

Population Genetics Homework, Week 1

Christian Polania

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```
# Question 1
unique(dat$pop) %>%
  length()
```

```
## [1] 12
```

```
# Question 2
table(dat$pop)
```

```
##
##      Boora      Bulla      Gnarl      Iron      MtCau      Rainy RainyMajor
##      20        9        20        1        9          1          1
##      Vict      Wagga      Warg      Yack      Yellow
##      30        5        33      29        30
```

```
# Question 3
boo <- subset(dat, pop == "Boora")
genotype.freq <- table(boo$GOT.1) %>%
  as.vector() %>%
  data.frame(row.names = c("AA", "Aa", "aa"))
allele.freq <- c(2 * genotype.freq[1, 1] + genotype.freq[2, 1], 2 * genotype.freq[3,
1] + genotype.freq[2, 1]) %>%
  data.frame(row.names = c("A", "a"))
genotype.freq
```

```
##      .
## AA   3
## Aa   2
## aa  15
```

```
allele.freq
```

```
##      .
## A     8
## a    32
```