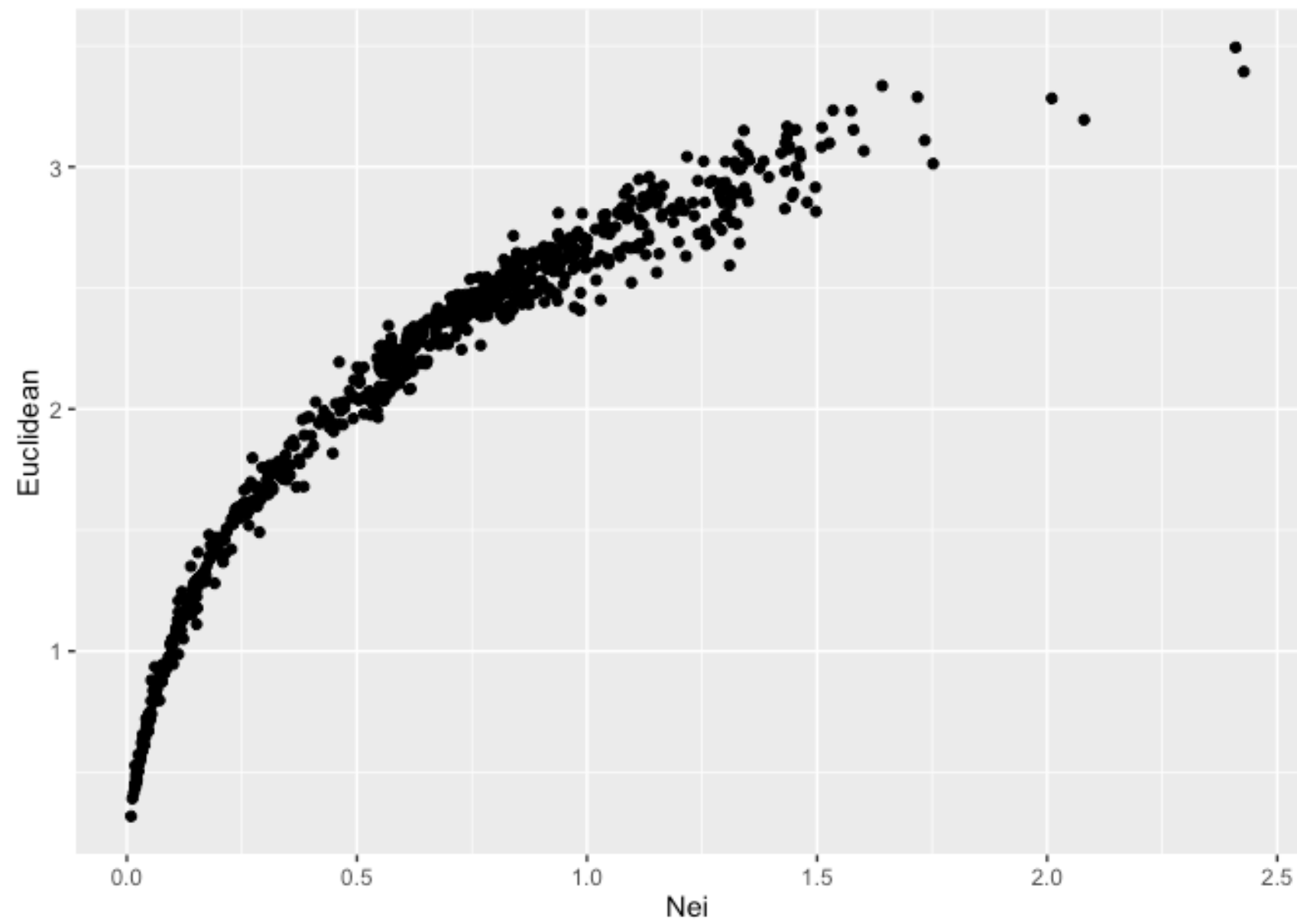


# Two Population Distances

```
D1 <- genetic_distance(arapat, stratum = "Population", mode = "Nei")
```

```
D2 <- genetic_distance(arapat, stratum = "Population", mode = "Euclidean")
```



```
df <- data.frame( Nei=D1[lower.tri(D1)], Euclidean=D2[ lower.tri(D2)] )  
ggplot(df,aes(x=Nei,y=Euclidean)) + geom_point()
```