

COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms

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Due to the ongoing COVID19 pandemic there is an urgent need to understand the nature of SARS-CoV-2 virus infection. The development of more efficient diagnosis and treatment depends heavily on a clear understanding of the multistep and multicellular processes implicated in the disease. However, to grasp the entire picture, the patched pieces of information need to be systematically collected, harmonized and combined together in an integrative picture.

The disease maps community initiated the COVID-19 Disease Map project that aims to develop a comprehensive standardized knowledge repository of mechanisms driving the coronavirus SARS-CoV-2 interactions with the human cell. It will enable domain experts, such as clinicians, virologists, and immunologists, to collaborate with data scientists and computational biologists.

Under this initiative, we are developing novel bioinformatic workflow for precise formulation of COVID-19 computational models, and accurate data interpretation that has the potential to suggest drug repositioning. This workflow integrates expert knowledge of molecular mechanisms of SARS-CoV-2 infection and host cell response, databases and data, and computational modeling. This will serve a basis for a computational model for tests and simulation of the response for drugs and predictions of response depending on patient's risk factor and predispositions.

References and useful links

[doi:10.17881/covid19-disease-map](https://doi.org/10.17881/covid19-disease-map)

<https://disease-maps.org>

<https://fairdomhub.org/projects/190>