FluEvidenceSynthesis-User's Notes

NWenzel

July 12, 2016

1 Performance Sites

This project was performed at the following sites:

1. Public Health England, Colindale (PHE Colindale), 61 Colindale Ave, London NW9 5EQ
2. Centre for the Mathematical Modelling of Infectious Diseases, London School of Hygiene and Tropical Medicine Keppel Street London, WC1E 7HT
3. Olympus High Performance Computing Cluster University of Pittsburgh, MIDAS INFORMATICS SERVICES GROUP, Models of Infectious Disease Agent Study (MIDAS)

2 fluEvidenceSynthesis Package Introduction

Installs directly from github thus `devtools` package is also needed.

```
library(devtools)
install_github("MJomaba/flu-evidence-synthesis", force=TRUE)
library(fluEvidenceSynthesis)
vignette(package="fluEvidenceSynthesis")
```

3 Model Assumptions

We assume:

1. Basic epidemiological model is a SEEIIR model.
2. Exposed and Infected split into two different groups; this gives gamma distributed waiting time between E I state and the I R state.
3. All-or-nothing vaccination assumption where vaccine efficacy for pathogenicity ($VE_P = 0$) is zero when individual is in any state except Recovered.

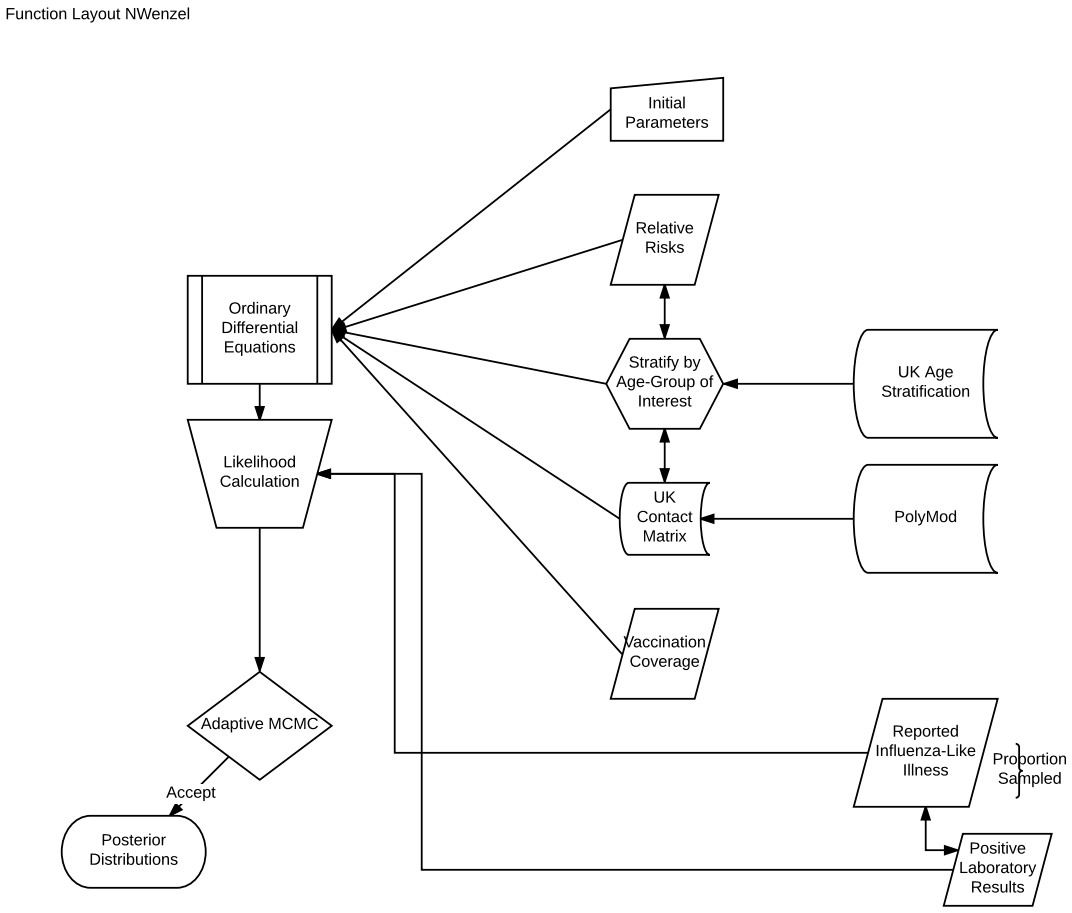

Figure 1: Code Diagram for NWenzel Reference

4. Duration of infectiousness is 1.8 days (Imperial Ferguson); this is not because of recovery, it assumes individuals self-sequester after this period.

, (Duration of immunity?)

4 Code Changes by NWenzel

Changes were made to the package to adapt to the question: It has been proposed that the indirect effect of vaccinating primary school children (age 5-11) vs a combination of primary and secondary school age children (2-17) may be a more cost-effective option. Focusing influenza vaccination resources on such a 'keystone' contact group[1] could moderate the logistical challenges of influenza vaccine distribution.

In particular, NWenzel implemented several structural changes such that varied combinations of parameters could be swapped through exterior functions leaving the base functions such as the log likelihood and the adaptive markov chain monte carlo (MCMC) isolated from potential errors that could occur with multiple parameter scenarios. Separate functions are marked with 'FUNC' in the file name, input data is marked with 'INPUT', and analysis/graphical code is marked with an 'AG' header in the file name. `R` code should be flexible enough to handle changes to age groups, initial parameters, vaccination strategy, Influenza-like-illness, coverage rates, with simple inputs to the top-level function. Additional flexibility adjustments were made to allow for either age-groups or risk-groups to be evaluated singularly while the other was held at zero.

4.1 Changes Waiting to be Implemented

Probability of case ascertainment, ϵ, and susceptibility are defined by the vector `pars` within master file. While `pars` can be set from the top level, the length of the vector and the corresponding susceptibility and epsilon to `pars` had to be changed within the likelihood function.

[1] By keystone we mean a contact group that has a disproportionately large effect on disease incidence relative to the contact's group size to the total population