**UNIVERSITY OF CAPE TOWN COMPUTATIONAL BIOLOGY DIVISION**

**Bioinformatics Support Request**

Please provide us with more information on your request for support. Complete the form as comprehensively as possible, and please indicate where there is still uncertainty.

**Please note, the earlier we are involved the better – for example, it would be better for us to be involved during the study design and even grant application stage**.

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| **CONTACT DETAILS** | |
| Date of request | **10 May 2021** |
| Name | **Michelle Mullins** |
| Email address | [**MLLMIC052@myuct.ac.za**](mailto:MLLMIC052@myuct.ac.za) |
| Research Group/Department | **Blackburn group** |
| Faculty | **Health Sciences** |
| IF student, name & email of supervisor | **Prof Jonathan Blackburn**  **jonathan.blackburn@uct.ac.za** |

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| **PROJECT DETAILS** |
| 1. What is the scientific question? |
| Longitudinal analysis of antibody titres in a convalescent COVID-19 health care worker cohort. |
| 2. Who are the partners on the project? |
| Prof Blackburn, Prof Burgers, Prof Ntusi |
| 3. What type of collaboration with CBIO is expected? For a project that is done as collaboration or for a fee, we will put the agreement in writing. |
| Assistance with combining two data sets.  TBC? |
| 4. Are there any ethical issues we should be aware of? |
| NA |
| 5. How much work is expected from CBIO and when? |
| All the data has been generated and pre-processed. The data was generated on two different platforms (in-house microarrays and Sengenics microarrays); but the same antigens and controls are present on both platforms. This data needs to be merged, so downstream analysis can be done. |
| 6. What type of data will be generated (e.g. sequencing, genotyping, expression, etc.) and what technology platform will be used? |
| Protein microarray data |
| 7. When do you expect the data? Does it need to be transferred from somewhere else? |
| NA |
| 8. How large will the data be? How long does it need to stored for, and have you made arrangements for storage? |
| Not large. We have data on ~ 45 samples at 4 timepoints, and an additional ~80 samples at one time point. Each sample has ~ 26 data points. |
| 9. What bioinformatics analysis needs to be done? Which tools are required? |
| Not sure of the exact tools that will be required. The idea was to treat the data generated on the different platforms as batches.  There is an overlap between the batches:  Data was generated from 4 different time points and a pre-pandemic control group.  On the one platform we have data for 3 time points (V1, V2, V3), and on the other platform we have data for three time points (V1, V3, V5) as well as pre-pandemic data. |
| 10. If a collaborative model is being used, what papers are envisaged and who will the authors be? |
| The original data was generated during my Honours project, and with this additional data (that will be merged with mine) we plan to publish a paper. The partners (2.) will be authors, along with other members from the Blackburn lab. |
| 11. Can we add a short description and objective of the project to the CBIO website? |
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**PLEASE FORWARD THE COMPLETED FORM TO:**

[Nicola.mulder@uct.ac.za](mailto:Nicola.mulder@uct.ac.za)