

# Plink

Na klasteru je dostupan programski paket PLINK. Informacije o samom programu mogu se pronaći na [službenoj stranici](#).

PLINK tool set is available for user. More info on how to run this tool set can be found [on official web pages](#).

## How to use:

Available versions and modules:

Version	Module
1.9	bioinfo/plink/1.9

Example data can be downloaded from <https://zzz.bwh.harvard.edu/plink/tutorial.shtml>

To use more than one thread you must use a mpisingle parallel environment as plink is not able to use more than one node. In this case you need to make sure plink uses the same number of threads as you requested. In this example we use \$NSLOTS variable for this:

### Primjer pokretanja

```
#!/bin/bash/
#$ -N test_plink
#$ -cwd
#$ -pe *mpisingle 5
module load plink/1.9

plink --file hapmap1 --threads $NSLOTS
plink --file hapmap1 --make-bed --out hapmap1 --threads $NSLOTS
plink --file hapmap1 --make-bed --mind 0.05 --out highgeno --threads $NSLOTS
plink --bfile hapmap1 --missing --out miss_stat --threads $NSLOTS
plink --bfile hapmap1 --chr 1 --out res1 --missing --threads $NSLOTS
plink --bfile hapmap1 --chr 2 --out res2 --missing --threads $NSLOTS
plink --bfile hapmap1 --freq --out freq_stat --threads $NSLOTS
plink --bfile hapmap1 --freq --within pop.phe --out freq_stat --threads $NSLOTS
plink --bfile hapmap1 --snp rs1891905 --freq --within pop.phe --out snp1_frq_stat --threads $NSLOTS
plink --bfile hapmap1 --assoc --out as1 --threads $NSLOTS
sort --key=7 -nr as1.assoc | head
plink --bfile hapmap1 --assoc --adjust --out as2 --threads $NSLOTS
plink --bfile hapmap1 --pheno pop.phe --assoc --adjust --out as3 --threads $NSLOTS
plink --bfile hapmap1 --model --snp rs2222162 --out mod1 --threads $NSLOTS
plink --bfile hapmap1 --model --cell 0 --snp rs2222162 --out mod2 --threads $NSLOTS
plink --bfile hapmap1 --cluster --mc 2 --ppc 0.05 --out str1 --threads $NSLOTS
plink --bfile hapmap1 --mh --within str1.cluster2 --adjust --out aac1 --threads $NSLOTS
plink --bfile hapmap1 --cluster --cc --ppc 0.01 --out version2 --threads $NSLOTS
plink --bfile hapmap1 --mh --within version2.cluster2 --adjust --out aac2 --threads $NSLOTS
plink --bfile hapmap1 --cluster --K 2 --out version3 --threads $NSLOTS
plink --bfile hapmap1 --mh --within pop.phe --adjust --out aac3 --threads $NSLOTS
plink --bfile hapmap1 --cluster --matrix --out ibd_view --threads $NSLOTS
```