

Practical Consequences

1. The more diverse the locus, the more individuals you need to sample to get a good estimate of diversity.
2. For rare alleles, you need very large samples sizes.

Rarefaction

Size-corrected estimates of diversity estimated by random subsampling of larger populations.

```
ae.cape <- genetic_diversity( arapat[ arapat$Species=="Cape", "WNT"] )  
ae.cape  
##           Ae  
## 1 1.305052
```

$N_{\text{Cape}} = 75$

$N_{\text{Mainland}} = 36$

```
ae.mainland <- genetic_diversity( arapat[ arapat$Species=="Mainland", "WNT"] )  
ae.mainland  
##           Ae  
## 1 1.033889
```