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# Supplement A: Simulations to Determine whether Average Familial Ancestry Provides Better Estimates of Progeny Ancestry than Direct Genotyping

## Background

Accurately estimating admixture can be difficult when using only a few genetic markers, but the use of average familial admixture provides a promising alternative. Recombination in hybrid individuals can produce genomic regions that are not representative of genome-wide admixture patterns. As a result, estimates of genomic ancestry may be incorrect if only a small number of loci are used to produce the estimates. An alternative approach is to use the familial admixture calculated by averaging the ancestry of both parents. By using both parents to estimate progeny admixture, twice as many genes will be used in the estimate. However, the accuracy of this technique may be influenced by the variation in admixture in the progeny produced or the effect of recombination on the variance of progeny admixture. Here, we simulated 10,000 $F_2$ and backcrossed progeny to identify whether using familial admixture provides better estimates of progeny admixture than genotyping progeny directly. $F_2$ offspring are expected to have the greatest variance in admixture, as an $F_1 \times F_1$ cross could produce offspring with admixture levels ranging from 0 to 1.

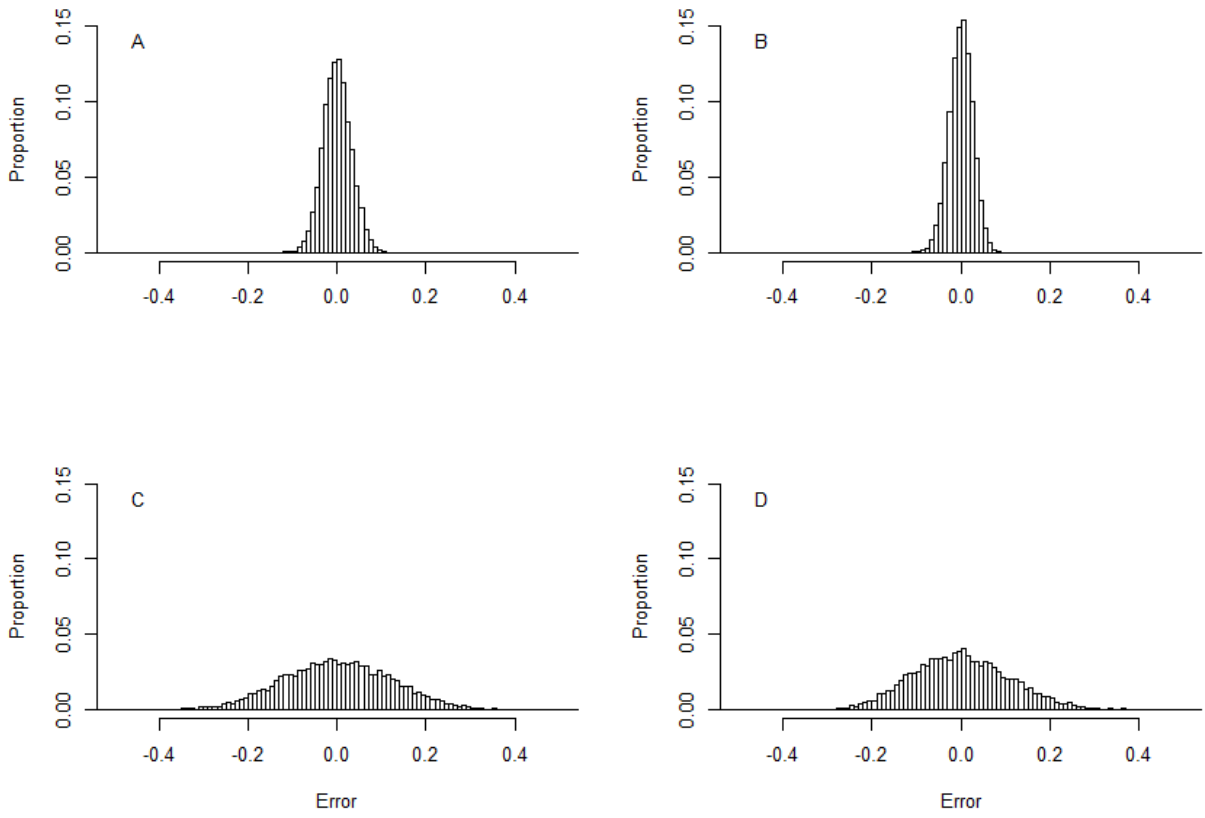
## Methods

To simulate progeny, we created pure and $F_1$ parents with 100 diagnostic loci per chromosome arm. We used a realistic number of chromosome arms for members of the genus *Oncorhynchus*, i.e., 50 pairs (Allendorf and Thorgaard 1984). Recombination was allowed to occur at previously published rates of 0.9, 0.026, and 0.074 for one, two, and zero crossovers per arm (Brieuc et al. 2014). Recombination was allowed to occur randomly across each chromosome arm.

The true admixture was identified for each progeny and compared with two different admixture estimates: (1) the average admixture in the parents estimated using 8 randomly selected SNPs and (2) the admixture estimated from 8 randomly selected SNPs in the progeny itself.

## Results

The variation in error (estimate minus true admixture) was smaller for familial admixture estimates than for admixtures estimated directly from the progeny (Figure S.A.1). The standard deviation of error for familial admixture estimates was 0.031 ($F_2$) and 0.026 (backcross), compared with 0.122 ($F_2$) and 0.108 (backcross) for admixture estimated directly from progeny.




Supplementary Figure S.A.1. Variation in error rates for different estimates of admixture in simulated progeny. Panel **(A)** shows the error in estimated admixture of $F_2$ progeny using the average admixture of both parents (familial admixture) calculated at 8 randomly selected loci, panel **(B)** the error in estimated admixture of backcrossed progeny using the average admixture of both parents calculated at 8 randomly selected loci, panel **(C)** the error in estimated admixture of $F_2$ progeny using the admixture calculated at 8 randomly selected loci in the individual itself,

and panel **(D)** the error in estimated admixture of backcrossed progeny using the admixture calculated at 8 randomly selected loci in the individual itself.

## Supplemental References


Allendorf, F. W., and G. H. Thorgaard. 1984. Tetraploidy and the evolution of salmonid fishes. Pages 1–27 *in* B. J. Turner, editor. Evolutionary genetics of fishes. Plenum, New York.

Brieuc, M. S. O., C. D. Waters, J. E. Seeb, and K. A. Naish. 2014. A dense linkage map for Chinook Salmon (*Oncorhynchus tshawytscha*) reveals variable chromosomal divergence after an ancestral whole genome duplication event. G3: Genes, Genomes, Genetics 4:447-460.


## R script

```
# recombination
recomb <- function(arm1, arm2){
 new_arm <- c()
 recomb <- runif(1)

 if (recomb > 0.974){ # double recombination
  positions <- sort(round(runif(2)*100))
  new_arm <- c(arm1[1:positions[1]], arm2[positions[1]+1:positions[2]], arm1[positions[1]+1:length(arm1)])
  if (runif(1)>0.5){
   new_arm <- c(arm2[1:positions[1]], arm1[positions[1]+1:positions[2]], arm2[positions[1]+1:length(arm2)])
  }
 }
 else if (recomb > 0.90){ # zero recombination
  new_arm <- arm1
  if (runif(1)>0.5){
   new_arm <- arm2
  }
 }
 else { # single recombination
  position <- round(runif(1)*100)
  new_arm <- c(arm1[1:position], arm2[position+1:length(arm2)])
  if (runif(1)>0.5){
   new_arm <- c(arm2[1:position], arm1[position+1:length(arm1)])
  }
 }
 return(new_arm[1:100])
}

trueAdmixture <- function(genome){
 return(mean(genome))
}

parentalAdmixture <- function(parent1, parent2){
 positions <- round(runif(8, min=1, max=5000))
 positions <- c(positions, positions+5000)
 value <- c()
```

```
 for (i in seq(1,16)){
  value <- c(value, parent1[positions[i]])
  value <- c(value, parent2[positions[i]])
 }
 value <- mean(value)

 return(value)
}


progenyAdmixture <- function(genome){
 positions <- round(runif(8, min=1, max=5000))
 positions <- c(positions, positions+5000)
 value <- c()

 for (i in seq(1,16)){
  value <- c(value, genome[positions[i]])
 }
 value2 <- mean(value)

 return(value2)
}


################################ F2 ############################
# run 1000 F2s to see how well we do at estimating admixture
f1_arm1 <- rep(0,100)
f1_arm2 <- rep(1,100)
genome <- c()
parent1 <- c(rep(0,5000), rep(1,5000))
parent2 <- c(rep(0,5000), rep(1,5000))

parental_true <- c()
true_true <- c()
progeny_true <- c()
parentVsTrue_F2 <- c()
progenyVsTrue_F2 <- c()

for (j in seq(1:10000)){
 if(j%%100==0){print(j)}
 genome <- c()

 # this creates a single progeny
 for (i in seq(1:100)){ # assuming 100 chromosome arms
  genome <- c(genome, recomb(f1_arm1, f1_arm2))
 }

 truth <- trueAdmixture(genome) # calculate true admixture
 parental <- parentalAdmixture(parent1, parent2) # calculate parental admixture
 progeny <- progenyAdmixture(genome)

 parental_true[j] <- parental
 true_true[j] <- truth
 progeny_true[j] <- progeny
 parentVsTrue_F2[j] <- parental-truth
 progenyVsTrue_F2[j] <- progeny-truth
}
```

```
################## BC1 ########################################
# run 1000 BC1's to see how well we do at estimating admixture
f1_arm1 <- rep(0,100)
f1_arm2 <- rep(1,100)
parent1 <- c(rep(0,5000), rep(1,5000))
parent2 <- rep(0, 10000)
genome <- c()

parentVsTrue_BC1 <- c()
progenyVsTrue_BC1 <- c()

for (j in seq(1:10000)){
 if(j%%100==0){print(j)}
 genome <- c()

 # this creates a progeny
 for (i in seq(1:100)){ # assuming 100 chromosome arms
  f2_arm <- recomb(f1_arm1, f1_arm2)
  genome <- c(genome, recomb(f2_arm, pure_arm))
 }

 truth <- trueAdmixture(genome) # calculate true admixture
 parental <- parentalAdmixture(parent1, parent2) # calculate parental admixture
 progeny <- progenyAdmixture(genome)

 parentVsTrue_BC1[j] <- parental-truth
 progenyVsTrue_BC1[j] <- progeny-truth
}


par(mfrow=c(2,2))
 hist(parentVsTrue_F2, xlim=c(-0.5,0.5), breaks=seq(-1, 1, 0.01), main="", xlab="", ylim=c(0,1500), ylab="Proportion", yaxt="n")
 axis(2, at=c(0,500,1000,1500), labels=c("0.00", "0.05", "0.10", "0.15"))
 legend("topleft", "A", bty="n")
 hist(parentVsTrue_BC1, xlim=c(-0.5,0.5), breaks=seq(-1, 1, 0.01), main="", xlab="", ylim=c(0,1500), ylab="Proportion", yaxt="n")
 axis(2, at=c(0,500,1000,1500), labels=c("0.00", "0.05", "0.10", "0.15"))
 legend("topleft", "B", bty="n")
 hist(progenyVsTrue_F2, xlim=c(-0.5,0.5), breaks=seq(-1, 1, 0.01), main="", xlab="Error", ylim=c(0,1500), ylab="Proportion", yaxt="n")
 axis(2, at=c(0,500,1000,1500), labels=c("0.00", "0.05", "0.10", "0.15"))
 legend("topleft", "C", bty="n")
 hist(progenyVsTrue_BC1, xlim=c(-0.5,0.5), breaks=seq(-1, 1, 0.01), main="", xlab="Error", ylim=c(0,1500), ylab="Proportion", yaxt="n")
 axis(2, at=c(0,500,1000,1500), labels=c("0.00", "0.05", "0.10", "0.15"))
 legend("topleft", "D", bty="n")
```