Database_RoundUp

Palmer Lab: Bonnie Lin

09 July, 2020

R Markdown

Broken down by cohort

of wake forest rfids

Cohort breakdown

```
## .
##  01  02  03  04  05
## 100 110 100 100 100
```

of subjects in raw data

Cohort breakdown

```
## .
##  01  02  03
##  89 110 100
```

of subjects in excel data

of tissue shipments

Spleen cohort breakdown

```
mitchell_shipments_spleen_df %>%
  mutate(cohort = str_match(sheet, "Shipment\\d+")[,1],
         cohort = str_pad(parse_number(cohort), 2, "left", "0")) %>%
  distinct(rfid, cohort) %>%
  select(cohort) %>% table()
```

```
## .
##  01  02  03  04
##  89 110 100 100
```

Ceca cohort breakdown

```
mitchell_shipments_ceca_df %>%
  mutate(cohort = str_match(sheet, "Shipment\\d+")[,1],
         cohort = str_pad(parse_number(cohort), 2, "left", "0")) %>%
  distinct(rfid, cohort) %>%
  select(cohort) %>% table()
```

```
## .
## 01  02  03  04
## 89 110 100 100
```
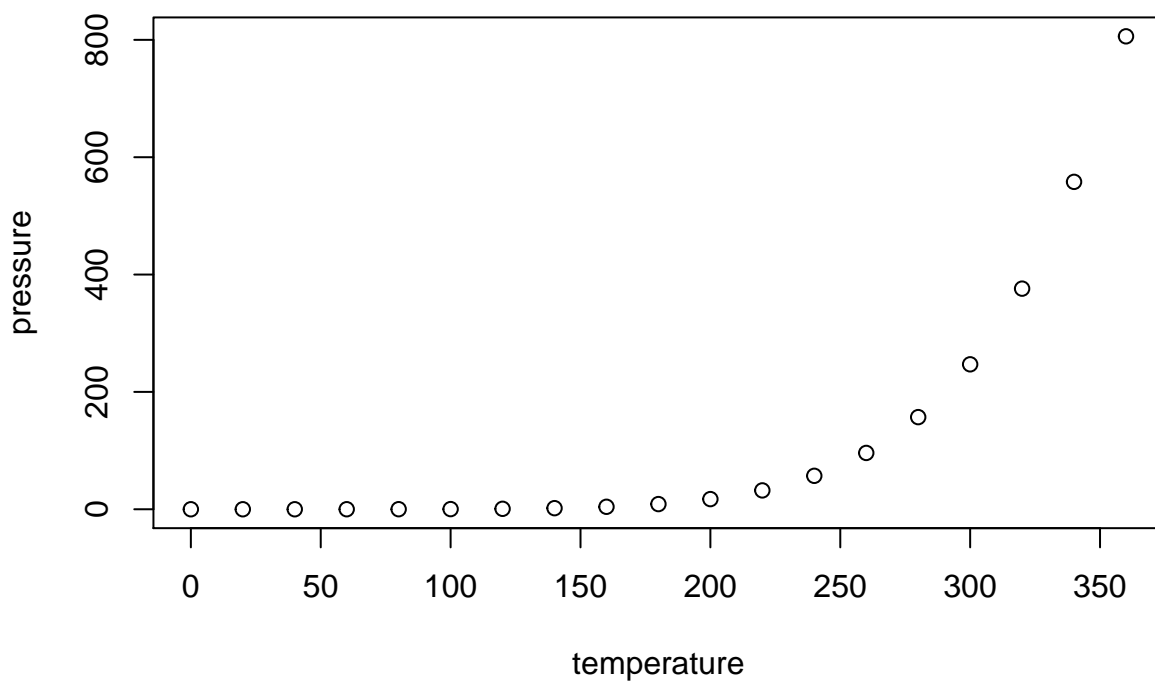
# of genotyping pipeline

```
summary(cars)
```

```
##      speed           dist
## Min.   : 4.0   Min.   :  2.00
## 1st Qu.:12.0   1st Qu.: 26.00
## Median :15.0   Median : 36.00
## Mean   :15.4   Mean   : 42.98
## 3rd Qu.:19.0   3rd Qu.: 56.00
## Max.   :25.0   Max.   :120.00
```

Experiments by Cohorts

You can also embed plots, for example:

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.