## Loading and Initializing Conda

1. cd /gpfs/data/bioinformatics/whan
2. module load gcc/6.2.0 java-jdk/1.11.0\_2 singularity/2.6.0
3. module load miniconda3/4.7.10
4. which conda

/apps/software/gcc-6.2.0/miniconda3/4.7.10/bin/conda

1. conda info

active environment : None

user config file : /home/whan/.condarc

populated config files :

conda version : 4.8.0

conda-build version : not installed

python version : 3.7.3.final.0

virtual packages : \_\_glibc=2.12

base environment : /apps/software/gcc-6.2.0/miniconda3/4.7.10 (read only)

channel URLs : https://repo.anaconda.com/pkgs/main/linux-64

https://repo.anaconda.com/pkgs/main/noarch

https://repo.anaconda.com/pkgs/r/linux-64

https://repo.anaconda.com/pkgs/r/noarch

package cache : /apps/software/gcc-6.2.0/miniconda3/4.7.10/pkgs

/home/whan/.conda/pkgs

envs directories : /home/whan/.conda/envs

/apps/software/gcc-6.2.0/miniconda3/4.7.10/envs

platform : linux-64

user-agent : conda/4.8.0 requests/2.22.0 CPython/3.7.3 Linux/2.6.32-573.12.1.el6.x86\_64 rhel/6.7 glibc/2.12

UID:GID : 788676860:788676860

netrc file : /home/whan/.netrc

offline mode : False

1. conda info --envs

(nextflow-21.04.0 envs can be seen)

Text

Description automatically generated

1. conda init bash

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/condabin/conda

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/bin/conda

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/bin/conda-env

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/bin/activate

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/bin/deactivate

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/etc/profile.d/conda.sh

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/etc/conda\_bash.sh

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/etc/bash\_completion.d/conda

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/etc/fish/conf.d/conda.fish

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/shell/condabin/Conda.psm1

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/shell/condabin/conda-hook.ps1

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/lib/python3.7/site-packages/xontrib/conda.xsh

no change /apps/software/gcc-6.2.0/miniconda3/4.7.10/etc/profile.d/conda.csh

modified /home/whan/.bashrc

==> For changes to take effect, close and re-open your current shell. <==

1. nano .condarc

channels:

- bioconda

- conda-forge

- defaults

pkgs\_dirs:

- /gpfs/data/bioinformatics/whan/conda/pkgs

envs\_dirs:

  - /gpfs/data/bioinformatics/whan/conda

env\_prompt: ‘({name})’

**Installing and activating a Conda environment**

1. conda activate nextflow-21.04.0

**Question: the target directory is needed to specify by using –prefix?**

**Or the envs automatically installed into** /gpfs/data/bioinformatics/whan/conda?

1. In nextflow-21.04.0 envs

Load java-jdk/1.11.0\_2

Conda install nextflow-21.04.0

Conda install nf-core

Nf-core download quantms



nextflow run nf-core/quantms -profile test,YOURPROFILE --input project.sdrf.tsv --database protein.fasta --outdir <OUTDIR>