HW1_code.R

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```r
# Start importing allele data
AA = 10
Aa = 25
aa = 81
Total_ind = sum(AA,Aa,aa)

# Find total allels
total_A = AA*2 + Aa
total_a = aa*2 + Aa
total_allels = total_a +total_A

# Find p and q
p = total_A/total_allels
q = 1-p

print(p)
```

```
## [1] 0.1939655
```

```r
print(q)
```

```
## [1] 0.8060345
```

```r
# Find expected frequencies
expected_AA = p**2*Total_ind
expected_Aa = 2*p*q*Total_ind
expected_aa = q**2*Total_ind

expected_aa
```

```
## [1] 75.36422
```

```r
expected_Aa
```

```
## [1] 36.27155
```

```r
expected_AA
```

```
## [1] 4.364224
```

```r
# Make a table of observed vs expected
observed = c(AA,Aa,aa)
expected = c(expected_AA,expected_Aa,expected_aa)
ob_ex_table = cbind(observed,expected)
ob_ex_table
```

```
##      observed  expected
## [1,]       10  4.364224
## [2,]       25 36.271552
## [3,]       81 75.364224
```

```
##
# Where r is the number of populations, and c is the number of levels for the categorical variable.
# DF = (r - 1) * (c - 1)
DF = (2 - 1) * (2 - 1)

# perform test
test_stat = 0
for (i in 1:3){
  test_val = (ob_ex_table[i,1] - ob_ex_table[i,2])**2 /(ob_ex_table[i,2])
  test_stat = test_stat + as.numeric(test_val)
}
test_stat
```

```
## [1] 11.20194
```

```
# Get p value
pchisq(test_stat,df=DF,lower.tail = FALSE)
```

```
## [1] 0.0008171198
```