

tracted from routinely collected electronic health records providing a highly accessible route to improve personalised disease prognostics in future models.

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A unified and flexible modelling framework for the analysis of malaria serology data

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Purpose: Serology data are an increasingly important tool in malaria surveillance, especially in low transmission settings where the estimation of parasite-based indicators is often problematic. Existing methods rely on the use of thresholds to identify seropositive individuals and estimate transmission intensity, while making assumptions about the temporal dynamics of malaria transmission that are rarely questioned. Here, we present a novel threshold-free approach for the analysis of malaria serology data which avoids dichotomization of continuous antibody measurements and allows us to model changes in the antibody distribution across age in a more flexible way.

Methods & Materials: We develop a unified mechanistic model which combines the properties of reversible catalytic and antibody acquisition models, and allows for temporally varying boosting and seroconversion rates. Additionally, as an alternative to the unified mechanistic model, we also develop an empirical approach to analysis where modelling of the age-dependency is informed by the data rather than biological assumptions. Using serology data from Western Kenya, we demonstrate both the usefulness and limitations of the novel modelling framework.

Results: The unified mechanistic model 1) eliminates the need to dichotomize continuous antibody measurements into seropositive and seronegative data, 2) removes assumptions about malaria transmission dynamics, 3) adds flexibility in how transmission intensity can be estimated using regression analysis, 4) incorporates age-dependency of the antibody distribution, and 5) allows for joint estimation of malaria transmission intensity from both the reversible catalytic and antibody acquisition models.

Conclusion: Our framework makes the best possible use of the data by avoiding the dichotomization of the continuous antibody measurements, a common practice in the analysis of malaria serology data. More importantly, the unified framework allows us to critically assess and evaluate assumptions on the dynamics of biological indicators of malaria transmission using a principled likelihood-based framework.

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Mathematical modelling of COVID-19: a systematic review and quality assessment in the early epidemic response phase

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Purpose: Epidemiological models have played a key role in informing national response strategies for the current COVID-19 pan-

demic. We aimed to identify how mathematical models were employed in the early phase of the pandemic, at a time of great epidemiological uncertainty, as well as to formally assess the quality of models used. Hence we aimed to identify areas for improvement in model-based decision-making for future unknown disease threats.

Methods & Materials: A systematic review of mathematical modelling studies estimating the epidemiological impact of COVID-19 (risk of importation/spread) and non-pharmaceutical interventions (NPI) was conducted. We systematically searched PubMed, Embase, and preprints in ARxiv, MedRxiv and bioRxiv. We adopted two published quality assessment frameworks to formally assess the extent in which modelling studies met minimal requirements for incorporation of uncertainty and good modelling practice.

Results: In total, 166 articles met our eligibility criteria. The vast majority (129 studies, 78%) of models evaluated the effectiveness NPIs. NPI effectiveness was predominantly modelled in China and Italy, but varied by global region. Asian studies largely evaluated the impact of quarantine and isolation (64 studies), whereas European modelling studies modelled the impact of containment (15 studies), quarantine of travellers, and the isolation of cases. Early models primarily concerned compartmental, deterministic frameworks using SEIR or variants of SEIR compartments (93 studies, 56%) assuming homogenous, symptomatic transmission. Incorporation of parameter uncertainty through model calibration (inference of unknown parameters by fitting models to data) and sensitivity analyses were relatively common (66% and 56% of studies respectively), the former mainly using Chinese data. In contrast, inclusion of structural uncertainty (uncertainty in disease characteristics) was relatively uncommon, as was validation of model output to external data.

Conclusion: This work allows for the identification of existing challenges in the mathematical modelling of emerging diseases, and emphasises minimal criteria for enhancing reliable model estimation and reporting. Limited availability of epidemiological data in the early phase of a new disease treat challenges model calibration to local, and validation to external data, emphasising the critical importance of enforcing standardised protocols for early epi-data collection, and raising awareness among modellers and decision-makers alike in handling uncertainty.

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Real-Time Forecasting of COVID-19 Cases Using Human Mobility in Ontario, Canada

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Purpose: To minimize the impact of the COVID-19 pandemic, local public health authorities are often required to make prompt and informed decisions on anticipated case-loads, resource allocation for surveillance and testing, and public health intervention appropriateness. The objective of this research was to develop a near-term forecasting model to predict COVID-19 cases using real-time human mobility information in Ontario, Canada to assist public health authorities with outbreak response.

Methods & Materials: We utilized a deep neural network model to generate a short-term forecast of new COVID-19 cases by two weeks from May to August 2021. Variable selection was informed by a recent literature review and our ongoing research associating COVID-19 cases with human mobility, demographic and socio-economic factors. A real-time human mobility statistics consisting of a weekly summary of short and long-distance movement,