

Rachael Aber
Exponent

Feilim Mac Gabhann and Jason Papin

PLOS
1875 Mission Street, Suite 103 #188
San Francisco, CA 94103
12/18/2024

Dear Dr. Mac Gabhann and Dr. Papin,

We wish to submit our original research manuscript entitled *Time-series modeling of epidemics in complex populations: detecting changes in incidence dispersion over time* for publication by *PLOS Computational Biology*.

We present a **novel computational method** that facilitates a **key finding about COVID-19 epidemic regimes** and thus constitutes a timely and suitable contribution to *PLOS Computational Biology*. In particular, we develop a metric of case clustering and a statistically validated method to identify changes in putative SARS-CoV-2 superspreading dynamics. The method we develop has application as a **public health leading indicator across infectious diseases**.

Contact-tracing data is often unavailable, so there is an urgent need to use available data to understand epidemics. Our method to quantify case clustering relies on **available population-level data**. Through application of our method to case counts from 144 US counties, we find that **case clustering is high at unexpected points of the COVID-19 pandemic** concurrently across US counties, suggesting predictable transmission heterogeneity and changes in epidemic regime.

Our findings give rise to many follow-on research avenues, such as investigating targeted control measures and surge capacity. Our research approach will catalyze further computational methodology to characterize epidemic dynamics based on available data, an area that is crucial to pandemic preparedness, one of the current priorities in epidemiology.

Thank you for your consideration.

Sincerely,

Rachael Aber
Statistical Scientist
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