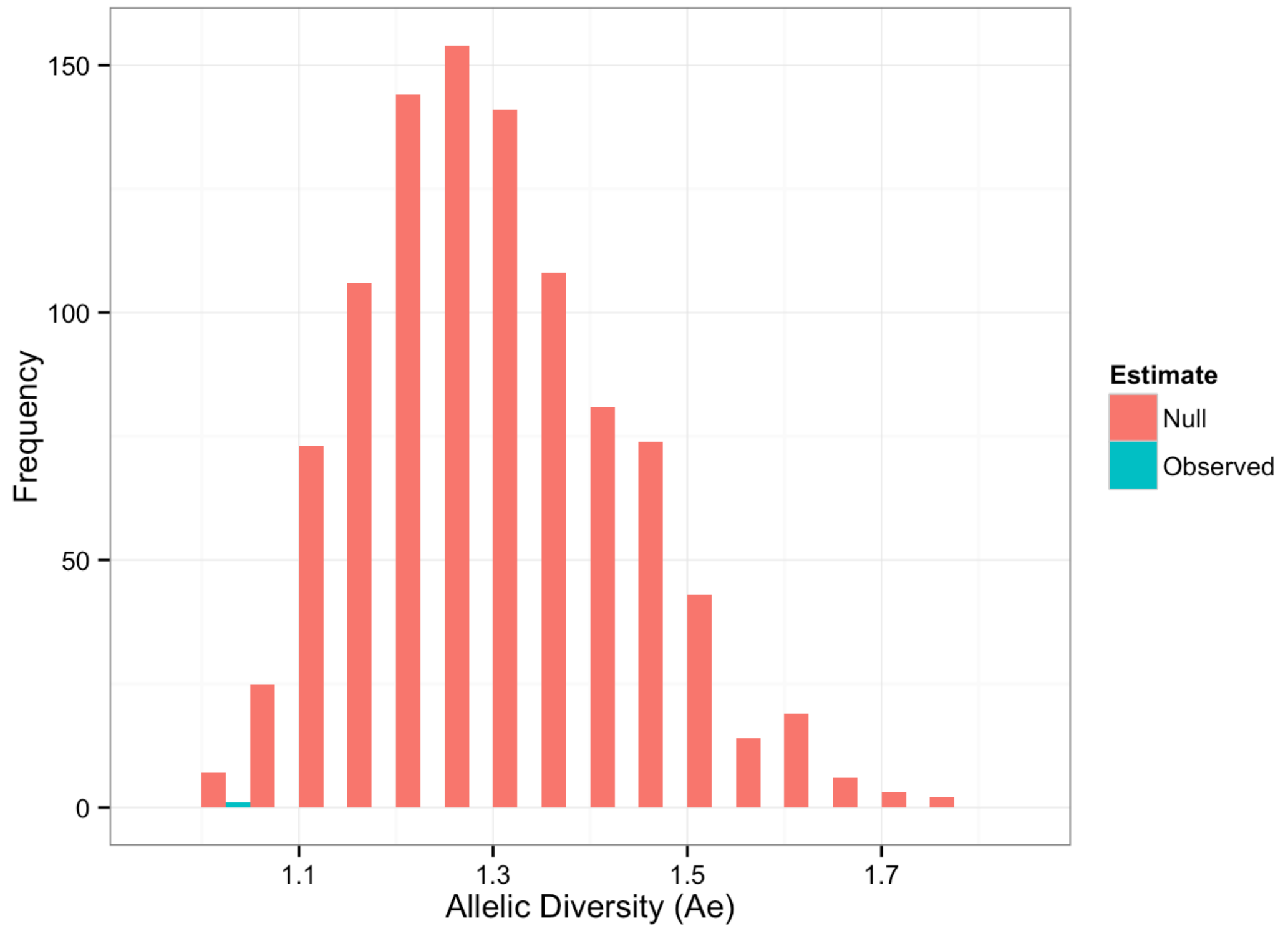# General Rarefaction

1. Select the smallest sample size.

2. Randomly select genotypes from larger populations and estimate diversity

3. Repeat a large number of times.

```
cape.pop <- arapat[ arapat$Species=="Cape","WNT"]
null.ae <- rarefaction( cape.pop, mode="Ae",size=36)
mean(null.ae)
## [1] 1.312669
```