Biomax
I N F O R M A T I C S

A human Coronavirus Disease Map to support SARS-CoV-2 vaccine development by combining literature mining with expert curation and semantic data integration.

Summary/Motivation

Development of SARS-CoV-2 vaccines would be supported by better knowledge about its pathobiology to enable rational antigen selection.

Disease maps are one way of representing pathobiological knowledge and make it available for integrative analysis and vaccine design. Within the EU funded PREPARE project Biomax is currently generating a SARS-CoV-2 disease map.

Here we propose to make this disease map available for vaccine design as well as extend and adapt it to specific needs of vaccine research organisations.

Background

Rational antigen selection for vaccine development
Within the collaborative European vaccine development project DRIVE Biomax and partners Artemis and Sabia are pioneering the use of disease maps for rational antigen selection.
A dengue disease map is used to explore and analyse host-pathogen interactions and enable integrative analysis of immunogenicity and vaccine safety profiles in the context of complex virus-host Interactions.

In addition to specific statistical profiles and predictive models an AI-based machine learning approach enables explorative antigen pattern identification from

maps and data visualisations to support an "informed guess" optimisation where data is not specific/extensive enough.
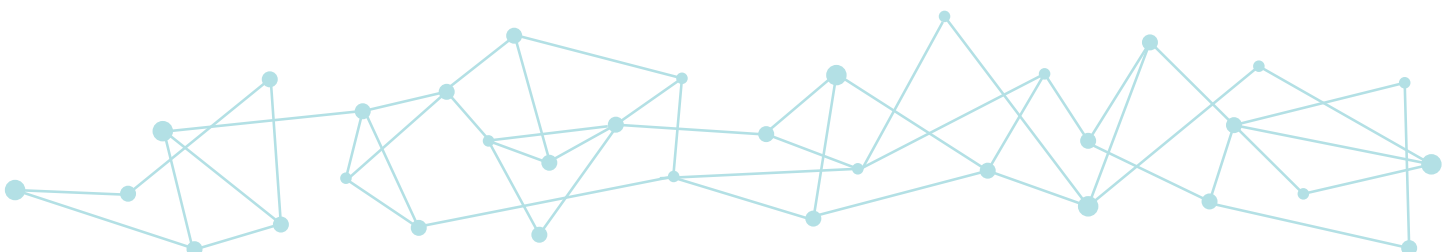
The approach was inspired by the analysis of a Zika disease map, generated within the FP7 PREPARE project, which identified several host-pathogen interactions that lead to hyperactivation of lymphocytes and macrophages. In addition the map provided information about the biological function of the corresponding antigens which enabled to prioritise the antigen profiles.

Disease map generation
Biomax is partner in the EU funded PREPARE project for harmonized large-scale clinical research studies on infectious diseases. The project focus is to rapidly respond to any severe infectious disease outbreak, providing real-time evidence for clinical management of patients and for informing public health responses.

Within PREPARE, Biomax has already generated and provided disease maps for a range of infectious diseases such as Zika or Influenza (submitted: „Informing epidemic (research) responses in a timely fashion by knowledge management - a Zika virus use case").

A disease map is a knowledge network, based on capturing, condensing and structuring of available information about disease facts, from symptoms to co-mor-

bidities, affected or involved organs, tissues and cell types to molecular processes, pathways and single molecules. The disease map thus makes this information available for research management decisions, integrative data analysis or computational modelling.

In the light of the current global SARS-CoV-2 spread the EC FP7 PREPARE project has switched into outbreak mode level 3 to start clinical research and support comparative human Coronavirus (h-CoV) pathobiological research including disease maps.

A h-CoV disease map is produced in a stepwise process starting with automatic literature mining based on available ontologies moving to optimization of ontologies for the h-CoV use case to manual curation and qualification of results.

Depending on the required use, completeness and quality of the disease map, different types of expertise and amounts of resources are required to reach corresponding significant impacts regarding SARS-CoV-2 pathobiology research. While PREPARE is focused on enabling pathobiology research other stakeholders may be interested to support further specific uses such as vaccine development.

Optimising the h-CoV disease map for vaccine development

To optimise the pathobiology focused h-CoV disease map currently being produced within PREPARE, a vaccine specific extension should focus on the immune system and its interaction with the SARS-CoV-2 antigens, addressing questions like: What kind of immune cells are involved, how is the communication between different immune cells influenced, and how is the ba-

lance between different cells regulated? Moreover, this disease map can serve as a reference tool throughout the vaccine development project to analyse data and to functionally relate it to existing biological knowledge and thereby capture the rational decision process during the vaccine development.

The disease map may also further guide customization of an immunogenicity package for evaluation of SARS-CoV-2 vaccine candidates.

Proposal
Based on the previously done work and the PREPARE h-CoV disease map, Biomax suggests to generate further customized h-CoV disease maps to address specific needs of, for example, vaccine development, research prioritization or drug-target identification.

Acknowledgement

References

https://www.biomax.com/project/prepare/

https://www.prepare-europe.eu/

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