

Epiverse-TRACE showcase

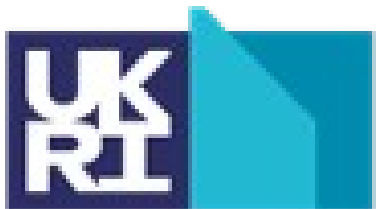
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November 2023

*MRCG
Pillar 1: data science
tools for field
epidemiology*



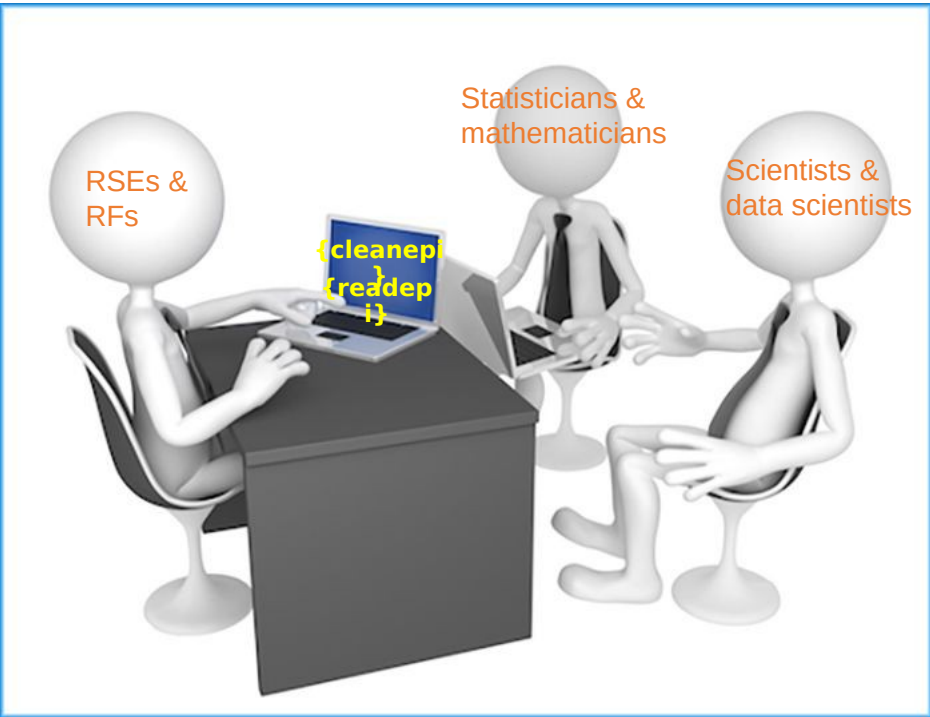
Bubacarr Bah



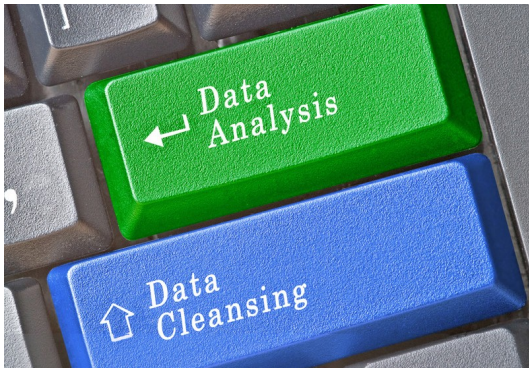
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Pillar 1:



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the challenges:

- Dealing with different HIS



Fingertips | Public health data



{readepi

0.0.1

Stage of
development:
Maturing }

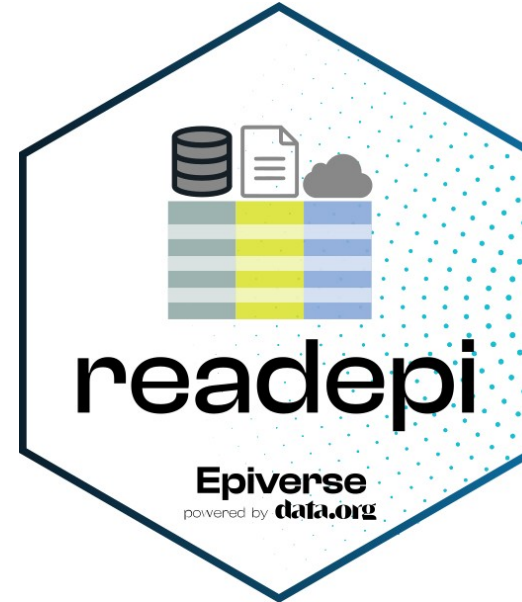
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**Importing data from health
information systems (HIS)**

RDBMS **including:** REDcap DHIS2 Fingertips



Fingertips | Public health data



<https://epiverse-trace.github.io/readepi>



[epiverse-trace/readepi](https://github.com/epiverse-trace/readepi)

Wants to use {readepi}: 3 requirements

- Assume that user is granted with read access to the HIS of interest
- User credentials to be saved in a file
- For MS servers, need installation of appropriate MS drivers on **Unix and OSX-based systems**

Return object type: **list**

{readepi}: main arguments

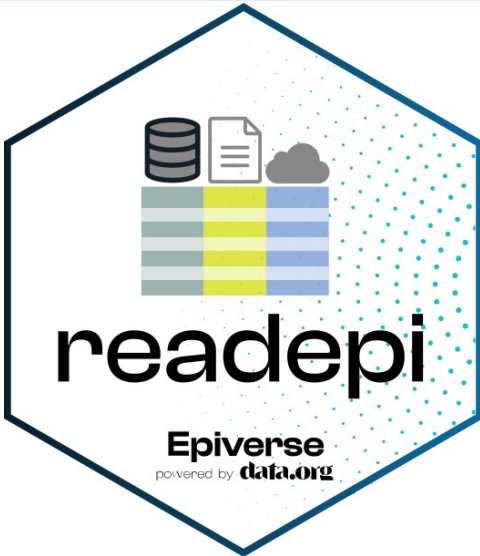
- **data_source**: the URL of the target HIS
- **records**: a vector of subject IDs
- **fields**: a vector of column names
- **id_position**: the column position of the variable that unique identifies the subjects
- **id_col_name**: the name of the column that unique identifies the subjects
- ... specific arguments to the HIS of interest



DISPLAY THE STRUCTUTRE OF THE TEMPLATE CREDENTIAL FILE

show_example_file()

user_name	password	host_name	project_id	comment	dbms	port
admin	district	https://play.dhis2.org/dev	DHIS2_DEMO	this is a test DHIS2 server	DHIS2	NA
rfamro		mysql-rfam-public.ebi.ac.uk	Rfam	this is a test MySQL server	MySQL	4497
kmane	9A81268476645C4E5F03428B8AC3AA7B	https://bbmc.ouhsc.edu/redcap/api/	SD_DATA	testing access to REDCap project	REDCap	NA



```
# DEFINE THE PATH TO THE CREDENTIAL FILE
```

```
credentials_file <- system.file("extdata", "test.ini", package = "readepi")
```

```
# READING FILE FROM A PROJECT IN A REDCap DATABASE
```

```
data <- readepi(data_source = "https://bbmc.ouhsc.edu/redcap/api/",  
               credentials_file = credentials_file)
```

```
project_data <- data$data # accessing the actual data  
project_metadata <- data$metadata # accessing the metadata  
                           associated with project
```

VIEWING THE LIST OF ALL TABLES IN A MySQL DATABASE

```
show_tables(data_source = "mysql-rfam-public.ebi.ac.uk",  
            credentials_file = credentials_file,  
            driver_name = "") # note that this example MySQL server  
does not require a driver
```

VISUALIZE FIRST 5 ROWS OF THE TABLE 'author'

```
visualise_table(data_source = "mysql-rfam-public.ebi.ac.uk",  
               credentials_file = credentials_file,  
               from = "author", # this is the table name  
               driver_name = "")
```



READING ALL FILES AND RECORDS FROM A MySQL SERVER

```
data <- readepi(data_source = "mysql-rfam-public.ebi.ac.uk",  
               credentials_file = credentials_file,  
               from = "author", # could also be an SQL query  
               driver_name = "")
```

READING DATA FROM DHIS2

```
data <- readepi(data_source = "https://play.dhis2.org/dev",  
               credentials_file = credentials_file,  
               dataset = "pBOMPrpg1QX",  
               organisation_unit = "DiszpKrYNg8",  
               data_element_group = NULL,  
               start_date = "2014",  
               end_date = "2023")
```



READING DATA FROM THE FINGERTIPS REPOSITORY

```
data <- readepi(indicator_id      = 90362,  
                area_type_id      = 202,  
                parent_area_type_id = 6) # optional
```

OPEN THE VIGNETTE WITHIN RSTUDIO

```
vignette("readepi")
```

OPEN THE VIGNETTE IN YOUR WEB BROWSER

```
browseVignettes("readepi")
```

