Notes

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# Infer mom's genotype by JRI

We have obs. mom and obs. (selfed) kids. We want to know , and , where is observed data. This consists of observed genotypes () of both mom and kids. So: This function is to impute mom's genotype from a progeny array of k kids at a single locus. inferred\_mom=1 -> 00, 2->01, 3->11

# Imputing Founder Genotypes

This function is to impute mom's genotype by finding the maximum likelihood of from a progeny array of k kids at a single locus. - Where denotes observed data. It consists of observed genotypes () of both mom and kids.  
- is the Hardy-Weinberg equilibrium estimated from the population.  
- is the error matrix estimated from the data, i.e. homozygote error = 0.02 and heterozygote error =0.6.  
- is the error matrix times Mendelian segregation rate.

# Phasing Founder Genotypes

* Where denotes observed data.
* is the haplotypes of a given window size .
* is the probability estimated from the error matrix times Mendelian segregation rate; denotes the heterozygote sites within the haplotype.
* We assume all the possible haplotypes of a given window size are equally likely.