

Using **AdhereR** with various database technologies for processing very large datasets

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Introduction

It is sometimes stated that **R** *cannot* be used with very large database as they don't fit in memory. Unfortunately, this has also been used as an argument against giving **AhereR** a try, especially in contexts where it would be most useful, namely for processing (very) large datasets.

Here we try to dispel this worry by presenting various methods for dealing with such cases, focusing on data stored in “classic” *relational databases* (such as [MySQL](#), [MariaDB](#), [SQLite](#), [PostgreSQL](#), [Microsoft SQL Server](#) or [Oracle Database](#)) as well as on a widely-used paradigm for processing large datasets in a distributed manner, namely [Hadoop’s MapReduce](#) paradigm.

We will present several techniques that can be used to access such data from **AdhereR** (without attempting to load the whole of it in memory!), to compute the adherence to medication and/or generate plots, and to optionally store the results back into the database.

Please note that while the code here was tested on an **Ubuntu 18.04** “server” (an AMD Ryzen 7 2700X CPU with 8 physical cores and 16 logical ones, and 32 GB RAM) and a **macOS High Sierra** “client” (an early 2015 Macbook Air 11" 7,1 with an Intel Core i7-5650U CPU with 2 physical cores and 4 logical ones, and 8 GB RAM), actually running it (and, thus, compiling this very **R**markdown script) requires a complex setup (detailed below). Therefore, we provide this vignette in compiled form as a **PDF** document¹ together with detailed instructions on how to install the required components for those users that want to reproduce or extend it.

Prerequisites: load **AdhereR** and **R**markdown setup bits

Before we start, load **AdhereR** and various options concerning the figures:

```
library(AdhereR);  
  
# Various Rmarkdown output options:  
# center figures and reduce their file size:  
knitr::opts_chunk$set(fig.align = "center", dpi=150, dev="jpeg");
```

Relational databases

Relational databases have a venerable history and are very popular² in a multitude of settings, including those of potential interest for the computation and visualization of patterns of adherence to treatment. In such databases, data is organized in one or more *tables*, each table comprising several *columns* (or *variables*) and *rows* (or *entries*) – a representation familiar to most users of statistical software such as **SPSS**, **SAS**, **Stata** and **R** (in the latter, this is implemented by **data.frame** and friends). The querying of such databases is usually done through **SQL** (or *Structured Query Language*), which allows, among others, the selection of entries from such tables that meet certain requirements (for an introduction see, for example, Viescas & Hernandez (2008) among many others).

Usually, in practice, there *already* exists such a relational database that contains the relevant patient info organized in one or more tables, hosted by one of the many commercial or free/open source solutions (or *Relational Database Management Systems*, **RDBMS**) available, and which we can access using **SQL**. For exemplification and reproducibility purposes, here we will also *create* these databases from the **med.events** dataset included in the **AdhereR** package (but these steps are obviously not part of the actual exploitation of the database).

We will focus here on [MySQL](#), but these can be applied to other **RDBMS** with minimal changes. **MySQL** is free and widely used, being a good example from the wider class of such systems. **MySQL** (and its close relative, [MariaDB](#)) is a stand-alone *server* that can be accessed (locally or remotely) by various *clients* who use **SQL** to manipulate the stored data. Thus, **MySQL** stands for the usual scenario where the patient, prescription and event data are stored in a centralized **RDBMS** (possibly hosted on a dedicated hardware and software

¹We provide only the **PDF** within the package itself as the **HTML** form is rather big due to the embedded images and generates a **NOTE** when building the package. Moreover, to void an unsuccessful attempt at compiling the vignette during the package build, the actual **.Rmd** source and related images are in the **specialVignettes** subfolder of the package.

²Despite the development of alternative architectures (generically known as “**NoSQL**”; see Harrison (2015)), **RDBMS**s are still extremely popular and will very probably continue to be so for the foreseeable future.

infrastructure) which can be queried (possibly over a network or even the Internet) by different specialized clients who perform particular tasks with (parts of) the data.

Currently, there are several ways of accessing a RDBMS from R, and we will focus here on two:

- a) using SQL directly, and
- b) transparently generating SQL queries through the `dplyr` front-end.

At the time of this writing (November 2018), the *MySQL Community Server* is a free version of the MySQL RDBMS which can be installed on several Operating Systems including Microsoft Windows, Apple's macOS and various flavors of Linux and BSD (for details, please see <https://dev.mysql.com/downloads/mysql/>). *MariaDB* is an open source RDBMS that started as a fork of MySQL (and is still very similar to it) and can as well be installed on a multitude of Operating Systems (for details, please see <https://mariadb.org/download/>).

Installing MySQL

Generic installation instructions can be found on the MySQL Community Server's [website](#), while step-by-step instructions geared towards R can be found, for example, in the [Introduction to MySQL with R](#) and [Connecting R to MySQL/MariaDB](#), among others. [How To Install MySQL on Ubuntu 18.04](#) is oriented specifically for Ubuntu 18.04 LTS (which we use on our test machine). In the following, we will assume that MySQL (Community Server) was successfully installed on the local machine.

In our case, we are on a machine running Ubuntu 18.04 LTS and we follow the procedure described in [How To Install MySQL on Ubuntu 18.04](#), with the difference that we create a user named `adherentuser` with password `AdhereR123!` using the command

```
CREATE USER 'adherentuser'@'localhost' IDENTIFIED BY 'AdhereR123!';
```

instead of the generic

```
CREATE USER 'sammy'@'localhost' IDENTIFIED BY 'password';
```

(and please make sure you do not forget to grant the new user the needed privileges:)

```
GRANT ALL PRIVILEGES ON *.* TO 'adherentuser'@'localhost' WITH GRANT OPTION;
```

Creating a sample database

Normally, this step is superfluous as the data should already be present in the RDBMS. Nevertheless, for illustration purposes, we transfer here the `med.events` example dataset that comes included with `AdhereR` into several tables in a MySQL database.

Use MySQL Workbench to connect to the database as user `adherentuser` using the password `AdhereR123!`. On our system, this means starting it either from the Desktop Environment's start menu or from the command prompt by typing:

```
mysql-workbench
```

after which, using the menu `Database -> Connect to Database...` we made a local connection using the desired user and credentials. Further, as described in [Introduction to MySQL with R](#), create a database:

```
CREATE DATABASE med_events;
```

which should become visible in the left-hand panel under "schemas" (see Figure).

Then, either using MySQL Workbench or SQL commands, create *four* tables within the `med_events` database:

- `event_patients` with two columns:
 - `id` of type `INT(11)`, primary key and non-null, and
 - `patient_id` of type `INT(11)` and non-null,

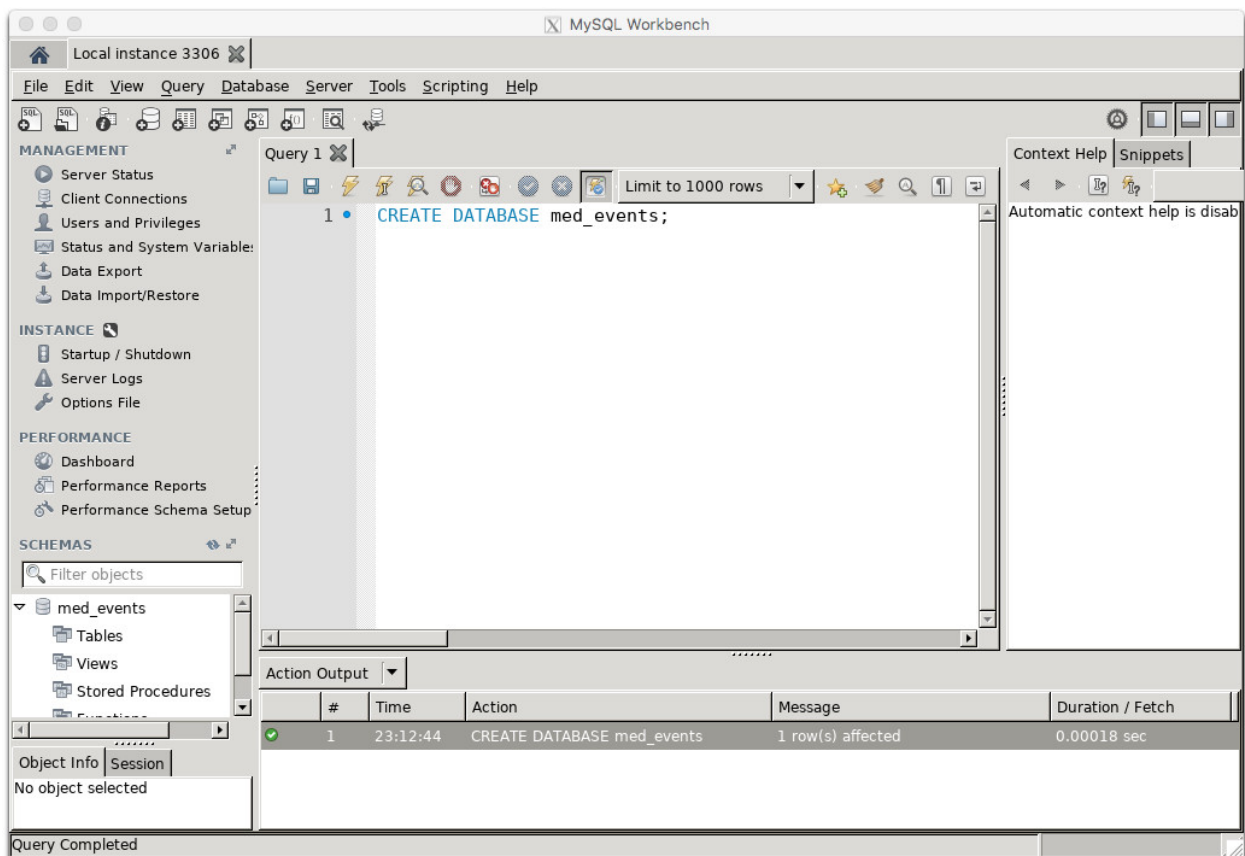


Figure 1: Creating a database using MySQL Workbench on Ubuntu 18.04 (screenshot taken on the macOS “client” using XQuartz for display).

- `event_date` with two columns:
 - `id` of type `INT(11)`, primary key and non-null, and
 - `date` of type `DATE` and non-null,
- `event_info` with four columns:
 - `id` of type `INT(11)`, primary key and non-null,
 - `perday` of type `INT(11)` and non-null,
 - `category` of type `VARCHAR(45)` and non-null, and
 - `duration` of type `INT(11)` and non-null.
- `patients` with two columns:
 - `id` of type `INT(11)`, primary key and non-null, and
 - `sex` of type `CHAR(1)` and non-null,

The SQL commands for these could be:

```
CREATE TABLE `med_events`.`event_patients` (
  `id` INT NOT NULL,
  `patient_id` INT NOT NULL,
  PRIMARY KEY (`id`));
```

```
CREATE TABLE `med_events`.`event_date` (
  `id` INT NOT NULL,
  `date` DATE NOT NULL,
  PRIMARY KEY (`id`));
```

```
CREATE TABLE `med_events`.`event_info` (
  `id` INT NOT NULL,
  `perday` INT NOT NULL,
  `category` VARCHAR(45) NOT NULL,
  `duration` INT NOT NULL,
  PRIMARY KEY (`id`));
```

```
CREATE TABLE `med_events`.`patients` (
  `id` INT NOT NULL,
  `sex` CHAR(1) NOT NULL,
  PRIMARY KEY (`id`));
```

Now, we will fill these tables using the data from AdhereR's `med.events` dataset from R itself. First, make sure the package `RMariaDB` is installed on your system (otherwise simply install it as usual, whether from RStudio or with `install.packages("RMariaDB")`) and load the library:

```
library(RMariaDB);
```

Then, connect to the database:

```
med_events_db <- dbConnect(RMariaDB::MariaDB(),      # works also for MySQL
                           user="adherentuser",      # the username
                           password="AdhereR123!",  # and password (insecure but ok here)
                           dbname='med_events',      # which database
                           host='localhost'          # on which host (here, local machine)
                           );
```

and, just to check that things are OK, list the tables:

```
db_res_tables <- dbListTables(med_events_db); db_res_tables;
```

```
## [1] "cma9_estimates" "event_date"      "event_info"      "event_patients"
## [5] "patients"
```

Clear the tables (in case there's some junk info in there):

```
# Truncate all the tables:
for( i in db_res_tables ) dbExecute(med_events_db, paste0("TRUNCATE ",i,";"));
```

Now, generate an extra column containing the event_id unique event id (really, just the row number) and make sure the format of the dates fits SQL's DATE type:

```
d <- med.events; # make working a copy
d$event_id <- 1:nrow(d); # simply the index of the event in med.events
d$DATE <- as.character(as.Date(d$DATE, format="%m/%d/%Y"),
                       format="%Y-%m-%d"); # use the expected format for SQL's DATE
```

Fill in the patients table (and allocate some random sexes which we won't really use at all):

```
tmp <- unique(d[,c("PATIENT_ID"),drop=FALSE]); # select the relevant info
tmp$sex <- sample(c("F","M"), size=nrow(tmp), replace=TRUE);
names(tmp) <- c("id", "sex"); # match the column names
# For convenience, write the whole data.frame in one go:
dbWriteTable(med_events_db, name="patients",
             value=tmp, row.names=FALSE, append=TRUE);
```

then spread the event info across the remaining tables:

```
# event_date:
tmp <- d[,c("event_id", "DATE")]; # select the relevant info
names(tmp) <- c("id", "date"); # match the column names
# For convenience, write the whole data.frame in one go:
dbWriteTable(med_events_db, name="event_date",
             value=tmp, row.names=FALSE, append=TRUE);

# event_info:
tmp <- d[,c("event_id", "PERDAY", "CATEGORY", "DURATION")]; # select the relevant info
names(tmp) <- c("id", "perday", "category", "duration"); # match the column names
# For convenience, write the whole data.frame in one go:
dbWriteTable(med_events_db, name="event_info",
             value=tmp, row.names=FALSE, append=TRUE);

# event_patients:
tmp <- d[,c("event_id", "PATIENT_ID")]; # select the relevant info
names(tmp) <- c("id", "patient_id"); # match the column names
# For convenience, write the whole data.frame in one go:
dbWriteTable(med_events_db, name="event_patients",
             value=tmp, row.names=FALSE, append=TRUE);
```

Check that the data was correctly written either using MySQL Workbench or from R:

```
# Fetch the whole results as they are small enough for display:
knitr::kable(dbGetQuery(med_events_db, "SELECT * FROM patients LIMIT 5;"),
             align=c("l","l"),
             caption="First 5 rows of the `patients` table (please note
                     that the `sex` may differ from your results and between runs).");
```

Table 1: First 5 rows of the `patients` table (please note that the `sex` may differ from your results and between runs).

| id | sex |
|----|-----|
| 1 | F |
| 2 | F |
| 3 | F |
| 4 | M |
| 5 | M |

```
knitr::kable(dbGetQuery(med_events_db, "SELECT * FROM event_date LIMIT 5;"),
  align=c("l","l"),
  caption="First 5 rows of the `event_date` table.");
```

Table 2: First 5 rows of the `event_date` table.

| id | date |
|----|------------|
| 1 | 2033-04-26 |
| 2 | 2033-07-04 |
| 3 | 2033-08-03 |
| 4 | 2033-08-17 |
| 5 | 2033-10-13 |

```
knitr::kable(dbGetQuery(med_events_db, "SELECT * FROM event_info LIMIT 5;"),
  align=c("l","l"),
  caption="First 5 rows of the `event_info` table.");
```

Table 3: First 5 rows of the `event_info` table.

| id | perday | category | duration |
|----|--------|----------|----------|
| 1 | 4 | medA | 50 |
| 2 | 4 | medB | 30 |
| 3 | 4 | medB | 30 |
| 4 | 4 | medB | 30 |
| 5 | 4 | medB | 30 |

```
knitr::kable(dbGetQuery(med_events_db, "SELECT * FROM event_patients LIMIT 5;"),
  align=c("l","l"),
  caption="First 5 rows of the `event_patients` table.");
```

Table 4: First 5 rows of the `event_patients` table.

| id | patient_id |
|----|------------|
| 1 | 1 |
| 2 | 1 |
| 3 | 1 |
| 4 | 1 |
| 5 | 1 |

Finally, don't forget to close the connection to the database:

```
dbDisconnect(med_events_db);
```

Access the database and estimate adherence using explicit SQL

The first method uses explicit SQL statements directed at the MySQL server through the R library RMariaDB (despite its name, it also works for MySQL).

First, make sure it is installed on your system (for example by running the following or, if you're using RStudio, by checking the Packages panel):

```
require(RMariaDB); # there should be no warnings
```

If not, install it either using RStudio's *Tools -> Install packages* menu, or by running:

```
install.packages("RMariaDB", dep=TRUE); # also install the dependencies
```

(please make sure you check for any errors and follow any indication; for example, on Ubuntu 18.04 it is necessary to install prior to this the libmysqlclient-dev package using, for example, `apt install libmysqlclient-dev`).

Now, load it:

```
library(RMariaDB);
```

We will next illustrate a few scenarios concerning the computation and plotting of patterns of adherence accessing data from the database.

Connect to the database

```
med_events_db <- dbConnect(RMariaDB::MariaDB(),      # works also for MySQL
                           user="adherentuser",      # the username
                           password="AdhereR123!",  # and password (insecure but ok here)
                           dbname='med_events',      # which database
                           host='localhost'         # on which host (here, local machine)
                           );
db_res_tables <- dbListTables(med_events_db); db_res_tables; # check things are ok

## [1] "cma9_estimates" "event_date"      "event_info"      "event_patients"
## [5] "patients"
```

How many patients are there?

```
no_patients <- dbGetQuery(med_events_db,
                          # overkill, as `id` is the primary key:
                          "SELECT COUNT(DISTINCT id) FROM patients;");
no_patients <- as.numeric(no_patients[1,1]); # single value: convert it to numeric
no_patients;

## [1] 100
```

How many events?

```
no_events <- dbGetQuery(med_events_db,
                        "SELECT COUNT(DISTINCT id) FROM event_info;");
```



```
no_events <- as.numeric(no_events[1,1]); # single value: convert it to numeric
no_events;
```

```
## [1] 1080
```

And how many events per patient?

```
dbGetQuery(med_events_db,
  "SELECT patient_id, COUNT(*) FROM event_patients GROUP BY patient_id;");
```

```
##      patient_id COUNT(*)
## 1             1      24
## 2             2       8
## 3             3      28
## 4             4       6
## 5             5       8
## 6             6       9
## 7             7       6
## 8             8      14
## 9             9       9
## 10            10      14
## 11            11       6
## 12            12       7
## 13            13       5
## 14            14      24
## 15            15      13
## 16            16      22
## 17            17      10
## 18            18       6
## 19            19       6
## 20            20      11
## 21            21      10
## 22            22       7
## 23            23      11
## 24            24       9
## 25            25      11
## 26            26      12
## 27            27      13
## 28            28      10
## 29            29      14
## 30            30      11
## 31            31       3
## 32            32       6
## 33            33       4
## 34            34      11
## 35            35      11
## 36            36      11
## 37            37       8
## 38            38       9
## 39            39      10
## 40            40      11
## 41            41       6
## 42            42       7
## 43            43      20
```

| | | |
|-------|----|----|
| ## 44 | 44 | 7 |
| ## 45 | 45 | 11 |
| ## 46 | 46 | 18 |
| ## 47 | 47 | 10 |
| ## 48 | 48 | 12 |
| ## 49 | 49 | 6 |
| ## 50 | 50 | 9 |
| ## 51 | 51 | 6 |
| ## 52 | 52 | 7 |
| ## 53 | 53 | 4 |
| ## 54 | 54 | 5 |
| ## 55 | 55 | 5 |
| ## 56 | 56 | 11 |
| ## 57 | 57 | 4 |
| ## 58 | 58 | 16 |
| ## 59 | 59 | 18 |
| ## 60 | 60 | 7 |
| ## 61 | 61 | 10 |
| ## 62 | 62 | 8 |
| ## 63 | 63 | 6 |
| ## 64 | 64 | 11 |
| ## 65 | 65 | 19 |
| ## 66 | 66 | 20 |
| ## 67 | 67 | 14 |
| ## 68 | 68 | 8 |
| ## 69 | 69 | 6 |
| ## 70 | 70 | 10 |
| ## 71 | 71 | 11 |
| ## 72 | 72 | 6 |
| ## 73 | 73 | 10 |
| ## 74 | 74 | 8 |
| ## 75 | 75 | 13 |
| ## 76 | 76 | 11 |
| ## 77 | 77 | 6 |
| ## 78 | 78 | 25 |
| ## 79 | 79 | 23 |
| ## 80 | 80 | 19 |
| ## 81 | 81 | 7 |
| ## 82 | 82 | 10 |
| ## 83 | 83 | 9 |
| ## 84 | 84 | 12 |
| ## 85 | 85 | 9 |
| ## 86 | 86 | 13 |
| ## 87 | 87 | 10 |
| ## 88 | 88 | 14 |
| ## 89 | 89 | 6 |
| ## 90 | 90 | 12 |
| ## 91 | 91 | 7 |
| ## 92 | 92 | 18 |
| ## 93 | 93 | 7 |
| ## 94 | 94 | 11 |
| ## 95 | 95 | 11 |
| ## 96 | 96 | 22 |
| ## 97 | 97 | 12 |

```
## 98      98      8
## 99      99      5
## 100     100     16
```

Get the list of patient_id's

```
patient_ids <- dbGetQuery(med_events_db, "SELECT id FROM patients;"); # a data.frame
patient_ids <- patient_ids$id; # convert it to a vector
patient_ids;
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## [18] 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
## [35] 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
## [52] 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68
## [69] 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85
## [86] 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
```

Retrieve the data for a given (set of) patient(s)

We don't assume here that we can load a lot of patients in memory at a time (after all, the whole point of this exercise is to keep the data in the database as much as possible), so we wrote a simple (but clearly not the most efficient!) function that retrieves the info for a given (set of) patient(s):

```
# Given a (set of) patient(s) ID(s) and a database connection,
# retrieve his/her/their info and
# return it as a data.frame (or NULL)
retrieve_patients_info <- function(patient_ids, # a single value or a vector
                                   db_connection) # the database connection
{
  s <- dbGetQuery(db_connection, paste0(" SELECT event_date.id,
                                           event_date.date,
                                           event_info.category,
                                           event_info.duration,
                                           event_info.perday,
                                           event_patients.patient_id,
                                           patients.sex
                                           FROM event_date
                                           JOIN event_info
                                           ON event_info.id = event_date.id
                                           JOIN event_patients
                                           ON event_patients.id = event_info.id
                                           JOIN patients
                                           ON patients.id = event_patients.patient_id
                                           WHERE patients.id IN (",
                                           paste0(patient_ids,collapse=","),
                                           ");"));

  if( nrow(s) < 1 )
  {
    return (NULL);
  } else
  {
    return (s);
  }
}
```

Compute CMA9 for all the patients and store it in the database

Also, for the sake of the exercise, we cannot assume that we can store the computed CMA values for all the patients in a vector in R, so, as soon as we estimate it for a single patient, we write it back to the database. For this, we will create a new table named `cma9_estimates` (with two columns: `patient_id` and `cma`) and we make sure it's empty:

```
dbExecute(med_events_db, "CREATE TABLE IF NOT EXISTS med_events.cma9_estimates (  
    patient_id INT NOT NULL,  
    cma REAL NULL,  
    PRIMARY KEY (patient_id));"); # create it if not already there
```

```
## [1] 0
```

```
dbExecute(med_events_db, "TRUNCATE cma9_estimates;"); # make sure it's empty
```

```
## [1] 0
```

For each patient in turn, extract his/her data from the database, estimate CMA9 and write back this estimate to the database (also, for the sake of illustration, we will assume that we can't even store the whole list of patient ID's, so we ask for each individual patient by selecting individual rows in the `patients` table):

```
# Time the whole thing:  
start.time <- Sys.time();  
  
# First (re)get the number of patients in the whole database:  
no_patients <- dbGetQuery(med_events_db, "SELECT COUNT(DISTINCT id) FROM patients;");  
no_patients <- as.numeric(no_patients[1,1]); # single value: convert it to numeric  
no_patients;  
  
## [1] 100  
  
# Select each patient in turn by its row number (remember: rows count starts at 0 in SQL!):  
for( i in 0:(no_patients-1) )  
{  
    # Get the patient ID in row i:  
    patient_id <- dbGetQuery(med_events_db,  
        paste0("SELECT id FROM patients LIMIT ",i,",1;"));  
    if( is.null(patient_id) || nrow(patient_id) < 1 )  
    {  
        warning(paste0("Cannot find patient number ",i+1,"!\n"));  
        next;  
    }  
    patient_id <- as.numeric(patient_id[1,1]); # single value: convert it to numeric  
  
    # Extract the patient's data:  
    s <- retrieve_patients_info(patient_id, med_events_db); # retrieve all the data  
    if( is.null(s) )  
    {  
        warning(paste0("Cannot retrieve data for patient '",patient_id,"'\n"));  
        cma <- NA;  
    } else  
    {  
        # Estimate the CMA:  
        cma <- CMA9(data=s, # compute the CMA  
            ID.colname="patient_id",  
            event.date.colname="date",  
            event.duration.colname="duration",
```

```

        event.daily.dose.colname="perday",
        medication.class.colname="category",
        followup.window.start=0,
        followup.window.start.unit="days",
        followup.window.duration=2*365,
        followup.window.duration.unit="days",
        observation.window.start=30,
        observation.window.start.unit="days",
        observation.window.duration=1*365,
        observation.window.duration.unit="days",
        date.format="%Y-%m-%d",
        parallel.backend="none");
if( is.null(cma) )
{
  warning(paste0("Cannot estimate CMA for patient '",patient_id,"'\n"));
  cma <- NA;
} else
{
  cma <- getCMA(cma)$CMA[1]; # retrieve the estimate
}
}

# Write back this estimate (with replacement,
# if there's an already existing estimate for this patient):
result <- dbExecute(med_events_db,
                    paste0("REPLACE INTO cma9_estimates (patient_id, cma) VALUES (",
                          patient_id,
                          ", ",
                          ifelse(is.na(cma),"NULL",cma),");"));
}

end.time <- Sys.time();
cat(paste0("The SQL-mediated computation of CMA9 on the whole database took: ",
          round(difftime(end.time, start.time, units="secs"),2),
          " seconds\n"));

```

The SQL-mediated computation of CMA9 on the whole database took: 2.17 seconds

Also, do it within R so we can compare the results of the two procedures:

```

# Also, time it using the same procedure:
start.time <- Sys.time();
cma9r <- CMA9(data=med.events,
              ID.colname="PATIENT_ID",
              event.date.colname="DATE",
              event.duration.colname="DURATION",
              event.daily.dose.colname="PERDAY",
              medication.class.colname="CATEGORY",
              followup.window.start=0,
              followup.window.start.unit="days",
              followup.window.duration=2*365,
              followup.window.duration.unit="days",
              observation.window.start=30,
              observation.window.start.unit="days",
              observation.window.duration=1*365,

```

```

        observation.window.duration.unit="days",
        date.format="%m/%d/%Y",
        parallel.backend="none");
end.time <- Sys.time();
cat(paste0("The computation of CMA9 in R on the whole database took: ",
        round(difftime(end.time, start.time, units="secs"),2),
        " seconds\n"));

## The computation of CMA9 in R on the whole database took: 0.3 seconds
# Retrieve the results from the database:
cma9sql <- dbGetQuery(med_events_db, "SELECT * FROM cma9_estimates;");
knitr::kable(merge(getCMA(cma9r),
        cma9sql,
        by.x="PATIENT_ID", by.y="patient_id", all=TRUE),
        align=c("c","c","c"),
        col.names=c("Patient ID", "CMA9 (R)", "CMA9 (MySQL)"),
        caption="The estimation of CMA9 on all the patients comparing
        the `MySQL` and `R` estimates (they are, as expected, **identical**).");

```

Table 5: The estimation of CMA9 on all the patients comparing the MySQL and R estimates (they are, as expected, **identical**).

| Patient ID | CMA9 (R) | CMA9 (MySQL) |
|------------|-----------|--------------|
| 1 | 0.9185229 | 0.9185229 |
| 2 | 0.7076512 | 0.7076512 |
| 3 | 0.9951294 | 0.9951294 |
| 4 | 0.2126893 | 0.2126893 |
| 5 | 0.3533546 | 0.3533546 |
| 6 | 0.2639304 | 0.2639304 |
| 7 | 0.6085971 | 0.6085971 |
| 8 | 0.9026890 | 0.9026890 |
| 9 | 0.6898670 | 0.6898670 |
| 10 | 0.7300316 | 0.7300316 |
| 11 | 0.1457626 | 0.1457626 |
| 12 | 0.4534314 | 0.4534314 |
| 13 | 0.2694568 | 0.2694568 |
| 14 | 0.6896727 | 0.6896727 |
| 15 | 0.4841183 | 0.4841183 |
| 16 | 1.0000000 | 1.0000000 |
| 17 | 0.4709437 | 0.4709437 |
| 18 | 0.2511233 | 0.2511233 |
| 19 | 0.2705104 | 0.2705104 |
| 20 | 0.3883306 | 0.3883306 |
| 21 | 0.4534097 | 0.4534097 |
| 22 | 0.3162253 | 0.3162253 |
| 23 | 0.6840264 | 0.6840264 |
| 24 | 0.2437649 | 0.2437649 |
| 25 | 0.4551645 | 0.4551645 |
| 26 | 0.6548924 | 0.6548924 |
| 27 | 0.6948941 | 0.6948941 |
| 28 | 0.7698630 | 0.7698630 |
| 29 | 0.8821918 | 0.8821918 |
| 30 | 0.9551252 | 0.9551252 |

| Patient ID | CMA9 (R) | CMA9 (MySQL) |
|------------|-----------|--------------|
| 31 | 0.2641743 | 0.2641743 |
| 32 | 0.1103753 | 0.1103753 |
| 33 | 0.1433427 | 0.1433427 |
| 34 | 0.6662712 | 0.6662712 |
| 35 | 0.4545709 | 0.4545709 |
| 36 | 0.9002090 | 0.9002090 |
| 37 | 0.5391753 | 0.5391753 |
| 38 | 1.0000000 | 1.0000000 |
| 39 | 0.6711226 | 0.6711226 |
| 40 | 0.7778944 | 0.7778944 |
| 41 | 0.1394641 | 0.1394641 |
| 42 | 0.7290265 | 0.7290265 |
| 43 | 1.0000000 | 1.0000000 |
| 44 | 0.3985459 | 0.3985459 |
| 45 | 0.7625689 | 0.7625689 |
| 46 | 1.0000000 | 1.0000000 |
| 47 | 0.8575342 | 0.8575342 |
| 48 | 0.6893408 | 0.6893408 |
| 49 | 0.3937378 | 0.3937378 |
| 50 | 0.8754789 | 0.8754789 |
| 51 | 0.5521455 | 0.5521455 |
| 52 | 0.7750355 | 0.7750355 |
| 53 | 0.1265823 | 0.1265823 |
| 54 | 0.2817497 | 0.2817497 |
| 55 | 0.3767123 | 0.3767123 |
| 56 | 0.4032023 | 0.4032023 |
| 57 | 0.2303609 | 0.2303609 |
| 58 | 0.8305149 | 0.8305149 |
| 59 | 0.9686888 | 0.9686888 |
| 60 | 0.3604903 | 0.3604903 |
| 61 | 0.6970132 | 0.6970132 |
| 62 | 0.3578026 | 0.3578026 |
| 63 | 0.2187364 | 0.2187364 |
| 64 | 0.3924057 | 0.3924057 |
| 65 | 1.0000000 | 1.0000000 |
| 66 | 0.9863014 | 0.9863014 |
| 67 | 0.9995849 | 0.9995849 |
| 68 | 0.3835616 | 0.3835616 |
| 69 | 0.4374202 | 0.4374202 |
| 70 | 0.7716222 | 0.7716222 |
| 71 | 0.4278826 | 0.4278826 |
| 72 | 0.3920769 | 0.3920769 |
| 73 | 0.5807266 | 0.5807266 |
| 74 | 0.3664650 | 0.3664650 |
| 75 | 1.0000000 | 1.0000000 |
| 76 | 0.8434442 | 0.8434442 |
| 77 | 0.1163283 | 0.1163283 |
| 78 | 0.8636008 | 0.8636008 |
| 79 | 1.0000000 | 1.0000000 |
| 80 | 0.9643836 | 0.9643836 |
| 81 | 0.3249420 | 0.3249420 |
| 82 | 0.8810842 | 0.8810842 |

| Patient ID | CMA9 (R) | CMA9 (MySQL) |
|------------|-----------|--------------|
| 83 | 0.4690076 | 0.4690076 |
| 84 | 0.5523369 | 0.5523369 |
| 85 | 0.3790906 | 0.3790906 |
| 86 | 0.6165855 | 0.6165855 |
| 87 | 0.8610212 | 0.8610212 |
| 88 | 0.3254529 | 0.3254529 |
| 89 | 0.2532995 | 0.2532995 |
| 90 | 0.4516032 | 0.4516032 |
| 91 | 0.1971892 | 0.1971892 |
| 92 | 0.6665592 | 0.6665592 |
| 93 | 0.5505812 | 0.5505812 |
| 94 | 0.9027050 | 0.9027050 |
| 95 | 0.5671233 | 0.5671233 |
| 96 | 0.9110578 | 0.9110578 |
| 97 | 0.5739005 | 0.5739005 |
| 98 | 0.6509310 | 0.6509310 |
| 99 | 0.3393666 | 0.3393666 |
| 100 | 0.9844865 | 0.9844865 |

Plot a set of patients

Here we generate some plots of patients from the database.

```
# Extract the data of the patient(s) to plot:
# (we relax the stringency and assume we can hold a the patient IDs in memory :)):
s <- retrieve_patients_info(patient_ids[1:5], med_events_db);
cma0 <- CMAO(data=s,
  ID.colname="patient_id",
  event.date.colname="date",
  event.duration.colname="duration",
  event.daily.dose.colname="perday",
  medication.class.colname="category",
  followup.window.start.unit="days",
  followup.window.duration=2*365,
  followup.window.duration.unit="days",
  observation.window.start=30,
  observation.window.start.unit="days",
  observation.window.duration=1*365,
  observation.window.duration.unit="days",
  date.format="%Y-%m-%d",
  parallel.backend="none");
plot(cma0);
```

```
# Extract the data of the patient(s) to plot:
# (we relax the stringency and assume we can hold a the patient IDs in memory :)):
s <- retrieve_patients_info(patient_ids[1:5], med_events_db);
cma9 <- CMA9(data=s,
  ID.colname="patient_id",
  event.date.colname="date",
  event.duration.colname="duration",
  event.daily.dose.colname="perday",
  medication.class.colname="category",
```

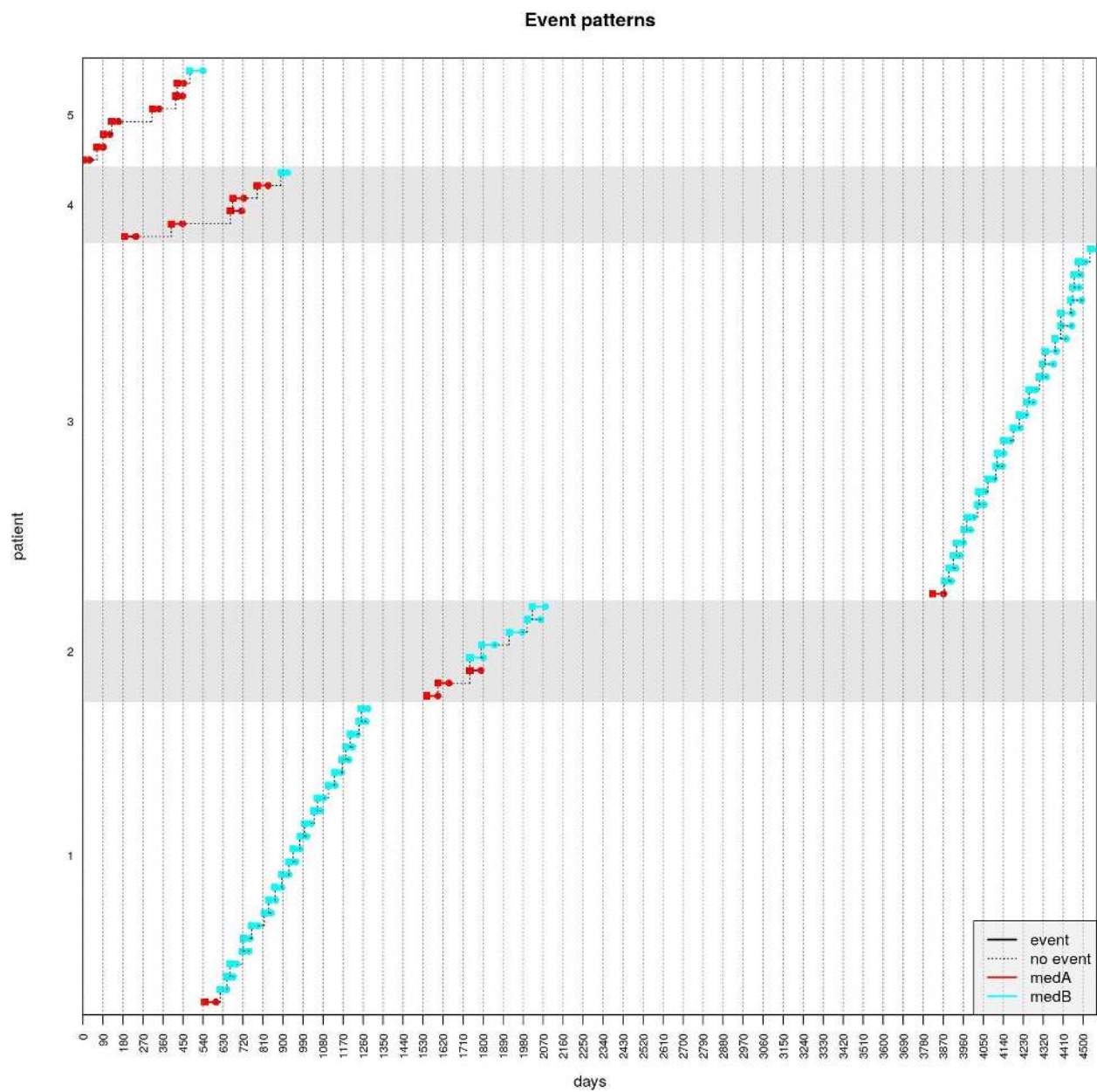



Figure 2: Plot of 'CMA0' for the first 5 patients in the 'MySQL' database using 'SQL'.

```

followup.window.start.unit="days",
followup.window.duration=2*365,
followup.window.duration.unit="days",
observation.window.start=30,
observation.window.start.unit="days",
observation.window.duration=1*365,
observation.window.duration.unit="days",
date.format="%Y-%m-%d",
parallel.backend="none");
plot(cma9);

```

Interactive plotting

For the interactive plotting of patients directly from the database (i.e., without local caching of data in R), we make use of the getter functions allowed by `plot_interactive_cma` through its function arguments `get.colnames.fnc`, `get.patients.fnc` and `get.data.for.patients.fnc`. As detailed in the help page for `plot_interactive_cma`, these arguments allow a user to use other types of data storage than the default `data.frame` by overriding the default behaviors for listing the data column names, listing all the patient IDs and getting the actual data for a (set of) patient ID(s), respectively.

Here, we redefined these functions as follows:

```

# Retrieve the column names of the data for the first patient:
get.colnames.fnc.MySQL <- function(d)
{
  return(names(retrieve_patients_info(
    as.numeric(dbGetQuery(med_events_db,
                          "SELECT id FROM patients LIMIT 0,1;"))[1,1]),
    d)
  ));
}
# List all the patient IDs:
get.patients.fnc.MySQL <- function(d, idcol)
{
  s <- dbGetQuery(d, "SELECT id FROM patients;");
  return(s$id);
}
# Retrieve the data for given (set of) patient ID(s):
get.data.for.patients.fnc.MySQL <- function(patientid, d, idcol)
{
  retrieve_patients_info(patientid, d);
}

```

resulting in the code (not run here as it needs an interactive R session with `AdhereR` and `Shiny`):

```

plot_interactive_cma(data=med_events_db, # use the MySQL connection as the data provider
  ID.colname="patient_id",
  event.date.colname="date",
  event.duration.colname="duration",
  event.daily.dose.colname="perday",
  medication.class.colname="category",
  date.format="%Y-%m-%d", # SQL's DATE specification
  backend=c("shiny","rstudio")[1], # use Shiny
  use.system.browser=TRUE, # use the system web browser
  # Override the getter functions to use the MySQL database

```

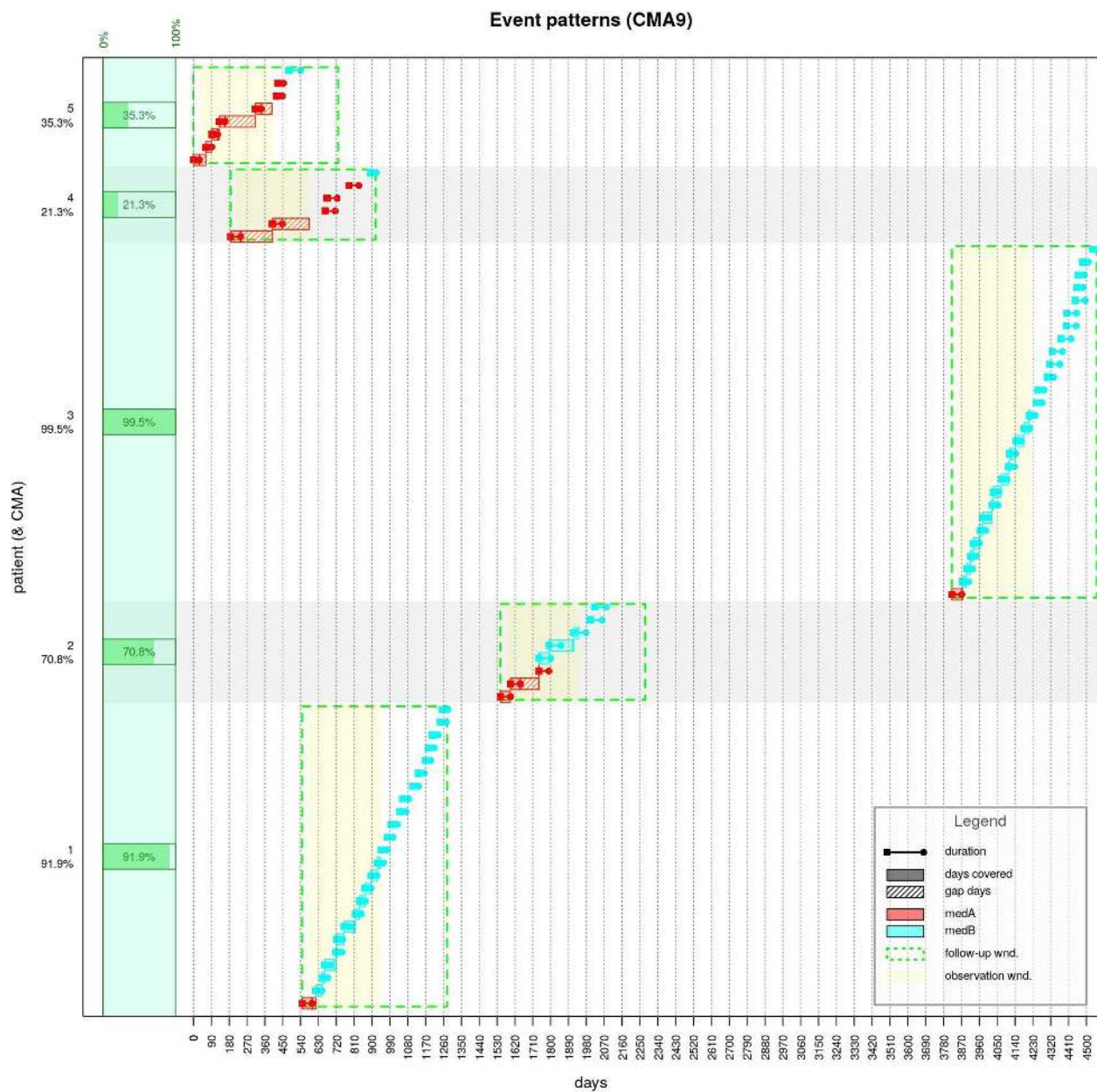


Figure 3: Plot of 'CMA9' for the first 5 patients in 'MySQL' database using 'SQL'.



Figure 4: Screenshot of interactive plotting directly from a MySQL database using Shiny and the system browser (here, Safari on a macOS High Sierra).

```
# (please note that, for consistency, we must keep the
# function arguments evens if we don't use all of them):
get.colnames.fnc=get.colnames.fnc.MySQL,
get.patients.fnc=get.patients.fnc.MySQL,
get.data.for.patients.fnc=get.data.for.patients.fnc.MySQL
);
```

Disconnect from the database

Finally, we need to disconnect from the database:

```
dbDisconnect(med_events_db);
```

Using a non-local MySQL database

Usually, the MySQL database is located on a *different* machine on a network (possibly even somewhere else on the Internet). We will show here how to access the same MySQL database we used so far (let's called it here the “*server*”) from a different machine (a Macbook Air 11" running macOS High Sierra with R 3.4.4; called the “*client*”).

First, make sure that the RMariaDB package is installed on the “*client*”.

Second, make sure that the user `adherentuser` is allowed to remotely access the MySQL database; for our setup, we did the following on the “*server*” (as suggested in <https://stackoverflow.com/questions/8380797/enable-remote-mysql-connection-error-1045-28000-access-denied-for-user> and <https://stackoverflow.com/>

[questions/8380797/enable-remote-mysql-connection-error-1045-28000-access-denied-for-user/21151255#21151255](https://stackoverflow.com/questions/8380797/enable-remote-mysql-connection-error-1045-28000-access-denied-for-user/21151255#21151255)):

- as root in MySQL (obtained by running, for example, `mysql -u root -p` in a terminal), execute:

```
GRANT ALL PRIVILEGES ON *.*
TO 'adherentuser'@'%'
IDENTIFIED BY 'AdhereR123!'
WITH GRANT OPTION;
FLUSH PRIVILEGES;
```

- also as root, edit the `/etc/mysql/my.cnf` (or the `/etc/mysql/mysql.conf.d/mysqld.cnf` on newer versions of MySQL) and replace the line `bind-address = 127.0.0.1` by `bind-address = 0.0.0.0`
- restart MySQL (for example, by `sudo service mysql restart`).

Now, on the “*client*” we should be able to connect to the remote “*server*”:

```
med_events_db <- dbConnect(RMariaDB::MariaDB(),      # works also for MySQL
                           user="adherentuser",      # the username
                           password="AdhereR123!",   # and password (insecure but ok here)
                           dbname='med_events',       # which database
                           host='remote.server.sql'   # the host's name or IP address
                           );
```

and check that everything is OK:

```
db_res_tables <- dbListTables(med_events_db); db_res_tables;
```

followed by all the other things you would do with a local database, including closing it at the end (as shown above). Of course, the access and data transfer times will be worse than for a local database, but this can be addressed by judiciously selecting the patients one needs to process and by processing them in chunks of more than one patient.

Optimisations and security

Especially for remote databases (but also for local ones), the access and data transfer are potentially very slow; moreover, **AdhereR** is heavily optimized for processing (possibly in parallel) multiple patients (using `data.table` and other techniques). Therefore, probably the following ideas may help speed up the processing:

- as far as possible, information extraction and preparation should be done server-side (i.e., using SQL) instead of client-side (i.e., transferring raw data and processing it in R);
- transfer locally only the data that is strictly needed for computing the adherence and/or plotting (e.g., if computing **CMA1**, it doesn't make any sense to also transfer the column containing the daily dose) and only for the patients for which this needs to be done (i.e., perform an SQL pre-selection of the patients and events);
- to minimize server querying and transfer, and to maximally use the optimization built in **AdhereR**, split the whole set of patients to process into chunks that are relatively large (but not too large so as not to fit comfortably in the client's RAM even when processed in parallel);
- collect the computation results in R as much as possible and only write them back to the database in large chunks.

In these examples we stored the server name, username and password in clear in the R code: while this OK for this demo, it is a *very bad idea* in a production environment! There are various techniques for mitigating this, ranging from storing these info in a separate file that is read at run-time, to asking the user to interactively give the username and password, to using the **keyring** package (<https://github.com/r-lib/keyring>) – see also <https://db.rstudio.com/best-practices/managing-credentials/> for a discussion. Please chose the most appropriate one for your use-case, but whatever you do, *don't store your credentials in the R script!!!*

Use dplyr and DBI to transparently access the database

This is based on the more extended discussion in <https://db.rstudio.com/dplyr/> . While using SQL for interacting with the database is very flexible and allows for fine-grained optimization, it requires a certain level of expertise and can be argued to create “chimeras” of R and SQL that might be more difficult to understand, debug and maintain.

The R packages dbplyr and DBI offer an alternative way, where the SQL is mostly “hidden” behind a familiar R code. Moreover, this allows to use the same code to access a variety of databases, such as MySQL, PostgreSQL and even Google’s BigQuery.

For example, we can connect and list the patients with (of course, you need to install first the needed packages, such as dbplyr, dplyr and RMySQL):

```
library(dplyr);

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
db_dplyer <- DBI::dbConnect(RMySQL::MySQL(),
                           user="adherentuser",      # the username
                           password="AdhereR123!",   # and password (insecure but ok here)
                           dbname='med_events'       # which database
);

DBI::dbListTables(db_dplyer); # list the tables in the database

## [1] "cma9_estimates" "event_date"      "event_info"      "event_patients"
## [5] "patients"

db_dplyer_patients <- tbl(db_dplyer, "patients"); # connect to the "patients" table
# db_dplyer_patients; # print it if you want to
```

Let’s get the data from patient with id 1, compute CMA9 and plot it:

```
# connect to the various event info tables as well:
db_dplyer_event_date <- tbl(db_dplyer, "event_date");
db_dplyer_event_info <- tbl(db_dplyer, "event_info");
db_dplyer_event_patients <- tbl(db_dplyer, "event_patients");

# Select and join the various pieces of info for patient with patient_id == 1
# (Please note that the data data is actually transfered from MySQL to R only
# at the end, when invoking collect()!!!)
s <- inner_join(inner_join(db_dplyer_event_info,
                           # filter the events for patient 1:
                           db_dplyer_event_patients %>% filter(patient_id == 1),
                           by="id"), # join with event_info
               db_dplyer_event_date, by="id") %>% collect();
cma9 <- CMA9(data=s, # compute CMA9 as usual
             ID.colname="patient_id",
             event.date.colname="date",
```

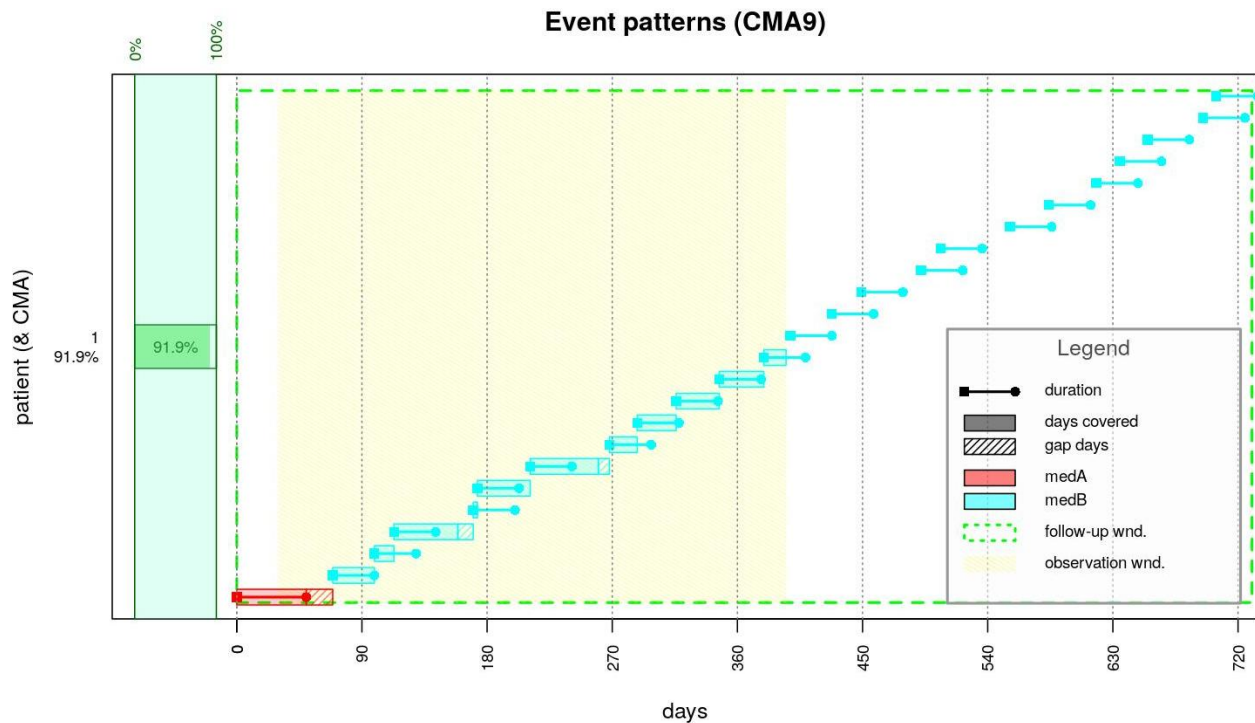


Figure 5: Plotting ‘CMA1’ for patient with id ‘1’ directly from a ‘MySQL’ database using ‘dbplyr’ and ‘DBI’.

```
event.duration.colname="duration",
event.daily.dose.colname="perday",
medication.class.colname="category",
followup.window.start.unit="days",
followup.window.duration=2*365,
followup.window.duration.unit="days",
observation.window.start=30,
observation.window.start.unit="days",
observation.window.duration=1*365,
observation.window.duration.unit="days",
date.format="%Y-%m-%d",
parallel.backend="none");
plot(cma9); # plot it
```

Finally, close the connection to the database:

```
DBI::dbDisconnect(db_dplyer);
```

```
## [1] TRUE
```

How about SAS and Stata

If the dataset is relatively small, probably the easiest is to export it into a format that R can read (such as CSV); if this is not possible, then maybe one of the methods for importing their native formats in R may work (see, for example, <https://www.statmethods.net/input/importingdata.html> or https://cran.r-project.org/doc/manuals/r-devel/R-data.html#EpiInfo-Minitab-SAS-S_002dPLUS-SPSS-Stata-Systat).

However, if the dataset is (very) large, then probably one should either:

- export it into a RDBMS such as MySQL where R can access it (as described above), or
- experimentally, use ODBC to access it directly from SAS (which might or might not work).

Finally, let's look at Hadoop and MapReduce!

[Apache Hadoop](#) is a general framework for the distributed processing of large datasets using a simple programming paradigm (MapReduce; see, for example, <https://wiki.apache.org/hadoop/ProjectDescription>). Given that **AdhereR** can compute adherence estimates for sets of at least one patient at a time, it is very easy to embed within the MapReduce framework using a variety of approaches (see, among others, the outlines [here](#) or [here](#)).

Just as an example, we will install here Hadoop 3.0.3 on the Ubuntu 18.04 machine and use it to compute CMA9 on all the patients.

Installing Hadoop 3.0.3 on Ubuntu 18.04

We are following the tutorial [here](#). All of these happen in a `shell` terminal.

Install Java

```
sudo apt update
sudo apt install default-jdk
java -version
```

Install Hadoop 3.0.3

Download the 3.0.3 *binary* version:

```
cd ~/Downloads
wget http://mirrors.ircam.fr/pub/apache/hadoop/common/hadoop-3.0.3/hadoop-3.0.3.tar.gz
```

then unpack and move it to `/usr/local/`:

```
tar -xzvf hadoop-3.0.3.tar.gz
sudo mv hadoop-3.0.3 /usr/local/hadoop
```

Configure Hadoop

Add to `/usr/local/hadoop/etc/hadoop/hadoop-env.sh` the line `export JAVA_HOME=$(readlink -f /usr/bin/java | sed "s:bin/java::")`.

Test Hadoop

Start it first:

```
/usr/local/hadoop/bin/hadoop
```

and test it:

```
/usr/local/hadoop/bin/hadoop jar /usr/local/hadoop/share/hadoop/mapreduce/hadoop-mapreduce-examples-3.0.3.jar grep ~/input ~/grep_example 'allowed[.]*'
cat ~/grep_example/*
```

which should produce:

Output

```
19 allowed.  
1 allowed
```

Installing RHadoop on Ubuntu 18.04

We are adapting here various guidelines for [RedHat](#) and [macOS](#). All these happen in R (unless specified).

Set the needed environment variables

```
Sys.setenv("HADOOP_HOME="/usr/local/hadoop"); # Hadoop HOME  
Sys.setenv("HADOOP_CMD="/usr/local/hadoop/bin/hadoop"); # Hadoop binary  
Sys.setenv("HADOOP_STREAMING=" # Streaming  
           "/usr/local/hadoop/share/hadoop/tools/lib/hadoop-streaming-3.0.3.jar");
```

Install the needed R packages

(You probably already have some installed).

```
install.packages(c("rJava",  
                  "Rcpp",  
                  "RJSONIO",  
                  "bitops",  
                  "digest",  
                  "functional",  
                  "stringr",  
                  "plyr",  
                  "reshape2"),  
                dep=TRUE);
```

Now, manually download the `rhdfs`, `rhbase` and `rmr2` packages from [Revolution Analytics' GitHub repository](#).

In a shell terminal:

```
cd ~/Downloads  
wget https://github.com/RevolutionAnalytics/rmr2/releases/download/3.3.1/rmr2_3.3.1.tar.gz  
wget https://github.com/RevolutionAnalytics/rhdfs/blob/master/build/rhdfs_1.0.8.tar.gz?raw=true  
wget https://github.com/RevolutionAnalytics/rhbase/blob/master/build/rhbase_1.2.1.tar.gz?raw=true
```

and then, in R:

```
install.packages(c("~/Downloads/HADOOP/rhdfs_1.0.8.tar.gz?raw=true",  
                  "~/Downloads/HADOOP/rmr2_3.3.1.tar.gz",  
                  "~/Downloads/HADOOP/rhbase_1.2.1.tar.gz"),  
                repos=NULL, dep=TRUE);
```

Using Hadoop through RHadoop to compute CMA9

With all these in place, we can compute CMA9 for each participant, as follows (of course, this is not optimized in any sense). Everything here takes place in R.

Load the libraries and initialize things

```
library(rhdfs); # access to HDFS
```

```
## Loading required package: rJava

##
## HADOOP_CMD=/usr/local/hadoop/bin/hadoop
##
## Be sure to run hdfs.init()
hdfs.init(); # initialize HDFS

library(rmr2); # MapReduce in R

## Warning: S3 methods 'gorder.default', 'gorder.factor', 'gorder.data.frame',
## 'gorder.matrix', 'gorder.raw' were declared in NAMESPACE but not found
## Please review your hadoop settings. See help(hadoop.settings)
```

Store the med.events data in HDFS

First, we will store the `med.events` example AdhereR dataset in HDFS (the [Hadoop Distributed File System](#)) as a set of *key-value* pairs:

```
# Transfer med.events to HDFS as a set of key-value pairs:
med_events_hdfs <- to.dfs(keyval(med.events$PATIENT_ID, med.events));
```

This is *not* a very efficient and scalable way of doing it, but it works for this example (normally, the data would be transferred to HDFS using specialized tools such as [Sqoop](#)). What this does is create a handler (`med_events_hdfs`) to a temporary HDFS storage where the rows of the `med.events` data.frame (the *values*) are stored paired with the corresponding `PATIENT_ID`s (the *keys*). Importantly the `med_events_hdfs` handler ensures that the actual data is never fully loaded in memory, which is very important for large databases.

Use MapReduce to compute CMA9

```
s <- mapreduce(input=med_events_hdfs, # read the data from med_events_hdfs
  # the mapping function here doesn't do much;
  # k (= the key) = PATIENT_ID; v (= value) = med.events rows:
  map=function(k,v) keyval(k,v),
  # the reduce function computes CMA9 on the data (the values v)
  # associated with a given PATIENT_ID (the key k):
  reduce=function(k,v)
  {
    cma <- CMA9(v,
      ID.colname="PATIENT_ID",
      event.date.colname="DATE",
      event.duration.colname="DURATION",
      event.daily.dose.colname="PERDAY",
      medication.class.colname="CATEGORY",
      followup.window.start=0,
      followup.window.start.unit="days",
      followup.window.duration=2*365,
      followup.window.duration.unit="days",
      observation.window.start=30,
      observation.window.start.unit="days",
      observation.window.duration=1*365,
      observation.window.duration.unit="days",
      date.format="%m/%d/%Y",
      parallel.backend="none");
```

```

# Return the computed CMA as the value paired with the PATIENT_ID key:
keyval(k, getCMA(cma)[1,"CMA"]);
});

```

The basic idea is to first *map* the (key, value) pairs in the input (here, the `PATEINT_ID`s with their associated event info) to (potentially) different (key, value) pairs (here, we don't do basically anything at this stage), followed by *reducing* all the data associated with a key to a summary value (here, `CMA9`), returning a new summary (key, value) pair. The result `s` is also a pointer to the actual results stored in HDFS (temporarily), so that again we don't load anything large in memory.

Load and use the results

Just for the sake of illustration, only now do we load the full results in memory for display as a `data.frame` (to be compared with the other ways of computing `CMA9`):

```

# Only *now* force the loading of the full results in memory!
s <- from.dfs(s);

# Convert the (key, value) pairs to a nice data.frame format:
cma9hadoop <- data.frame("PATIENT_ID"=s$key, "CMA9"=s$val);

# And plot them for comparison with the other methods discussed here:
knitr::kable(merge(merge(getCMA(cma9r),
                        cma9sql,
                        by.x="PATIENT_ID", by.y="patient_id", all=TRUE),
                    cma9hadoop,
                    by="PATIENT_ID", all=TRUE),
              align=c("c","c","c","c"),
              col.names=c("Patient ID", "CMA9 (R)", "CMA9 (MySQL)", "CMA9 (Hadoop)"),
              caption="The estimation of CMA9 on all the patients comparing the `R`,
`MySQL` and `Hadoop` estimates (they are, as expected, identical!).");

```

Table 6: The estimation of CMA9 on all the patients comparing the R, MySQL and Hadoop estimates (they are, as expected, **identical**!).

| Patient ID | CMA9 (R) | CMA9 (MySQL) | CMA9 (Hadoop) |
|------------|-----------|--------------|---------------|
| 1 | 0.9185229 | 0.9185229 | 0.9185229 |
| 2 | 0.7076512 | 0.7076512 | 0.7076512 |
| 3 | 0.9951294 | 0.9951294 | 0.9951294 |
| 4 | 0.2126893 | 0.2126893 | 0.2126893 |
| 5 | 0.3533546 | 0.3533546 | 0.3533546 |
| 6 | 0.2639304 | 0.2639304 | 0.2639304 |
| 7 | 0.6085971 | 0.6085971 | 0.6085971 |
| 8 | 0.9026890 | 0.9026890 | 0.9026890 |
| 9 | 0.6898670 | 0.6898670 | 0.6898670 |
| 10 | 0.7300316 | 0.7300316 | 0.7300316 |
| 11 | 0.1457626 | 0.1457626 | 0.1457626 |
| 12 | 0.4534314 | 0.4534314 | 0.4534314 |
| 13 | 0.2694568 | 0.2694568 | 0.2694568 |
| 14 | 0.6896727 | 0.6896727 | 0.6896727 |
| 15 | 0.4841183 | 0.4841183 | 0.4841183 |
| 16 | 1.0000000 | 1.0000000 | 1.0000000 |
| 17 | 0.4709437 | 0.4709437 | 0.4709437 |
| 18 | 0.2511233 | 0.2511233 | 0.2511233 |

| Patient ID | CMA9 (R) | CMA9 (MySQL) | CMA9 (Haddop) |
|------------|-----------|--------------|---------------|
| 19 | 0.2705104 | 0.2705104 | 0.2705104 |
| 20 | 0.3883306 | 0.3883306 | 0.3883306 |
| 21 | 0.4534097 | 0.4534097 | 0.4534097 |
| 22 | 0.3162253 | 0.3162253 | 0.3162253 |
| 23 | 0.6840264 | 0.6840264 | 0.6840264 |
| 24 | 0.2437649 | 0.2437649 | 0.2437649 |
| 25 | 0.4551645 | 0.4551645 | 0.4551645 |
| 26 | 0.6548924 | 0.6548924 | 0.6548924 |
| 27 | 0.6948941 | 0.6948941 | 0.6948941 |
| 28 | 0.7698630 | 0.7698630 | 0.7698630 |
| 29 | 0.8821918 | 0.8821918 | 0.8821918 |
| 30 | 0.9551252 | 0.9551252 | 0.9551252 |
| 31 | 0.2641743 | 0.2641743 | 0.2641743 |
| 32 | 0.1103753 | 0.1103753 | 0.1103753 |
| 33 | 0.1433427 | 0.1433427 | 0.1433427 |
| 34 | 0.6662712 | 0.6662712 | 0.6662712 |
| 35 | 0.4545709 | 0.4545709 | 0.4545709 |
| 36 | 0.9002090 | 0.9002090 | 0.9002090 |
| 37 | 0.5391753 | 0.5391753 | 0.5391753 |
| 38 | 1.0000000 | 1.0000000 | 1.0000000 |
| 39 | 0.6711226 | 0.6711226 | 0.6711226 |
| 40 | 0.7778944 | 0.7778944 | 0.7778944 |
| 41 | 0.1394641 | 0.1394641 | 0.1394641 |
| 42 | 0.7290265 | 0.7290265 | 0.7290265 |
| 43 | 1.0000000 | 1.0000000 | 1.0000000 |
| 44 | 0.3985459 | 0.3985459 | 0.3985459 |
| 45 | 0.7625689 | 0.7625689 | 0.7625689 |
| 46 | 1.0000000 | 1.0000000 | 1.0000000 |
| 47 | 0.8575342 | 0.8575342 | 0.8575342 |
| 48 | 0.6893408 | 0.6893408 | 0.6893408 |
| 49 | 0.3937378 | 0.3937378 | 0.3937378 |
| 50 | 0.8754789 | 0.8754789 | 0.8754789 |
| 51 | 0.5521455 | 0.5521455 | 0.5521455 |
| 52 | 0.7750355 | 0.7750355 | 0.7750355 |
| 53 | 0.1265823 | 0.1265823 | 0.1265823 |
| 54 | 0.2817497 | 0.2817497 | 0.2817497 |
| 55 | 0.3767123 | 0.3767123 | 0.3767123 |
| 56 | 0.4032023 | 0.4032023 | 0.4032023 |
| 57 | 0.2303609 | 0.2303609 | 0.2303609 |
| 58 | 0.8305149 | 0.8305149 | 0.8305149 |
| 59 | 0.9686888 | 0.9686888 | 0.9686888 |
| 60 | 0.3604903 | 0.3604903 | 0.3604903 |
| 61 | 0.6970132 | 0.6970132 | 0.6970132 |
| 62 | 0.3578026 | 0.3578026 | 0.3578026 |
| 63 | 0.2187364 | 0.2187364 | 0.2187364 |
| 64 | 0.3924057 | 0.3924057 | 0.3924057 |
| 65 | 1.0000000 | 1.0000000 | 1.0000000 |
| 66 | 0.9863014 | 0.9863014 | 0.9863014 |
| 67 | 0.9995849 | 0.9995849 | 0.9995849 |
| 68 | 0.3835616 | 0.3835616 | 0.3835616 |
| 69 | 0.4374202 | 0.4374202 | 0.4374202 |
| 70 | 0.7716222 | 0.7716222 | 0.7716222 |

| Patient ID | CMA9 (R) | CMA9 (MySQL) | CMA9 (Hadoop) |
|------------|-----------|--------------|---------------|
| 71 | 0.4278826 | 0.4278826 | 0.4278826 |
| 72 | 0.3920769 | 0.3920769 | 0.3920769 |
| 73 | 0.5807266 | 0.5807266 | 0.5807266 |
| 74 | 0.3664650 | 0.3664650 | 0.3664650 |
| 75 | 1.0000000 | 1.0000000 | 1.0000000 |
| 76 | 0.8434442 | 0.8434442 | 0.8434442 |
| 77 | 0.1163283 | 0.1163283 | 0.1163283 |
| 78 | 0.8636008 | 0.8636008 | 0.8636008 |
| 79 | 1.0000000 | 1.0000000 | 1.0000000 |
| 80 | 0.9643836 | 0.9643836 | 0.9643836 |
| 81 | 0.3249420 | 0.3249420 | 0.3249420 |
| 82 | 0.8810842 | 0.8810842 | 0.8810842 |
| 83 | 0.4690076 | 0.4690076 | 0.4690076 |
| 84 | 0.5523369 | 0.5523369 | 0.5523369 |
| 85 | 0.3790906 | 0.3790906 | 0.3790906 |
| 86 | 0.6165855 | 0.6165855 | 0.6165855 |
| 87 | 0.8610212 | 0.8610212 | 0.8610212 |
| 88 | 0.3254529 | 0.3254529 | 0.3254529 |
| 89 | 0.2532995 | 0.2532995 | 0.2532995 |
| 90 | 0.4516032 | 0.4516032 | 0.4516032 |
| 91 | 0.1971892 | 0.1971892 | 0.1971892 |
| 92 | 0.6665592 | 0.6665592 | 0.6665592 |
| 93 | 0.5505812 | 0.5505812 | 0.5505812 |
| 94 | 0.9027050 | 0.9027050 | 0.9027050 |
| 95 | 0.5671233 | 0.5671233 | 0.5671233 |
| 96 | 0.9110578 | 0.9110578 | 0.9110578 |
| 97 | 0.5739005 | 0.5739005 | 0.5739005 |
| 98 | 0.6509310 | 0.6509310 | 0.6509310 |
| 99 | 0.3393666 | 0.3393666 | 0.3393666 |
| 100 | 0.9844865 | 0.9844865 | 0.9844865 |

Conclusions

We hope to have shown here that, far from being constrained by the “‘R’ can’t process large datasets that don’t fit in memory” myth, **AdhereR** can, in fact, nicely and easily interface with both “classical” relational databases (such as **MySQL**) and with newer technologies (such as Apache **Hadoop**), allowing it to access potentially huge databases (even across the Internet) and process them efficiently (even across massively parallel heterogeneous computational infrastructures).

Thus, **AdhereR** can seamlessly scale up from being used for the real-time visualization and computation of adherence of a small-to-medium local database (stored either in a “flat” CSV file or in an **SQLite** database) on a *consumer-grade laptop*, up to running on *large heterogenous computer clusters* where it can process huge amounts of data stored across several RDBMS tables (managed by, for example, **MySQL**) or as (key, value) pairs in a **Hadoop** **HDFS** file system. The examples (with actual code and step-by-step instructions) presented here should provide a starting point for real-world implementations optimized for the problems at hand.

There is a vast literature concerning both “classic” **SQL** and newer **NoSQL** databases, and there is an already mature ecosystem for accessing them from **R**. However, even for very specific cases where this is not feasible, we have provided a flexible framework for seamlessly using **AdhereR** from other programming languages (such as **Python**) for the computation and plotting of adherence.

References

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