

Testing LD structure

a first approach

First I'm going to take a chunk of the 1000 genome database. So I do,

```
plink --noweb --bfile /nas/data/GNlib/1000Genome/ALL/1000genome_all_merged -  
-chr 6 --from-kb 20000 --to-kb 22000 --make-bed --out 1kg_chr6_20_22 --  
allow-no-sex
```

to get the chromosome 6 from 20 to 22 megabases.

From this small piece I want to calculate the LD matrix. Let me see, $2\text{MB}^2 = 4\text{e}12$ bases. So I will end with a theoretical matrix of $4\text{e}12$ elements. Must be a little less cause no all the positions are filled.

So my next step will be

```
plink --bfile 1kg_chr6_20_22 --r2 --matrix --allow-no-sex --out  
1kg_chr6_20_22_ldmap
```

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