

RImmPort: Quick Start Guide

Ravi Shankar

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1 Introduction

ImmPort study data is available for download in two formats currently: MySQL and TSV (Tab) formats. The RImmPort workflow is as follows: 1) MySQL formatted study data: User downloads one or more studies in MySQL zip files. Unzips the files. Loads local database instance. Connects to the database. Sets the ImmPort data source to the connection handle. Invokes RImmPort functions. 2) Tab: User downloads one or more studies in Tab format. Passes the folder where the zip files are located to an RImmPort function that builds SQLite database. Connects to the database. Sets the ImmPort data source to the connection handle. Invokes RImmPort functions.

User downloads study data of interest from the ImmPort website (<http://www.immport.org>) **. Depending on the file format MySQL or Tab the data is loaded into a local MySQL and SQLite database respectively. The user installs the RImmPort package, loads the RImmPort library, connects to the ImmPort database, and calls RImmPort methods to load study data from the database into R. Please refer to RImmPort_Article.pdf for a detailed discussion on RImmPort.

** User need to regisiter to the ImmPort website for downloading the datasets.

2 Initial Steps

- Download MySQL or Tab formatted data of studies of interest from the ImmPort website
- If working with MySQL-format, load the data in to a local MySQL database
- Install and load RImmPort package, and other required packages.

3 Load the RImmPort library

```
library(RImmPort)
library(DBI)
library(sqldf)
library(plyr)
```

4 Setup ImmPort data source that all RImmPort functions will use

4.1 Option 1: ImmPort MySQL database

4.1.1 Download zip files of ImmPort study data in MySQL format. e.g. 'SDY139' and 'SDY208'

4.1.2 Load the data into a local MySQL database

4.1.3 Connect to the ImmPort MySQL database.

```
# provide appropriate connection parameters
mysql_conn <- dbConnect(MySQL(), user="username", password="password",
                        dbname="database", host="host")
```

4.1.4 Set the data source as the ImmPort MySQL database.

```
setImmPortDataSource(mysql_conn)
```

4.2 Option 2: ImmPort SQLite database

4.2.1 Download zip files of ImmPort data, in Tab format. e.g. 'SDY139' and 'SDY208'

```
# get the directory where ImmPort sample data is stored in the directory structure of RImmPort package
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")

# set tab_dir to the folder where the zip files are located
tab_dir <- file.path(studies_dir, "Tab")
list.files(tab_dir)

## [1] "SDY139-DR16_Tab.zip" "SDY208-DR16_Tab.zip"
```

4.2.2 Build a local SQLite ImmPort database instance.

```
# set db_dir to the folder where the database file 'ImmPort.sqlite' should be stored
db_dir <- file.path(studies_dir, "Db")

# build a new ImmPort SQLite database with the data in the downloaded zip files
buildNewSqliteDb(tab_dir, db_dir)

list.files(db_dir)

## [1] "ImmPort.sqlite"
```

4.2.3 Connect to the ImmPort SQLite database

```
# connect to the private instance of the ImmPort database
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
```

4.2.4 Set the data source to the ImmPort SQLite DB

```
setImmPortDataSource(sqlite_conn)
```

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

5 NOTE: In rest of the script, all RImmPort functions will use the SQLite ImmPort database as the data source.

6 Get all study ids

```
getListOfStudies()
```

```
## [1] "SDY139" "SDY208"
```

7 Get all data of a specific study

The `getStudyFromDatabase` queries the ImmPort database for the entire dataset of a specific study, and instantiates the `Study` reference class with that data.

```
?Study
```

```
# load all the data of study: `SDY139`
study_id <- 'SDY139'
sdy139 <- getStudy(study_id)
```

```
## loading Study ID = SDY139
## loading Demographics data....done
## loading Subject Visits data....done
## loading Concomitant Medications data....done
## loading Exposure data....done
## loading Substance Use data....done
## loading Adverse Events data....done
## loading Protocol Deviations data....done
## loading Medical History data....done
## loading Associated Persons Medical History data....done
## loading Laboratory Test Results data....done
## loading Physical Examination data....done
## loading Vital Signs data....done
## loading Questionnaires data....done
## loading Findings About data....done
## loading Skin Response data....done
## loading Genetics Findings data....loading HLA Typing Results data....done
## loading Array Results data....done
## done
```

```
## loading Protein Quantification data....loading ELISA Results data....done
## loading MBAA Results data....done
## done
## loading Cellular Quantification data....loading FCS Results data....done
## loading ELISPOT Results data....done
## done
## loading Nucleic Acid Quantification data....loading PCR Results data....done
## done
## loading Titer Assay Results data....loading HAI Assay Results data....done
## loading Neut. Ab Titer Results data....done
## done
## loading TrialArms data....done
## loading TrialInclusionExclusionCriteria data....done
## loading TrialSummary data.... SDY139 done
## done loading Study ID = SDY139
```

```
# access Demographics data of SDY139
dm_df <- sdy139$special_purpose$dm_l$dm_df
head(dm_df)
```

```
## STUDYID DOMAIN USUBJID AGE AGEU SEX RACE ETHNIC SPECIES
## 1 SDY139 DM SUB118053 2 Months Unknown NA NA Mus musculus
## 2 SDY139 DM SUB118054 2 Months Unknown NA NA Mus musculus
## 3 SDY139 DM SUB118055 2 Months Unknown NA NA Mus musculus
## 4 SDY139 DM SUB118056 2 Months Unknown NA NA Mus musculus
## 5 SDY139 DM SUB118057 2 Months Unknown NA NA Mus musculus
## 6 SDY139 DM SUB118058 2 Months Unknown NA NA Mus musculus
## STRAIN SBSTRAIN ARMCD ARM
## 1 BALB/c NA ARM678 BALB/c
## 2 BALB/c NA ARM678 BALB/c
## 3 BALB/c NA ARM678 BALB/c
## 4 BALB/c NA ARM678 BALB/c
## 5 BALB/c NA ARM678 BALB/c
## 6 BALB/c NA ARM678 BALB/c
```

```
# access Concomitant Medications data of SDY139
cm_df <- sdy139$interventions$cm_l$cm_df
head(cm_df)
```

```
## NULL
```

```
# get Trial Title from Trial Summary
ts_df <- sdy139$trial_design$ts_l$ts_df
title <- ts_df$TSVAL[ts_df$TSPARMCD== "TITLE"]
title
```

```
## [1] "The peptide specificity of the endogenous T follicular helper cell repertoire generated after p
```

8 Get the list of Domain names.

Note that some RImmPort functions take a domain name as input.

```
# get the list of names of all supported Domains
getListOfDomains()
```

```
## Domain Name Domain Code
```

```
## 1          Adverse Events          AE
## 2      Concomitant Medications      CM
## 3          Demographics            DM
## 4          Exposure                EX
## 5          Medical History          MH
## 6 Associated Persons Medical History APMH
## 7          Laboratory Test Results  LB
## 8          Physical Examination     PE
## 9          Protocol Deviations     DV
## 10         Trial Arms                TA
## 11 Trial Inclusion Exclusion Criteria TI
## 12         Trial Summary             TS
## 13         Subject Visits           SV
## 14         Substance Use            SU
## 15         Vital Signs              VS
## 16         Questionnaires           QS
## 17         Findings About           FA
## 18         Skin Response            SR
## 19         Genetics Findings        PF
## 20         Protein Quantification   ZA
## 21         Cellular Quantification  ZB
## 22         Nucleic Acid Quantification ZC
## 23         Titer Assay Results      ZD
```

```
? "Demographics Domain"
```

9 Get list of studies with specific domain data

The Domain name should be exact to what is found in the list of Domain names.

```
# get list of studies with Cellular Quantification data
domain_name <- "Cellular Quantification"
study_ids_l <- getStudiesWithSpecificDomainData(domain_name)
study_ids_l
```

```
## [1] "SDY139" "SDY208"
```

10 Get specific domain data of one or more studies

The Domain name should be exact to what is found in the list of Domain names.

```
# get Cellular Quantification data of studies `SDY139` and `SDY208`

# get domain code of Cellular Quantification domain
domain_name <- "Cellular Quantification"
getDomainCode(domain_name)
```

```
## [1] "ZB"
```

```
study_ids <- c("SDY139", "SDY208")
domain_name <- "Cellular Quantification"
zb_l <- getDomainDataOfStudies(domain_name, study_ids)
```

```

## loading Cellular Quantification data....loading FCS Results data....done
## loading ELISPOT Results data....done
## done
## loading Cellular Quantification data....loading FCS Results data....done
## loading ELISPOT Results data....done
## done

if (length(zb_1) > 0)
  names(zb_1)

## [1] "zb_df"      "suppbz_df"

head(zb_1$zb_df)

##   STUDYID DOMAIN   USUBJID ZBSEQ      ZBTEST      ZBCAT ZBMETHOD
## 1 SDY139      ZB SUB118078      1 Figure-7_FCM Cellular_Phenotype      FCM
## 2 SDY139      ZB SUB118078      2 Figure-7_FCM Cellular_Phenotype      FCM
## 3 SDY139      ZB SUB118078      3 Figure-7_FCM Cellular_Phenotype      FCM
## 4 SDY139      ZB SUB118078      4 Figure-7_FCM Cellular_Phenotype      FCM
## 5 SDY139      ZB SUB118079      1 Figure-7_FCM Cellular_Phenotype      FCM
## 6 SDY139      ZB SUB118079      2 Figure-7_FCM Cellular_Phenotype      FCM
##   ZBPOPDEF ZBPOPNAM ZBORRES ZBORRESU ZBBASPOP ZBSPEC VISITNUM
## 1                               Cell          1
## 2                               Cell          1
## 3                               Cell          1
## 4                               Cell          1
## 5                               Cell          1
## 6                               Cell          1
##                                     VISIT ZBELTM
## 1 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
## 2 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
## 3 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
## 4 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
## 5 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
## 6 Day 0 Protein/peptide inoculation, SL_Sant_Plos1_2012_d0      POD
##                                     ZBTPTREF ZBREFID      ZBXFN
## 1 Time of initial vaccine administration ES662746      Tfh_Tfh CLN D0-1.fcs
## 2 Time of initial vaccine administration ES662766      Tfh 1_Tfh EAR D0-1.fcs
## 3 Time of initial vaccine administration ES662786      Tfh_Tfh ILN D0-1.fcs
## 4 Time of initial vaccine administration ES666052      Tfh_Tfh SPLEEN D0-1.fcs
## 5 Time of initial vaccine administration ES662747      Tfh_Tfh CLN D0-2.fcs
## 6 Time of initial vaccine administration ES662767      Tfh 1_Tfh EAR D0-2.fcs

```

11 Get the list of assay types from ImmPort studies

```

getListOfAssayTypes()

## [1] "ELISA"      "ELISPOT"    "Array"      "PCR"
## [5] "HLA Typing" "MBAA"       "HAI"        "Neut Ab Titer"
## [9] "Flow"

```

12 Get specific assay data of one or more Immport studies

The assay type should be exact to what is found in the list of supported assay types.

```
# get 'ELISPOT' data of study `SDY139`
assay_type <- "ELISPOT"
study_id = "SDY139"
elispot_l <- getAssayDataOfStudies(study_id, assay_type)

## loading Protein Quantification data....done
## loading Cellular Quantification data....loading ELISPOT Results data....done
## done
## loading Nucleic Acid Quantification data....done
## loading Titer Assay Results data....done
## loading Genetics Findings data....done

if (length(elispot_l) > 0)
  names(elispot_l)

## [1] "zb_df"      "suppzb_df"

head(elispot_l$zb_df)
```

##	STUDYID	DOMAIN	USUBJID	ZBSEQ	ZBTEST	ZBCAT
## 1	SDY139	ZB	SUB118053	8681	Figure-4_ELISPOT Cellular_Quantification	
## 2	SDY139	ZB	SUB118053	8666	Figure-4_ELISPOT Cellular_Quantification	
## 3	SDY139	ZB	SUB118053	8690	Figure-4_ELISPOT Cellular_Quantification	
## 4	SDY139	ZB	SUB118053	8668	Figure-4_ELISPOT Cellular_Quantification	
## 5	SDY139	ZB	SUB118053	8661	Figure-4_ELISPOT Cellular_Quantification	
## 6	SDY139	ZB	SUB118053	8692	Figure-4_ELISPOT Cellular_Quantification	
##	ZBMETHOD	ZBPOPDEF	ZBPOPNAM	ZBORRES	ZBORRESU	ZBBASPOP
## 1	ELISPOT	IL-4	IL-4	1300.0000	1000000 TfH cells	TfH cells
## 2	ELISPOT	IL-21	IL-21	170.0000	1000000 Non-TfH cells	Non-TfH cells
## 3	ELISPOT	IFNg	IFNg	1162.5000	1000000 TfH cells	TfH cells
## 4	ELISPOT	IL-2	IL-2	7125.0000	1000000 TfH cells	TfH cells
## 5	ELISPOT	IL-21	IL-21	1931.2500	1000000 TfH cells	TfH cells
## 6	ELISPOT	IFNg	IFNg	277.1429	1000000 Non-TfH cells	Non-TfH cells
##	ZBSPEC	VISITNUM	VISIT	ZBELTM		
## 1	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
## 2	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
## 3	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
## 4	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
## 5	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
## 6	Cell	3 Day 8 Sample collection,	SL_Sant_Plos1_2012_d8	P8D		
##	ZBPTREF	ZBREFID	ZBXFN			
## 1	Time of initial vaccine administration	ES661776				
## 2	Time of initial vaccine administration	ES661761				
## 3	Time of initial vaccine administration	ES661785				
## 4	Time of initial vaccine administration	ES661763				
## 5	Time of initial vaccine administration	ES661756				
## 6	Time of initial vaccine administration	ES661787				

13 Serialize RImmPort-formatted study data as .rds files

```
# serialize all of the data of studies `SDY139` and `SDY208`
study_ids <- c('SDY139', 'SDY208')

# the folder where the .rds files will be stored
rds_dir <- file.path(studies_dir, "Rds")

serializeStudyData(study_ids, rds_dir)
list.files(rds_dir)
```

14 Load the serialized data (.rds) files of a specific domain of a study from the directory where the files are located

```
# get the directory where ImmPort sample data is stored in the directory structure of RImmPort package
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")

# the folder where the .rds files will be stored
rds_dir <- file.path(studies_dir, "Rds")

# list the studies that have been serialized
list.files(rds_dir)
```

```
## [1] "SDY139" "SDY208"
```

```
# load the serialized data of study `SDY208`
study_id <- 'SDY208'
dm_1 <- loadSerializedStudyData(rds_dir, study_id, "Demographics")
```

```
##
```

```
## domain_file_path = C:/Users/biocbuild/bbs-3.4-bioc/tmpdir/Rtmp0SkpsD/Rinst2140293e3755/RImmPort/extdata
## suppdomain_file_path = C:/Users/biocbuild/bbs-3.4-bioc/tmpdir/Rtmp0SkpsD/Rinst2140293e3755/RImmPort/extdata
```

```
head(dm_1[[1]])
```

```
##   STUDYID DOMAIN  USUBJID AGE  AGEU  SEX    SPECIES STRAIN SBSTRAIN
## 1  SDY208     DM SUB120516  6 Weeks Female Mus musculus <NA>    NA
## 2  SDY208     DM SUB120517  6 Weeks Female Mus musculus <NA>    NA
## 3  SDY208     DM SUB120518  6 Weeks Female Mus musculus <NA>    NA
## 4  SDY208     DM SUB120519  6 Weeks Female Mus musculus <NA>    NA
## 5  SDY208     DM SUB120520  6 Weeks Female Mus musculus <NA>    NA
## 6  SDY208     DM SUB120521  6 Weeks Female Mus musculus <NA>    NA
##   ARMCD
## 1 ARM881
## 2 ARM882
## 3 ARM883
## 4 ARM884
## 5 ARM885
## 6 ARM886
##
## 1                               Microneedle vaccination- 5 ug inactivated A/Califor
## 2                               Subcutaneous vaccination- 5 ug inactivated A/Califor
```


3 Uncoated microneedle vacci
4 Microneedle vaccination- 5 ug inactivated A/California/04/09 virus, Challenged: 10x LD50 A/Califo
5 Subcutaneous vaccination- 5 ug inactivated A/California/04/09 virus, Challenged: 10x LD50 A/Califo
6 Uncoated microneedle vaccination- Placebo, Challenged: 10x LD50 A/Califo