

## Solutions for exercises day3 ##

#2

```
awk '{print $1,0,0}' genotypes.txt > ped.gen  
awk '{print $1}' genotypes.txt | sort +0 -1 > sgen.temp  
sort +0 -1 phenotypes.txt > sphen.temp  
join -1 +1 -2 +1 sgen.temp sphen.temp > phen.gen
```

#3

```
sed -i 's:phenotypes.txt:phen.gen:g' renum.par  
sed -i 's:pedigree.txt:ped.gen:g' renum.par  
sed -i '24s/5/1/' renum.par  
echo renum.par | renumf90 | tee renum.log
```

#4

```
cp renf90.par pre.par  
echo 'OPTION createG 0  
OPTION createGInverse 0  
OPTION createA22 0  
OPTION createA22Inverse 0  
OPTION createGimA22i 0' >> pre.par  
echo pre.par | preGSf90 | tee pre.log
```

```
grep 'Number of SNPs' pre.log  
grep 'Number of effective SNPs' pre.log
```

#5

```
echo 'OPTION saveCleanSNPs' >> pre.par  
echo pre.par | preGSf90 | tee pre1.log
```

```
awk '{if (NR==1) print length($2)}' genotypes.txt_clean  
wc -l genotypes.txt_clean_XrefID  
#or awk 'END {print NR}' genotypes_new.txt_clean_XrefID
```

#6

```
cp renf90.par gblup.par  
sed -i 's:genotypes.txt:genotypes.txt_clean:g' gblup.par  
echo 'OPTION no_quality_control' >> gblup.par  
echo 'OPTION tunedG 0' >> gblup.par  
echo 'OPTION AlphaBeta 1 0' >> gblup.par  
echo gblup.par | blupf90 | tee gblup.log
```

```
sed -i '28s/1 0/0.99 0.01/' gblup.par  
echo gblup.par | blupf90 | tee gblup.log
```

```
mv solutions solutions1
```

```
#7
```

```
cp renf90.par pre2.par
sed -i 's:genotypes.txt:genotypes.txt_clean:g' pre2.par
echo 'OPTION no_quality_control' >> pre2.par
echo 'OPTION tunedG 0' >> pre2.par
echo 'OPTION AlphaBeta 0.99 0.01' >> pre2.par
echo 'OPTION saveG' >> pre2.par
echo pre2.par | preGSf90 | tee pre2.log
```

```
cp renf90.par gblup2.par
sed -i 's:genotypes.txt:genotypes.txt_clean:g' gblup2.par
echo 'OPTION no_quality_control' >> gblup2.par
echo 'OPTION readG' >> gblup2.par
echo gblup2.par | blupf90 | tee gblup2.log
mv solutions solutions2
```

```
#8
```

```
cp renf90.par pre3.par
sed -i 's:genotypes.txt:genotypes.txt_clean:g' pre3.par
echo 'OPTION no_quality_control' >> pre3.par
echo 'OPTION tunedG 0' >> pre3.par
echo 'OPTION AlphaBeta 0.99 0.01' >> pre3.par
echo 'OPTION saveAscii' >> pre3.par
echo 'OPTION saveGInverse' >> pre3.par
echo pre3.par | preGSf90 | tee pre3.log
```

```
awk '{print $1,NR}' genotypes.txt_clean_XrefID | sort +0 -1 > index.gen
awk '{print $3,$0}' renf90.dat | sort +0 -1 > srenf90.temp
join -1 +1 -2 +1 srenf90.temp index.gen | awk '{print $2,$3,$5,$4}' | sort -n +2 -3 > srenf90.dat
```

```
cp renf90.par gblup3.par
sed -i 's:renf90.dat:srenf90.dat:g' gblup3.par
sed -i '/OPTION SNP_file genotypes.txt/d' gblup3.par
sed -i '20s/add_animal/user_file/' gblup3.par
sed -i '22s/renadd02.ped/Gi/' gblup3.par
echo gblup3.par | blupf90 | tee gblup3.log
mv solutions solutions3
```

```
#matching the ID back with renumbered IDs
```

```
awk '{if (NR>1 && $2==2) print $3,$4}' solutions3 | sort +0 -1 > sol3.temp
awk '{print NR,$1}' genotypes.txt_clean_XrefID | sort +0 -1 > index.line.gen
```

```
join -1 +1 -2 +1 index.line.gen sol3.temp | awk '{print $2,$1,$3}' | sort -n +0 -1 > solutions3.new
```