20019803_A1

Code

Load data and dplyr

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```
setwd("/Users/kelli/Desktop/Biol343/Assignment_1")
decDat=read.csv("DecodonAsexualityData.csv")
library(dplyr)
```

Check class, dimensions, head and tail for errors

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```
class(decDat)
```

```
[1] "data.frame"
```

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```
dim(decDat)
```

```
[1] 46  8
```

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```
head(decDat)
```

	PopType <fctr>	PopName <fctr>	LatN <dbl>	LongE <dbl>	OvaryWidthMM <dbl>	OvaryHeightMM <dbl>
1	A	MI M2	43.264	-84.884	3.62	3.48
2	A	MI M3	45.615	-84.689	3.61	3.59
3	A	MI M5	42.418	-84.013	2.98	2.68
4	A	MI M7	45.623	-84.705	3.48	4.08
5	A	MI M8	43.350	-85.935	3.43	2.94
6	A	MI M9	45.600	-84.709	3.87	3.11

6 rows | 1-7 of 8 columns

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```
tail(decDat)
```

	PopType <fctr>	PopName <fctr>	LatN <dbl>	LongE <dbl>	OvaryWidthMM <dbl>	OvaryHeightMM <dbl>
41	S	ON T14	43.966	-77.035	3.18	2.46
42	S	ON T15	43.418	-80.262	3.16	2.67
43	S	ON T16	44.902	-75.870	3.34	3.11
44	S	ON T3	43.208	-80.650	3.35	2.83
45	S	ON T7	42.049	-83.106	3.78	3.18
46	S	ON T8	42.257	-81.859	3.30	2.88

6 rows | 1-7 of 8 columns

Add the ovary area measure to the dataset

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```
decDat$OvaryAreaMM <- decDat$OvaryWidthMM*decDat$OvaryHeightMM
```

Calculate the minimum, maximum, mean, median and standard deviation of ovary area and flower number

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```
decDat %>% filter(!is.na(FlowerNum))  %>%  summarise( min_OA = min(OvaryAreaMM), min_
FN = min(FlowerNum), max_OA = max(OvaryAreaMM), max_FN = max(FlowerNum), avg_OA = mea
n(OvaryAreaMM), avg_FN = mean(FlowerNum), med_OA = median(OvaryAreaMM), med_FN = medi
an(FlowerNum), sd_OA = sd(OvaryAreaMM), sd_FN = sd(FlowerNum)
)
```

min_OA <dbl>	min_FN <dbl>	max_OA <dbl>	max_FN <dbl>	avg_OA <dbl>	avg_FN <dbl>	med_OA <dbl>	med_FN <dbl>
7.524	12.4	12.903	181.76	10.20399	58.0156	10.5625	47.68

1 row | 1-8 of 10 columns

Calculate the mean ovary area, flower number, and August temperature for sexual and asexual populations

Asexual data

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```
decDat %>% filter(!is.na(FlowerNum))  %>% filter(PopType=="A") %>% summarise(meanOA_a
s = mean(OvaryAreaMM), meanFN_as = mean(FlowerNum), meanAT_as = mean(MeanTempC))
```

meanOA_as <dbl>	meanFN_as <dbl>	meanAT_as <dbl>

meanOA_as <dbl>	meanFN_as <dbl>	meanAT_as <dbl>
10.31834	44.57467	19.72667

1 row

Sexual data

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```
decDat %>% filter(!is.na(FlowerNum))  %>% filter(PopType=="S") %>% summarise(meanOA_s
= mean(OvaryAreaMM), meanFN_s = mean(FlowerNum), meanAT_s = mean(MeanTempC))
```

meanOA_s <dbl>	meanFN_s <dbl>	meanAT_s <dbl>
10.03246	78.177	20.16

1 row

Draw some conclusions with regards to the hypothesis you are testing. Is there a potentially confounding factor that a full analysis of these data should take into account?

Sexual populations produce 54% more flowers than asexual populations. Interestingly, the ovary area of the average asexually produced flower is ~3% larger than that of the average sexually produced flower. Considering the small sample size (n=25), this second difference is likely not statistically significant.

It is worth considering that local variables like altitude or even latitude based circadian rythm shifts could be playing a role in dictating flowering amount and potentially reproductive type determination.