**VIMC – RfP (Request for Proposals) for Modelling Groups – 2022/23**

**Guide for Applicants**

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**Other languages:**

**English:** Section 1 of this guide will be available in French, Portuguese and Spanish in due course. Please note that VIMC’s working language is English, and application forms must be completed in English.

**Français**: La section 1 de ce guide sera disponible en français, portugais et espagnol en temps utile. Veuillez noter que la langue de travail de VIMC est l'anglais et que les formulaires de candidature doivent être remplis en anglais.

**Português:** A Secção 1 deste guia estará disponível em francês, português e espanhol em breve. Observe que o idioma de trabalho do VIMC é o inglês e os formulários de inscrição devem ser preenchidos em inglês.

**Español**: La Sección 1 de esta guía estará disponible en francés, portugués y español a su debido tiempo. Tenga en cuenta que el idioma de trabajo de VIMC es el inglés y los formularios de solicitud deben completarse en inglés.

1. **Requests for Proposals (RfP)**

Overview and Guidance

**Background**

The Vaccine Impact Modelling Consortium (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. As of 2022, VIMC provides ‘core-funding’ for modelling groups in eight disease areas: cholera, HPV, hepatitis B, meningitis A / multivalent meningococcal conjugate vaccine (MMCV), measles, rubella, typhoid, and yellow fever.

The Consortium will now see a greater focus on modelling to address questions for vaccine policy and practice, working with a more diverse international community of modellers, for a wider range of diseases (including malaria and COVID-19). It will also take on additional groups focusing on of operational, health economic, climate/disease, or geospatial aspects. The Consortium will also establish a new research programme on the impact of climate change on vaccine-preventable diseases. Funding for VIMC 2.0 comes from the Bill & Melinda Gates Foundation; Gavi, the Vaccine Alliance; and the Wellcome Trust.

**About this Request for Proposals (RfP)**

Through this RfP, the Consortium seeks to recruit both groups with disease-specific models of vaccine impact for malaria, COVID-19, meningitis A / MMCV, and hepatitis B, and other cross-cutting groups that will add value to the Consortium.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Number & type of models sought** | **Geographic considerations/constraints** | **Funding period** | **Prime funder** | **Funding available** |
| **Disease-specific modelling groups** | | | | |
| 2 x malaria models | Applications open to all. Funding for one of the two models is ring-fenced for an LMIC-based modelling group (with preference given to those in countries experiencing a high burden of malaria). | Mar 2023 – Aug 2025 [[1]](#footnote-1) | Gavi | Up to USD $73,000 per modelling group per year[[2]](#footnote-2) |
| 2 x COVID-19 models | Applications open to all |
| 1 x model for meningitis A / MMCV | Applications restricted to LMIC-based modelling groups (with preference given to those in countries experiencing a high burden of meningitis). | Sep 2023 – Aug 2025 1 |
| 1 x Hepatitis B model | Applications open to all |
| **Cross-cutting groups** | | | | |
| 2 x cross-cutting groups, e.g. focusing on:   * Operational aspects * Health economics * Impact of climate on disease dynamics * Geospatial aspects | Applications restricted to LMIC-based groups, with preference given to those in sub-Saharan Africa. | Mar 2023 – Aug 2025 1 | Wellcome Trust | Up to GBP £60,000 per group per year[[3]](#footnote-3) |

**Eligibility**

**Criteria for all applicants:**

* Applicants must be based in a university or other academic/research institution.
* Please note the geographic considerations/constraints shown in the table above. By ‘LMIC-based modelling group’, the Consortium expects both that the lead institution is based in a [low- or middle-income country](https://wellcome.org/grant-funding/guidance/low-and-middle-income-countries), and that all the budget will be spent in an LMIC context. Preference will be given to groups in countries experiencing a high burden of the disease in consideration.
* 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 in 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 to make decisions about model selection.

**Additional criteria for cross-cutting applicants:**

* Applications are restricted to LMIC-based modelling groups, with preference given to those in sub-Saharan Africa.
* Prior experience of producing policy-relevant research is desirable. Applicants will be asked to provide evidence and state how this has influenced policy.
* Experience of modelling or working with vaccine-preventable diseases (including arboviruses such as dengue fever) would be beneficial.

**Additional criteria for disease-specific applicants:**

Priority will be given to modelling groups that can provide standardised outputs for the Consortium’s next major update (in 2023-2024). We will also consider applications from groups with models currently in development, which are working towards being able to provide these outputs. This will entail providing age-disaggregated estimates of deaths, DALYs and cases for 117 countries (or an agreed subset of endemic countries), for the period 2000-2100, for multiple vaccine coverage scenarios. As well as central (point) estimates, we require estimates of uncertainty. As model inputs, we provide demographic data and estimates of vaccine coverage. We do not provide disease-specific data. For more details, please see ‘[Output specifications guidance](#Appendix_2_Output_spec_guidance)’.

Given one of the Consortium’s goals to become a diverse international community of vaccine impact modellers, we are also interested in hearing from modellers who are focusing on disease burden and/or vaccine impact for only one country, or a more limited period or age range. Although the Consortium may not be able to offer core-funding in these cases, there may be other funded opportunities to collaborate with the Consortium, for example to produce or advise on modelling in response to specific policy questions.

**Malaria models**: we hope to take on at least one model that is compatible with the model used by the Global Fund for global strategy targets/reporting, to further collaboration between Gavi and the Global Fund. This criteria is desirable but not essential, and we encourage applicants who do not meet it to apply.

**COVID models:** we hope to take onat least one model that aligns with other models or methods used by existing major global initiatives collaborating with Gavi. This criteria is desirable but not essential, and we encourage applicants who do not meet it to apply.

**Scope of work for successful applicants**

**Disease-specific groups:** If selected to join the Consortium, applicants will then be expected to carry out the scope of work detailed under ‘[Sample scope of work for modelling groups](#Sample_scope_of_work)’. This is a standard scope of work for all disease-specific VIMC models that receive core-funding.

**Cross-cutting groups:** If selected to join the Consortium, applicants will be expected to carry out a similar scope of work to the one detailed under ‘[Sample scope of work for modelling groups](#Sample_scope_of_work)’. Please note this may be adapted to be more appropriate for the disciplinary area in question.

**Funding**

Successful models will be invited to join the Consortium as full members and will receive core-funding as set out in the table above. Funding will be arranged via a subcontract between Imperial College London and the modelling group’s institution, with either Gavi or Wellcome Trust as the prime 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 this Guide for Applicants and separate [FAQ](https://www.vaccineimpact.org/resources/VIMC-RfP-FAQs.docx). If you are eligible and wish to apply for the RfP, you should then email us to register your group’s interest. We encourage all groups to register their interest as soon as possible. Please note that Imperial College London will be closed from 5pm on Friday 23 December 2022 and will reopen on 3 January 2023.

**To register your group’s interest:**

**Disease-specific groups** should send one email per group to [vimc@imperial.ac.uk](mailto:vimc@imperial.ac.uk), stating the following:

* Disease area (COVID, hepatitis B, malaria, or meningitis A/MMCV)
* 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.)

**Cross-cutting groups** should send one email per group to [vimc@imperial.ac.uk](mailto:vimc@imperial.ac.uk), stating the following:

* Disciplinary focus (e.g. operational aspects, health economics, impact of climate on disease dynamics, or geospatial aspects)
* 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)
* 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 slides and a recording from a webinar held on 6 December 2022. For disease-specific groups, we will also give you access to Montagu (VIMC’s delivery platform) and advise you how to use this to submit the draft burden estimates that will form part of your application.

**To submit your application:**

After you have registered your interest, you will then need to submit the following by 31 January 2023:

**Disease-specific groups:**

* Application form for disease-specific groups. This should state basic information about the model and the applicants.
* Model documentation that will allow assessment against the Consortium model standards (e.g. a published paper, report, or custom-written documentation).
* Draft burden estimates for one pre-defined country for 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

**Cross-cutting groups:**

* Application form for cross-cutting groups. This should describe the applicants’ modelling and policy experience, including up to 10 relevant publications, and up to 10 links to policy documents that have been influenced by your research.
* Brief CVs for all applicants (max. 2 pages each).
* Institutional / departmental letter of support

**Timeline**

|  |  |
| --- | --- |
|  | |
| 23 November 2022 | RfP published |
| 6 Dec 2022 | VIMC webinar for potential applicants (to be recorded and available afterwards) |
| 9 December 2022 | Application period opens:   * Groups register their interest (see ‘[Next Steps](#Next_Steps)’). * VIMC gives groups access to standalone application forms, and the webinar recording and slides. * VIMC gives disease-specific groups access to Montagu (VIMC’s delivery platform) and advises on how to upload draft burden estimates. |
| 31 January 2023 | RfP closing date for all applicants |
| By 28 February 2023 | Applicants informed of outcomes |
| March 2023 | Subcontracts drafted |

Application period: ~10 weeks

Review period (application deadline to finalised outcome): 4 weeks

**External reviewers:**

External expert reviewers will be sought by the VIMC secretariat and may include members of the new VIMC Stakeholder Group. External reviewers will be selected to ensure a breadth of expertise in relevant fields and 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, considering the external reviewers’ recommendations.

**Conflicts of interest:**

The Consortium will avoid institutional conflicts of interest. Other minor conflicts of interest (i.e. collaborative work) will be noted. Prime funders will have sight of all applications.

*This application form is included for reference only. Please register your group’s interest to receive a standalone Word document version.* [*See ‘Next Steps’ for more details*](#Next_Steps)*.*

1. **Application Form for Disease-Specific Modelling Groups**

|  |  |  |  |
| --- | --- | --- | --- |
| **APPLICANT INFORMATION**  Principal Investigator | | | |
| Name: |  | | |
| Preferred contact email: |  | | |
| Title/position: |  | | |
| Institutional affiliation: |  | | |
| Institutional address: |  | | |
| Co-Investigator | | | |
| Name: |  | | |
| Preferred contact email: |  | | |
| Title/position: |  | | |
| Institutional affiliation: |  | | |
| Institutional address: |  | | |
| Please add further Investigators as appropriate by duplicating the relevant table.  **BUDGET** | | | |
| If invited to join the consortium, we can offer up to $73,000 per year. Any Gavi-eligible overheads (up to 10% for universities and research centres) must be taken from with this total. Do you expect to require this full amount? | | | Y/N |
| If no, please indicate a ballpark figure: | | | USD $ |
| **MODEL SPECIFICATIONS** | | | |
| Disease / Antigen: | | * Malaria * COVID-19 * Meningitis A / multivalent meningococcal conjugate vaccine (MMCV) * Hepatitis B | |
| Does your model produce all of the following burden outcomes?\* | |  | |
| Severe cases: | |  | |
| Deaths: | |  | |
| DALYs: | |  | |
| Other: | |  | |
| Age range modelled: | | *(if not 0-100, please provide a brief justification)* | |
| Does the model include herd effects? | |  | |
| Programming language/ software: | |  | |
| Brief model description (max 100 words): | |  | |
| Can your model use the standardised demography provided? | | Y/N *(if no, please provide a brief justification)* | |
| This RfP requires standardised outputs for one country only. Are you currently able to provide similar outputs for 117 countries (or all endemic countries)? | | * Yes * No, but working towards this goal * No   *If you are working towards this goal, please give brief details of the model development needed, and your timescale.* | |

*\* Please specify if the model produces the relevant outcome, and elaborate if appropriate (e.g. short case definition of severe cases). Please also indicate if any outcomes are gender-specific.*

|  |  |
| --- | --- |
| **POLICY EXPERIENCE** | |
| What is your experience of producing modelling to address vaccine policy decisions? (max 200 words) |  |
| Please describe your links to policymakers, e.g. committees you are on (max 200 words) |  |

|  |
| --- |
| **ALIGNMENT WITH OTHER MODELS** |

***Malaria models only:***

|  |  |
| --- | --- |
| Is your model compatible with the model used by the Global Fund for global strategy targets/reporting? | * Yes * No * Unsure   Please add any comments: |

***COVID models only:***

|  |  |
| --- | --- |
| Does your model align with other models or methods used by existing major global initiatives collaborating with Gavi? | * Yes * No * Unsure   Please add any comments: |

**Checklist:**

In addition to this application form, you will need to submit:

* **Model documentation** that will allow assessment against the Consortium model standards (e.g. a published paper, report, or custom-written documentation).
* **Draft burden estimates** for one pre-defined country for your specified disease area. (Standardised template to be provided by VIMC.)
* **Brief CVs** for all applicants (max 2 pages per person)
* **A letter of support** from your department or institution

Please email your application documents (including this form) to [vimc@imperial.ac.uk](mailto:vimc@imperial.ac.uk) by 31 January 2023.

1. **Application Form for Cross-Cutting Groups**

*This application form is included for reference only. Please register your group’s interest to receive a standalone Word document version.* [*See ‘Next Steps’ for more details*](#Next_Steps)*.*

|  |  |  |  |
| --- | --- | --- | --- |
| **APPLICANT INFORMATION**  **Principal Investigator** | | | |
| Name: |  | | |
| Preferred contact email: |  | | |
| Title/position: |  | | |
| Institutional affiliation: |  | | |
| Institution address: |  | | |
| **Co-Investigator** | | | |
| Name: |  | | |
| Preferred contact email: |  | | |
| Title/position: |  | | |
| Institutional affiliation: |  | | |
| Institution address: |  | | |
| Please add further Investigators as appropriate by duplicating the relevant table.  **BUDGET** | | | |
| If invited to join the consortium, we can offer up to GBP £60,000 per year. (Any [Wellcome-eligible overheads](https://wellcome.org/grant-funding/guidance/overheads-policy) (up to a maximum of 20% of direct research costs) must be taken from within this total.) Do you expect to require this full amount? | | | **Y/N** |
| If no, please indicate a ballpark figure: | | | **GBP £** |
| Please confirm that the budget will be spent in LMIC settings only: | | | **Y/N** |
| **ABOUT YOUR MODELLING EXPERTISE** | | | |
| Disciplinary focus: | | * Operational aspects * Health economics * Impact of climate on disease dynamics * Geospatial aspects * Other (please state) | |
| Please list up to 10 relevant publications, including links: | |  | |
| Description of research focus and relevance to VIMC (max 300 words): | |  | |
| How will you add value to VIMC and help it achieve its goals? (max 200 words) | |  | |
| What is your experience of modelling or working with vaccine-preventable diseases? | |  | |
| **ABOUT YOUR POLICY EXPERIENCE** | | | |
| What is your experience of producing evidence to address vaccine policy decisions? (max 200 words) | |  | |
| Please describe your links to policymakers, e.g. committees you are on (max 200 words) | |  | |
| Please list up to 10 policy documents that have been influenced by your research, including links where possible: | |  | |

**Checklist:**

In addition to this application form, you will need to submit:

* **Brief CVs** for all applicants (max 2 pages per person)
* **A letter of support** from your department or institution

Please email your application documents (including this form) to [vimc@imperial.ac.uk](mailto:vimc@imperial.ac.uk) by 31 January 2023.

1. **Vaccine Impact Modelling Consortium (VIMC) 2.0 - Project Summary**

**Background**

The Vaccine Impact Modelling Consortium (VIMC) was established in 2016, to deliver a more sustainable, efficient, and transparent approach to generating estimates of disease burden and vaccine impact, for vaccines supported by Gavi, the Vaccine Alliance. In its first phase (VIMC 1.0, 2016-2022) VIMC successfully created a rigorous methodology and platform for combining and analysing modelled estimates across 12 vaccine antigens and 112 countries. These impact estimates were core to Gavi’s 2021-2025 replenishment, which raised USD $8.8billion for immunisation in low and low-middle income countries.

VIMC has now secured renewed funding of £12.8 million (USD $15.4 million) for a new project phase (2022-2027). Funding comes from the Bill & Melinda Gates Foundation; Gavi, the Vaccine Alliance; and the Wellcome Trust.

This new phase – ‘VIMC 2.0’ – will see a greater focus on modelling to address questions for vaccine policy and practice, working with a more diverse international community of modellers. The Consortium will also establish a new research programme on the impact of climate change on vaccine-preventable diseases.

The VIMC secretariat is based at Imperial College London. Professor Caroline Trotter will take on the role of Consortium Director. Professor Neil Ferguson will act as Deputy Director of the Consortium, leading on the climate-related research programme.

**Vision for VIMC by 2027**

By 2027, VIMC’s 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 will be dynamically engaged in our work
* to translate the Consortium’s 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 (LMICs),
* to provide training in infectious disease modelling and its application to vaccine-preventable diseases for both modellers and policymakers.

In addition, more 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.

**VIMC scope**

**Vertical research programme:**

VIMC 2.0 will produce high-quality vaccine impact estimates across 117 countries and multiple antigens, incorporating new vaccines including malaria and COVID, and responding to policy-relevant questions that require infectious disease modelling. Estimates of the health impact of vaccines will be in terms of cases, deaths and disability-adjusted life years (DALYs) averted. These may include both direct effects in immunized individuals and indirect effects of vaccination in the population.

This programme will be led by core-funded modelling groups, including groups involved in VIMC 1.0, and new disease-specific groups to be recruited via Requests for Proposals (RfPs). In addition, VIMC will collaborate with a wider network of modellers on specific policy questions.

Vaccine policy-relevant research questions often incorporate health economic and operational considerations (e.g. vaccine stockpiles) alongside infectious disease modelling. The VIMC secretariat will coordinate these efforts, working with key technical partners and new core-funded cross-cutting models to be recruited via Requests for Proposals (RfPs).

**Horizontal programmes of work:**

These will involve all modelling groups and be led by the VIMC secretariat, will encompass four major themes:

(1) **stakeholder engagement**, to disseminate VIMC outputs, to identify and refine vaccine impact modelling questions posed by decision-makers and to help ensure that timely answers to these questions are well communicated and understood

(2) **coordination** of the modelling response to address vaccine policy-relevant questions within our community, networks and partners, ensuring questions are prioritized in a systematic process and duplication is avoided

(3) **ecosystem building** to ensure the consortium is more inclusive of modelling groups in low- and middle-income countries (LMICs), that there are appropriately skilled and supported modellers in countries where the burden of vaccine-preventable disease is highest and that policymakers are well-informed about modelling

(4) **shared learning agenda** to optimize use of available vaccines and respond to future challenges in vaccine impact modelling, such as population displacement and climate change.

**Consortium Structure**

The **VIMC secretariat** is based at Imperial College London and will manage day-to-day operations. It will include the VIMC’s central science & policy team, who will coordinate and standardise estimates across diseases.

A **Stakeholder Group** (SG) will advise on VIMC’s strategic direction; set high-level priorities for addressing policy-relevant questions; and assist in the dissemination of outputs and provide feedback as ‘consumers’ of vaccine impact estimates.

**Project working groups** will be set up on an ad-hoc basis, to tackle policy-relevant questions. Core-funded modellers will take a leading role in project working groups; this will be written into their subcontracts. Other project working group members may include disease focal points, secretariat members, SG members with specific expertise, and relevant individuals from the program or policy side.

**Modelling groups** will be subcontracted by Imperial. Modelling groups that are core-funded are expected to respond to vaccine policy-related questions (through leading and actively participating in project working groups), and to be on hand to respond to other ad-hoc disease-specific questions, including providing context and explanations of modelled results. (A more detailed scope of work is provided in a separate document.) VIMC’s current core-funded modelling groups are listed below.

As part of its goal to work with a more diverse international community of modellers, VIMC will collaborate with a broad range of modelling groups, not limited to core-funded groups. This may include funded opportunities to produce or advise on modelling in response to specific policy questions, for a specific country or region.

**List of core-funded VIMC modelling groups (as of September 2022):**

|  |  |  |
| --- | --- | --- |
| **Disease area** | **Organisation of modelling group** | **Lead modeller** |
| Cholera | International Vaccine Institute (IVI) | Jong-Hoon Kim |
| Johns Hopkins University | Elizabeth Lee |
| COVID | **To be recruited** | TBC |
| **To be recruited** | TBC |
| Hepatitis B | Imperial College London | Timothy Hallett |
| **To be recruited** | TBC |
| HPV | Harvard University | Allison Portnoy |
| London School of Hygiene & Tropical Medicine | Mark Jit |
| Malaria | **To be recruited** | TBC |
| **To be recruited (LMIC-based)** | TBC |
| Measles | London School of Hygiene & Tropical Medicine | Mark Jit |
| Pennsylvania State University | Matthew Ferrari |
| Meningitis A / MMCV | University of Cambridge | Caroline Trotter |
| **To be recruited (LMIC-based)** | **TBC** |
| Rubella | UK Health Security Agency | Emilia Vynnycky |
| University of Georgia | Amy Winter |
| Typhoid | International Vaccine Institute (IVI) | Jong-Hoon Kim |
| Yale University | Virginia Pitzer |
| Yellow fever | Imperial College London | Katy Gaythorpe |
| University of Notre Dame | Alex Perkins |
| Cross-cutting modelling groups | **To be recruited (LMIC-based)** | **TBC** |
| **To be recruited (LMIC-based)** | **TBC** |

**Structure of VIMC 2.0:**

**A picture containing text

Description automatically generated**

Diagram

Description automatically generated**Overlap between Project Working Groups and other VIMC stakeholders.** A project working group will be convened to address a specific research question. For simplicity, only two project working groups are shown for illustration.

**Answering vaccine-policy questions with modelling**

**SG discusses questions to be answered**

Prioritization based on suitability for VIMC’s remit, capability within the consortium and the broader modelling landscape, availability of data to inform models and the potential for impact (in terms of providing evidence for a policy change/ to inform programmatic discussions and the impact on lives saved / costs saved). Time sensitive questions may be rapidly evaluated by email.

)

**Mechanism for proposing questions established**

At regular intervals (e.g. before each SG) the VIMC secretariat will solicit research questions from modelling groups, the SG and the broader vaccine impact modelling consumer community. These will be filtered by the central science & policy team to ensure that they fall within VIMC’s scope.

**Project Working Group (PWG) set up to address each question**

SG to advise on PWG members from SG and wider stakeholders; VIMC secretariat to advise on / invite relevant VIMC modellers and science & policy team members. For priority questions that fall outside of existing capability, RfPs will be issued.

**Project Working Group to refine questions**

(iterative process with wider SG if necessary)

**Project Working Group to carry out modelling**

**and presents results to SG**

(results also shared with other PWGs)

**SG advises on wider dissemination and any new questions to be tackled**

**Project Working Group refines its work**

(iterative process with wider SG if necessary)

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**Wider dissemination of results**

E.g. briefings to policymakers, blog posts, research publications

**Response to wider dissemination assessed by SG**

(May lead to further questions to be answered)

1. **Sample scope of work for modelling groups**

***Disease-specific groups:*** *If selected to join the Consortium, applicants will then be expected to carry out the scope of work detailed below. This is a standard scope of work for all disease-specific VIMC models that receive core-funding.*

***Cross-cutting groups:*** *If selected to join the Consortium, applicants will be expected to carry out a similar scope of work to the one detailed below. Please note this may be adapted to be more appropriate for the disciplinary area in question. For example, deliverable 11 will not be included for cross-cutting groups.*

**Deliverables for each core-funded modelling group**

The following broad deliverables are expected of each core-funded VIMC modelling group in Years 1-3, in relation to the disease area(s) noted on page 1 of this scope of work. 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. This represents a significant shift from VIMC 1.0.

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

1. 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::
   1. Refine policy-relevant questions (in an iterative process, if necessary)
   2. Carry out modelling and lead on presenting results to VIMC’s Stakeholder Group (SG)
   3. Refine the modelling work (in an iterative process, if necessary)
   4. Disseminate results widely
2. 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:
   1. Contribute to refining policy-relevant questions (in an iterative process, if necessary)
   2. Carry out modelling
   3. Refining the modelling work (in an iterative process, if necessary)
   4. Contribute to disseminating results widely
3. 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.
4. Carry out model comparisons and comparisons of results with other modellers.
5. Work collaboratively with the VIMC science & policy team on our shared learning agenda.
6. Apply to VIMC to host a visiting fellow for one month, including participation in a shorter reciprocal visit.
7. Present findings at VIMC webinars and consortium-wide meetings, with an expectation of at least one presentation every year per disease area.
8. Contribute to VIMC training activities and ecosystem building, including collaborating with groups working with the Consortium for the first time.
9. Engage with the VIMC secretariat on tailored reviews of estimates, including reviewing vaccine coverage scenarios.
10. 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.
11. ***For disease-specific modelling groups only:***

Provide modelled vaccine impact estimates for VIMC’s major update in 2023/2024, 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 117 countries (or an agreed subset where the disease in not endemic in every country) and be stratified by age (0-100) and year (2000-2100).

1. Submit brief progress reports every four months (to be shared with all VIMC members by default) covering all the activities listed above.
2. **Appendix 1 – Model Standards**

**(for disease-specific modelling groups only)**

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[[4]](#footnote-4).

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.

**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** 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.

1. **Appendix 2 – Output specifications guidance**

**(for disease-specific modelling groups only)**

*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 117 countries (or all endemic countries). Please note:*

* *We will also consider applications from groups with models currently in development, which are working towards being able to provide these outputs for 117 countries.*
* *We are also interested in hearing from modellers who are focusing on disease burden and/or vaccine impact for only one country, or a more limited period or age range. Although we may not be able to offer core-funding in these cases, there may 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** |
| disease1 | Disease – will be constant across the file |
| year1 | Calendar year – the default period is 2000 to 2100, but this may differ between models depending on the age range modelled |
| age1 | Age in years of the birth cohort in the calendar year in question.  The default age range is 0-100 years. |
| country1 | 3-letter ISO country code. |
| country\_name1 | Country name spelled out |
| cohort\_size2 | The national population size of the cohort in question, irrespective of disease or vaccination status |
| cases2 | Number of severe cases in a given year and age group. This should be incidence rather than prevalence. |
| deaths2 | Number of deaths in a given year and age group. |
| dalys2 | 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 of a template:

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

Graphical user interface, text, application

Description automatically generated

Output columns for modellers to complete.

Pre-filled columns

**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](mailto: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, ML 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.

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](mailto: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](https://www.vaccineimpact.org/resources/VIMC_RfP2020_DALYs-guidance-12-diseases.pdf) (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](mailto:montagu-help@imperial.ac.uk).

1. All VIMC models will be assessed in a mid-term review in 2025; some models may then be offered extended funding for a further two years (September 2025 – August 2027). [↑](#footnote-ref-1)
2. Any Gavi-eligible overheads (up to 10% for universities and research centres) must be taken from with this total. [↑](#footnote-ref-2)
3. Any [Wellcome-eligible overheads](https://wellcome.org/grant-funding/guidance/overheads-policy) (up to 20% of direct research costs) must be taken from within this total. [↑](#footnote-ref-3)
4. 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. [↑](#footnote-ref-4)