
CID: 02001365

Modual Code: CMEE

Modual Name: Computational Methods in Ecology and Evolution

Question Number: C3

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(a)

```
Qa <- function(fA1, fA2){  
  HS <- (2*fA1*(1-fA1)+2*fA2*(1-fA2))/2  
  D <- abs(fA1-fA2)  
  HT <- HS + (D^2/2)  
  FST <- (HT-HS)/HT  
  return(c(HS,D,HT,FST))  
}
```

(b)

Qa(fA1 = 0.2, fA2 = 0.1)

```
[1] 0.25000000 0.10000000 0.25500000 0.01960784
```

Qa(fA1 = 0.3, fA2 = 0.3)

```
[1] 0.42 0.00 0.42 0.00
```

Qa(fA1 = 0, fA2 = 1)

```
[1] 0.0 1.0 0.5 1.0
```

(c)

The mean standardized variance in allele frequencies F_{ST} of the second population equals 0, ($D=0$, $HT = HS$), means there is no subdivision, it is structured, it means the population is in HWE, random mating with respect to genotype. The other two population are not structured.

For the third population, $D=1$, means the population is totally not in HWE.

Mating, inbreeding, spatial distribution, migration, Natural selection etc. can influence levels of population structure at the genomic level.

(d)

A useful way of summarizing genetic variability among different populations is through estimates of the inbreeding coefficient, F_{ST} . However, the promise of this approach has yet to be fully realized owing to the pervasive dogma that this distribution is highly dependent on

demographic history. Recent theoretical results that indicate that the distribution of estimates of F_{ST} is generally expected to be robust to the vagaries of demographic history.