

Visualizations of Topologic Entropy on SARS-CoV-2 Genomes in Multiple Regions

Mu Qiao

Yunnan University

Renyang Liu

Yunnan University

Zhenhui Wang

Yunnan University

Xinmei Li

Yunnan University

Jeffrey Zheng (✉ conjugatelogic@yahoo.com)

Yunnan University <https://orcid.org/0000-0003-4225-7077>

Research Article

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Abstract

The outbreak of novel coronavirus (SARS-CoV-2) developed into a global pandemic in a few months. The latest study found that the virus belongs to the beta coronavirus family. SARS-CoV-2 is highly similar to Pangolin CoV and BatCoV RaTG. Advanced scientific studies help traceability and vaccine development. In addition to the subgenus classification analysis of the virus, it is interesting for further exploration to focus attention on mutations and their transmissions in different regions. New mutations may be likely to affect the symptoms of the disease and the effectiveness of vaccination. This paper is focused on the study to make error bars and scatter graphs with the support of the metagenetic analysis system MAS. Using SARS-CoV-2 genomes in different countries and regions as input datasets, topological entropy values provide global characteristic quantities based on C4 module for visualization. Sample results show that the method is powerful and useful for consistently integrating all genomes on one unique genomic index map. Various countries have confirmed their specific positions and projections under topologic entropies. Further explorations are required.

Full Text

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Figures

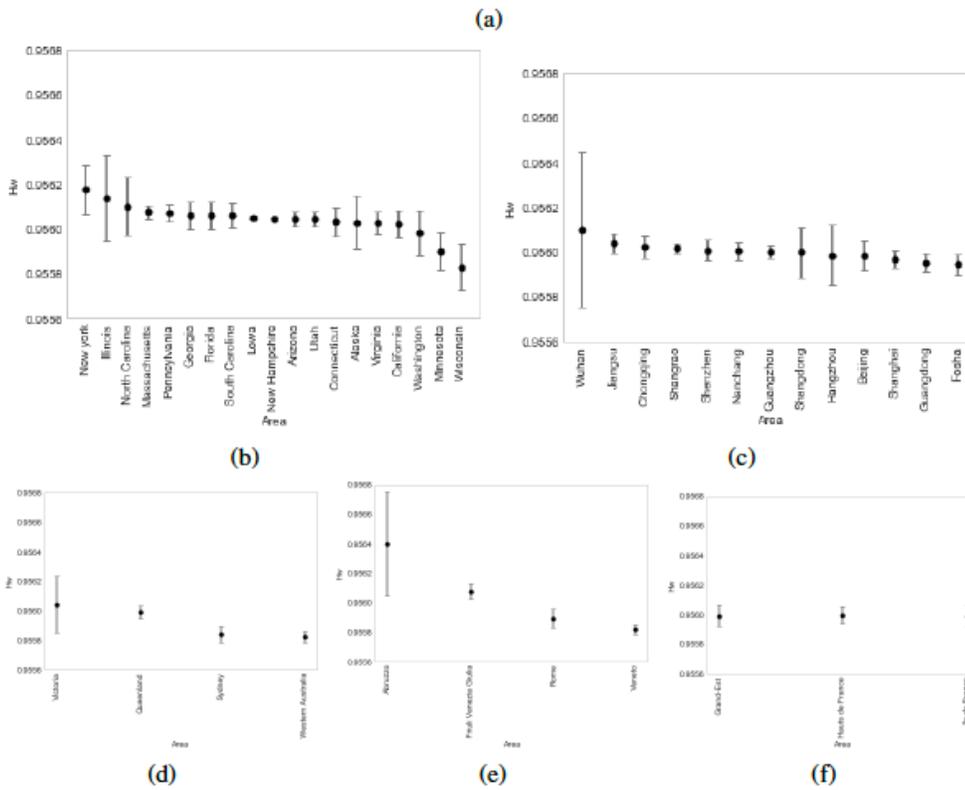
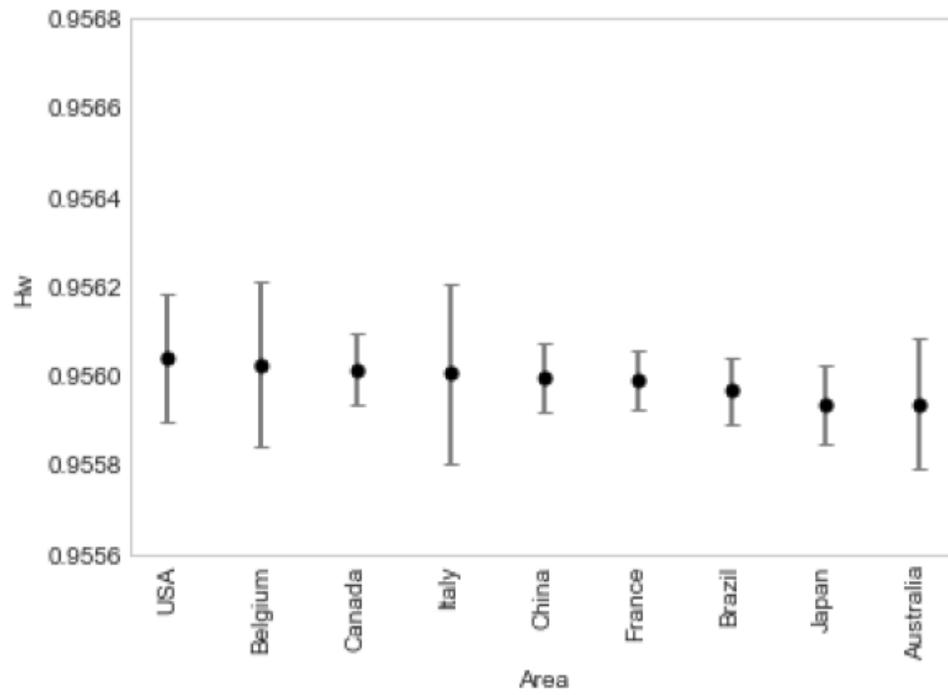


Figure 1

Error bar diagram of topological entropy in six maps (a)-(f); (a) different countries; (b) USA; (c) China; (d) Australia; (e) Italy; (f) France

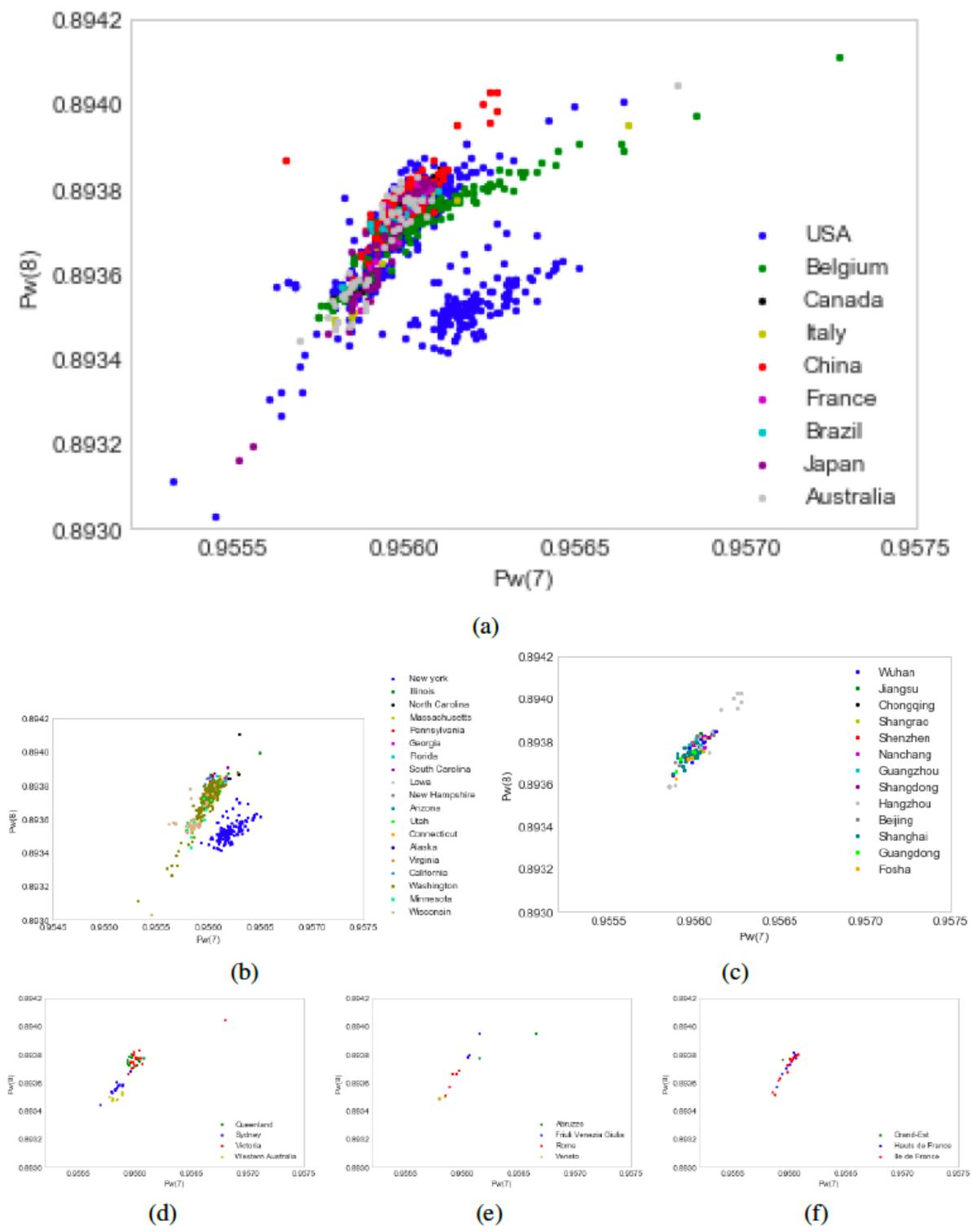


Figure 2

scatter distribution of topological entropy in six maps (a)-(f); (a)different countries; (b) USA; (c) China; (d) Australia;(e)Italy; (f)France