Explaination of portfolio exercises:

D, Normally I would start with a log dosis response curve, but im trying to show answers to the question but make the RMD seem like it a report. Which is why I start with a normal dot plot, even though it doesn’t add any useful information to the report

E, Correction of data types was already done before plotting so the explanation and answer to E are missing in the report.

My answer would be as follows:

The data type of compConcentration is character, this means per concentration value it adds a point is added on the x-axis.

G+H, answer left out of RMD.

My answer would be as follows:

Fill in: (G) The positive control for this experiments is "ethanol (H) The negative control for this experiment is "S-medium"

I: answer left out of RMD.

My answer would be as follows:  
I would plot the dose response curves (is done in RMD). I would identify the concentrations between which the effect of offspring seems significant. Then I would check for significant differences in offspring count between those concentrations of the same compound. I would do this as follows: 1. Check if the data is normally distrubted, perform an independent t-test or a 2-independent mann-whitney test. The result of this test would tell me if the effect of the compound is significant.

J+K: answer left out of RMD.

I could find a way to include this naturally in my ‘report’: my answer would be:

```{r}

#calculating mean of control negative outside of mutate because mutate doesn't like filter function

CN\_mean <- ce\_data %>% dplyr::filter(expType == "controlNegative") %>% dplyr::select("RawData") %>% colMeans()

normalized\_ce\_data <- ce\_data %>%

dplyr::mutate(norm\_data = RawData/CN\_mean)

#checking if it's correct

normalized\_ce\_data %>% dplyr::group\_by(expType) %>% dplyr::summarise(m = mean(norm\_data, na.rm = T))

#making first plot

normalized\_ce\_data %>% slice\_sample(prop = 0.40) %>%

ggplot(aes(x = compConcentration, y = norm\_data)) +

geom\_jitter(aes(color = compName, shape = expType), alpha = 0.7, size = 1, width = 0.3) +

labs(x = "Compand concentration",

y = "Number of offspring,",

title = "Counted offspring after incubation with compound")

#making the log plot

normalized\_ce\_data %>% ggplot(aes(x = log10(compConcentration), y = norm\_data)) +

geom\_jitter(aes(color = compName, shape = expType), alpha = 0.7, size = 1, width = 0.2) +

labs(x = "Compand concentration",

y = "Number of offspring,",

title = "Counted offspring after incubation with compound")

```

\*\*K. Why would you want to take the step under J?\*\*

this eliminates natural and extraneous variation between groups. After normalization all groups fall on the same scale of 0 - 1.

1.2

O: answer left out of RMD:

My answer would be 5 very easy, the code used uses common packages and is very readable.