

# Inference on allele frequency (INCLASS-2)

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```
nAA=3
nAa=16
naa=31

# Sample size (number of diploid genotypes)
n=(nAA+nAa+naa)

# Total number of alleles is 2n
nAlleles=n*2

# Allele frequency
pHat=(2*nAA+nAa)/nAlleles

VAR=pHat*(1-pHat)/nAlleles
SE=sqrt(VAR)

NormalCI=pHat+c(-1,1)*1.96*SE

AlternativeCI=binom.test(x=c(nAA*2+nAa,nAa+2*naa))$conf.int

message(pHat, ' +/-', SE)

## 0.22 +/-0.041424630354416
message('Normal CI:', round(NormalCI,4))

## Normal CI:0.13880.3012
message('Alternative CI:', round(AlternativeCI,4))

## Alternative CI:0.14330.3139
```