

Pseudacris output from populations with -p 1 -r 0.5, then plink filters in order

1. filter loci with less than 65% sequenced

```
Options in effect:
--ped Pr.all.short-z.ped
--map Pr.all.short-z.map
--geno 0.35  ##results directly below were done with 0.4, but rest of
results are accurate
--out Pr-03.18
--recode
--noweb
Before frequency and genotyping pruning, there are 37597 SNPs
132 founders and 0 non-founders found
Total genotyping rate in remaining individuals is 0.388049
35841 SNPs failed missingness test ( GENO > 0.4 )##at first I did this
but then decided to filter more SNPs on the first step so that I would
retain more of the poorly genotyped Legacy (mainland) populations later
on.
0 SNPs failed frequency test ( MAF < 0 )
After frequency and genotyping pruning, there are 1756 SNPs
```

2. filter individuals that have less than 50% data

```
Options in effect:
--ped Pr-03.18.ped
--map Pr-03.18.map
--mind 0.5
--out Pr-03.18-b
--recode
--noweb
Before frequency and genotyping pruning, there are 1756 SNPs
132 founders and 0 non-founders found
Writing list of removed individuals to [ Pr-03.18-b.irem ]
38 of 132 individuals removed for low genotyping ( MIND > 0.5 )
Total genotyping rate in remaining individuals is 0.804131
0 SNPs failed missingness test ( GENO > 1 )
0 SNPs failed frequency test ( MAF < 0 )
After frequency and genotyping pruning, there are 1756 SNPs
```

3. filter loci genotyped in less than 50% individuals and MAF < 0.02 in remaining individuals

Options in effect:

--ped Pr-03.18-b.ped

--map Pr-03.18-b.map

--geno 0.5

--maf 0.02

--out Pr-03.18-c

--recode

--noweb

Before frequency and genotyping pruning, there are 1756 SNPs

94 founders and 0 non-founders found

Total genotyping rate in remaining individuals is 0.804131

0 SNPs failed missingness test (GENO > 0.5)

68 SNPs failed frequency test (MAF < 0.02)

After frequency and genotyping pruning, there are 1688 SNPs

Final proportion of missing data in matrix:

Total genotyping rate in remaining individuals is 0.817583