

What is JAGS?

JAGS is Just Another Gibbs Sampler. It is a program for analysis of Bayesian hierarchical models using Markov Chain Monte Carlo (MCMC) simulation. It is similar to the BUGS program (<http://www.mrc-bsu.cam.ac.uk/software/bugs/>) developed by the UK Medical Research Council.

JAGS was written with three aims in mind:

- To have a cross-platform engine for the BUGS language
- To be extensible, allowing users to write their own functions, distributions and samplers
- To be a platform for experimentation with ideas in Bayesian modelling.

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This guide to running JAGS provides instructions on how to run a standard JAGS test case on the HPC Wales systems.

Step 1 - Log in

The example used in this guide is configured to run on the Swansea Sandy Bridge cluster. Connect to *login.hpcwales.co.uk* with your HPC Wales user credentials using your preferred method (e.g. PuTTY from a Windows machine or ssh from any Linux terminal), then **ssh sw-sb-log-001** to connect to the Swansea system.

The steps below involve typing commands (**in bold font**) in the terminal window.

Step 2 - Load a JAGS module

A number of JAGS binary packages are available.

- List preinstalled JAGS versions:
module avail JAGS
- Load your preferred version (version 3.4.0 is used in this example):
module load JAGS/3.4.0
- Confirm the loaded modules:
module list

Note: Dependent modules, such as the compiler environment, are loaded automatically.

Step 3 - Create a directory

Create a directory to hold any user data files. For this example, a directory called JAGS should be created in your home directory:

```
cd ~  
mkdir JAGS
```

Step 4 - Obtain a test case

A test case for JAGS is provided with the installation at

```
/app/genomics/JAGS/3.4.0/example/
```

Copy the SLURM job script and input files to the JAGS directory:

```
cd ~/JAGS  
cp -r /app/genomics/JAGS/3.4.0/example/run_JAGS.SLURM.q .  
cp -rp /app/genomics/JAGS/3.4.0/example/inputFiles .
```

The test case runs one of the examples available at <http://sourceforge.net/projects/mcmc-jags/files/Examples/3.x/>. Note that the job will be run using the scratch directory `/scratch/$USER/run_JAGS_id-< JobID>`, where `<JobID>` is the ID generated by the queuing system.

Step 5 - Submit a job

JAGS is a serial application (i.e. it runs using just one core). The supplied test should run for less than one minute.

- Submit the job using:

```
sbatch run_JAGS.SLURM.q
```
- Check the job queue using:

```
squeue
```
- When completed, output can be found in a file called `JAGS.o.<JobID>` and errors, if any, can be found in `JAGS.e.<JobID>`. If your job is successful, its output can be found in the output file `JAGS.out.<JobID>`.
- Compare your output that that found in the file

```
/app/genomics/JAGS/3.4.0/example/JAGS.out.592
```

Further info

Further information on JAGS can be found at the website <http://mcmc-jags.sourceforge.net/>.