Setting up a portable RNA-Seq pipeline for CBIO - Support #24

Setting up the NGI-RNAseq pipeline on UCT Hex

03/14/2018 10:13 PM - Gerrit Botha

Status:	New	**Start date:**	04/09/2018
Priority:	Normal	**Due date:**	
Assignee:	Katie Lennard	**% Done:**	0%
Category:		**Estimated time:**	0.00 hour
Target version:		**Spent time:**	12.60 hours

Description

Katie received a support request to analyse human RNA-Seq data. We do not have a pipeline ready for just pushing RNA-Seq data through.

We have also seen in the CBIO 2017 bioinformatics needs survey that there are many users interested in RNA-Seq analysis.

To get ready for the Katie's analysis and also doing planning ahead we need to start setting up a portable/robust RNA-Seq pipeline that initially does analysis on human data only. We can look into existing pipelines or develop our own.

Existing pipelines that might get things done

- https://github.com/SciLifeLab/NGI-RNAseq/ is developed by a bioinformatician that is very active in the Nextflow community. Jon had a look at the pipeline and said it is worth getting it up and running.
- Jenny Drnevich mentioned that they have a Nextflow pipeline based on the new version of the H3ABioNet RNA-Seq SOP. Might also be worth looking into that. Gerrit can follow up on this.

For now Katie is setting up the NGI-RNAseq pipeline on UCT Hex and will check if we can just use the pipeline as is.

Subtasks:

Support # 25: Configure NGI-RNAseq pipeline to run on hex	**In Progress**
Support # 30: Update Nextflow to version 0.27.6	**In Progress**

History

#1 - 03/15/2018 04:39 PM - Gerrit Botha

Katie I've talked to Chris Fields he is working with Jenny. He will check if he can make their pipeline available. He says it is basically a template from the one that you are currently working but expanded to include Salmon counts and more QC. If he shares the code we can see what he means.