Bowtie2 runtime environment

Name	APPS/BIO/BOWTIE-2.2.3
Description	Bowtie2 short read mapper
Status	Production
Last update	2014-09-22

Usage example

Here is a simple test case for the runtime environment.

Download the example job here.

The job description file *bowtie2.xrs*l:

```
&
(executable=run_bowtie2.sh)
(jobname=bowtie2)
(stdout=std.out)
(stderr=std.err)
(gmlog=gridlog)
(cputime=60)
(memory=4000)
(runtimeenvironment=APPS/BIO/BOWTIE-2.2.3)
(inputfiles=
  ("chr_18.fa" "chr_18.fa")
  ("reads100k.fq" "reads100k.fq")
)
(outputfiles=
  ("output.sam" "output.sam")
)
```

Corresponding execution script *run_bowtie.sh*

```
#!/bin/sh

echo "Hello Bowtie2"
bowtie2-build -p $BOWTIE_NUM_CPUS chr_18.fa chr_18
bowtie2 -p $BOWTIE_NUM_CPUS chr_18 reads100k.fq > output.sam
exitcode=$?
echo "Bye Bowtie2!"
exit $exitcode
```

Here the actual run consists of two steps: 1. Indexing the reference genome (*bowtie-build*), 2. Running the mapping task (*bowtie)*, The exitcode from bowtie is used as the exit code for the script, this way ARC knows whether the job has succeeded or failed.

Interface definition

The runtime environment sets the following environment variables:

- BOWTIE_DIR points to the BOWTIE base directory
- PATH is set so that the $BOWTIE_DIR is included in the path

- BOWTIEDB is set to a suitable temporary directory for unpacking the datasets
- BOWTIE_NUM_CPUS is set to the number of allocated CPUs for this job. Remember to use bowtie2 -p BOWTIE_NUM_CPUS ... when running.

System administrator guide for installing the RE

Bowtie2 executables

Pre-compiled Bowtie2 executables can be downloaded from the Bowtie home page

```
wget
http://downloads.sourceforge.net/project/bowtie-bio/bowtie2/2.2.3/bowtie2-2.2.3-linux-
x86_64.zip
unzip bowtie2-2.0.5-linux-x86_64.zip
```

Sample runtime environment for SLURM.

Modify the scripts as needed and save the main script in your ARC runtime directory as APPS/BIO/BOWTIE-2.0.0.

Contact information

Contact helpdesk@csc.fi if you have any Bowtie pecific questions.