Exercise II:

Open a terminal:

Copy data package for exercise 1 to your Desktop:

cp /tmp/ex2.tar.gz ~/Desktop

Navigate to Desktop:

cd Desktop

Unpack package:

tar -xzvf ex2.tar.gz

Inspect content of directory:

ls -la .

Inspect content of all files:

More filename.txt

Please note that linux commands can be aggregated and scripted into a text file. The file can be executed as a new command then.

Design and configure a (embarrassingly) parallel compute job. Use the script launcher file template to create a Matlab job (uncomment where appropriate):

1. Open the file launchScripts.sh in a text editor:

gedit lanchScripts.sh

Make adjustment for the appropriate program type (uncomment).

1. Save the file.

Submit the set of compute jobs to the wait queue:

./launchScripts.sh

Monitor the queue and the submitted jobs:

qstat

showq

Upon completion (C status in qstat) examine the result output/error files (replace “<jobid>” with proper number from qstat):

more myscript\_1.e<jobid>

more myscript\_1.o<jobid>

Assess the outcome of your compute jobs. Describe how the batch scheduler was used to run the computation. What happened at each step of the procedure? Describe how a hierarchy of scripts was used to automate parallel job submission and execution.

Submit R and Python jobs.

Think about bioinformatics computations where these parallelization concepts could be useful.