

Identification of therapeutic targets and drug repurposing against Covid19 based on proteins, diseases, drugs, and symptoms network analysis

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Network medicine aims at using networks to uncover patterns in diseases and use them to understand their biology and propose new drugs.

Press release by [Inserm – Cancer Research Center of Toulouse \(F\)](#)

Manlio De Domenico, Giulia Bertagnolli, Arsham Ghavasieh ([FBK CoMuNeLab](#)) and Giuseppe Jurmann ([FBK DSH Unit](#)) coauthored the paper about [*“Identification of therapeutic targets and drug repurposing against Covid19 based on proteins, diseases, drugs, and symptoms network analysis”*](#) published in [“**Network and systems medicine**”](#)

Since the appearance of Covid19, the disease provoked by the SARS-Cov-2 virus, the research community all around the globe has been on a race to develop treatments or repurpose existing drugs for this new challenge.

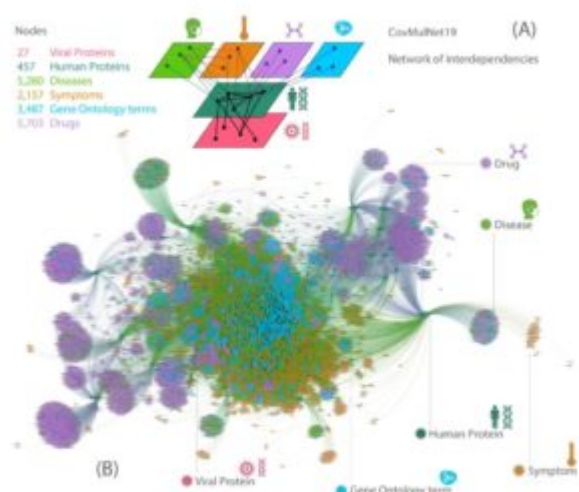
We are now relieved by the existence of effective vaccines, but better understanding of this disease will improve treatment of patients who keep succumbing to it while the logistic challenge of world-wide vaccination is met.

We therefore suggest the use of network medicine to reveal the biological processes affected by this disease by compiling information from multiple public databases collecting information on protein and drug interactions as well as symptoms for other diseases.

In this study we introduce **CovMulNet19**, a comprehensive **COVID-19 network containing all available known interactions involving the SARS-CoV-2 virus proteins, interacting-human proteins, related diseases, symptoms and drugs** that can potentially target them.

We used **extensive network analysis** methods to prioritize a list of diseases that display a high similarity to COVID-19 and a list of drugs that could potentially be beneficial to treat patients. Amongst the diseases that have high similarity with COVID-19, we find some of the conditions that were reported to be risk factors in patients to develop severe forms of COVID-19, including intestinal, hepatic, and neurological diseases as well as other respiratory conditions.

The database CovMulNet19 can be used as a valuable tool for exploring drug repurposing options but also to better understand the symptomatology of COVID-19, especially in the long-term forms. The network approach accounts for the intertwined relationships between molecular interactions, diseases and symptoms of this and all other diseases.



Giuseppe Jurman, FBK: *“The FBK team, formed by **Manlio De Domenico, Giulia Bertagnolli** and **Arsham Ghavasieh (CoMuNeLab)** and **Giuseppe Jurman (DSH)** first collected the publicly available data sources, processed them and made them uniform by building a new unified database of molecules/compounds, target proteins and pharmacological principles. This database was then analyzed with complex network techniques to identify all possible interactions between proteins, symptoms and similar diseases in order to draw up a list of drugs potentially candidates to be used as treatments for Covid-19.”*

Discover the published article:

[Netw Syst Med](#). 2020 Nov 17;3(1):130-141.doi: 10.1089/nsm.2020.0011. eCollection 2020. CovMulNet19, Integrating Proteins, Diseases, Drugs, and Symptoms: A Network Medicine Approach to COVID-19

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