Genotype and Allele Frequencies

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Compute allele frequencies

```
#Set population size
N=60
#Set total number of alleles in the population
DN=N*2
#Number of A allele obeserved in the population
A=70
#Number of a allele observed in the population
a=50

fA=A/DN
fA
```

```
## [1] 0.5833333
```

```
fa=a/DN
fa
```

```
## [1] 0.4166667
```

```
fA+fa
```

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

Compute genotype frequencies

```
#Set population size
N=60
#AA genotypes obeserved in the population
AA=25
#aa genotypes observed in the population
aa=25
#Aa genotypes observed in the population
Aa=10

fAA=AA/N
fAA
```

```
## [1] 0.4166667
```

```
faa=aa/N
fa
```

```
## [1] 0.4166667
```

```
fAa=Aa/N
fAa #heterozygosity
```

```
## [1] 0.1666667
```

```
hom=1-fAa
hom
```

```
## [1] 0.8333333
```

```
fAA+faa+fAa
```

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

Compute allele frequency from genotype frequency

```
#Set population size
N=60
#AA genotypes obeserved in the population
AA=25
#aa genotypes observed in the population
aa=25
#Aa genotypes observed in the population
Aa=10
#Number of A allele obeserved in the population
A=70
#Number of a allele observed in the population
a=50

fA=A/DN
fA
```

```
## [1] 0.5833333
```

```
fA=fAA+fAa/2
fA
```

```
## [1] 0.5
```

Testing if there is deviation from HWE

```
#Set population size
N=60
#AA genotypes obeserved in the population
AA=25
#aa genotypes observed in the population
aa=25
#Aa genotypes observed in the population
Aa=10
#Number of A allele obeserved in the population
A=70
#Number of a allele observed in the population
a=50

observed=c(AA,Aa,aa)
observed
```

```
## [1] 25 10 25
```

```
#Calculate allele frequencies:

#total number of alleles = 2*Population size (N) = 2*sum(observed)

n=2*sum(observed)
n
```

```
## [1] 120
```

```
#compute freq. of A from genotypes
fA=(2*AA+Aa)/n
fA
```

```
## [1] 0.5
```

```
fa=(2*aa+Aa)/n
fa
```

```
## [1] 0.5
```

```
#Generate expected genotype frequencies:

AA_e=fA^2
AA_e
```

```
## [1] 0.25
```

```
aa_e=fa^2
aa_e
```

```
## [1] 0.25
```

```
Aa_e=2*(fA*fa)
Aa_e
```

```
## [1] 0.5
```

```
expected=c(AA_e,aa_e,Aa_e) * 120
expected
```

```
## [1] 30 30 60
```

```
#combine observed and expected
final=cbind(expected,observed)
final
```

```
##      expected observed
## [1,]       30       25
## [2,]       30       10
## [3,]       60       25
```

```
#test if this is significant:
```

```
chit= chisq.test(observed, p = c(AA_e,aa_e,Aa_e))
str(chit)
```

```
## List of 9
##  $ statistic: Named num 9.17
##   ..- attr(*, "names")= chr "X-squared"
##  $ parameter: Named num 2
##   ..- attr(*, "names")= chr "df"
##  $ p.value  : num 0.0102
##  $ method   : chr "Chi-squared test for given probabilities"
##  $ data.name: chr "observed"
##  $ observed : num [1:3] 25 10 25
##  $ expected : num [1:3] 15 15 30
##  $ residuals: num [1:3] 2.582 -1.291 -0.913
##  $ stdres   : num [1:3] 2.98 -1.49 -1.29
##  - attr(*, "class")= chr "htest"
```