JE MODEL DESCRIPTION FOR THE PAPER: “ESTIMATING THE GLOBAL BURDEN OF JAPANESE ENCEPHALITIS AND THE IMPACT OF VACCINATION: A SYSTEMATIC REVIEW COMBINED WITH MATHEMATICAL MODELLING”   
(submitted at Dec 21th 2018)

# SUMMARY:

There are two main stages:

1. We first conducted a systematic review to collate age-stratified case data and a literature review to obtain vaccination information. We then fit a model to this data to estimate the transmission intensity or force of infection (FOI) for each study.
2. We extrapolated the FOI for all endemic areas from our previous estimates. Finally, using the processed population and vaccination data in all endemic areas, we generated burden quantities (cases and deaths) in two scenarios, with or without JE vaccination.

# DATA FOLDER:

* age case: age-stratified case data for every countries. There are 5 subfolders, all have the same age case data but different susceptible population:
  + d10, d30: susceptible population when vaccine coverage is decreased by 10% or 30%
  + u10, u30: susceptible population when vaccine coverage is increased by 10% or 30%
  + or: original susceptible population – no change in vaccine coverage.

In each subfolder, **“All\_sel\_studies\_JE.xlsx”** contains age case data for all studies selected to generate FOI. There is a tab for data description. *The susceptible population after vaccination in this file (column “Pop\_all\_age\_year\_sum”) is modified by* ***“JE\_vaccinated\_population\_sum.R”*** *in the codes folder.*

* Map\_GADM: gadm map, used to generate burdens map plot, *used in* ***“JE\_map.R”*** *in the codes folder.*
* Population: population with or without vaccination, used to generate susceptible population after vaccination for each study catchment area and to generate population of 30 endemic areas in 2 scenarios.
  + **“UN\_WPP\_24\_JE\_endemic\_1\_pop\_both\_sexes.xlsx”** raw population data. *Used in* ***“JE\_vac\_pop\_24\_ende\_regions.R”*** *and* ***“JE\_vaccinated\_population\_sum.R”*** *in the code folders.*
  + **Naive\_pop\_24ende\_1950\_2015.rds, After\_vac\_pop\_24ende\_or\_1950\_2015.rds,** **After\_vac\_pop\_24ende\_d10\_1950\_2015.rds, After\_vac\_pop\_24ende\_d30\_1950\_2015.rds, After\_vac\_pop\_24ende\_u10\_1950\_2015.rds, After\_vac\_pop\_24ende\_u30\_1950\_2015.rds:** population in no vaccination scenario; susceptible population after vaccination (or); with decreased 10%, 30% coverage (d10, d30); with increased 10%, 30% coverage (u10, u30). *Generated by* ***“JE\_vac\_pop\_24\_ende\_regions.R”*** *code and used in* ***“JE\_FOI\_infe\_quantities\_gen.R”***
* Systematic review: table of selected studies and subfolder with all fulltext paper collected.
* Uncertainty\_quantities:
  + **“FOI\_arbit\_0\_0.5.rds”**: stored FOI sampled from uniform(0, 0.5), used for sensitivity analysis, *used in* ***“JE\_FOI\_infe\_quantities\_gen.R”*** *code.*
  + **“Group\_B\_dist.rds”:** stored FOI of Group B – extremely low incidence, sampled from . Used in ***“JE\_FOI\_infe\_quantities\_gen.R”*** *code.*
  + **“mort\_rate\_dist.rds”, “symp\_rate\_dist.rds”:** Stored mortality and symptomatic rates, sampled from and . Used in ***“JE\_FOI\_infe\_quantities\_gen.R”*** *code.*
  + Vaccine: additional vaccination population from national report in Nepal, India. *Used in* ***“JE\_vac\_pop\_24\_ende\_regions.R”*** *and* ***”JE\_vaccinated\_population\_sum.R”*** *code.*

# CODES FOLDER (please change the working directory for every codes):

* JE\_FOI\_infe\_quantities\_gen: FOI inference and generating burden estimates.

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| --- | --- | --- | --- |
| Code trunk | description | input | output |
| FOI for endemic regions | FOI inference | FOI of all studies:  **“prior\_cov\_every\_studies\_",tag,".rds”**  FOI of Group B:  **“Group\_B\_dist.rds”** | FOI of all endemic areas:  **“ende\_24\_regions\_lambda\_extr\_or.rds”** |
| Burdens estimation | estimating burden like cases, deaths for 2 scenarios | Symptomatic rate: **” symp\_rate\_dist.rds"**  Death rate: **“mort\_rate\_dist.rds"**  Naïve population: **“Naive\_pop\_24ende\_1950\_2015.rds”**  Susceptible population after vaccinating: **“After\_vac\_pop\_24ende\_",tag,"\_1950\_2015.rds"** | Cases and deaths for 2 scenarios:  **“no\_vac\_cases\_gen\_",tag,".rds"**  **“vac\_cases\_gen\_",tag,".rds"**  **“no\_vac\_deaths\_gen\_",tag,".rds"**  **“vac\_deaths\_gen\_",tag,".rds"**  Cases and deaths for 2 scenarios, aggregated by age:  **“no\_vac\_cases\_gen\_age\_sum\_",tag,".rds"**  **“vac\_cases\_gen\_age\_sum\_",tag,".rds"**  **“no\_vac\_deaths\_gen\_age\_sum\_",tag,".rds"**  **“vac\_deaths\_gen\_age\_sum\_",tag,".rds"** |
| Sensitivity analysis | generate cases in with alternated population (from subnational data vs subnation data) |  | **“all\_regions\_no\_vac\_cases\_age\_sum.rds”**  **“all\_regions\_vac\_cases\_age\_sum.rds”** |
| Subnational vs national data, Different geography stratifications | **“all\_regions\_no\_vac\_cases\_age\_sum.rds”** |  |
| changing FOI of unknown regions | **“FOI\_arbit\_0\_0.5.rds”**: stored FOI sampled from uniform(0, 0.5), |  |
| Decrease the number of vaccinated people by 10%, 30%, change FOI => vaccine effectiveness 70, 90% |  | **“vac\_cases\_gen\_age\_sum\_diffFOI\_d10.rds”**  **“vac\_cases\_gen\_age\_sum\_diffFOI\_d30.rds”** |
| Different coverage for Japan, Malaysia, South Korea => decrease and increase vaccine coverage by 10, 30% | Population after vaccination:  **"After\_vac\_pop\_24ende\_",tag,"\_1950\_2015.rds"**  FOI for J, K, M:  **prior\_cov\_JKM\_", tag, ".rds"** | **vac\_cases\_gen\_age\_sum\_JKM\_", tag,".rds"** |
| Different doses number in VN | Naïve population:  **Naive\_pop\_24ende\_1950\_2015.rds**  **Je package,** data from Marchosy | **prior\_cov\_VNM\_", doses, "doses.rds"**  **vac\_cases\_gen\_age\_sum\_VNM\_", doses,"\_doses.rds"** |
| Comparing cases gen | Compare with previous estimates in 2011 by incidence group | **"all\_regions\_no\_vac\_cases\_age\_sum.rds"**  **"all\_regions\_vac\_cases\_age\_sum.rds"** | A table in supplement information. |
| case averted | Calculate the total number of case averted for every years worldwide | **"no\_vac\_cases\_gen\_age\_sum\_or.rds"**  **"vac\_cases\_gen\_age\_sum\_or.rds"** | Numbers to report in the manuscript |
| deaths averted | Calculate the total number of deaths averted for every years worldwide | **"no\_vac\_deaths\_gen\_age\_sum\_or.rds"**  **"vac\_deaths\_gen\_age\_sum\_or.rds"** | Numbers to report in the manuscript |

* JE\_map:
  + Endemic places: create a vanilla shapefile to draw a map of 30 endemic area
  + Gen data for Shiny map: create a shapefile to create a shiny map of FOI in study’s catchment area.
* JE\_plots\_for\_papers: draw all plots for manuscript and supplement.
  + FOI plot: Figure 3
  + Reporting rate plot: Figure S2
  + Burdens plot: Figure 4
  + SENSITIVITY ANALYSIS plots:
    - Different stratifications: C, D
    - Changing FOI of unknown regions: A, B
    - Different coverage vaccine analysis: E-J
    - Vaccine effectiveness: K, L
  + Annual FOI estimates: Figure M
  + Model convergence, susceptible proportion, fit: section model converge in SI, Figure S1, S3
  + Map plot: Figure 5
* JE\_vac\_pop\_24\_ende\_regions: Naïve population and population after vaccination of 30 endemic areas + other areas
* JE\_vaccinated\_population\_sum: susceptible population after vaccination by age group of all studies.
* JEV\_cases\_model\_cov\_prior: model with prior distribution for susceptible proportion after vaccination, constant FOI
* JEV\_cases\_model\_cov\_prior\_annual\_FOI: model with prior distribution for susceptible proportion after vaccination, time-dependent FOI.

# RESULTS FOLDER

* Annual FOI: time-dependent FOI model results
* Areas\_lambda: FOI of 30 endemic areas (or), with changed coverage data (d10, d30). FOI with changed coverage data for Japan, South Korea and Malaysia. FOI for Vietnam with 2 doses and 3 doses coverage data.
* Cases\_gen: cases generated for the main manuscript and sensitivity analysis
* Deaths\_gen: deaths generated for the main manuscript
* Map\_data: “shapefiles\_FOI\_data\_merged\_region.rds” => vanilla shapefile data, “lambda\_every\_catchment\_areas.rds” => shapefile data with FOI for every studies.
* Plots
* Studies\_lambda: “All\_model\_results\_or” => save the whole stan fit model; prior\_cov\_every\_studies => only save extracted FOI, expected cases, and susceptible proportion.

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* Raw documents: Figure, SI, cover letter
* Submitted documents: Figure, SI, cover letter, JE manuscript.