VIMC – RfP (Request for Proposals) for a Meningitis Modelling Group

Guide for Applicants

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1. Requests for Proposals (RfP) Overview and Guidance

Background

The Vaccine Impact Modelling Consortium (VIMC) is an international community of modellers providing high-quality estimates of the public health impact of vaccination, to inform and improve decision making.

VIMC was originally established in 2016, to deliver a more sustainable, efficient, and transparent approach to generating estimates of disease burden and vaccine impact, for investments by Gavi, the Vaccine Alliance. VIMC is now in its second phase – VIMC 2.0 – from 2022 – 2027, supported by grants from Gavi, the Gates Foundation and the Wellcome Trust.

By 2027, our core aims are:

- to provide reliable and accessible estimates of vaccine impact across the Gavi portfolio
- to address critical modelling-related vaccine policy questions raised by stakeholders who are dynamically engaged in our work
- to translate our modelling to real-world policy that improves health outcomes
- to foster a diverse international community of vaccine impact modellers, inclusive of modellers in low- and middle-income countries
- to provide training in infectious disease modelling and its application to vaccine-preventable diseases for both modellers and policymakers.

Specific aims of our research programme on climate change are:

- to better characterise the mechanistic relationship between environment, climate and disease transmission
- to assess implications of long-term climate change for disease burden, range and routine vaccination
- to optimise control programmes to respond to seasonal variation in disease burden and the consequences of increasingly frequent extreme climate events.

As of 2024, VIMC provides 'core funding' for modelling groups in ten disease areas: cholera, COVID-19, HPV, hepatitis B, malaria, meningitis A / multivalent meningococcal conjugate vaccine (MMCV), measles, rubella, typhoid, and yellow fever. The research programme on climate change and vaccine-preventable diseases focuses on malaria, dengue, yellow fever, meningitis and cholera.

For more information on the VIMC, please refer to our website: https://www.vaccineimpact.org/

About this Request for Proposals (RfP)

Through this RfP, the Consortium seeks to recruit one new group to evaluate the impact of meningitis A / MMCV in the 26 countries of the African meningitis belt. Applications from LMIC-based modelling groups will be given priority, with preference given to those in countries experiencing a high burden of meningitis. Up to USD $73,000 per year is available in funding. The new group will join the consortium from early 2025 to August 2027. The primary funder of this work is Gavi, the Vaccine Alliance.

Eligibility

- Applicants must be based at a university or another academic/research institution.
- The Consortium anticipates that the lead institution is based in a low- or middle-income country, with the expectation that the majority of the budget will be allocated within an LMIC context. Preference will be given to groups in countries experiencing a high burden of meningitis.
- Prior modelling experience is essential; models must already be developed and in use.

One of VIMC's goals is to become a diverse community of vaccine impact modellers, inclusive of modellers from LMICs, and we are committed to embedding equality, diversity and inclusion (EDI) in our practices. As such, we encourage applications and expressions of interest from applicants who may be underrepresented among the mathematical modelling community. This includes female modellers in countries/regions where the gender balance is currently skewed towards male modellers. We will monitor EDI (including gender balance and geographical location) by asking all applicants to complete a separate anonymous EDI form. Information provided on the EDI form will not be used in the model selection process.

Priority will be given to modelling groups that can provide standardised outputs. However, we will also consider applications from groups with models currently in development that are working towards being able to provide these outputs. This will entail providing age-disaggregated estimates of deaths, DALYs and cases for 26 countries for the period 2000-2100, for multiple vaccine coverage scenarios and for both MenA vaccine and MMCVs. As well as central (point) estimates, we require estimates of uncertainty. As model inputs, we provide demographic data and estimates of vaccine coverage. However, we do not provide disease-specific data. For more details, please refer to the 'Output Specifications Guidance'.

Scope of Work for Successful Applicants

If selected to join the Consortium, applicants will then be expected to carry out the scope of work detailed in the 'Sample Scope of Work for Modelling Groups'. This is the standard scope of work for all disease-specific VIMC models that receive core funding.

Funding

Successful models will be invited to join the Consortium as full members and will receive core funding. Funding will be arranged via a subcontract between Imperial College London and the modelling group's institution, with Gavi as the primary funder. (The level of funding and subcontract arrangement aligns with the Consortium's approach for its current modelling groups).

Next Steps / How to Apply

First, please check your eligibility by reading the Guide for Applicants and the separate FAQ. If you are eligible and wish to apply for the RfP, please email us at vimc@imperial.ac.uk to register your group's interest.

To register your group's interest:

Please send one email per group to vimc@imperial.ac.uk, with 'RfP Meningitis' in the subject line, including the following:

- 1 paragraph describing your group's modelling and policy experience
- Lead organisation name
- Name of each applicant (please indicate the lead applicant if known)

- Email of each applicant (or simply cc all co-applicants)
- GitHub IDs of each applicant (if known)
- How you heard about the RfP (e.g. direct email from VIMC / email from another source / via Twitter or Mastodon, etc.)

We will then ensure all registered applicants have access to standalone application forms, and access to Montagu (VIMC's delivery platform). We will also provide guidance on how to use the platform to submit the draft burden estimates, which will form part of your application.

To submit your application:

After you have registered your interest, you will need to submit the following by 29 November 2024:

- Application form for disease-specific groups stating basic information about the model and the applicants.
- Model documentation that allows assessment against the Consortium model standards (e.g., a published paper, report, or custom-written documentation).
- Draft burden estimates for one pre-defined country in the specified disease area, to be submitted on Montagu (standardised template provided by VIMC).
- Brief CVs for all applicants (max. 2 pages each).
- Institutional / departmental letter of support.

Timeline

27 September 2024	- RfP published - Groups register their interest (see 'Next Steps').
7 October 2024	Application period opens: - VIMC gives groups access to standalone application forms - VIMC gives disease-specific groups access to Montagu (VIMC's delivery platform) and advises on how to upload draft burden estimates.
29 November 2024	RfP closing date for all applicants
By 20 December 2024	Applicants informed of outcomes
January 2025	Subcontracts drafted

External Reviewers:

External expert reviewers will be sought by the VIMC Secretariat and may include members of the VIMC Stakeholder Group. Reviewers will be selected to ensure a breadth of expertise in relevant fields and will be asked to provide both technical and non-technical feedback.

Decision-making Panel

The Consortium Director and funders will make the final decisions on model selection, taking into account the recommendations of the external reviewers.

Conflicts of Interest:

The Consortium will avoid institutional conflicts of interest. Other minor conflicts of interest (e.g. collaborative work) will be noted. Primary funders will have access to all applications.

2. Appendix 1 - Sample Scope of Work for Modelling Groups

Deliverables for each core-funded modelling group

The following broad deliverables are expected of each core-funded VIMC modelling group. Groups are expected to be consistently engaged in policy-relevant work, and able to respond flexibly as needs evolve. As such, deliverables 1, 2, and 3 below represent the main focus of modelling groups in VIMC 2.0.

More detailed group-specific deliverables will be discussed and agreed with each group and kept in a separate live document.

1. Provide modelled vaccine impact estimates for VIMC in 2025, in VIMC'S standardised format. This includes central and stochastic estimates of the number of deaths, cases and DALYs for different vaccination scenarios. Estimates should span all 26 countries of the African meningitis belt and be stratified by age (0-100) and year (2000-2100).
2. Respond to vaccine policy-related questions through leading one project working group per disease area at all times. Project working group leads are expected to:
    a. Refine policy-relevant questions (in an iterative process, if necessary)
    b. Carry out modelling and lead on presenting results to VIMC's Stakeholder Group (SG)
    c. Refine the modelling work (in an iterative process, if necessary)
    d. Disseminate results widely
3. Support VIMC's response to vaccine policy-related questions through active participation in one further project working group, if required. Active participants are expected to:
    a. Contribute to refining policy-relevant questions (in an iterative process, if necessary)
    b. Carry out modelling
    c. Refining the modelling work (in an iterative process, if necessary)
    d. Contribute to disseminating results widely
4. Be on hand to respond to other ad-hoc disease-specific questions raised by funders and other VIMC partners, including providing context and explanations of modelled results.
5. Carry out model comparisons and comparisons of results with other modellers.
6. Work collaboratively with the VIMC science & policy team on our shared learning agenda.
7. Apply to VIMC to host a visiting fellow for one month, including participation in a shorter reciprocal visit.
8. Present findings at VIMC webinars and consortium-wide meetings, with an expectation of at least one presentation every year per disease area.
9. Contribute to VIMC training activities and ecosystem building, including collaborating with groups working with the Consortium for the first time.
10. Engage with the VIMC Secretariat on tailored reviews of estimates, including reviewing vaccine coverage scenarios.
11. For groups included in VIMC 1.0, maintain the model to meet VIMC's quality standards (see separate document). For all other groups, agree with the VIMC Secretariat on a plan for model development to bring the model closer to VIMC's quality standards.

12. Submit brief progress reports every four months (to be shared with all VIMC members by default) covering all the activities listed above.

3. Appendix 2 – Model Standards

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, the Bill and Melinda Gates Foundation and other global health partners. For comparison purposes, the Consortium aims to employ at least two models per disease area included in its portfolio[1].

Models included in the first phase of VIMC (VIMC 1.0, 2016-2022) are required to maintain the model to meet the standards outlined below. Models joining the Consortium in its second phase (VIMC 2.0, 2022-2027) should either meet the minimum standards below, or alternatively agree with the VIMC Secretariat on a plan for model development to bring the model closer to these standards. Meeting these standards does not guarantee that new applicants will be selected to join the Consortium.

Model Minimum Standards:

- Model generates the **outputs** required for each of the specified 117 countries, or the subset of countries in which the disease in question is considered endemic or of strategic interest:
  - 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 should 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 publicly 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).
    - 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.

[1] For the second phase of the Consortium ('VIMC 2.0', 2022 – 2027), the core-funded disease areas will be cholera, COVID, hepatitis B, HPV, malaria, measles, meningitis A / MMCV, rubella, typhoid, and yellow fever. Additional non-core-funded disease areas will also be included in VIMC work through other means.

Desirable Characteristics:

- 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 117 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 117 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** can be shared with the VIMC Secretariat. Models coded in a mainstream programming language (e.g. R, C/C++, Java, JavaScript, Python) are preferred.

4. Appendix 3 – Output Specifications Guidance

This appendix sets out the outputs that we require from disease-specific modelling groups. For this RfP, you will need to submit standardised outputs for one country only, to demonstrate that your model is able to produce these. If you are then selected to join the Consortium, you will be expected to provide similar outputs for or all endemic countries (26 for meningitis). Please note:

- *We will also consider applications from groups with models currently in development, that are working towards being able to provide these outputs for 26 countries.*
- *We are also interested in hearing from modellers who are focusing on disease burden and/or vaccine impact for a single country, or for a more limited period or age range. Although we may not be able to offer core funding in these cases, there could be other funded opportunities to collaborate with the Consortium - for example, to produce or advise on modelling in response to specific policy questions.*

The burden outcomes modelled within the VIMC across all diseases include deaths, (severe) cases, and DALYs, and we also ask modellers to record the underlying population size assumed in the model. These outcomes are stratified by annual age cohort, year and country.

The standard burden estimate templates contain the following columns:

Table 1: Columns of the standard burden estimate templates:

Column name	Comment/explanation
disease[1]	Disease – will be constant across the file
year[1]	Calendar year – the default period is 2000 to 2100, but this may differ between models depending on the age range modelled
age[1]	Age in years of the birth cohort in the calendar year in question. The default age range is 0-100 years.
country[1]	3-letter ISO country code.
country_name[1]	Country name spelled out
cohort_size[2]	The national population size of the cohort in question, irrespective of disease or vaccination status
cases[2]	Number of severe cases in a given year and age group. This should be incidence rather than prevalence.
deaths[2]	Number of deaths in a given year and age group.
dalys[2]	Number of disability adjusted life years (DALYs) lost, associated with the incidence of severe cases and deaths in a given year and age group. For a death occurring in year y and age a, the total number of life years lost until the end of the life expectancy should be recorded in year y and age a, rather than spread across future years and ages. Similarly, years lived with a disability should also be accounted for at the time of infection.

[1] will be pre-filled

[2] model outcomes to be provided by the modellers

The default age and year range are as above. If you do not model the same ranges, please specify this in the cover sheet of your application and delete the empty rows from the output template before uploading.

We provide the burden estimate templates as CSV files. Below is an example of the first few rows and columns of a template:

Table 2: Example burden estimate template (for central estimates)

	A	B	C	D	E	F	G	H	I
1	disease	year	age	country	country_name	cohort_size	cases	deaths	dalys
2	Malaria	2000	0	RFP	Request for Proposal				
3	Malaria	2001	0	RFP	Request for Proposal				
4	Malaria	2002	0	RFP	Request for Proposal				
5	Malaria	2003	0	RFP	Request for Proposal				

Pre-filled columns

Output columns for modellers to complete.

For meningitis, the outcomes in the template are stratified by serotypes (eg. cases and cases_cwyx) and where possible we would ask applicants to supply burden outcomes in the same stratification. Where this is not possible, applicants should provide estimates in the cases, deaths and DALYs fields and set the cases_cwyx, deaths_cwyx and DALYs_cwyx fields to 0.

Montagu (online delivery platform)

Montagu is our online delivery platform. To access the demographic and coverage data, the upload templates, and to submit the burden estimates generated by your model, please contact vimc@imperial.ac.uk to request an account, which will enable you to log in to Montagu. Please provide your name, the organisation (if applicable), and the disease area.

Scenarios

For the RfP, applicants will need to provide burden estimates for two scenarios:

- Default
- No vaccination

Uploads Required

We require central estimates and probabilistic outputs. The central estimates should be either means or medians of stochastic runs or posterior distributions arising in the model fitting, maximum likelihood estimates or similar or based on best estimate parameters. For the probabilistic outputs for this RfP, we require a small sample of 30 probabilistic realisations per scenario. For models explicitly fitted to data, probabilistic outputs can be a sample from the posterior distribution. If no explicit model fitting has taken place, input parameters should be sampled from reasonable ranges.

For this RfP, applicants will need to provide the following:

Table 3: Required uploads

Item	How to create	Where to upload complete file(s)
Central estimates (multiple files)	Download central burden estimate template from Montagu, use this to create one file per scenario	Montagu
Stochastic estimates (multiple files)	Download stochastic burden estimate template from Montagu, use this to create as many files as you need.	Dropbox
Parameter set (1 file per disease)	Download stochastic parameters template from Montagu, use this to create your parameter set.	Montagu
Parameter certificate (1 file per disease)	You will be able to download this from Montagu once you have uploaded your parameter set.	Dropbox

Central Estimates (also known as deterministic estimates)

First, download your central burden estimate template from the Responsibilities page of Montagu (listed under 'Scenarios'). The template is illustrated in Table 2.

You will need to use this template to create one file for each scenario, ensuring that you fill in all rows and columns.

Your scenarios are shown in the grey headings on the Responsibilities page of Montagu. Details of the coverage sets are shown after you click the '**Download coverage data**' buttons.

Once you have completed one output file for each scenario, you should upload each file to Montagu, using the '**Upload burden estimates**' buttons on the Responsibilities page.

There is no specific filename format to use. This is because when you upload through Montagu, the URL of the page you are on will determine the scenario.

Montagu will confirm whether each central burden estimate file uploads successfully and show you some quick diagnostic graphs.

When uploading your central estimates, you will need to register how these have been calculated. If possible, please generate your central estimates as the average of your stochastic estimates. If this is not possible, please specify in your answer to the registration questions how your central estimates have been calculated. If your answers to the registration questions change between uploading your central estimates and your stochastic estimates, you should complete this registration step again and re-upload your central estimates to Montagu.

Stochastic Estimates (also known as probabilistic estimates)

For the stochastic runs, we require 30 model runs for each scenario, each of which represents a random sample from the uncertainty distribution of your model outputs. Optimally, this would be samples of a posterior distribution representing all the parameter uncertainty in your model. As we want to compare the runs across scenarios

to calculate the impact, the same parameter samples must be used across all scenarios, and the runs labelled to ensure we can identify them.

The aim of the stochastic estimates is to help us understand the drivers of uncertainty. The stochastic estimates should therefore represent the full range of uncertainty, and include any parameters that may affect burden estimates, not just efficacy parameters, e.g. case fatality ratios. Please note you must not vary demography or vaccine coverage; instead, you should use only the standardised demography and coverage provided.

The format of the stochastic burden estimate is almost identical to the central burden estimate template, but there is one additional column: 'run_id'. This column labels the particular run and should link the run to the parameter value detailed in the parameter set file. Importantly, the runs across all scenarios with the same run id should be based on the same parameter values and have the same random seed.

For the RfP, we require 30 independent realisations for the stochastic estimates. The stochastic estimate template only contains all rows for a single realisation, so you will need to generate 30 times as many rows.

You will need to use the stochastic burden estimate template to create one or more files for each scenario, ensuring that you fill in all required rows and columns. If you choose to break the data up into multiple files it does not matter how you distribute the rows among files (e.g. by country, by run_id, by year or even randomly), as long as the data are complete, and scenarios are kept separate. The scenarios are the same as for your central estimates.

Next, rename your stochastic estimate files. The filename format should be, for example, *stochastic_burden_est_malaria-IC-Smith_malaria-default_1.csv*. The first part is from the template filename, the second part is the scenario ID (as it appears in Montagu), the final number is an arbitrary way to distinguish between different files for the same scenario if you choose to split the estimates across several files.

Once you have completed all files for each scenario, you should upload each one to Dropbox, to the specific folder that we will email you. We will then use scripts to automatically process the uploaded files and import them into Montagu.

Parameter Set

First, download your stochastic parameters template from the Responsibilities page of Montagu. You should use this template to create one file (a parameter set) that will show us the underlying parameter values of your stochastic runs.

It is essential that the runs across all scenarios with the same 'run id' are based on the same parameter values.

Your parameters file should contain 30 rows (i.e. in addition to the row showing the column headings).

The column headings in the template are labelled <param_1> and <param_2> but you should rename these to the actual parameters you are using and add extra columns if necessary.

Once you have completed your parameter set, you should upload this file via Montagu.

Montagu will then give you a 'parameter certificate'. After you have downloaded this, please upload it to Dropbox, to the specific folder that we will email you.

You should only upload one parameter certificate to Dropbox. This must correspond to the exact parameters that underlie your stochastic estimates. If you discover a mistake in your stochastic files or parameter set after you have uploaded these to Dropbox, please let us know (montagu-help@imperial.ac.uk).

Age Groups

The age groups in your burden estimate templates must be 1-year age groups. If your model uses larger age groups, you will need to disaggregate these.

DALYs Guidance

Download report with detailed guidance on DALYs (includes disability weights)

Cohort Size

The cohort size is the number of people alive in a given birth cohort specified by the calendar year and age during that year – so it will be the same across all scenarios. We will then be able to calculate the number of FVPs (fully vaccinated persons) by multiplying this with the relevant coverage. The cohort size should be comparable to the interpolated population provided on Montagu. The cohort size should reflect the age range, time range and gender (female, male or both) for which your model is tracking the population.

Demography, Coverage and Target Population

We provide demography and coverage as model inputs, via our delivery platform, Montagu. The coverage downloads include target population. Coverage and target population are always specified at a national level. For example, where a campaign targets all ages in Region A (population 1,000,000) and achieves 90% coverage, and where the population of the whole country is 5,000,000, the coverage would appear on Montagu as 0.18 (18%) and the target population as 5,000,000.

For routine vaccination, target is always shown as NA, which means you should assume the target population matches the population shown in the demographic data downloads for the corresponding ages (age_first and age_last).

Checklist for avoiding errors when uploading to Montagu:

- Your file should not contain any empty columns
- Values should not contain commas (e.g. 1395 not 1,395)
- The demographic/coverage data may include years that are outside the scope we are asking you to provide estimates for. Therefore, you should go by the years that appear in the burden estimate templates (or the ages/years you have indicated on your cover sheet).

If you have any questions or any problems uploading your burden estimates, please email montagu-help@imperial.ac.uk.