

Instructions for running GBS-PLAID

(Note these instructions are mac specific. You will need to consult with someone familiar with windows if you are not using a mac)

First you need to build the program from the source code in online resource 7. Building follows GNU autoconfigure/automake process.

1. Open the terminal and 'cd' into the GBS-PLAID directory. Then run './configure' When that command has completed run 'make', then 'make install' .
If you run make install, you might want to run './configure --prefix=/usr/local' in the first step so that the program installs into /usr/local/bin rather than /usr/bin which is where the OS and managed packages install their binaries. You will likely need to be root or use "sudo make install" to install into /usr/local/bin or /usr/bin.
2. the command to run GBS-PLAID is 'gbs-plaid-impute'. Run the command without any arguments to see a list of options. You must at least specify the VCF input file and the output directory. One parameter that is not listed in the on-screen output is the flag for specifying the parent names. Specify parent names using the flag --parents= parent1, parent2
3. When you have decided on the parameters for your run of GBS-PLAID, you can run the program as you would any command-line based script, e.g.,

```
gbs-plaid-impute -f /Users/me/myproject/mygenotypes.vcf -m 15 -n 60 -w 5 --output-  
directory=/Users/me/myproject/ --parents= IR64, Azucena
```

Final Note: GBS-PLAID was designed for imputation in RIL populations. Care should be taken if using for other population types.