Model Standards | Vaccine Impact Modelling Consortium

The Vaccine Impact Modelling Consortium (VIMC) aims to generate transparently developed and well-documented vaccine impact and disease burden estimates for Gavi, the Vaccine Alliance, and the Bill and Melinda Gates Foundation. For comparison purposes, the Consortium aims to employ at least two models per disease area included in its portfolio[1]. The below check-list is proposed for the baseline evaluation of models included in the Consortium.

The model review process is outlined separately in the "Model Review Process" document.

Meeting these standards does not guarantee that new applicants will be selected to join the Consortium.

Model minimum standards - for any model included in the Consortium:

- Model generates the **outputs** required for each of the 96 Gavi and DoV (Decade of Vaccines) countries, or the subset of countries in which the disease in question is considered endemic:
  - Deaths, cases (by year of current age and year of chronological time);
  - DALYs (by year of current age and year of chronological time, ideally at infection, or alternatively at symptom onset);
  - The above outputs should be estimated for a number of different scenarios regarding vaccination coverage;

- Model can make use of **the standardised demographic data** provided by VIMC;

- Model includes comprehensive **documentation**:
  - Published scientific paper (with detailed Supplementary Information, if needed), or other comparably detailed documentation that can be made publically available.
  - Documentation should include:
    - A full model description to enable replication of the results in principle.
    - Details of how the model represents key aspects of the natural history and epidemiology (including definitions of what a 'case' represents) of the disease in question.
    - Details of model parameterisation/fitting (see below), including how fitting accounts for data limitations (e.g. under-reporting of cases).

[1] As of 2016, the diseases included in the portfolio are *HPV, Japanese encephalitis, measles, meningitis A, hepatitis B, Hib (Haemophilus influenzae type b), pneumococcus, rubella, rotavirus, and yellow fever.* Over the course of the Consortium the disease portfolio might be updated and expanded.

- A description of data sets used to parameterise/validate the model, with references and/or details if these can be made available.
- Comprehensive tables of all parameter estimates.

Desirable characteristics - for quality improvement target setting:

- The model has been **rigorously fitted to epidemiological data**. Approaches that capture and propagate data uncertainty in a statistically meaningful way (e.g. likelihood-based methods such as MCMC) are strongly preferred.

- **Model complexity** is appropriate for the data available.

- **Data used in model fitting** has the following characteristics:
  - Geography: optimally data from the 96 countries of interest are used. Where extrapolation from one country to others is needed, this should be justified in the documentation.
  - Data types: for many diseases, case incidence, serological, and mortality data may be available. Optimally models will make use of the full range of different types of data.
  - Data on vaccine efficacy/effectiveness: optimally models will fit vaccine efficacy parameters using data on vaccine impact from the 96 countries of interest, or else from efficacy trials.

- Model **validation**: out-of-sample validation is desirable (i.e. fit the model to one set of data, and evaluate ability to predict relevant outputs in another setting).

- Model **captures quantifiable uncertainty**, e.g. regarding:
  - Ability to generate multiple (100s) versions of the outputs, each of which represents a random sample from the joint uncertainty distribution (e.g. posterior) of the input parameters.
  - For stochastic models, the ability to generate multiple (100s) versions of the outputs, each of which represents a single stochastic realisation.
  - Representation of structural uncertainty and uncertainty in future non-vaccination related intervention scenarios is also desirable.

- **Indirect effects** of vaccination/herd-immunity are represented in the model, where epidemiologically relevant.

- **Model source code** is able to be shared with the VIMC Secretariat to allow the model to be run centrally. Models coded in a mainstream programming language (e.g. R, C/C++, Java, JavaScript, Python) are preferred.