11 April 2025

Dear Editors,

We would like to submit our paper entitled "The influence of model structure and geographic specificity on predictive accuracy among European COVID-19 forecasts", for your consideration for publication in *PLOS Computational Biology*. Our work addresses epidemiological prediction, and the challenge of disentangling and evaluating influences on forecasting models' accuracy.

Accurately predicting the spread of infectious disease is essential to supporting public health. However, comparing the accuracy of different forecasting models is challenging. Existing evaluations have struggled to isolate the impact of model design choices from the inherent difficulty of predicting complex outbreak dynamics. This study introduces a novel approach to address this by systematically adjusting for common factors affecting epidemiological forecasts, accounting for multi-layered and non-linear effects on predictive difficulty.

We applied this approach to a large dataset of forecasts from 47 different models submitted to the European COVID-19 Forecast Hub. We adjusted for variation across epidemic dynamics, forecast horizon, location, time, and model-specific effects. This allowed us to isolate the impact of model structure and geographic specificity on predictive performance. We found that after adjustment, apparent differences in performance between model structures became minimal, while models that were specific to a single location showed a slight performance advantage over multi-location models. Our work highlights the importance of considering predictive difficulty when evaluating across forecasting models, with a framework for more robust evaluations.

We have made the manuscript available on the medRxiv preprint server (MEDRXIV/2025/325611), while all code and data are available on Github and Zenodo (DOI: 10.5281/zenodo.14903161). We note that to maintain the flow of the paper, we have moved the Methods section before Results to help readers contextualise the data and statistical approach.

We believe our study will be of interest to a broad range of readers with interests in epidemiology and the role of predictive modelling in infectious disease response, and we hope that *PLOS Computational Biology* would be the ideal platform for communicating this work. We appreciate your consideration and look forward to hearing from you.

Yours sincerely,

Katharine Sherratt, on behalf of all the authors