**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 | **28 January 2019** |
| Name | **Dr. Clinton Moodley** |
| Email address | **clintonmoodley@yahoo.com** |
| Research Group/Department | **Medical Microbiology** |
| Faculty | **Health Sciences** |
| IF student, name & email of supervisor | **Prof. M Nicol (Study PI)** |

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| **PROJECT DETAILS** |
| 1. What is the scientific question? |
| The characterization of pathogenic bacteria as potential outbreak or novel bacterial strains causing infection. |
| 2. Who are the partners on the project? |
| All collaborators are UCT and NHLS joint staff, or affiliated staff:Prof. Mark NicolDr. Clinton MoodleyDr. Chad CentnerDr. C. OppermanDr. M ZampoliDr. S Chaya |
| 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. |
| This will be conducted in a collaborative way. The bioinformatic data analysis will be included in relevant publications, with the contributing bioinformatician included as co-author on the manuscript. |
| 4. Are there any ethical issues we should be aware of? |
| Ethics approval has been obtained from the UCT HREC. |
| 5. How much work is expected from CBIO and when? |
| The data analysis will involve WGS de novo and remapping to reference sequences. The genomes generated will need to be annotated and phylogenetic trees constructed. |
| 6. What type of data will be generated (e.g. sequencing, genotyping, expression, etc.) and what technology platform will be used? |
| Prokaryotic nucleic acid will be sequenced on the Illumina platform using a shotgun approach, to generate reads of bacterial genomes present. |
| 7. When do you expect the data? Does it need to be transferred from somewhere else? |
| Some preliminary data has already been generated, and can be used to initiate the analysis pipeline, as soon as is possible. The primary data will be generated over the next 2 months, with additional sequencing later this year. |
| 8. How large will the data be? How long does it need to stored for, and have you made arrangements for storage?  |
| The Division of Medical Microbiology has its own server and all data and analyses will be stored there, with limited access. |
| 9. What bioinformatics analysis needs to be done? Which tools are required? |
| Bacterial WGS assembly and mapping from RAW Illumina reads, as well as exploratory metagenomic taxonomic data analysis, with phylogenetic tree assembly. |
| 10. If a collaborative model is being used, what papers are envisaged and who will the authors be? |
| There are 2 smaller publications envisaged for the preliminary data analysis, as well as 2 larger publications on the outbreak and metagenomic analyses. The author list will include all contributors to the manuscript, with the bioinformatician included as co-author on all relevant publications. |
| 11. Can we add a short description and objective of the project to the CBIO website? |
| Bacterial outbreak and Metagenomic Investigation of Pathogenic Bacteria. |

**PLEASE FORWARD THE COMPLETED FORM TO:**

Nicola.mulder@uct.ac.za