

Analysis of communities of countries with similar dynamics of the COVID-19 pandemic evolution

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This work addresses the spread of the coronavirus through a non-parametric approach, with the aim of identifying communities of countries based on how similar their evolution of the disease is. The analysis focuses on the number of daily new COVID-19 cases per ten thousand people during a period covering at least 250 days after the confirmation of the tenth case. Dynamic analysis is performed by constructing Minimal Spanning Trees (MST) and identifying groups of similarity in contagions evolution in 95 time windows of a 150-day amplitude that moves one day at a time. The intensity measure considered was the number of times countries belonged to a similar performance group in constructed time windows. Groups' composition is not stable, indicating that the COVID-19 evolution needs to be treated as a dynamic problem in the context of complex systems. Three communities were identified by applying the Louvain algorithm. Identified communities analysis according to each country's socioeconomic characteristics and variables related to the disease sheds light on whether there is any suggested course of action. Even when strong testing and tracing cases policies may be related with a more stable dynamic of the disease, results indicate that communities are conformed by countries with diverse characteristics. The best option to counteract the harmful effects of a pandemic may be having strong health systems in place, with contingent capacity to deal with unforeseen events and available resources capable of a rapid expansion of its capacity.

Palabras clave

COVID-19, hierarchical clustering, minimal spanning trees

Características de la colaboración

Este trabajo se generó a partir de autores y coautores que ya colaboraban antes de la pandemia

Interinstitucionalidad

Si

Interdisciplina

No

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