Running Busco

A Singularity container is available for version 4.0.6 of Busco. To run it, you need to proceed as follows:

```
$ module load singularityce
$ export SINGULARITY_BINDPATH="/scratch,/users,/work"
```

Some configuration files included in the container must be copied in a writable location. So create a directory in your /scratch, e.g. called "busco_config"

```
$ mkdir /path/to/busco_config
```

Then we copy the stuff out of the container to the newly created directory:

```
$ singularity exec /dcsrsoft/singularity/containers/busco-4.0.6 cp -rv /opt/miniconda/config/.
/path/to/busco_config
```

Now we need to set the AUGUSTUS_CONFIG_PATH environment variable to the newly created and populated busco_config directory:

```
$ export AUGUSTUS_CONFIG_PATH=/path/to/busco_config
```

Finally, you should now be able to run a test dataset from busco (see
https://gitlab.com/ezlab/busco/-/tree/master/test_data/eukaryota):

```
$ curl -O https://gitlab.com/ezlab/busco/-/raw/master/test_data/eukaryota/genome.fna
```

And launch the analysis.
Note: in `$AUGUSTUS_CONFIG_PATH` you have a copy of the default `config.ini` used here, so you can copy, modify it and use it in the `--config` option in the following command:

```
$ singularity exec /dcsrsoft/singularity/containers/busco-4.0.6 busco --config /opt/miniconda/config/config.ini -i
genome.fna -c 8 -m geno -f --out test_eukaryota
```

Then download the reference log:

```
curl -O https://gitlab.com/ezlab/busco/-/raw/master/test_data/eukaryota/expected_log.txt
```

And compare to the one you generated.

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