

Setting up a portable metagenome assembly pipeline for CBIO - Support #60

Setup Nextflow metagenomics pipeline YAMP on hex

07/24/2018 12:13 PM - Katie Lennard

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| <b>Status:</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | New    | <b>Start date:</b>     | 07/24/2018 |
| <b>Priority:</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Normal | <b>Due date:</b>       |            |
| <b>Assignee:</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |        | <b>% Done:</b>         | 0%         |
| <b>Category:</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |        | <b>Estimated time:</b> | 0.00 hour  |
| <b>Target version:</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |        | <b>Spent time:</b>     | 0.00 hour  |
| <b>Description</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |        |                        |            |
| Setup yet another metagenomics pipeline (YAMP), see <a href="https://www.biorxiv.org/content/biorxiv/early/2017/11/21/223016.full.pdf">https://www.biorxiv.org/content/biorxiv/early/2017/11/21/223016.full.pdf</a> , on hex for testing. This pipeline should suffice for most of the project requests we get. YAMP performs QC (BBmap suite, FastQC), taxonomic binning and profiling (MetaPhlAn2) - this is reference-based, not de novo; functional profiling (HUMAN2); and diversity estimates (QIIME) |        |                        |            |
| Pipeline repo: <a href="https://github.com/kviljoen/YAMP/blob/dev/conf/uct_hex.conf">https://github.com/kviljoen/YAMP/blob/dev/conf/uct_hex.conf</a>                                                                                                                                                                                                                                                                                                                                                        |        |                        |            |