het

TMJ

April 18, 2016

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```r
genos <- read.delim("out.012", header=FALSE)
indiv <- read.table("out.012.indv", quote="\"", comment.char="")
genos$V1 <- NULL
gi <- cbind(indiv, genos)
row.names(gi) <- gi$V1
gi=gi[,-1]
tgi <- as.data.frame(t(gi))
```

divide into seperate files

```r
samBC <- tgi[ ,1:3]
samBM <- tgi[ ,4:6]
gatBC <- tgi[ ,7:9]
gatBM <- tgi[ ,10:12]
```

samBCt <- samBC[samBC[,1]==0 & samBC[,2]==2 & samBC[,3]!=-1,] dim(samBCt) totLoci <- sum(samBCt[,1]==0) totLoci refAllele <- sum(samBCt[,3]==0) refAllele altAllele <- sum(samBCt[,3]==2) altAllele hetAllele <- sum(samBCt[,3]==1) hetAllele

hetaccuracy <- hetAllele/totLoci hetaccuracy*100

function for finding het accuracy rate for each file

```r
hfx<-function(file){
filet <- file[file[,1]==0 & file[,2]==2 & file[,3]!=-1,]
dim(filet)
refAllele <- sum(filet[,3]==0)
refAllele
altAllele <- sum(filet[,3]==2)
altAllele
hetAllele <- sum(filet[,3]==1)
hetAllele
totLoci <- sum(filet[,1]==0)
totLoci
hetaccuracy <- hetAllele/totLoci
hetaccuracy*100
}
```

run teh funciton across the 4 subfiles

```
hetfiles <- list(samBC, samBM, gatBC, gatBM)
result <- lapply(hetfiles, hfx)
hetfilenames <- list("samBC", "samBM", "gatBC", "gatBM")
results <- as.data.frame(cbind(hetfilenames, result))
results$result <- as.numeric(results$result)
```

calculate averages for each method/method

```
samavg <- (results[1,2]+results[2,2])/2
samavg
```

```
## [1] 82.03585
```

```
gatavg <- (results[3,2]+results[4,2])/2
gatavg
```

```
## [1] 96.49624
```