Open Research Assistant or Postdoc position to do statistical/computational analysis of coronavirus immune response

We have a position available to understand the serologic response to SARS-CoV-2 in collaboration with the Overbaugh lab. They have developed a phage display library that encodes all seven CoV clades, including genetic circulating variants, to comprehensively examine the response to SARS-CoV-2 infections.

The project will define the epitopes that are targeted by antibodies during SARS-CoV-2 infection, as well as search for cross-reactive epitopes. We will then examine whether specific responses to SARS-CoV-2 or other CoVs modulate SARS-CoV-2 outcomes.

The second component will be to use the Phage-DMS method recently developed by the Overbaugh group, to characterize SARS-CoV-2 epitopes at single amino acid resolution and to define potential pathways of immune escape.

There will also be opportunities to apply similar serological analysis to HIV and Zika. For all of this work we have an excellent collection of samples through a network of collaborators. These projects mesh with other interests in the group, including B cell repertoire analysis, and more recently analysis of deep mutational scanning data.

We have a range of collaborators available for discussion with many different backgrounds, including Jesse Bloom, Phil Bradley, and Noah Simon.

We are not expecting any specialized biological knowledge, however we would like to find someone with strong computational and statistical/machine learning skills who is motivated to advance biology in this area.

We especially encourage applications from groups underrepresented in science.

Please get in touch directly as soon as possible if you are interested– we’re interviewing!

Here's a link to the post: https://matsen.fredhutch.org/general/2020/06/01/ncov-postdoc.html