

BGC on HPC cluster:

What is Bgc?

bgc implements Bayesian estimation of genomic clines to quantify introgression at many loci. Models are available for linked loci, genotype uncertainty and sequence errors. Models for genotype uncertainty and sequence error can be used to estimate genomic cline parameters from next-generation sequence data. The basic models implemented in *bgc* are described in detail in [Gompert & Buerkle 2011](#), [Gompert et al. 2012](#), and [Gompert et al. 2012](#). Use of the software will require good familiarity with the models described in these papers. The software is described and evaluated in [Gompert & Buerkle 2012b](#).^[source]

The official documentation can be found on:

[Official Site](#)

[Documentation](#)

Versions Available:

- Bgc v-1.03

How to load a version of Bgc?

To load a version of Bgc on the HPC, use the following command:

```
module load bio/bgc/1.03
```

Verify by using this command:

```
module list
```

It should load gsl and hdf5 as additional dependencies.

How to use Bgc on the cluster?

For this demonstration, copy the test file from the following directory,

```
cp /share/apps/bgcdist/example/*.txt ~/test
```

This should copy all the required input files to the test directory.

Use the following sbatch script for using Bgc,

```
#!/bin/bash
#SBATCH --job-name=bgctest      # create a short name for your job
#SBATCH --nodes=1              # node count
#SBATCH --task's=1             # total number of task
#SBATCH --cpus-per-task=24     # cpu-cores per task
#SBATCH --mem-per-cpu=1G       # memory per cpu-core (4G is default)
#SBATCH --mail-type=begin      # send email when job begins
#SBATCH --mail-type=end        # send email when job ends
#SBATCH --mail-user=<user_email>

#Load modules
module purge
module load bio/bgc/1.0.3

# Assuming all the files are in script submission directory, move to
# the current directory
cd $SLURM_SUBMIT_DIR

# Run bgc on the test files
bgc -a p0in.txt -b plin.txt -h admixedin.txt -M map.txt -O 0 -x 50000
-n 25000 -p 1 -q 1 -N 1 -m 1 -D 0.5 -t 5 -E \
0.0001 -d 1 -s 1 -I 0 \
-u 0.04.
```

The output should be in the job submission directory along with the log file. Users can see additional information about this test run on the [documentation](#) of this software.

Where to find help?

If you are stuck on some part or need help at any point, please contact OIT at the following address.

<https://ua-app01.ua.edu/researchComputingPortal/public/oitHelp>