

# Tables

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## Tables for FishTrapsFoodSec

```
# Load packages
library(readr)
library(knitr)
library(plotrix)
library(kableExtra)

# Import data
TripData <- read_csv("04_DataExploration_Out/TripDataForAnalysis_GatedTraps_Galligan.csv")

## Rows: 1839 Columns: 68
## -- Column specification -----
## Delimiter: ","
## chr  (12): TripID, Country, Site, Observer, Fisher, TrapLocation, Depth_m, S...
## dbl  (55): Latitude, Longitude, TotalCrew, TrapsOwned, TrapsFished, BrowserM...
## date  (1): Date
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

# Subset by trap type
trad.trip <- subset(TripData, TripData$TrapType == "Traditional")
gated.trip <- subset(TripData, TripData$TrapType == "Gated")

# Table columns
GatedTrapConcentration <- c(
  mean(gated.trip$CaConc_mgPer100g),
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mean(gated.trip$FeConc_mgPer100g),
mean(gated.trip$Omega3Conc_gPer100g),
mean(gated.trip$VAConc_ugPer100g),
mean(gated.trip$SeConc_ugPer100g),
mean(gated.trip$ZnConc_ugPer100g))

SE_GTC <- c(
  std.error(gated.trip$CaConc_mgPer100g),
  std.error(gated.trip$FeConc_mgPer100g),
  std.error(gated.trip$Omega3Conc_gPer100g),
  std.error(gated.trip$VAConc_ugPer100g),
  std.error(gated.trip$SeConc_ugPer100g),
  std.error(gated.trip$ZnConc_ugPer100g)
)

TraditionalTrapConcentration <- c(
  mean(trad.trip$CaConc_mgPer100g),
  mean(trad.trip$FeConc_mgPer100g),
  mean(trad.trip$Omega3Conc_gPer100g),
  mean(trad.trip$VAConc_ugPer100g),
  mean(trad.trip$SeConc_ugPer100g),
  mean(trad.trip$ZnConc_ugPer100g)
)

SE_TTC <- c(
  std.error(trad.trip$CaConc_mgPer100g),
  std.error(trad.trip$FeConc_mgPer100g),
  std.error(trad.trip$Omega3Conc_gPer100g),
  std.error(trad.trip$VAConc_ugPer100g),
  std.error(trad.trip$SeConc_ugPer100g),
  std.error(trad.trip$ZnConc_ugPer100g)
)

GatedTrapYield <- c(
  mean(gated.trip$CaPUE),
  mean(gated.trip$FePUE),
  mean(gated.trip$Omega3PUE),
  mean(gated.trip$VAPUE),

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    mean(gated.trip$SePUE),
    mean(gated.trip$ZnPUE)
)

SE_GTY <- c(
  std.error(gated.trip$CaPUE),
  std.error(gated.trip$FePUE),
  std.error(gated.trip$Omega3PUE),
  std.error(gated.trip$VAPUE),
  std.error(gated.trip$SePUE),
  std.error(gated.trip$ZnPUE)
)

TraditionalTrapYield <- c(
  mean(trad.trip$CaPUE),
  mean(trad.trip$FePUE),
  mean(trad.trip$Omega3PUE),
  mean(trad.trip$VAPUE),
  mean(trad.trip$SePUE),
  mean(trad.trip$ZnPUE)
)

SE_TTY <- c(
  std.error(trad.trip$CaPUE),
  std.error(trad.trip$FePUE),
  std.error(trad.trip$Omega3PUE),
  std.error(trad.trip$VAPUE),
  std.error(trad.trip$SePUE),
  std.error(trad.trip$ZnPUE)
)

RDI <- c(700, 7, 0.7, 300, 20, 3)

# Make a data frame
tab1 <- data.frame(GatedTrapConcentration, SE_GTC, TraditionalTrapConcentration, SE_TTC, GatedTrapYield, SE_GTY, TraditionalTrapYield, SE_TTY, RDI)

# Row names
rownames(tab1) <- c("Calcium (mg)", "Iron (mg)", "Omega-3 (g)",

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paste("Vitamin A (", "\u00b5", "g)", sep = ""),
paste("Selenium (", "\u00b5", "g)", sep = ""),
"Zinc (mg)")

# Column names
colnames(tab1) <- c(
  "Gated Trap Concentration (100g-1)",
  "±SE",
  "Traditional Trap Concentration (100g-1)",
  "±SE",
  "Gated Trap Yield (Trap-1)",
  "±SE",
  "Traditional Trap Yield (Trap-1)",
  "±SE",
  "Recommended Daily Intake (Child 1-3 yrs)"
)

# Render a table
kable(tab1, digits = 2)

```

	Gated Trap Concentration (100g <sup>-1</sup> )	±SE	Traditional Trap Concentration (100g <sup>-1</sup> )	±SE	Gated Trap Yield (Trap <sup>-1</sup> )	±SE	Traditional Trap Yield (Trap <sup>-1</sup> )	±SE
Calcium (mg)	7.45	0.18	7.18	0.17	278.31	10.54	278.31	10.54
Iron (mg)	0.14	0.00	0.13	0.00	5.20	0.20	5.20	0.20
Omega-3 (g)	0.04	0.00	0.03	0.00	1.38	0.05	1.38	0.05
Vitamin A (µg)	9.32	0.40	8.88	0.36	448.64	32.33	448.64	32.33
Selenium (µg)	5.69	0.15	5.78	0.14	259.27	12.46	259.27	12.46
Zinc (mg)	0.29	0.01	0.26	0.01	11.15	0.48	11.15	0.48