LLIN_Analses

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Load the Data

```
library(readr)
ig2.df <- read_csv("Burkina Faso_bio_ig2_master_m36_anonym.csv")
```

```
Rows: 322 Columns: 35
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (4): Province, netid, Mosquitospeciesstrain, NetType
dbl (31): round, loc, splace, splacegr, uselast, usergr, usegr2, freq, seaso...

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.
```

```
pn3.df <- read_csv("Burkina Faso_bio_pn3_master_m36_anonym.csv")
```

```
Rows: 590 Columns: 33
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (4): Province, netid, Mosquitospeciesstrain, NetType
dbl (29): round, loc, splace, splacegr, uselast, usergr, usegr2, freq, seaso...

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.
```

```
interceptor.df <- read_csv("Burkina Faso_bio_interceptor_master_m36_anonym.csv")
```

```
Rows: 120 Columns: 26
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (3): Province, netid, Mosquitospeciesstrain
dbl (23): round, loc, splace, splacegr, uselast, usergr, usegr2, freq, seaso...

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.
```

IG2 Data Preliminary Analyses

Strucutre of IG2 Data

```
colnames(ig2.df)
```

```
 [1] "Province"            "netid"               "round"
 [4] "loc"                 "splace"              "splacegr"
 [7] "uselast"             "usergr"              "usegr2"
[10] "freq"                "season"              "wash"
[13] "times"               "soap"                "soapgr"
[16] "dried"               "res"                 "Mosquitospeciesstrain"
[19] "NetType"             "nettype"             "ig2_filter"
[22] "n"                   "n_penetrated"        "n_blood_fed"
[25] "n_dead24h"           "n_dead72h"           "penetrated"
[28] "bloodfed"            "mort24h"             "mort72"
[31] "bfi"                 "alpha_g_kg"          "alpha_mg_m2"
[34] "chlor_g_kg"          "chlor_mg_m2"
```

```
table(ig2.df$NetType, ig2.df$Mosquitospeciesstrain)
```

	An. coluzzii VKPER	An. gambiae Kisumu	An.kisumu
.	1	0	0
Interceptor	14	10	2
Interceptor G2	133	96	32
New	0	0	3
Untreated	2	0	2
Untreated net	13	14	0

```
# An.kisumu is the same as An.gambiae Kisumu in "Mosquitospeciesstrain".
# Merge them.
ig2.df$Mosquitospeciesstrain[
  ig2.df$Mosquitospeciesstrain == "An. gambiae Kisumu"] <- "An. Kisumu"
ig2.df$Mosquitospeciesstrain[
  ig2.df$Mosquitospeciesstrain == "An.kisumu"] <- "An. Kisumu"
# Untreated and Untreated net are the same as in "NetType".
ig2.df$NetType[ig2.df$NetType == "Untreated"] <- "Untreated Net"
ig2.df$NetType[ig2.df$NetType == "Untreated net"] <- "Untreated Net"
```

```
# One "NetType" is . and another is New. Remove it.
ig2.df <- ig2.df[ig2.df$NetType != ".", ]
ig2.df <- ig2.df[ig2.df$NetType != "New", ]

# Filter > 100 vales in "mort24h" and "mort72"
ig2.df <- ig2.df[ig2.df$mort24h <= 100, ]
ig2.df <- ig2.df[ig2.df$mort72 <= 100, ]

table(ig2.df$NetType, ig2.df$Mosquitospeciesstrain)
```

```
                  An. coluzzii VKPER An. Kisumu
  Interceptor                    14         12
  Interceptor G2                133        127
  Untreated Net                  15         16
```
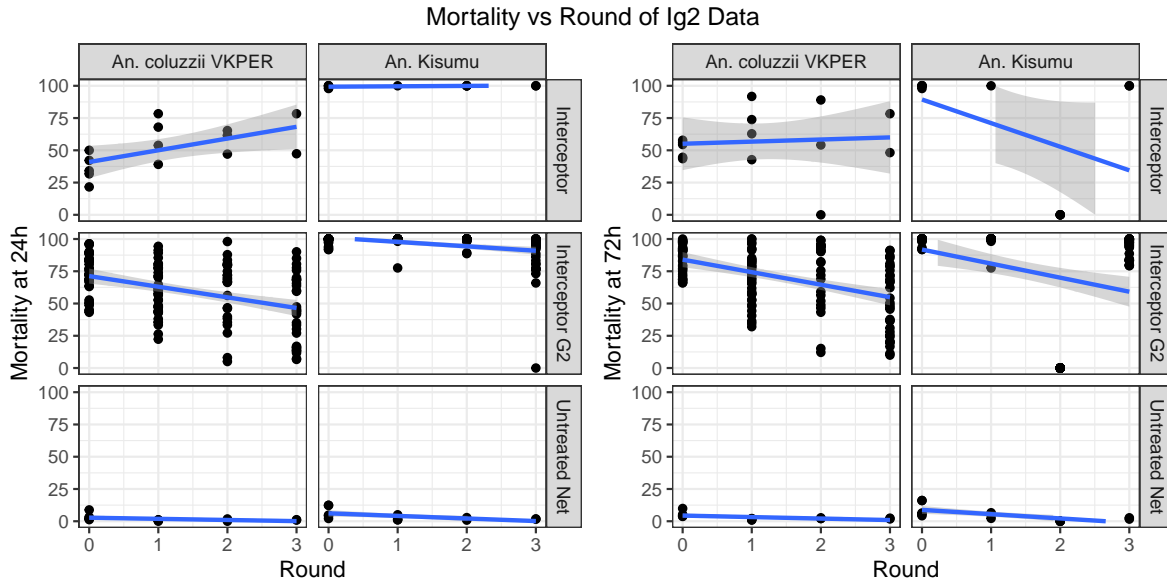
Plot mortality at 24h and 72h v.s. round by type and mosquito species strain

```
# Plot "mort24h" & "mort72" v.s. "round" by "NetType" & "Mosquitospeciesstrain"

library(ggplot2)
library(gridExtra)

m1 <- ggplot(ig2.df, aes(x = round, y = mort24h)) +
  geom_point() + geom_smooth(method = "lm") +
  facet_grid(NetType ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 24h") + xlab("Round") +
  theme_bw()
m2 <- ggplot(ig2.df, aes(x = round, y = mort72)) +
  geom_point() + geom_smooth(method = "lm") +
  facet_grid(NetType ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 72h") + xlab("Round") +
  theme_bw()

grid.arrange(m1, m2, ncol = 2,
             top = "Mortality vs Round of Ig2 Data")
```

Mortality vs Round of Ig2 Data

```
ggsave("1_IG2_Mortality_vs_Round.png", width = 8, height = 4)
```

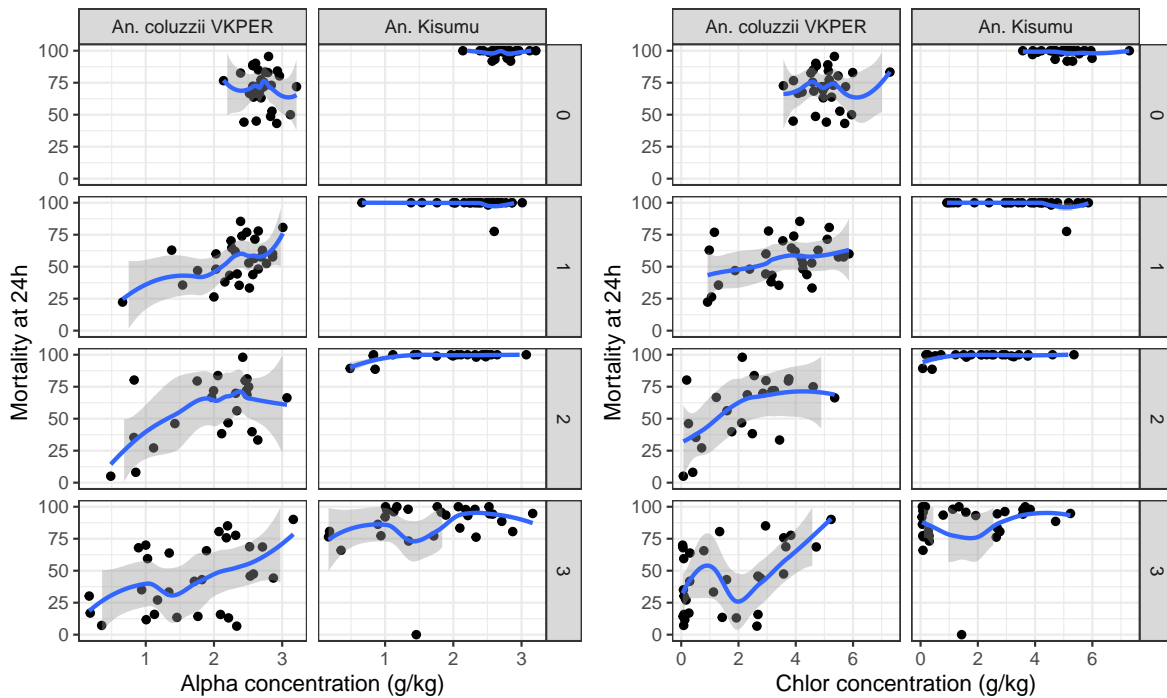**Plot mortality at 24h and 72h v.s. drug conc. by round and mosquito species strain**

```
# Plot "mort24h" v.s. "alpha_g_kg" & "chlor_g_kg" by "round" & "Mosquitospeciesstrain".

n1 <- ggplot(ig2.df, aes(x = alpha_g_kg, y = mort24h)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 24h") + xlab("Alpha concentration (g/kg)") +
  theme_bw()
n2 <- ggplot(ig2.df, aes(x = chlor_g_kg, y = mort24h)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 24h") + xlab("Chlor concentration (g/kg)") +
  theme_bw()

grid.arrange(n1, n2, ncol = 2,
             top = "Mortality vs Drug Concentration of IG2 Data")
```
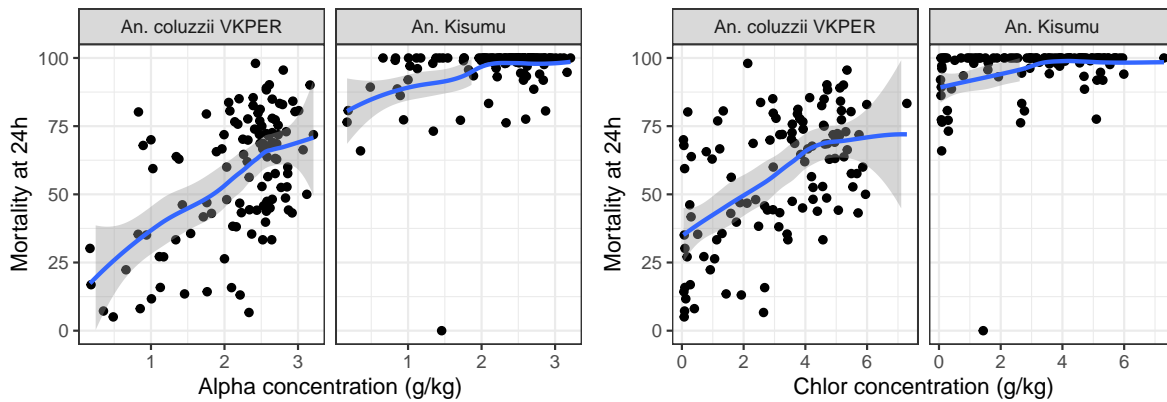
Mortality vs Drug Concentration of IG2 Data

```r
ggsave("2_IG2_Mortality_24h_vs_Drug_Concentration.png", width = 8, height = 5)
```

```r
# Plot "mort24h" v.s. "alpha_g_kg" & "chlor_g_kg" by "Mosquitospeciesstrain".

n1.2 <- ggplot(ig2.df, aes(x = alpha_g_kg, y = mort24h)) +
  geom_point() + geom_smooth() +
  facet_wrap(~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 24h") + xlab("Alpha concentration (g/kg)") +
  theme_bw()
n2.2 <- ggplot(ig2.df, aes(x = chlor_g_kg, y = mort24h)) +
  geom_point() + geom_smooth() +
  facet_wrap(~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality at 24h") + xlab("Chlor concentration (g/kg)") +
  theme_bw()

grid.arrange(n1.2, n2.2, ncol = 2,
             top = "Mortality vs Drug Concentration of IG2 Data")
```

Mortality vs Drug Concentration of IG2 Data

```
ggsave("3_IG2_Mortality_vs_Drug_Concentration.png", width = 8, height = 3)
```

PN3 Data Preliminary Analyses

```
colnames(pn3.df)
```

```
 [1] "Province"            "netid"               "round"
 [4] "loc"                 "splace"              "splacegr"
 [7] "uselast"             "usergr"              "usegr2"
[10] "freq"                "season"              "wash"
[13] "times"               "soap"                "soapgr"
[16] "dried"               "res"                 "Mosquitospeciesstrain"
[19] "NetType"             "nettype"             "panel_1side_2roof"
[22] "pn3_filter"          "n"                   "n_kd"
[25] "kd60"                "n_m"                 "mort"
[28] "delta_side_g_kg"     "delta_side_mg_m2"    "delta_roof_g_kg"
[31] "delta_roof_mg_m2"    "pbo_roof_g_kg"       "pbo_roof_mg_m2"
```

```
table(pn3.df$NetType, pn3.df$Mosquitospeciesstrain)
```

	An. coluzzii VKPER	An. gambiae Kisumu
Contrôle	4	4
PermaNet 2.0	6	4
PermaNet 3.0	286	252
Untreated Net_Control	20	14

```
# Change An. gambiae Kisumu to An. kisumu in "Mosquitospeciesstrain".
pn3.df$Mosquitospeciesstrain[
  pn3.df$Mosquitospeciesstrain == "An. gambiae Kisumu"] <- "An. Kisumu"
# Contrôle is the same as Untreated Net_Control  in "NetType".
# Merge them and name as "Untreated Net".
pn3.df$NetType[pn3.df$NetType == "Contrôle"] <- "Untreated Net"
pn3.df$NetType[pn3.df$NetType == "Untreated Net_Control"] <- "Untreated Net"

# Filter > 100 vales in "mort" and "kd60"
pn3.df <- pn3.df[pn3.df$mort <= 100, ]
pn3.df <- pn3.df[pn3.df$kd60 <= 100, ]

# Remove NA in "NetsType" and "Mosquitospeciesstrain"
pn3.df <- pn3.df[!is.na(pn3.df$NetType), ]
pn3.df <- pn3.df[!is.na(pn3.df$Mosquitospeciesstrain), ]

table(pn3.df$NetType, pn3.df$Mosquitospeciesstrain)
```

```
              An. coluzzii VKPER An. Kisumu
  PermaNet 2.0                4          4
  PermaNet 3.0              285        251
  Untreated Net             22          16
```

Plot knock out rate at 60 min and moratality v.s. round by type and mosquito species strain

```
# Plot "kd60" & "mort" v.s. "round" by "NetType" & "Mosquitospeciesstrain"

o1 <- ggplot(pn3.df, aes(x = round, y = kd60)) +
  geom_point() + geom_smooth(method = "lm") +
  facet_grid(NetType ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Knock Down Rate at 60 min") + xlab("Round") +
  theme_bw()
o2 <- ggplot(pn3.df, aes(x = round, y = mort)) +
  geom_point() + geom_smooth(method = "lm") +
  facet_grid(NetType ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Round") +
```
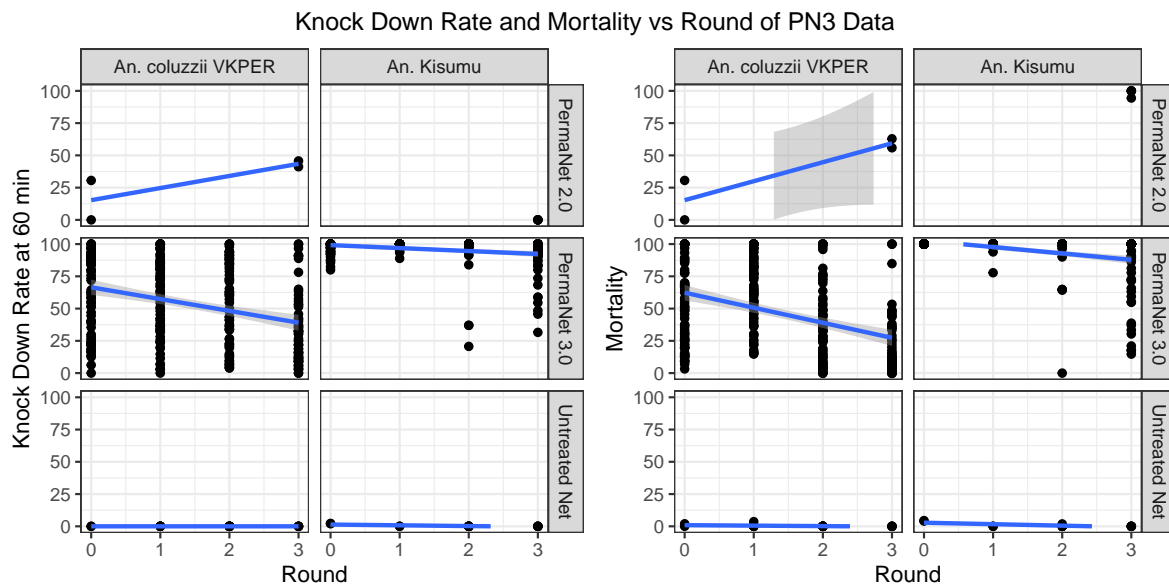
```
    theme_bw()

grid.arrange(o1, o2, ncol = 2,
             top = "Knock Down Rate and Mortality vs Round of PN3 Data")
```


Knock Down Rate and Mortality vs Round of PN3 Data

```
ggsave("4_PN3_Knock_Down_Rate_and_Mortality_vs_Round.png",
       width = 8, height = 4)
```

Plot knock out rate at 60 min and mortality v.s. drug conc. by round and mosquito species strain

```
# Plot "kd60" v.s. "delta_side_g_kg" & "delta_roof_g_kg" & "pbo_roof_g_kg"
# by "round" & "Mosquitospeciesstrain".

p1 <- ggplot(pn3.df, aes(x = delta_side_g_kg, y = kd60)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Knock Down Rate at 60 min") + xlab("Delta Side concentration (g/kg)") +
  theme_bw()
p2 <- ggplot(pn3.df, aes(x = delta_roof_g_kg, y = kd60)) +
  geom_point() + geom_smooth() +
```
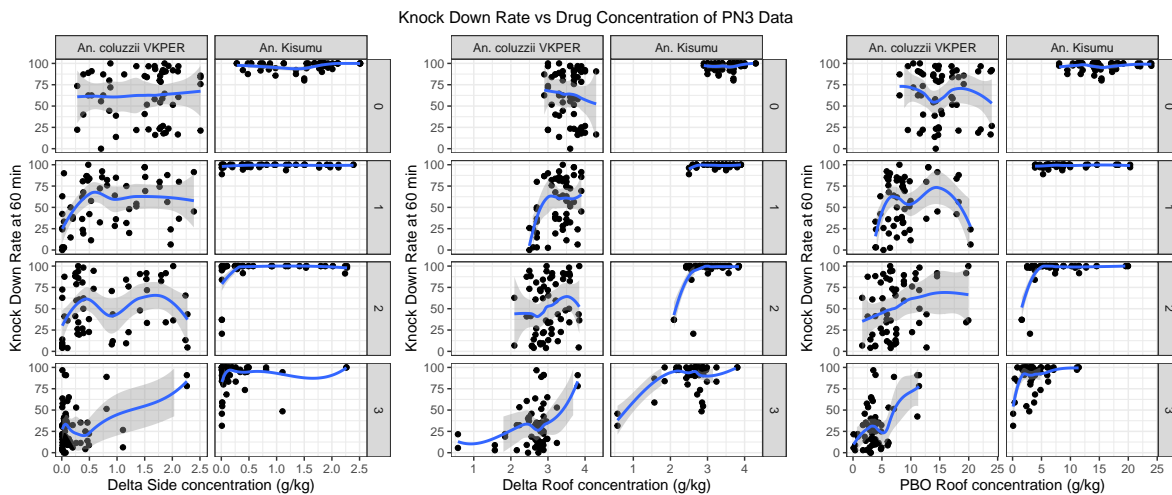
```
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Knock Down Rate at 60 min") + xlab("Delta Roof concentration (g/kg)") +
  theme_bw()
p3 <- ggplot(pn3.df, aes(x = pbo_roof_g_kg, y = kd60)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Knock Down Rate at 60 min") + xlab("PBO Roof concentration (g/kg)") +
  theme_bw()

grid.arrange(p1, p2, p3, ncol = 3,
             top = "Knock Down Rate vs Drug Concentration of PN3 Data")
```



```
ggsave("5_PN3_Knock_Down_Rate_vs_Drug_Concentration.png",
       width = 12, height = 5)
```

```
# Plot "mort" v.s. "delta_side_g_kg" & "delta_roof_g_kg" & "pbo_roof_g_kg"
# by "round" & "Mosquitospeciesstrain".

q1 <- ggplot(pn3.df, aes(x = delta_side_g_kg, y = mort)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Delta Side concentration (g/kg)") +
  theme_bw()
q2 <- ggplot(pn3.df, aes(x = delta_roof_g_kg, y = mort)) +
```
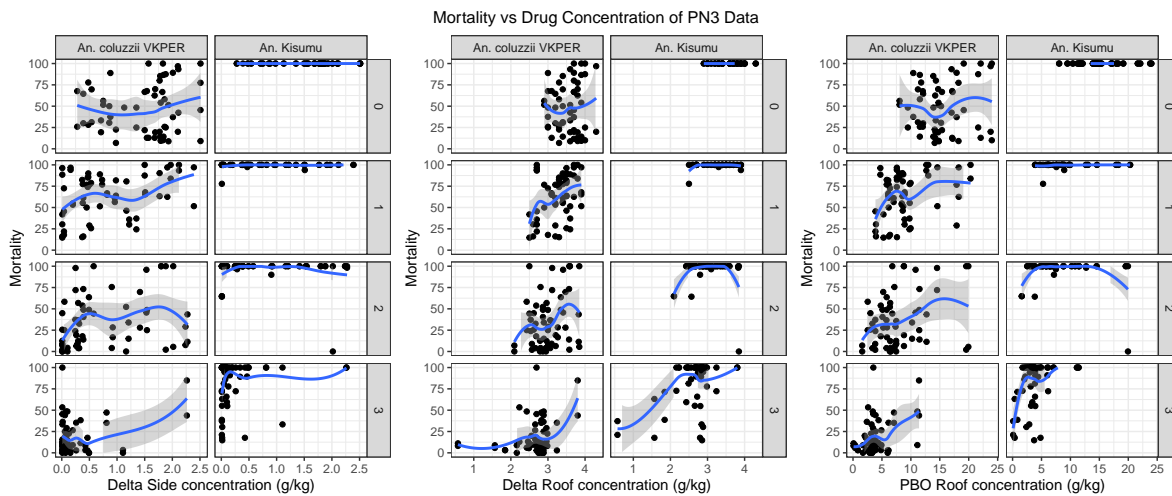
```
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Delta Roof concentration (g/kg)") +
  theme_bw()
q3 <- ggplot(pn3.df, aes(x = pbo_roof_g_kg, y = mort)) +
  geom_point() + geom_smooth() +
  facet_grid(round ~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("PBO Roof concentration (g/kg)") +
  theme_bw()

grid.arrange(q1, q2, q3, ncol = 3,
             top = "Mortality vs Drug Concentration of PN3 Data")
```



```
ggsave("6_PN3_Mortality_vs_Drug_Concentration.png", width = 12, height = 5)
```

```
# Plot "mort" v.s. "delta_side_g_kg" & "delta_roof_g_kg" & "pbo_roof_g_kg"
# by "Mosquitospeciesstrain".

q1.2 <- ggplot(pn3.df, aes(x = delta_side_g_kg, y = mort)) +
  geom_point() + geom_smooth() +
  facet_wrap(~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Delta Side concentration (g/kg)") +
  theme_bw()
q2.2 <- ggplot(pn3.df, aes(x = delta_roof_g_kg, y = mort)) +
```

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```
  geom_point() + geom_smooth() +
  facet_wrap(~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Delta Roof concentration (g/kg)") +
  theme_bw()
q3.2 <- ggplot(pn3.df, aes(x = pbo_roof_g_kg, y = mort)) +
  geom_point() + geom_smooth() +
  facet_wrap(~ Mosquitospeciesstrain) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("PBO Roof concentration (g/kg)") +
  theme_bw()

grid.arrange(q1.2, q2.2, q3.2, ncol = 3,
             top = "Mortality vs Drug Concentration of PN3 Data")
```
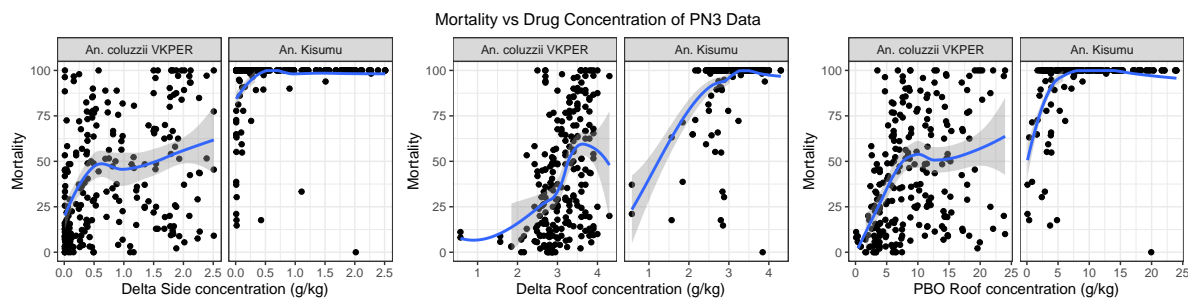


```
ggsave("7_PN3_Mortality_vs_Drug_Concentration.png", width = 12, height = 3)
```

Comparison of IG2 and PN3 Data

Data structure

```
library(dplyr)
```

```
Attaching package: 'dplyr'
```

```
The following object is masked from 'package:gridExtra':

    combine
```

```
The following objects are masked from 'package:stats':

    filter, lag


The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```r
# Select An. coluzzii VKPER from "Mosquitospeciesstrain" in ig2.df.
# Select Interceptor G2 from "NetType" in ig2.df.
# Extract "NetType", "round", and "mort24h" from ig2.df
# Name 3 columns as "NetType", "round", and "mort" respectively.
ig2.mort <- ig2.df %>%
  filter(Mosquitospeciesstrain == "An. coluzzii VKPER") %>%
  filter(NetType == "Interceptor G2") %>%
  select(NetType, round, mort24h) %>%
  rename(mort = mort24h)


# Select An. coluzzii VKPER from "Mosquitospeciesstrain" in pn3.df.
# Select PermaNet 3.0 from "NetType" in pn3.df.
# Extract "NetType", "round", and "mort" from pn3.df
pn3.mort <- pn3.df %>%
  filter(Mosquitospeciesstrain == "An. coluzzii VKPER") %>%
  filter(NetType == "PermaNet 3.0") %>%
  select(NetType, round, mort)


# Combine ig2.mort and pn3.mort
ig2.pn3.mort <- rbind(ig2.mort, pn3.mort)
```
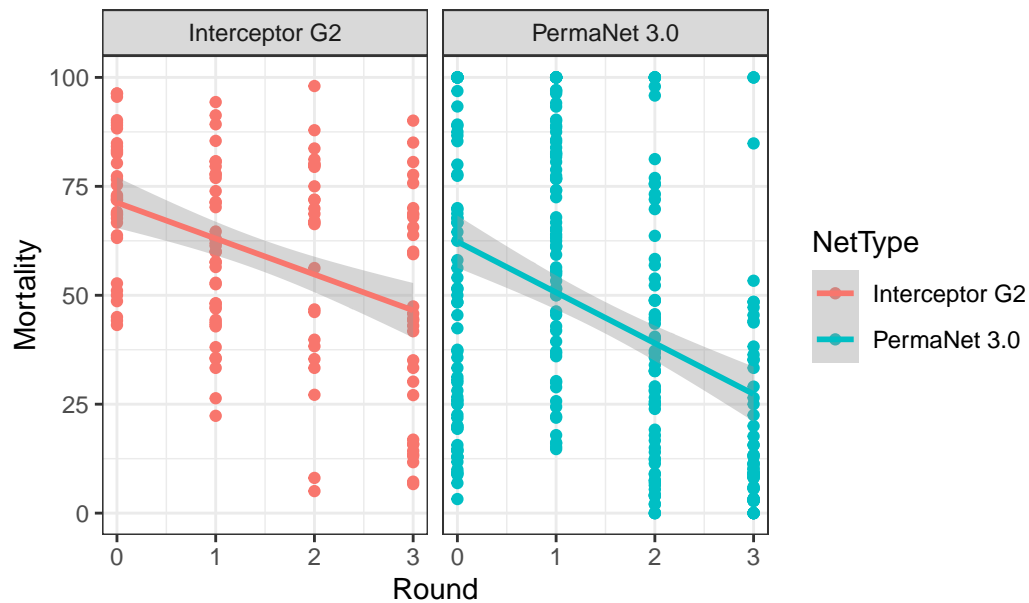
Dot plot Mortality Comparison of IG2 and PN3 Data

```r
# Plot "mort" v.s. "round" by "NetType" of ig2.pn3.mort.

ggplot(ig2.pn3.mort, aes(x = round, y = mort, color = NetType,)) +
  geom_point() + geom_smooth(method = "lm") +
  facet_wrap(~ NetType) +
  ylim(0, 100) +
  ylab("Mortality") + xlab("Round") +
  theme_bw() +
  ggtitle("Mortality Comparison of IG2 and PN3 Data")
```

Mortality Comparison of IG2 and PN3 Data

```
ggsave("8_Mortality_Comparison_of_IG2_and_PN3_Data.png", width = 6, height = 3)
```

Statistical inference

```
# Perform t-test to compare mortality between IG2 and PN3 for each round.
# t.test ~ 2 independent samples
cat("t-test: IG2 vs PN3\n")
```

```
t-test: IG2 vs PN3
```

```
cat("p-value for each round:\n")
```

```
p-value for each round:
```

```
t.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 0, ])$p.value
```

```
[1] 3.381515e-06
```

```r
t.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 1, ])$p.value
```

```
[1] 0.08416484
```

```r
t.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 2, ])$p.value
```

```
[1] 0.001256952
```

```r
t.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 3, ])$p.value
```

```
[1] 3.384657e-05
```

```r
cat("\n")
```

```r
# Perform U-test to compare mortality between IG2 and PN3 for each round.
# wilcox.test ~ 2 independent samples
cat("U-test: IG2 vs PN3\n")
```

```
U-test: IG2 vs PN3
```

```r
cat("p-value for each round:\n")
```

```
p-value for each round:
```

```r
wilcox.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 0, ])$p.value
```

```
[1] 0.0006484355
```

```r
wilcox.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 1, ])$p.value
```

```
[1] 0.0647963
```

```r
wilcox.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 2, ])$p.value
```

```
[1] 0.002721057
```

```
wilcox.test(mort ~ NetType, ig2.pn3.mort[ig2.pn3.mort$round == 3, ])$p.value
```

```
[1] 2.463179e-06
```

Violin plot Mortality Comparison of IG2 and PN3 Data

```
# Plot "mort" v.s. "round" of ig2.pn3.mort by "NetType".
library(ggpubr)

ggviolin(ig2.pn3.mort, x = "round", y = "mort", color = "NetType",
         palette = "jco", add = "mean_sd", error.plot = "crossbar",
         add.params = list(size = 0.5)) +
  geom_jitter(aes(color = NetType), position = position_jitterdodge(0.2),
              size = 0.5) +
  theme_bw() + ylim(0, 100) +
  labs(x = "Round", y = "Mortality",
       title = "Mortality Comparison of IG2 and PN3 Data",
       subtitle = "An. coluzzii VKPER") +
  # U test of 2 independent samples for each round
  stat_compare_means(method = "wilcox.test", label = "p.signif",
                     aes(group = NetType), label.y = 99)
```


Mortality Comparison of IG2 and PN3 Data
An. coluzzii VKPER
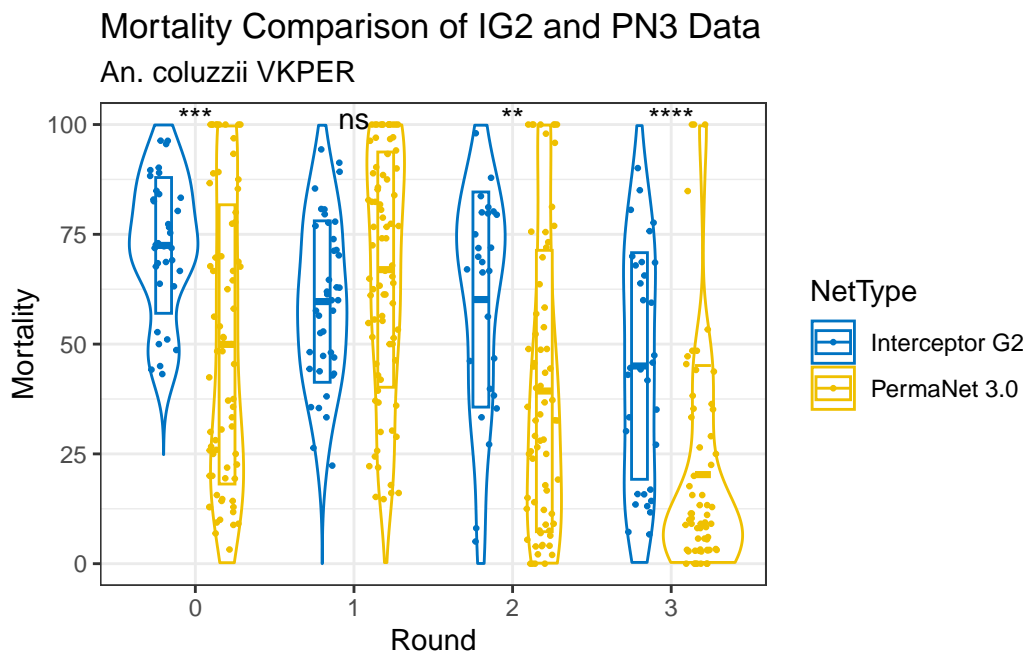
```
ggsave("9_Mortality_Comparison_of_IG2_and_PN3_Data_Violin.png",
       width = 6, height = 4)
```

Box plot Mortality Comparison of IG2 and PN3 Data

```
# Plot "mort" v.s. "round" of ig2.pn3.mort by "NetType".

ggboxplot(ig2.pn3.mort, x = "round", y = "mort", color = "NetType",
          palette = "jco") +
  geom_jitter(aes(color = NetType), position = position_jitterdodge(0.2),
              size = 1) +
  theme_bw() + ylim(0, 100) +
  labs(x = "Round", y = "Mortality",
       title = "Mortality Comparison of IG2 and PN3 Data",
       subtitle = "An. coluzzii VKPER") +
  # U test of 2 independent samples for each round
  stat_compare_means(method = "wilcox.test", label = "p.signif",
                     aes(group = NetType), label.y = 99)
```
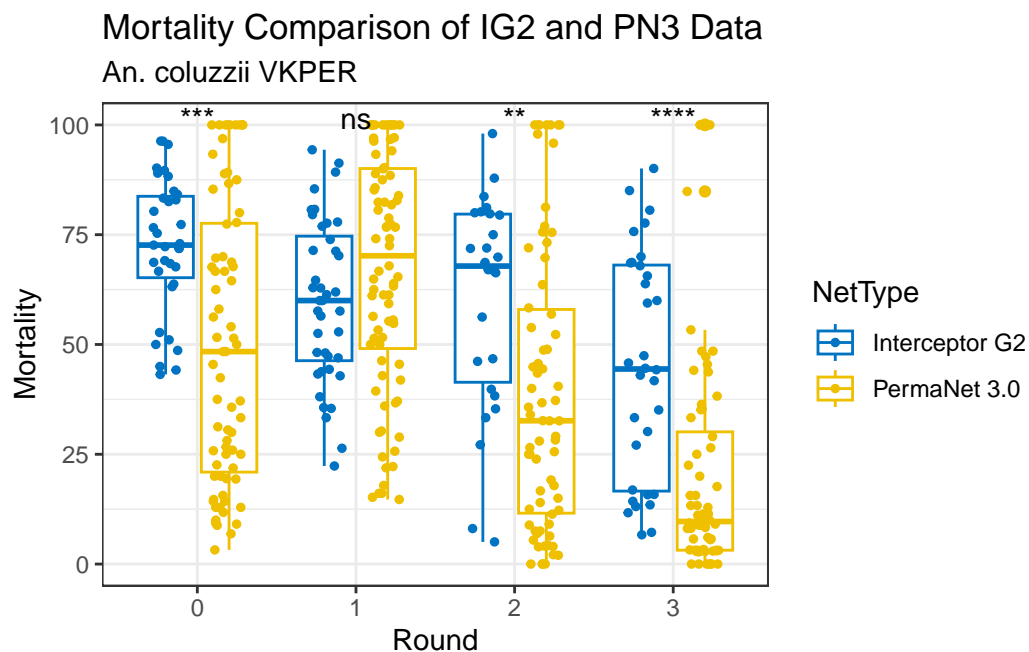

Mortality Comparison of IG2 and PN3 Data
An. coluzzii VKPER

```
ggsave("10_Mortality_Comparison_of_IG2_and_PN3_Data_Box.png",
       width = 5, height = 3)
```

Interceptor Data Preliminary Analyses

Structure of Interceptor Data

```
colnames(interceptor.df)
```

```
 [1] "Province"                "netid"                   "round"
 [4] "loc"                     "splace"                  "splacegr"
 [7] "uselast"                 "usergr"                  "usegr2"
[10] "freq"                    "season"                  "wash"
[13] "times"                   "soap"                    "soapgr"
[16] "dried"                   "Mosquitospeciesstrain"   "n"
[19] "n_kd"                    "n_m"                     "kd60"
[22] "mort"                    "opt"                     "min"
[25] "g_kg"                    "mg_m2"
```

```
table(interceptor.df$Mosquitospeciesstrain)
```

```
An. gambiae Kisumu
               120
```