P-MEDDS User Manual

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1 Introduction

P-MEDDS provides a robust set of of tools for modeling the spread of infectious diseases. Using a determenistic compartmental S-I-R model and a robust Markov-Chain-Monte-Carlo (MCMC) fitting procedure P-MEDDS can quickly characterize an incidence profile a in real time providing estimates for the:

- individual level epidemic severity (as described by the proportion p_C of infections that result in clinical cases)
- and the epidemic transmissibility (measured by the basic reproduction number R_0)

Publicaly available weekly influenza-like-ilness (ILI) data is included in the package (from the CDC, Google Flu Trends (GFT), and the World Health Organization (WHO)) along with weekly averaged specific humidity and school opening/closing schedule. The last two sets of data are needed for three of the five different models for the time dependence of the reproduction number $R(t)$ that the user can choose from.

Upon completion of the MCMC fitting procedure the P-MEDDS pacakge analyses the results and produces an extensive set of publication quality plots (in PDF and PNG formats) and tables (in csv format). The complete history of the run and the fitting procedure is saved as an '`.RData`' file which the user can later load and further analyze.

P-MEDDS also provides a computationally efficient version of the Wallinga-Teunis (W-T) likelihood-based procedure for estimating the daily effective reproduction number using an observed epidemic curve [insert ref.]. This algorithm can be applied to the 2003 SARS epidemic data which is inlcuded in the P-MEDDS package. As in the case of influenza modeling, P-MEDDS will produce a set of publicaition quality figures and tables when the estimation procedure is completed.

2 Examples

P-MEDDS includes an examples directory with three sample R drivers that demonstarte how to use the package:

- `example.driver.R`: This script can be used to model any of the ILI data in the P-MEDDS data base: Military, CDC or GFT. The script explains every parameter that the package requires and shows the default values foreach one.
- `example.interactive.R`: This is an interactive version of the example.driver.R: it will prompt the user to select each of the parameters for a P-MEDDS run. It will explain the options and use their defaults if the user provides an incorrect value.
- `example.wt.R`: This script demonstartes how the P-MEDDS package can be used to model the 2003 SARS data using the Wallinga-Teunis procedure.

For more information on each of these R scripts see `README.example.md` file in the `examples` directory. Inside the `examples` directory there is a sub-directory `tests.output` with sample output files for the different models supported by P-MEDDS. After reading this manual we suggest that the User familiarize him/her-self with the package by using these scripts and modifying them as needed.

3 Influenza Modeling

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3.1 ILI Methods

3.2 ILI Data

We obtained data from the Armed Forces Health Surveillance Center (AFHSC) consisting of outpatient visits to permanent military treatment facilities (MTFs) by active duty military personnel for a range of ICD (international classification of diseases)-9 codes associated with respiratory-related ilnesses between January 1, 2009 and April 30, 2011. For each record, the data contained: a unique staudy identifier for the individual; ICD-9 codes associated with that visit; and the zip code (5 digits) of the clinic location. We used the zip code of the reporting clinic as a proxy with which to define a military installation: we do not explicitly represent military installations or bases, rather, we assume that the case reports from the same zip code are from the same military installation. Each record (an anonymized Study ID) was assigned as either "ILI-large" ($n = 1,336,471$) or "ILI-small" ($n = 27,582$) using a set of classifications based on ICD-9 codes [ref here]. The definition of ILI-large was broader and inluded non-specific diagnosis such as 'viral infection' and 'acute nasopharyngitis'. The definition of ILI-small was more constrained and included: 'influenza w/other respiratory manifestations' ($n = 25,293$), 'influenza with manifestation not elsewhere classified (NEC)' ($n = 1,006$), ' infectious upper repiratory, multiple sites, acute NEC' ($n = 897$), and 'influenza with pneumonia' ($n = 404$). We further trimmed the data temprally to cover the period from April 1, 2009 through June, 1, 2010 which is the 2009 H1N1 pandemic period. We ranked the military installations by size according to the total number of ILI-small cases they reported.

In the P-MEDDS data base we provide the data for the top-50 largest profiles, 47 of which, were located within the USA. Of the remaining three, one was located in Landstuhl, Germany, and two were located in Japan (Misawa and Yokosuka).

For each of these 50 military installations we provide our estimate of the total population (N_{total}), the "denominator data". Our method for estimating these sizes relied on the use of the total number of visits to a clinic for all causes as a proxy for the total number of active duty

personnel at that location [ref]. The coefficient of proportionallity Ω was estimated by using a subset of the installations for which reasonably reliable estimates for the total population have been published.

We obtained civilian data through a variety of means. County- and State-level data were generally acquired directly from the appropriate public health services department . CDC ILI data (for the ten HHS regions) were obtained from the flu activity and surveillance website: http://www.cdc.gov/flu/.

Google Flu Trends data (at the national, state and city level) was also obtained directly from the GFT web site: http://www.google.org/flutrends/us/#US.

Denominator civilian data was obtained from the US 2010 census data center: http://www.census.gov/2010census/data/

3.3 ILI Results

4 SARS Modeling

4.1 SARS Methods

4.2 SARS Data

4.3 SARS Results