ranges(arr) <- list(Mnemonic=cbind(”BMW”, ”BMW”),
                             Datetime=cbind(as.POSIXct(”2020-11-04 09:00”),
                                            as.POSIXct(”2020-11-04 10:00”)))
BMW <- arr[]
```

Time Series

```
suppressMessages({
    library(rtsplot)                          # for nicer financial plot
    library(xts)                              # used by rtsplot
})
setDT(BMW)
symbol <- ”BMW”
rt <- as.xts(BMW[Mnemonic==symbol,
                 .(Datetime, Open=StartPrice, High=MaxPrice,
                   Low=MinPrice, Close=EndPrice, Volume=TradedVolume)])

cols <- rtsplot.colors(2)
layout(c(1,1,1,1,2))
rtsplot(rt, type=”n”)
rtsplot.ohlc(rt, col=rtsplot.candle.col(rt))
rtsplot.legend(symbol, cols[1], list(rt))
rt <- rtsplot.scale.volume(rt)
rtsplot(rt, type = 'volume', plotX = FALSE, col = 'darkgray')
rtsplot.legend('Volume', 'darkgray', quantmod::Vo(rt))
```



GWAS

What *is* a GWAS?

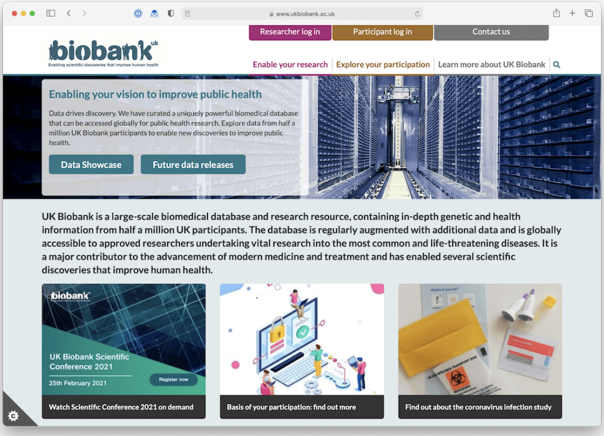
Overview

- *GWAS*: Genome-wide Association Study
- Used to identify regions of the genome that are associated with a particular trait (e.g., hair color)
- Requires:
  1) sequencing data on a large population of samples to identify genetic variants
  2) measurements for the trait of interest across the same samples

GWAS Results Example

```
variant       beta         se          tstat        pval
1:15791:C:T   -1.70174e+01 5.66755e+01 -3.00260e-01 7.63979e-01
1:69487:G:A   -5.70053e-02 1.11014e-01 -5.13496e-01 6.07605e-01
1:69569:T:C   -2.30684e-03 1.99098e-02 -1.15865e-01 9.07760e-01
1:139853:C:T  -5.62416e-02 1.11017e-01 -5.06603e-01 6.12434e-01
1:692794:CA:C 7.72562e-04  9.22074e-04 8.37852e-01  4.02114e-01
1:693731:A:G  1.31202e-03  8.71218e-04 1.50596e+00  1.32078e-01
1:707522:G:C  8.77269e-04  9.79498e-04 8.95631e-01  3.70450e-01
1:717587:G:A  -8.32431e-05 2.33724e-03 -3.56160e-02 9.71589e-01
1:723329:A:T  -1.15975e-02 6.88597e-03 -1.68422e+00 9.21406e-02
1:730087:T:C  4.23934e-05  1.21371e-03 3.49286e-02  9.72137e-01
```

Data source: UK Biobank


www.ukbiobank.ac.uk
Researcher log in
Participant log in
Contact us
biobank uk
Enabling scientific discoveries that improve human health
Enable your research
Explore your participation
Learn more about UK Biobank
Data Showcase
Future data releases
biobank
UK Biobank Scientific Conference 2021
25th February 2021
Register now
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Basis of your participation: find out more
Find out about the coronavirus infection study

Enabling your vision to improve public health

Data drives discovery. We have curated a uniquely powerful biomedical database that can be accessed globally for public health research. Explore data from half a million UK Biobank participants to enable new discoveries to improve public health.

UK Biobank is a large-scale biomedical database and research resource, containing in-depth genetic and health information from half a million UK participants. The database is regularly augmented with additional data and is globally accessible to approved researchers undertaking vital research into the most common and life-threatening diseases. It is a major contributor to the advancement of modern medicine and treatment and has enabled several scientific discoveries that improve human health.

About

Provides an incredibly rich source of biomedical data collected from hundred of thousands of volunteers in the United Kingdom.

[tile]DB

UK Biobank GWAS Dataset Stats

- Contains ~12,000 GWAS results files
- Analyzed over >4,000 traits across >350,000 individuals
- Also includes different versions of each analysis (e.g., sex-specific results)
- Each file:
  - contains ~10 million rows
  - ~500Mb gzipped (1.7Gb uncompressed)

UK Biobank announcement:

`http://www.nealelab.is/uk-biobank/ukbround2announcement`

Data Accessibility Goals

- Available on a remote cloud bucket
- Facilitate comparisons across phenotypes
- Query variants by their genomic location
- Query traits by their descriptive names

Tutorial Files

Copy GWAS tutorial to your working directory

```
# library(tiledb.user2021)
file.copy(
  from = system.file(”examples/exGWAS.R”, package = ”tiledb.user2021”)
  to = ”exGWAS.R”
)
```

Download GWAS results files

```
dir.create(”gwas-tutorial/data”, showWarnings = FALSE, recursive = TRU
download_gwas_files(”gwas-tutorial/data”)
```

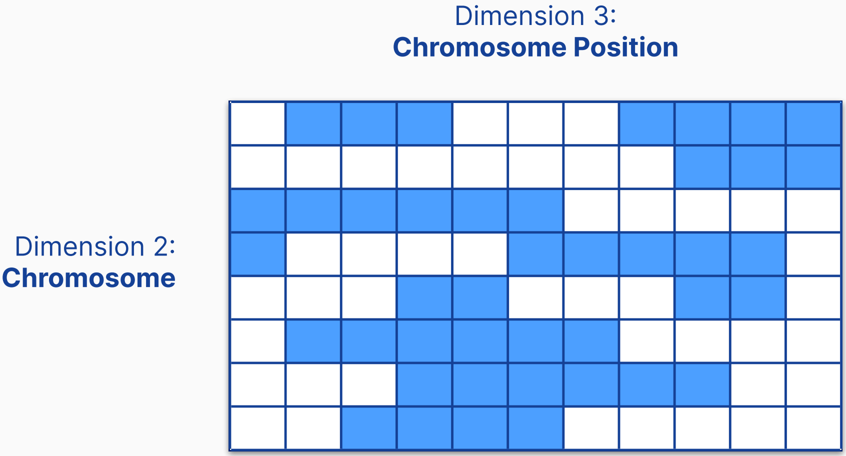
Extracting Genomic Location Data

```
variant
1:15791:C:T
1:69487:G:A
1:69569:T:C
1:139853:C:T
1:692794:CA:C
1:693731:A:G
1:707522:G:C
1:717587:G:A
```

becomes

```
chr pos    ref alt
1   15791  C   T
1   69487  G   A
1   69569  T   C
1   139853 C   T
1   692794 CA  C
1   693731 A   G
1   707522 G   C
1   717587 G   A
```

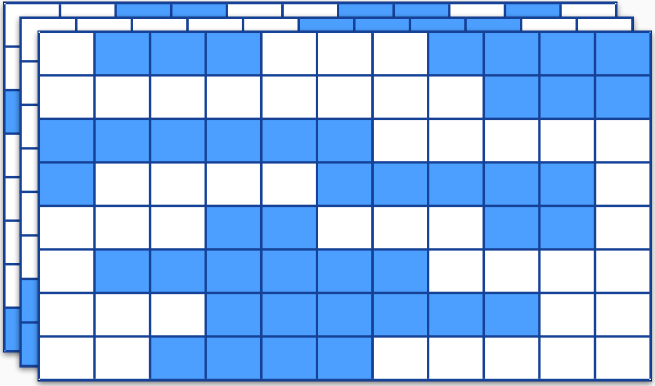
Array Layout



Dimension 3:
Chromosome Position

Dimension 2:
Chromosome

GWAS Array Layout

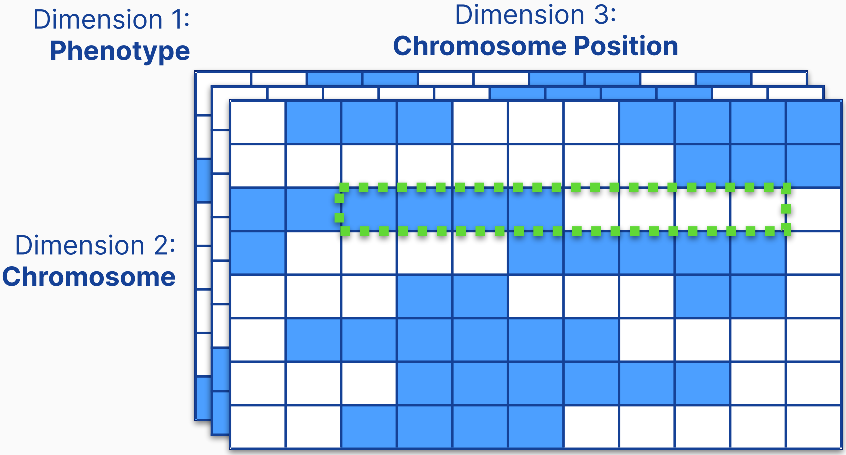


Dimension 1:
Phenotype

Dimension 3:
Chromosome Position

Dimension 2:
Chromosome

GWAS Array Layout



[tile]DB

Array Dimensions

1. GWAS Phenotype (e.g., *Ventricular rate*)
2. Variant chromosome (e.g., *chromosome 1*)
3. Chromosome location (e.g., 43,113,410 bp)

GWAS Array Dimension 1

Phenotype (the descriptive name for each analyzed trait)

```
dim_pheno <- tiledb_dim(
  name = ”phenotype”,
  domain = NULL,
  tile = NULL,
  type = ”ASCII”
)
```

GWAS Array Dimension 2

Chromosome labels

```
dim_chr <- tiledb_dim(
    name = ”chr”,
    domain = NULL,
    tile = NULL,
    type = ”ASCII”
  )
```

GWAS Array Dimension 3

Chromosome position

```
dim_pos <- tiledb_dim(
  name = ”pos”,
  domain = c(1L, 249250621L),
  tile = 1e5L,
  type = ”UINT32”
)
```

GWAS Array Attributes

```
attr_filters <- tiledb_filter_list(tiledb_filter(”ZSTD”))

all_attrs <- list(
  ref = tiledb_attr(”ref”, type = ”CHAR”, filter_list = attr_filters),
  alt = tiledb_attr(”alt”, type = ”CHAR”, filter_list = attr_filters),
  minor_AF = tiledb_attr(”minor_AF”, type = ”FLOAT64”, filter_list = attr_filters),
  pval =  tiledb_attr(”pval”, type = ”FLOAT64”, filter_list = attr_filters),
  tstat = tiledb_attr(”tstat”, type = ”FLOAT64”, filter_list = attr_filters),
  se   =  tiledb_attr(”se”, type = ”FLOAT64”, filter_list = attr_filters),
  beta =  tiledb_attr(”beta”, type = ”FLOAT64”, filter_list = attr_filters)
)
```

GWAS Array Creation

```r
# assemble the schema
gwas_schema <- tiledb_array_schema(
  domain = tiledb_domain(dims = c(dim_pheno, dim_chr, dim_pos)),
  attrs = all_attrs,
  sparse = TRUE,
  allows_dups = TRUE
)

# create the array
gwasdb_uri <- ”ukbiobank-gwasdb”
tiledb_array_create(gwasdb_uri, schema = gwas_schema)
```

Download GWAS Results Files

A set of 6 slimmed down results files created for this tutorial can be downloaded using the helper package:

```
dir.create(”gwas_files”, showWarnings = FALSE)
tiledb.user2021::download_gwas_files(”gwas_files”)
```

These files were processed to:

- include only chromosomes 20, 21, and 22
- remove variants flagged as *low confidence*
- parse chromosomal location from the `variant` identifiers
- add a `phenotype` column with GWAS trait description

Open GWAS Array

Let’s return the results as a `data.frame` that includes the subset of attributes we’re interested in.

```r
gwasdb <- tiledb_array(
  gwasdb_uri,
  is.sparse = TRUE,
  as.data.frame = TRUE,
  attrs = c(”beta”, ”se”, ”tstat”, ”pval”)
)
```

GWAS Query #1

Use `[]` indexing to query the first 2 dimensions (e.g., `phenotype` and `chr`).

```
gwasdb[”Water intake”, ”20”]
```

```
# A tibble: 295,761 x 7
  phenotype     chr     pos       beta      se   tstat  pval
  <chr>         <chr> <int>      <dbl>   <dbl>   <dbl> <dbl>
1 Water intake  20    61098  0.00199   0.00246  0.812  0.417
2 Water intake  20    61270 -0.00113   0.00719 -0.157  0.876
3 Water intake  20    61795  0.000381  0.00218  0.175  0.861
4 Water intake  20    62731 -0.00200   0.00328 -0.611  0.541
5 Water intake  20    63231  0.00219   0.00683  0.320  0.749
```

GWAS Query #2

Use `selected_ranges` to query all 3-dimensions and extract data for a specific genomic region.

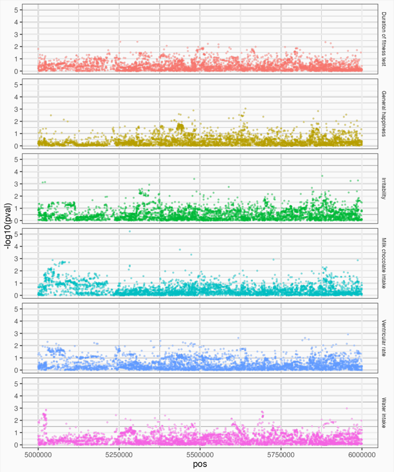
```
selected_ranges(gwasdb) <- list(
  phenotype = cbind(”Water intake”, ”Water intake”),
  chr = cbind(”20”, ”20”),
  pos = cbind(5e6, 6e6)
)
gwasdb[]
```

```
# A tibble: 5,198 x 7
  phenotype     chr         pos     beta      se  tstat   pval
  <chr>         <chr>     <int>    <dbl>   <dbl>  <dbl>  <dbl>
1 Water intake 20     5000142  0.0138  0.0103   1.34  0.180
2 Water intake 20     5000146 -0.00457 0.00529 -0.864 0.388
3 Water intake 20     5000279  0.00523 0.0181   0.288 0.773
4 Water intake 20     5000280 -0.00605 0.00246 -2.46  0.0139
5 Water intake 20     5000337 -0.00459 0.00529 -0.867 0.386
```

GWAS Query #3

Examine p-values across all phenotypes for the same genomic region.

```
selected_ranges(gwasdb) <- list(
  phenotype = NULL,
  chr = cbind(”20”, ”20”),
  pos = cbind(5e6, 6e6)
)
gwas_results <- gwasdb[]
manhattan_plot(gwas_results)
```



GWAS Resources

1. UK Biobank (`https://www.ukbiobank.ac.uk`)
2. Neale Lab UK Biobank GWAS results (`https://www.nealelab.is/uk-biobank`)
3. GWAS Results Manifest

Wrap-Up

In Summary

TileDB

- an open-source embeddable storage engine
- an open-source format for modeling any type of data
- fully cloud-native on AWS, GCS, Azure
- limitless scalability
- offers time travel
- offers Encryption

In Summary

TileDB R Package

- available on CRAN, and already used by Bioconductor
- high-level R-friendly interface for creating/query TileDB arrays
- also includes low-level access to the full TileDB API
- fully interoperable with DBI, Arrow, ...

In Summary

Use cases

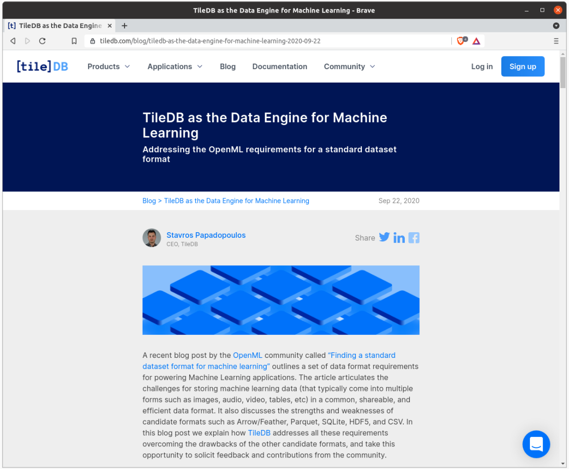
- limitless 😉 – just get in touch with TileDB for a demo

Use cases covered today

- Data Frames
- LiDAR and Geospatial uses
- Finance and Time Series
- Population Genomics and GWAS

Further Resources

Resources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Addressing the OpenML requirements for a standard dataset format

Blog > TileDB as the Data Engine for Machine Learning

Sep 22, 2020

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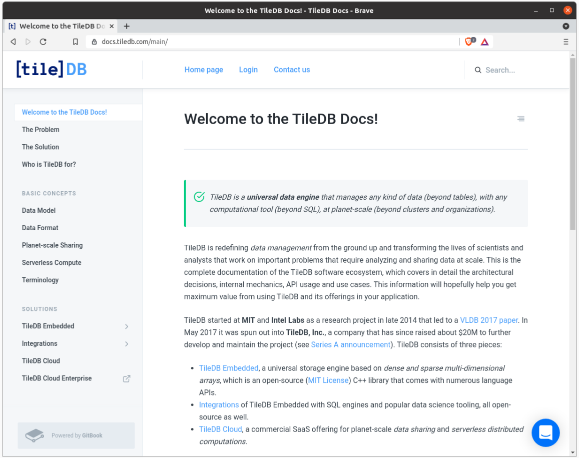
CEO, TileDB

A recent blog post by the OpenML community called "Finding a standard dataset format for machine learning" outlines a set of data format requirements for powering Machine Learning applications. The article articulates the challenges for storing machine learning data (that typically come into multiple forms such as images, audio, video, tables, etc) in a common, shareable, and efficient data format. It also discusses the strengths and weaknesses of candidate formats such as Arrow/Feather, Parquet, SQLite, HDF5, and CSV. In this blog post we explain how TileDB addresses all these requirements overcoming the drawbacks of the other candidate formats, and take this opportunity to solicit feedback and contributions from the community.

Blog post describing how TileDB answers the data format requirements for scientific data as layed out in an earlier post by the OpenML team.

Documentation



Welcome to the TileDB Docs!

> *TileDB is a **universal data engine** that manages any kind of data (beyond tables), with any computational tool (beyond SQL), at planet-scale (beyond clusters and organizations).*

TileDB is redefining *data management* from the ground up and transforming the lives of scientists and analysts that work on important problems that require analyzing and sharing data at scale. This is the complete documentation of the TileDB software ecosystem, which covers in detail the architectural decisions, internal mechanics, API usage and use cases. This information will hopefully help you get maximum value from using TileDB and its offerings in your application.

TileDB started at **MIT** and **Intel Labs** as a research project in late 2014 that led to a VLDB 2017 paper. In May 2017 it was spun out into **TileDB, Inc.**, a company that has since raised about $20M to further develop and maintain the project (see Series A announcement). TileDB consists of three pieces:

- TileDB Embedded, a universal storage engine based on *dense and sparse multi-dimensional arrays*, which is an open-source (MIT License) C++ library that comes with numerous language APIs.
- Integrations of TileDB Embedded with SQL engines and popular data science tooling, all open-source as well.
- TileDB Cloud, a commercial SaaS offering for planet-scale *data sharing* and *serverless distributed computations*.

Extensive documentation on TileDB, APIs, Usage, and more

`docs.tiledb.com`

`github.com/TileDB-Inc/TileDB-R`

`github.com/TileDB-Inc/TileDB`

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we’re hiring!!