Now you submitted successfully one job, you can do something a litle more difficult.

You will create a blast environment that submits 10 jobs for 10 sequences. You wil write program that does it automatically.
You can develop this in the programmation language you want.

This program will do the following:
- copy the 10 .fasta file in your home directory.
- make a loop (for each file, create .sh .jdl, submit (use -o option to set the jobID in an output file)
- make a loop to check the job status (edg-job-status)
- get the result of each job

--> line commands in order of appearance:
    - cp (for the .fasta files)
    - edg-job-submit --vo apesci -o id ...jdl
    - edg-job-status -i id
    - edg-job-get-output --dir . -i id