#!/bin/bash

# 1) renumf90

echo renum.par | renumf90 | tee renum.log

# 2) regular\_blup

cp renf90.par blup.par

sed '/OPTION /d' -i blup.par

echo OPTION conv\_crit 1e-15 >> blup.par

echo OPTION use\_yams >> blup.par

echo blup.par | blup90iod2 | tee blup.log

cp solutions solutions\_blup

rm solutions

# 3) preparing parameter files for ssGBLUP

#prepblup

cp renf90.par itpre.par

echo OPTION no\_quality\_control >> itpre.par

echo OPTION saveGInverse >> itpre.par

echo OPTION weightedG W >> itpre.par

#preppost

cp renf90.par itpos.par

sed '/OPTION /d' -i itpos.par

echo OPTION SNP\_file ../snp.2k >> itpos.par

echo OPTION chrinfo ../mrkmap.txt >> itpos.par

echo OPTION readGInverse >> itpos.par

echo OPTION weightedG W >> itpos.par

echo OPTION windows\_variance 20 >> itpos.par

# 4) WssGBLUP (or ssGWAS)

awk 'BEGIN { for (i==1;i<45000;i++) print 1}' > W #should have the same number of SNPs from the marker file...in this case 45000

 for j in {1..3} #3 is the number of iterations

 do

 echo itpre.par | blup90iod2 | tee blup.log1\_$j

 cp Gi Gi1\_$j

 cp solutions solutions1\_$j

 echo itpos.par | postGSf90 | tee post.log1\_$j

 cp snp\_sol snp\_sol1\_$j

 cp W W1\_$j

 awk '{ if ($1==1) print $7}' snp\_sol > W

 mkdir plot1\_$j

 cp chrsnp plot1\_$j/chrsnp

 cp chrsnpvar plot1\_$j/chrsnpvar

 done