R Code Reference

Win Khaing

```
if (!require("pacman")) install.packages("pacman")
  pacman::p_load(ggplot2, tidyr, dplyr, tidyverse, knitr, finalfit, here)
```

Contigency Table (2x2 Table)

```
library(tidyverse)
library(gtsummary)

data(CO2)
head(CO2)
```

```
Grouped Data: uptake ~ conc | Plant
  Plant   Type  Treatment conc uptake
1   Qn1 Quebec nonchilled   95   16.0
2   Qn1 Quebec nonchilled  175   30.4
3   Qn1 Quebec nonchilled  250   34.8
4   Qn1 Quebec nonchilled  350   37.2
5   Qn1 Quebec nonchilled  500   35.3
6   Qn1 Quebec nonchilled  675   39.2
```

```
# basic summary table
CO2 %>% select(!c(Plant, conc)) %>% tbl_summary()
```

Characteristic	**N = 84**
Type	
Quebec	42 (50%)
Mississippi	42 (50%)
Treatment	

Characteristic	**N = 84**
nonchilled	42 (50%)
chilled	42 (50%)
uptake	28 (18, 37)

```
# summary split by a categorical variable
CO2 %>% select(!c(Plant, conc)) %>% tbl_summary(by = Type)
```

Characteristic	**Quebec**, N = 42	**Mississippi**, N = 42
Treatment		
nonchilled	21 (50%)	21 (50%)
chilled	21 (50%)	21 (50%)
uptake	37 (30, 40)	19 (14, 28)

```
# summary split by a categorical variable with p-value
CO2 %>% select(!c(Plant, conc)) %>%
  tbl_summary(by = Type) %>% add_p()
```

Characteristic	**Quebec**, N = 42	**Mississippi**, N = 42	**p-value**
Treatment			>0.9
nonchilled	21 (50%)	21 (50%)	
chilled	21 (50%)	21 (50%)	
uptake	37 (30, 40)	19 (14, 28)	<0.001

```
# include overall, extra heading, custom stats
CO2 %>% select(!c(Plant, conc)) %>%
  tbl_summary(
    by = Type,
    statistic = list(
      all_continuous() ~ "{mean} ({sd})",
      all_categorical() ~ "{n} / {N} ({p}%)"
    ),
    digits = all_continuous() ~ 2
  ) %>%
  add_p() %>% add_overall() %>%
  modify_spanning_header(c("stat_1", "stat_2") ~ "**Location**") %>%
  bold_labels()
```

Characteristic	**Overall**, N = 84	**Quebec**, N = 42	**Mississippi**, N = 42	**p-value**
Treatment				>0.9
nonchilled	42 / 84 (50%)	21 / 42 (50%)	21 / 42 (50%)	
chilled	42 / 84 (50%)	21 / 42 (50%)	21 / 42 (50%)	
uptake	27.21 (10.81)	33.54 (9.67)	20.88 (7.82)	<0.001

```
# crosstabs
CO2 %>%
  tbl_cross(
    row = Type,
    col = Treatment, percent = "cell"
  ) %>%
  add_p() %>%
  bold_labels()
```

	nonchilled	chilled	**Total**	**p-value**
Type				>0.9
Quebec	21 (25%)	21 (25%)	42 (50%)	
Mississippi	21 (25%)	21 (25%)	42 (50%)	
Total	42 (50%)	42 (50%)	84 (100%)	