imputeR Documentation

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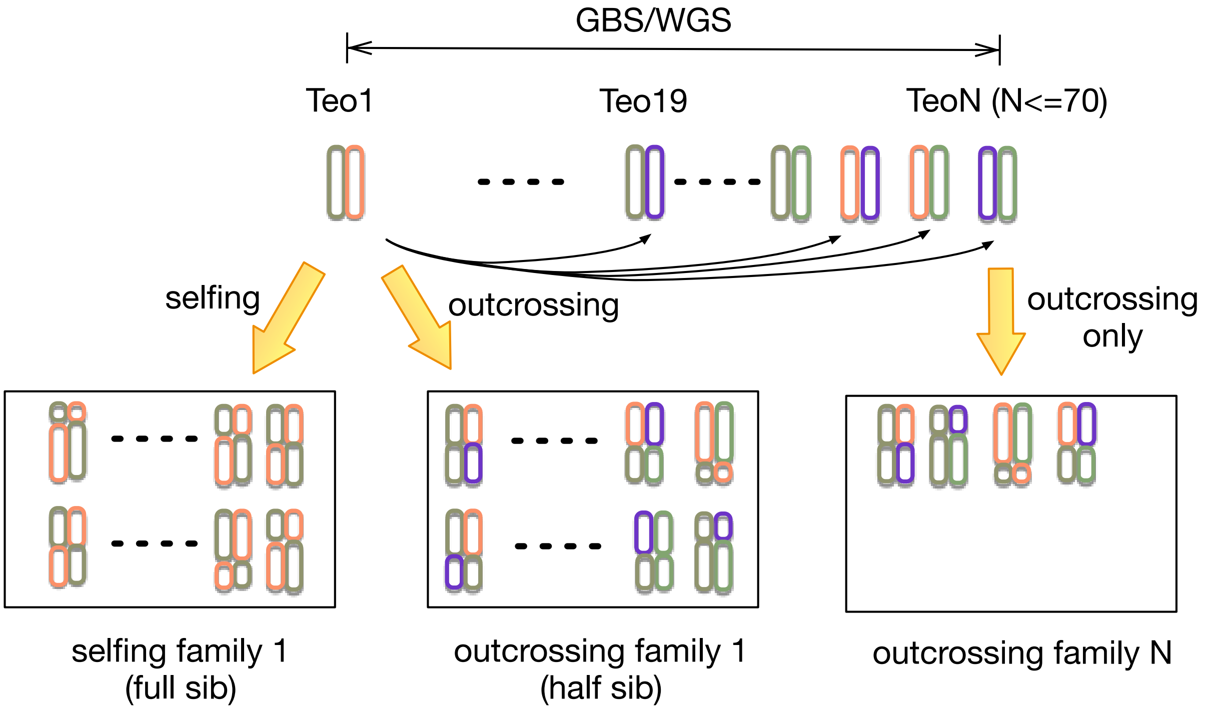
Contents

1 Crossing Scheme and the Experimental Design



In this experiment, we selfed and outcrossed a set of ~70 teosinte landraces to get a progeny array composed of 4,875 individuals. The ~70 founders and all the progeny were genotyped using GBS. We also re-sequenced

20/70 founder lines (the others will be re-sequenced soon). Because of the high error rate of the GBS data, especially problematic for calling heterozygous sites, we employed a phasing and imputation strategy to infer the expected genotypes by combining parentage and GBS information.

This file is to document the R codes we used to solve the problems step by step.

2 Infer mom's genotype from GBS data

If we got mom's WGS data , this step can be skipped.

We have obs. mom and obs. (selfed) kids. We want to know $P(G|\theta)$, or the probability of the mom's genotype given observed data θ. And according to Bayes' theorem,

$P(G|\theta) \propto P(\theta|G) \times P(G)$,

where $P(G)$ is the probability of the genotype according to the Hardy-Weinberg equilibrium estimated from the population. This consists of observed genotypes (G') of both mom and kids. So:

$P(G|\theta) \propto \left(\prod_{i=1}^{k} P(G'_k|G)\right) \times P(G'_{mom}|G) \times P(G)$,

where, $P(G'_{mom}|G)$ is the probability of the mom's observed genotype given genotype G by considering error rates, i.e. GBS homozygote error = 0.02 and heterozygote error = 0.8.
And $P(G'_k|G)$ is the probability of kid's observed genotype given genotype G by considering error rates and Mendelian segregation rate.

k and all the

```r
# set the path
setwd("../")
# loading all the R functions from folder "lib"
f <- sapply(list.files(pattern="[.]R$", path="lib", full.names=TRUE), source)


set.seed(123456)
sim <- SimSelfer(size.array=10, het.error=0.7, hom.error=0.002, numloci=100, rec=1.2, imiss=0.3)

plotselfer(sim, kids=6:10, snps=40:100, cols=c("green", "blue"))


#install.packages(c("devtools", "roxygen2", "testthat", "knitr"))
```

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

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3 Imputing Founder Genotypes

$P(G|\theta) \propto P(\theta|G) \times P(G)$

$$P(G|\theta) \propto \left(\prod_{i=1}^{k} P(G'_i|G)\right) \times \left(\sum_{n=1}^{mom} P(G'_{mom}|G)\right) \times P(G)$$

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

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4 Phasing Founder Genotypes

$P(H|\theta) \propto P(\theta|H) \times P(H)$
$P(H|\theta) \propto \left(\prod_{i=1}^{k} P(H'_k|H)\right) \times P(H)$
$P(H|\theta) \propto \left(\prod_{i=1}^{k} \prod_{l=1}^{n} P(G'_{i,l}|H)\right) \times P(H)$

- Where θ denotes observed data.
- $P(H)$ is the probability of the haplotype for a given window size of n.
- $P(G'_{i,l}|H)$ is the probability of kid i at locus l for a given haplotype H.
- We assume all the possible haplotypes of a given window size are equally likely.

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5 Imputing and Phasing Kids

$P(H_k|\theta) \propto P(\theta|H_k) \times P(H_k)$
$P(H_k|\theta) \propto \left(\prod_{i=k} P(H'_k|H_k)\right) \times P(H_k)$
$P(H_k|\theta) \propto \left(\prod_{i=k} \prod_{l=1}^{n} P(G'_{i,l}|H_k)\right) \times P(H_k)$

- Where θ denotes observed data.
- $P(H)$ is the probability of the haplotype for a given window size of n.
- $P(G'_{i,l}|H)$ is the probability of kid i at locus l for a given haplotype H.
- We assume all the possible haplotypes of a given window size are equally likely.

```r
phase <- read.csv("../data/sim_phasing_res.csv")

hist(phase$er, breaks=30, main="Simulation (N=100)",col="#faebd7", xlab="Phasing Error Rate")
abline(v=mean(phase$er), col="red", lwd=2)
abline(v=median(phase$er), col="darkblue", lwd=2)
```

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6 Phasing Dad of outcrossing progeny array

$$P(H_d|\theta) \propto P(\theta|H_d) \times P(H_d)$$
$$P(H_d|\theta) \propto \left(\prod_{i=1}^{k} P(H'_k|H_d, H_m) \right) \times P(H_m) \times P(H_d)$$
$$P(H|\theta) \propto \left(\prod_{i=1}^{k} \prod_{l=1}^{n} P(G'_{i,l}|H) \right) \times P(H)$$

- Where θ denotes observed data.
- $P(H_d)$ is the probability of the dad's haplotype for a given window size of n.
- $P(G'_{i,l}|H)$ is the probability of kid i at locus l for a given haplotype H.
- We assume all the possible haplotypes of a given window size are equally likely.