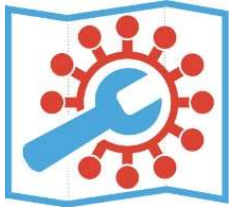


COVID-19 Disease Map, an explorable computational repository of SARS-CoV-2 virus-host interactions



Researchers around the world join forces to construct the molecular picture of the coronavirus SARS-CoV-2 interactions with the human body aiming to combat the cause of the ongoing pandemic. The Computational Systems Biology of Cancer group of Institut Curie/Inserm takes part in this initiative.

Due to the ongoing COVID19 pandemic there is an urgent need to understand the nature of SARS-CoV-2 virus infection, life cycle and mechanisms of human body response and recovery. The development of more efficient diagnosis, proper tests, treatment and vaccines 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. 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.

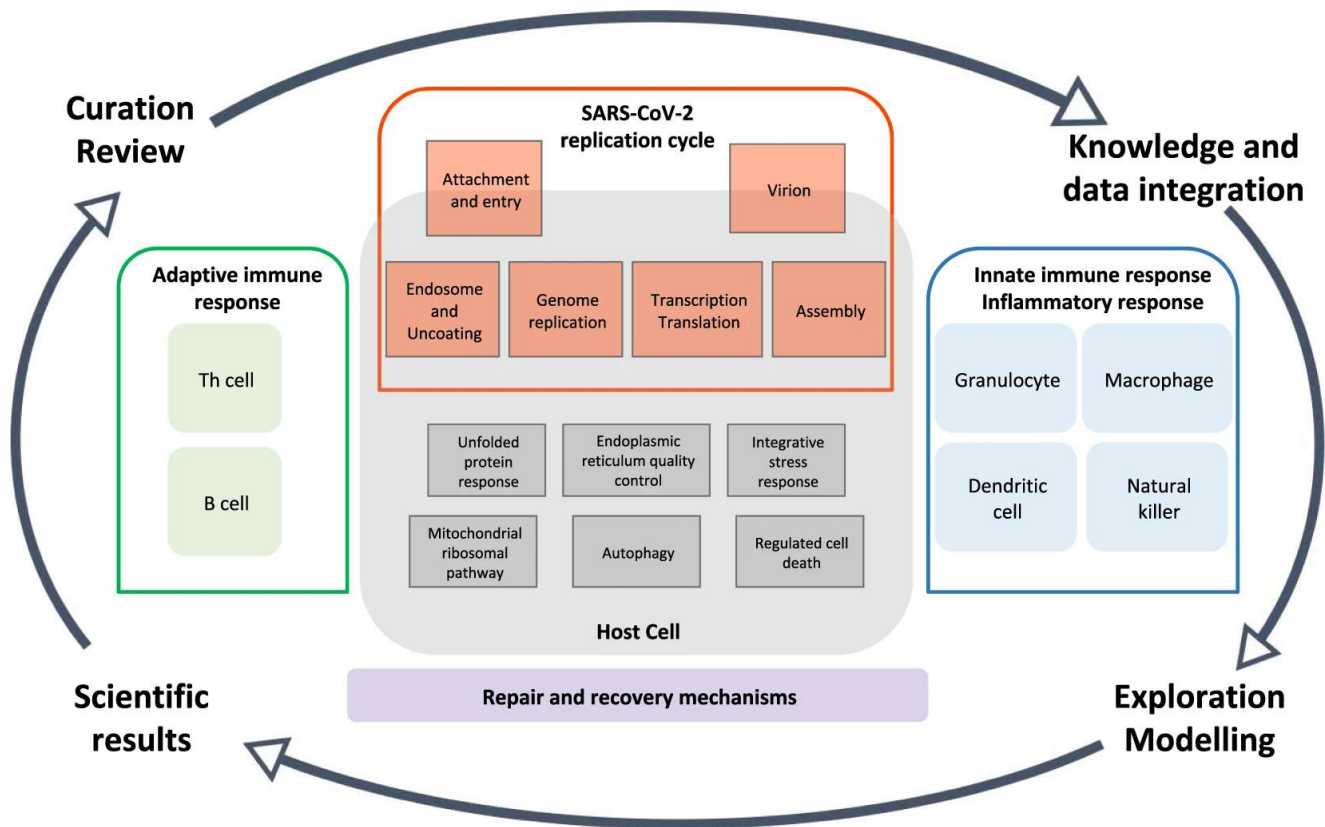
The project relies on the initiative and enthusiasm of the community members and involves multiple contributors from around the globe. In fact, currently above 150 researchers from 24 countries are implicated. The COVID-19 Disease Map community involves computational biologists, data analysts, modellers, practising physicians and clinical researchers that work together remotely.

The members of the Computational Biology Department in Institut Curie, headed by Emmanuel Barillot, were among the researchers that stepped in at the very initial steps. Cristobal Monraz-Gomez and Inna Kuperstein participated in the conceptualisation and setting the logistics of the project and now actively contributing to the realisation of the COVID-19 disease map.

Once constructed, this computational resource the COVID-19 disease map, will provide a basis for modelling drug repositioning, to enable fast and efficient use of already approved treatment for other diseases, part of the project where Laurence Calzone, together with other specialists in the mathematical modelling, will apply their expertise.

Thousands of persons touched by the disease were monitored for various biological markers and clinical factors. Obviously, these stacks of data need to be analysed and interpreted, among other, using the COVID-19 disease map. Andrei Zinovyev from Institut Curie will contribute together with other data scientists to this part of the project.

The initiative is driven by the community, this is a natural response to the ongoing pandemic, the Covid-19 disease maps project has been announced in the *Nature Scientific Data* publication ([link here](#)) with aim to seek for new contributors.



Workflow of the COVID-19 Disease Map project

Reference :

Ostaszewski, M., Mazein, A., Gillespie, M.E. et al. **COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms.** *Sci Data* 7, 136 (2020). <https://doi.org/10.1038/s41597-020-0477-8>

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