



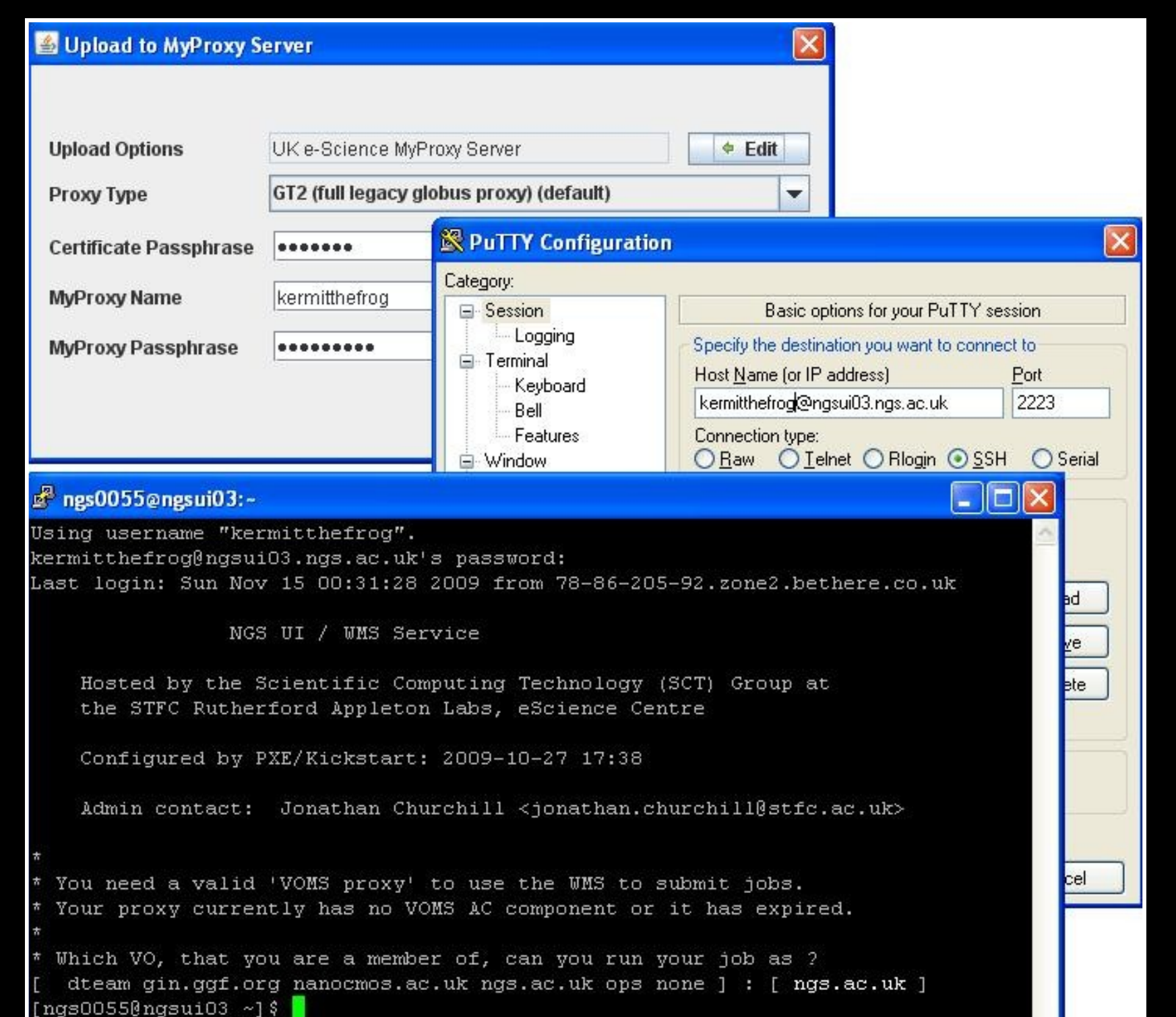
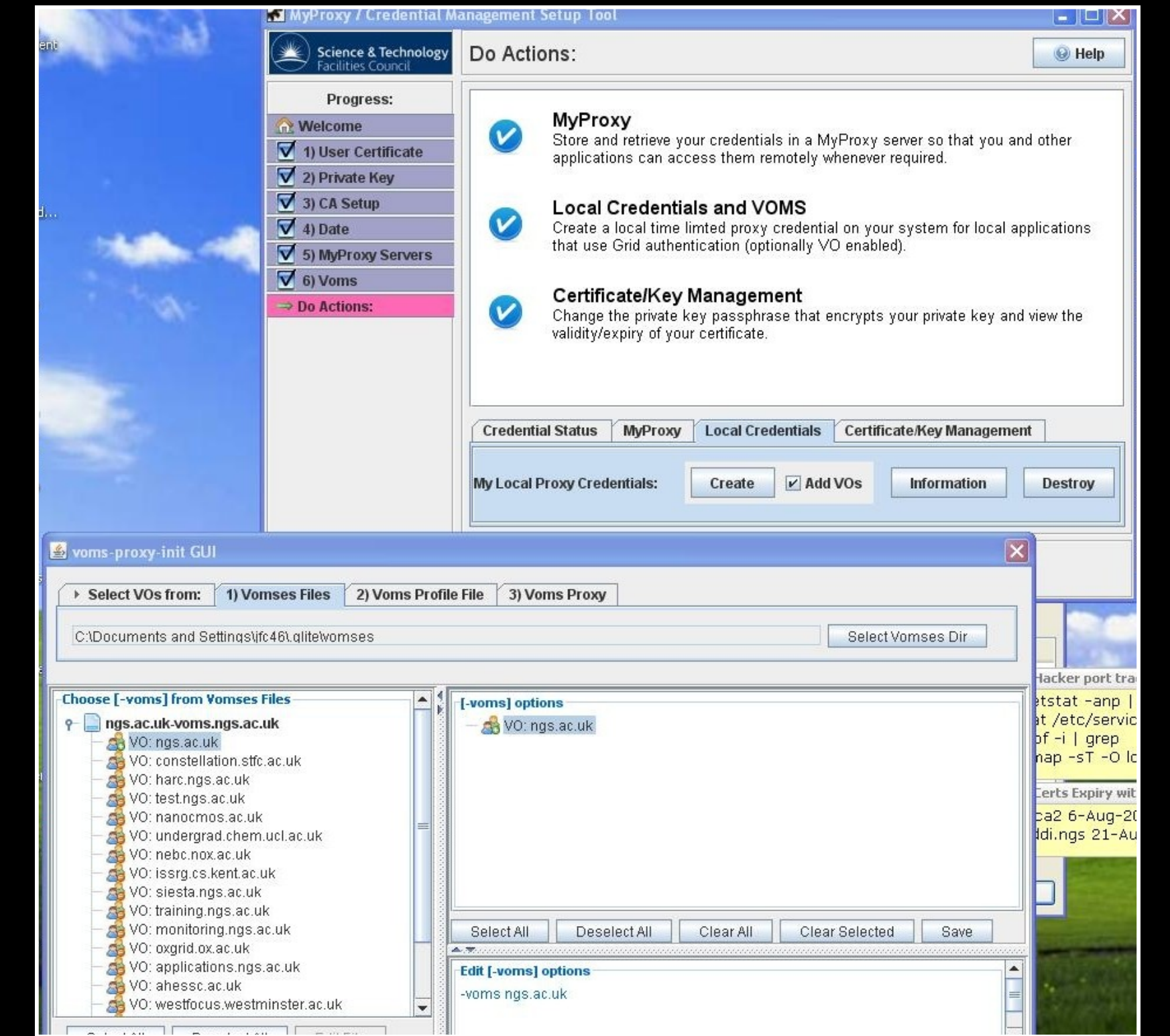
# NGS

# Workload Management System (WMS)

Submit jobs to the NGS easily and automatically retrieve output:

- log onto User Interface (UI) to interact with the WMS using any SSH client
- specify jobs and any files required
- describe any additional requirements such as hardware or software
- the WMS then automatically selects the best resources to run the job.

The UI/WMS has many powerful features allowing large parameter sweeps of 1000's of jobs to be submitted, monitored, analysed and retrieved.



Paul Wilkinson at Exeter University is studying mRNA in insects that are crop pests. By comparing their genetic sequences against known protein sequences they hope to discover enzymes for use in pest control.

```

Input file segment for
WMS 'JDL' file, describing
1000 jobs

Executable = "/usr/ngs/BLAST-NCBI";
Arguments = "blastall -p blastx -d
uniprot -i flydna- PARAM_ .fsa -a
1";
StdOutput = " flydna- PARAM_ .out";
StdError = " flydna- PARAM_ .err";
Parameters = 1000;
ParameterStart = 1;
ParameterStep = 1;
....

Submit all 1000 using:
glite-wms-job-submit -o jobIDs -a
ParamBlast.jdl

Monitoring all 1000 using:
Glite-wms-job-status -i jobIDs

```

- the 55,000 contigs (DNA segments) were previously analysed individually in sequence, taking over a month
- Jonathan Churchill from the NGS helped by splitting these into 1000 jobs of 55 contigs
- they used the WMS to execute the jobs in BLAST across all of the NGS resources in parallel using parametric job submission
- the analysis was complete in under 10 hours



To find out more about the NGS visit our website at [www.ngs.ac.uk](http://www.ngs.ac.uk)



