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To
Feilim Mac Gabhann, PhD
Editor-in-Cheif
PLOS Computational Biology

Submission: Flexible Bayesian Nowcasting with leading indicators applied to COVID-19 fatalities in Sweden.

Dear Mr Gabhann,

Hereby we submit our research article entitled *Flexible Bayesian Nowcasting with leading indicators applied to COVID-19 fatalities in Sweden* for publication in PLOS Computational Biology. We confirm that the work is original and has not been published, nor is under consideration, elsewhere.

In our work, we propose a computationally intensive method for real-time analysis of infectious disease surveillance data, a task that is often challenged by reporting delays. The method tackle the problem of reporting delays and extends, and improves, existing nowcasting methods by using leading indicators. The different disease stages (infected, exposed, symptomatic/asymptomatic, hospital, ICU, death) have a time order which can be exploited in order to provide better nowcasts. We apply our method to COVID-19-related fatalities in Sweden during the winter season 2020–2021 and use time series of reported cases and ICU admissions as leading indicators. The method is flexible in terms of its application and thus can be a helpful tool for future pandemic stress situations. We support this by providing open-source software for the real-time analysis of surveillance data.

As part of the COVID-19 pandemic response PLOS Computational Biology has recently published several nowcasting related papers. We therefore think our work is well suited for publication in your journal.

Since Mr Claudio José Struchiner seems to have handled previous manuscripts about nowcasting, we recommend him as Associate Editor, to handle the submission. Alternative suggestions are Mr Don Klinkenberg, Ms Cecil Viboud and Mr Benjamin Althouse.

We look forward to your reply on our work.

Best regards,

Fanny Bergström

(on behalf of all authors; Felix Günther, Michael Höhle, and Tom Britton)