

## **Cover Letter: How Not to Forecast the Flu**

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Dear Editor,

In recent years, flu forecasting competitions have attracted a lot of interest in the scientific community. We were part of two such efforts (organized by CDC and by IARPA) and were declared the winning team in the IARPA forecasting tournament. As a participant in these competitions, our team has come to appreciate several key facets of flu forecasting that pose unique challenges and opportunities for computational, statistical, and modeling researchers. Exiting research often makes simplifying assumptions that are easily violated. For example, most studies on flu forecasting are retrospective/or do not model instabilities associated with flu surveillance – rendering such approaches impractical for a real-time forecasting system.

In this paper, we have gathered together some of our "lessons learned" in the form of a "what not to do" manifesto and presented evidence to support our lessons using surveillance data from several Latin American countries (where surveillance is more unstable) and the United States (where surveillance is relatively more stable). We hope that these insights help communicate the underlying complexity of the problem to a broader audience and will help lower the bar for new flu modelers. Relevant prior work from our group and others' are cited in the article and will be provided in the supplementary information.

We recommend that this manuscript would be of interest to PLOS Computational Biology editorial board member

Dr. Justin Lessler,  
Johns Hopkins Bloomberg School of Public Health,  
Baltimore, MD, USA.

We submitted this manuscript for a presubmission inquiry (PCOMPBIOL-D-16-00924) and submitting the full manuscript with this letter.

Sincerely,

The authors