NextFlow Pipelines on aurora-ls2

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March 2022

1 Introduction

Nextflow pipelines are installed in `/projects/fs1/common/nextflow/`. To execute these nextflow pipelines wherever you are you need to add this folder to your `$PATH`. The easiest way to add this line to your `~/.bashrc` is:

```
echo "export PATH=/projects/fs1/common/nextflow:$PATH" >> ~/.bashrc
```

This are the pipelines currently available:

1. nf-core-atacseq-1.2.1

2. nf-core-chipseq-1.2.2

3. nf-core-cutandrun-1.1

4. nf-core-hic-1.3.0

5. nf-core-methylseq-1.6.1

6. nf-core-rnafusion-1.2.0

7. nf-core-rnaseq-3.6

8. nf-core-scrnaseq-1.1.0

9. nf-core-smrnaseq-1.1.0

2 Usage

The usage might best be explained using the nextflow test cases. Therefore I have installed all test files on aurora-ls2.lunarc.lu.se. The test cases can be run in two settings: on the front-end (not recommended) and using the blades. All test cases are run using the script `test_all_local.sh` and `test_all_blade.sh`.

The json parameter files called by this script lie in `/projects/fs1/common/nextflow/test.json` and should be a good starting point to create your on ones.

3   Future

Watching a nextflow pipeline in action is great as it spawns small sbatch jobs for every step allowing for rather short blade use cycles. Using these pipelines and implementing our own pipelines in nextflow should enable us to use the blades in a more fair way without single jobs blocking the server for a long period of time. Hence please try to use the pipelines if you can.

I will try to convert some of my pipelines to a nextflow pipeline in the future. So stay tuned.