

# Equivalence Relations among Phylogenetic Trees and Genomic Index Maps

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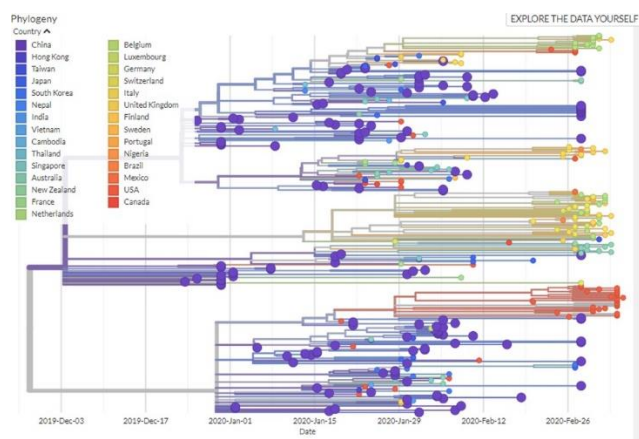
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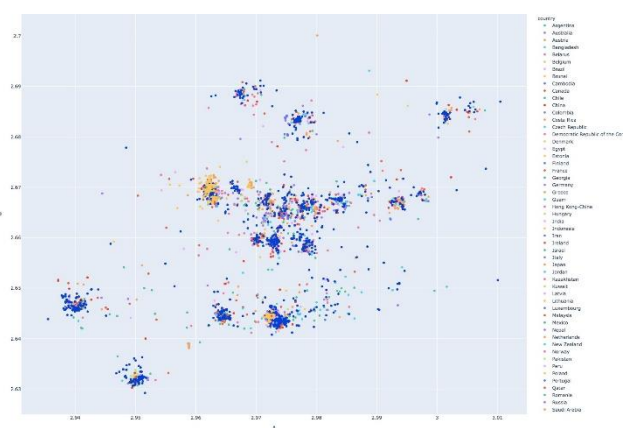
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## Graphical Abstract

Phylogenetic Tree for SARS-CoV-2 worldwide Countries/Regions.



Genomic Index Map for 72



## Abstract

Visual technology of variant construction [1] for complicated sequences plays an assistant role in various applications to be useful in both scientific researches and advanced technologies especially for advanced bioinformatics [2]. Measuring schemes provide hierarchical tools to analyse complicated sequences as characteristic eigenvalues in wider applications.

In this talk, equivalence relations among phylogenetic trees and genomic index maps are discussed. Using diversity measure to a given set of genomes, equivalent clusters and complementary visual effects are provided between genomic index maps and phylogenetic trees. In this hierarchical framework, it is possible to use a unified framework and a visual tool to represent any selected region for clustering genomes on refined effects. A sample projection is illustrated to analyse three UK variation lineages of SARS-CoV-2 genomes in both BLAST phylogenetic trees and genomic index maps in comparisons. This equivalence relation can be wider applied to any genome and other complex sequences.

**Keywords:** Equivalence relation; phylogenetic tree; genomic index; SARS-CoV-2; visual maps.

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## **References**

1. J. Zheng, Variant Construction from Theoretical Foundation to Applications, *Springer Nature*, **2019**.
2. J. Zheng, M.H. Zhu, Viral Evolution of Multiple Coronavirus Genomes on Genomic Index Maps, *Advanced Materials Letters*, **2021**, *12*(2), 600.

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