

Procedure for all tests

- First we took the every provided file (listTEST5.txt, listTEST6.txt, listTEST15.txt, listTEST16.txt) and look for the proxies for every marker at <http://www.broadinstitute.org/mpg/snap/ldsearch.php> with,

```
SNP data set: 1000 Genomes Pilot 1
r2 threshold: 0.7
Population panel: CEU
Distance limit: 100
```

- We substitute every marker for all its proxies and construct every possible pair for each file
- Then, for every database, we choose the pairs which contains both makers in database. Aparently interSNP do this but it is very slow. We make this with a simple perl script. (download below)
- Now we run intersnp with the obtained pairs and each database. Here we run all those test using a template for the selection file and writing the tags as needed.

```
BFILE <Database> // put path and name of plink bfile there
TWO_MARKER 1
PRINTTOP 50000
TEST <Test>
COMBIFILE <Pairs> // if file is in working dir, else put path
COMBILIST 1
OUTPUTNAME <Output>
END
```

- Results and other files could be downloaded from <https://docs.google.com/folder/d/0B8-42LjtMhdZSTVrZEZCU3d6NUE/edit>

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