## MMC Benchmarking Call

*1 April 2020*

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### Agenda

1. Feedback and comments on this round of benchmarking.
2. Discussion of a template for benchmarking submissions.
3. Citing data sources.

### Discussion

#### Feedback and comments

* Should we standardize treatment assumptions for benchmarking submissions? Start with zero care seeking and treatment, then move up.
* Axis scales should be the same for all plots, to give a common visual basis.
* How can we make this somewhat comparable? How to communicate what’s accounting for the variability in plots from different groups? There is real uncertainty in the models that produce these relationships, and we need to send the message that we are dealing with that uncertainty in credible ways.

#### Submission template

* The MMC Secretariat can write some introductory text that discusses uncertainty and what to expect when viewing the plots.
* Groups can write supportive text for each model to explain how fitting was done and how data were used.
* Secretariat will come up with an example of a documentation template and spend time with each group to work on their submission, then come to a common format.

#### Citing data sources

* Secretariat is working on a way to organize data sources.
* Each group should cite the data used for calibration, as well as inclusion/exclusion criteria.

### Next Steps

1. Secretariat to draft introductory text.
2. Secretariat to contact each group individually over the next several weeks to work on their submissions and documentation.
3. Secretariat to work on developing a template for documentation (see below).
4. Next call to be scheduled for mid-May.

### Benchmarking submission template

*Following the call, the Secretariat discussed specific elements that should go into benchmarking submissions (listed below). As we reach out to each group, we will use this list as a basis for developing documentation.*

1. Free form opening paragraph that briefly describes the model, how the fitting was done, and how various data sources were used (*e.g.* fitting vs. validation). High level overview of what kind of model this is?
   1. “briefly describes the model” is a little open ended, as well as various data sources, over the years this is so many uses for both fitting and validation, by so many, it would be prohibitively burdensome on me to do this just for mmc
   2. The fitting procedures are so layered especially for most recent versions of the model. The many parameters have each been fit modularly to different data different times (ie Seasonality and heterogeneity in Garki, Incidence in Senegal, Durations in Malariatherapy, model calibration to age-stratified measurements of parasite prevalence and clinical incidence at a variety of independent sites in Tanzania and Garki and Senegal across arrange of transmission intensities.
   3. From Kevin McCarthy et al Malaria J 2015 (<https://malariajournal.biomedcentral.com/articles/10.1186/1475-2875-14-6>)
      1. : First, age-stratified prevalence and fever incidence curves were used to calibrate parameters governing antigenic dynamics and immune response, and then age-stratified severe disease incidence curves were used to calibrate model parameters governing the probabilistic presentation of a severe malarial incident.
      2. For health seeking configuration individuals who present fever begin parasite-clearing treatment with a 30% probability per day from the fever onset, meant to roughly capture the ‘time to next visit’ for fever detection.
   4. From Philip Eckhoff Malaria J 2011 \*<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3224385/>
      1. The habitat scaling parameters and habitat-specific time constants were obtained by simulation of one species at a time, comparing to measurements of local EIR by species. Parameters which exhibit high uncertainty or geographic variability, such as the host preference of An. arabiensis, are studied over broad numerical ranges for their impact on results. A simplified human disease model is used in all simulations, with a constant latent period of 22 days from bite to infectiousness to mosquitoes, and exponentially-distributed period of infectiousness with mean 180 days. Infectiousness is a constant 0.2, without development of immunity to allow resolution of vector-specific effects. Superinfection is allowed, with a maximum of five simultaneous infections. General model and simulation-specific parameters and their values are summarized in Table [​Table11](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3224385/table/T1/).
2. Does the benchmark curve represent the true PR, or the PR as it would be observed (*i.e.* detected by light microscopy, RDT, or another method).
   1. True PfPR 2-10
3. Does the benchmark curve assume that the population is open or closed to migration?
   1. Closed to migration currently can incorporate spatial relatedness with travel to a migration node
4. What levels of case management are represented?
   1. No case management currently, but can do age/individual property binned health care seeking (rates can be attenuated as mentioned above)
5. How was the probability of disease calibrated and with which data sets?
   1. See above description
6. What was the seasonal pattern for EIR used to produce these patterns?
   1. Namawala, Tanzania

monthly\_EIR = [43.8, 68.5, 27.4, 46.6, 49.4, 24.7, 13.7, 11, 11, 2.74, 13.7, 16.5]

1. Did the models show substantial variation in PR by age within 2-10 year olds?
   1. Didn’t plot but can do
2. Did the model make any assumptions about heterogeneous biting by age, or among individuals within a population?
   1. Surface-area dependent biting creates heterogeneity in biting risk by age, but within the node, biting is distributed similarly across individuals of similar ages
3. What decisions were made that are unique to this particular exercise?
   1. Burnin of 40 years, population of 1000
4. What other caveats or clarifications are there?