

1 Bioinformatics Essentials

No exercises in this section.

2 Conda

2.1

2.2

2.3

2.4

2.5

2.6 Exercises

1. List all the software packages installed in the base environment

```
conda list -n base
```

2. List all the software packages installed in the samtools-1.17 environment

```
conda list -n samtools-1.17
```

3. Install the ARIBA software package in a new environment

```
conda create -n ariba ariba
```

4. What version of Python was installed with ARIBA? Is this different to the version installed in the base environment?

```
conda list -n ariba | grep -i python conda list -n base | grep -i python
```

5. How many software packages were installed with ARIBA?

```
conda list -n ariba | wc -l
```

6. What channel was ARIBA installed from?

```
conda list -n ariba | grep -i ariba
```

7. In the ARIBA environment, what channel was Python installed from?

```
conda list -n ariba | grep -i python
```

8. How many conda environments have been created?

```
conda info --envs | wc -l
```

3 Nextflow

3.1

3.2

3.3

3.4 Exercises

1. Use the `nf-core help` flag to print the list command usage

```
nf-core list --help
```

2. List all available `nf-core` pipelines

```
nf-core list
```

3. How many `nf-core` pipelines are there?

There are 74 pipelines. Try:

```
nf-core list | grep -c dev
```

4. Sort the pipelines by popularity (stars)

```
nf-core list --sort stars
```

5. Filter pipelines for those that work with RNA

```
nf-core list RNA
```

4 Nextflow Pipelines

No exercises in this section.