

Inference on Allele Frequencies

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1) Using A Normal Approximation

```
nA=20
nG=80

nAlleles=nA+nG #total number of alleles
pA=nA/nAlleles
V=pA*(1-pA) # the variance in one Bernoulli trial
vMean=V/nAlleles # the sampling variance of the mean
SE=sqrt(vMean) # standard error
normalCI=pA+c(-1,1)*1.96*SE
round(normalCI,4)

## [1] 0.1216 0.2784
```

2) Using binom.test()

The CI reported by this function uses a method proposed by Clopper and Pearson (1934).

```
binom.test(x=nA,n=nAlleles,conf.level=0.95)

##
## Exact binomial test
##
## data:  nA and nAlleles
## number of successes = 20, number of trials = 100, p-value = 1.116e-09
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.1266556 0.2918427
## sample estimates:
## probability of success
##                0.2
```

3) Let's increase sample size

First, let's write a function to return a CI based on a normal approximation.

```
normalCI=function(x,n,conf.level=0.95){
  p=x/n
  V=p*(1-p)
  vMean=V/n
  SE=sqrt(vMean)
```

```

a=(1-conf.level)/2
CI= qnorm(mean=p,sd=SE,p=c(a,1-a))
return(CI)
}

binom.test(x=nA*100,n=nAlleles*100,conf.level=0.95)

##
## Exact binomial test
##
## data: nA * 100 and nAlleles * 100
## number of successes = 2000, number of trials = 10000, p-value < 2.2e-16
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.1921984 0.2079767
## sample estimates:
## probability of success
## 0.2

normalCI(x=nA*100,n=nAlleles*100,conf.level=0.95)

## [1] 0.1921601 0.2078399

binom.test(x=nA/10,n=nAlleles/10,conf.level=0.95)

##
## Exact binomial test
##
## data: nA/10 and nAlleles/10
## number of successes = 2, number of trials = 10, p-value = 0.1094
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.02521073 0.55609546
## sample estimates:
## probability of success
## 0.2

normalCI(x=nA/10,n=nAlleles/10,conf.level=0.95)

## [1] -0.04791801 0.44791801

```