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library(genetics)

data<-matrix(0,1000,100)

for ( i in 1:100 ){
  data[,i]<-sample(c("A/A","A/a","a/A", "a/a"),1000,replace=TRUE)
}

data<-makeGenotypes(data)

af<-matrix(0,2,100);gf<-list()

het<-c(); pic<-c()

for( i in 1:ncol(data)){
  r<-summary(data[,i])
  af[,i]<-r$allele.freq[,2]
  gf[[i]]<-r$genotype.freq[,2]
  het[i]<-r$Hu
  pic[i]<-r$pic
}

plot(af[1,],af[2,],ylim=c(0,1))

abline(h=0.5,col="blue")

unlist(gf[[1]])

class(gf[[1]])

unlist(gf)

matrix(unlist(gf),3,100)

gf[[100]]

gf1<-matrix(unlist(gf),3,100)

plot(het,ylim=c(0,1));abline(h=0.5,col="maroon")

plot(log(het))

abline(h=log(0.5),col="maroon")

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#polymorphism informative content
plot(pic,ylim=c(0,1));abline(h=0.5,col="maroon")

#r1<-HWE.test(data[,1])
#r1$diseq
#r1$test$p.value
phwe<-c()
for(i in 1:ncol(data)){
  phwe[i]<-HWE.test(data[,i])$test$p.value
}
plot(phwe,ylim=c(0,1));abline(h=0.05,col="maroon")

# Install and load required package
if(!require(genetics)) install.packages("genetics", dependencies = TRUE)
library(genetics)

# ---- Simulate Genotype Data ----
set.seed(97)
data <- matrix(0, 1000, 100)
for (i in 1:100) {
  data[, i] <- sample(c("A/A", "A/a", "a/A", "a/a"), 1000, replace = TRUE)
}

# Convert to genotype format
data <- makeGenotypes(data)

# ---- Calculate Allele Frequencies ----

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allele_freqs <- data.frame(SNP = paste0("SNP_", 1:100),
                           A_freq = numeric(100),
                           a_freq = numeric(100))

for (i in 1:ncol(data)) {
  r <- summary(data[, i])

  allele_freqs$A_freq[i] <- r$allele.freq["A", 2]
  allele_freqs$a_freq[i] <- r$allele.freq["a", 2]
}

# ---- Prepare Data for ggplot ----

if(!require(reshape2)) install.packages("reshape2", dependencies = TRUE)
library(reshape2)

allele_freqs_melt <- melt(allele_freqs, id.vars = "SNP",
                          variable.name = "Allele",
                          value.name = "Frequency")

# ---- Plot Overlapping Bar Plot ----

if(!require(ggplot2)) install.packages("ggplot2", dependencies = TRUE)
library(ggplot2)

ggplot(allele_freqs_melt, aes(x = SNP, y = Frequency, fill = Allele)) +
  geom_bar(stat = "identity", position = "dodge", color = "black") +
  scale_fill_manual(values = c("#1f77b4", "#ff7f0e")) +
  labs(title = "Allele Frequencies per SNP",

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    x = "SNP",
    y = "Allele Frequency") +
theme_minimal() +
theme(axis.text.x = element_blank(), # Hide x-axis labels (too many SNPs)
      axis.ticks.x = element_blank(),
      legend.position = "top",
      plot.title = element_text(hjust = 0.5, face = "bold"))
ggplot(allele_freqs_melt, aes(x = SNP, y = Frequency, fill = Allele)) +
  geom_bar(stat = "identity", position = "identity", alpha = 0.5, color = "black") +
  scale_fill_manual(values = c("#1f77b4", "#ff7f0e")) +
  labs(title = "Overlapping Allele Frequencies per SNP",
       x = "SNP",
       y = "Allele Frequency") +
theme_minimal() +
theme(axis.text.x = element_blank(),
      axis.ticks.x = element_blank(),
      legend.position = "top",
      plot.title = element_text(hjust = 0.5, face = "bold"))

##Genotype Frequency plot
# Your existing code up to gf1
library(genetics)
data <- matrix(0, 1000, 100)
for (i in 1:100) {
  data[, i] <- sample(c("A/A", "A/a", "a/A", "a/a"), 1000, replace = TRUE)
}
data <- makeGenotypes(data)

```

```
af <- matrix(0, 2, 100)
```

```
gf <- list()
```

```
het <- c()
```

```
pic <- c()
```

```
for (i in 1:ncol(data)) {  
  r <- summary(data[, i])  
  af[, i] <- r$allele.freq[, 2]  
  gf[[i]] <- r$genotype.freq[, 2]  
  het[i] <- r$Hu  
  pic[i] <- r$pic  
}
```

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# Combine genotype frequencies into a matrix (3 genotypes x 100 SNPs)
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gf1 <- matrix(unlist(gf), nrow = 3, ncol = 100, byrow = FALSE)
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rownames(gf1) <- c("A/A", "A/a", "a/a")
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colnames(gf1) <- paste0("SNP_", 1:100)
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# ---- Convert to data frame for plotting ----
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geno_freqs <- as.data.frame(gf1)
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```
geno_freqs$Genotype <- rownames(geno_freqs)
```

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# Reshape into long format
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if(!require(reshape2)) install.packages("reshape2", dependencies = TRUE)
```

```
library(reshape2)
```

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geno_long <- melt(geno_freqs, id.vars = "Genotype",
  variable.name = "SNP",
  value.name = "Frequency")

# ---- Plot genotype frequencies ----

if(!require(ggplot2)) install.packages("ggplot2", dependencies = TRUE)
library(ggplot2)

ggplot(geno_long, aes(x = SNP, y = Frequency, fill = Genotype)) +
  geom_bar(stat = "identity", position = "identity", alpha = 0.6, color = "black") +
  scale_fill_manual(values = c("#1f77b4", "#2ca02c", "#ff7f0e")) +
  labs(title = "Overlapping Genotype Frequencies per SNP",
    x = "SNP",
    y = "Genotype Frequency") +
  theme_minimal() +
  theme(axis.text.x = element_blank(),
    axis.ticks.x = element_blank(),
    legend.position = "top",
    plot.title = element_text(hjust = 0.5, face = "bold"))

##another plot

geno_freqs <- as.data.frame(gf1)
geno_freqs$Genotype <- rownames(geno_freqs)
geno_long <- melt(geno_freqs, id.vars = "Genotype",
  variable.name = "SNP",
  value.name = "Frequency")

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# ---- Side-by-side bar plot ----

ggplot(geno_long, aes(x = SNP, y = Frequency, fill = Genotype)) +
  geom_bar(stat = "identity", position = position_dodge(width = 0.8), color = "black") +
  scale_fill_manual(values = c("#1f77b4", "#2ca02c", "#ff7f0e")) +
  labs(title = "Genotype Frequencies per SNP (Side-by-Side)",
        x = "SNP",
        y = "Genotype Frequency") +
  theme_minimal() +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        legend.position = "top",
        plot.title = element_text(hjust = 0.5, face = "bold"))

```