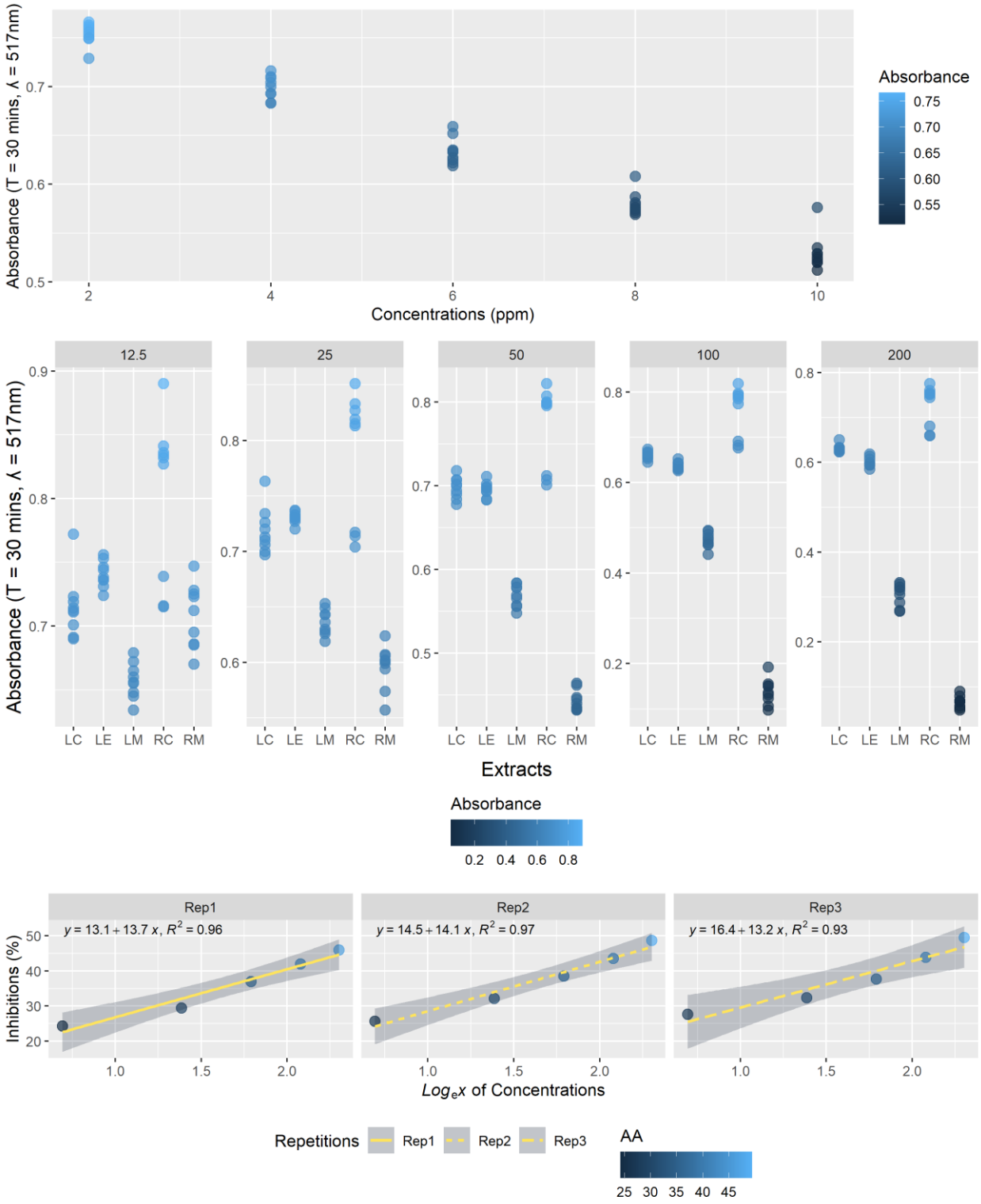
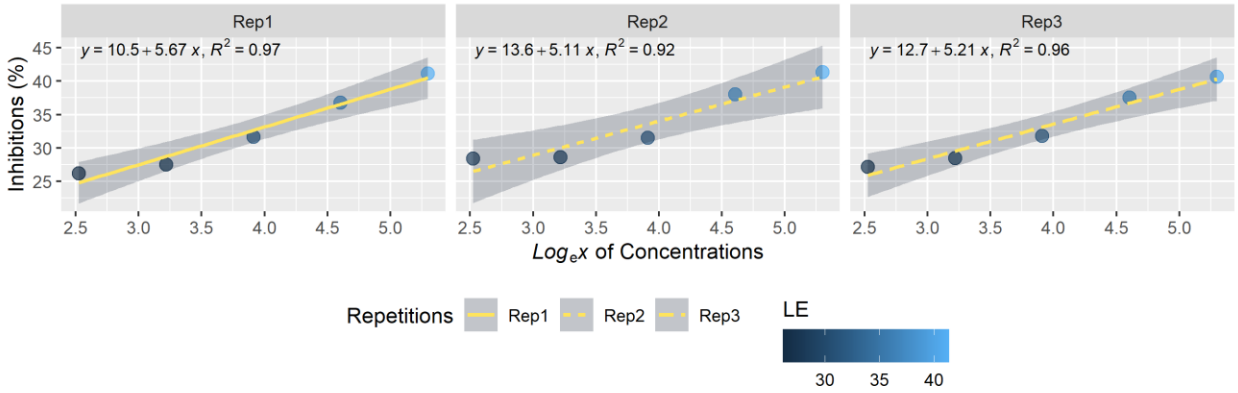
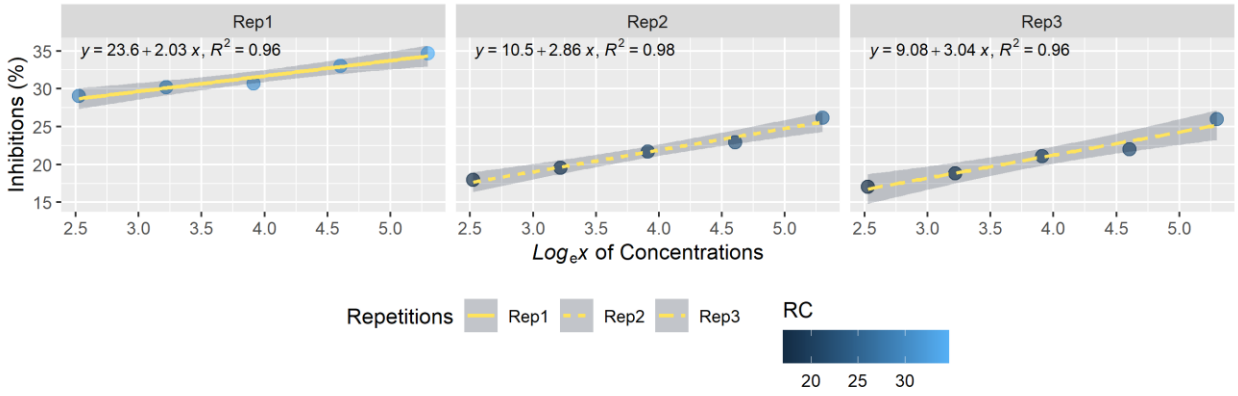
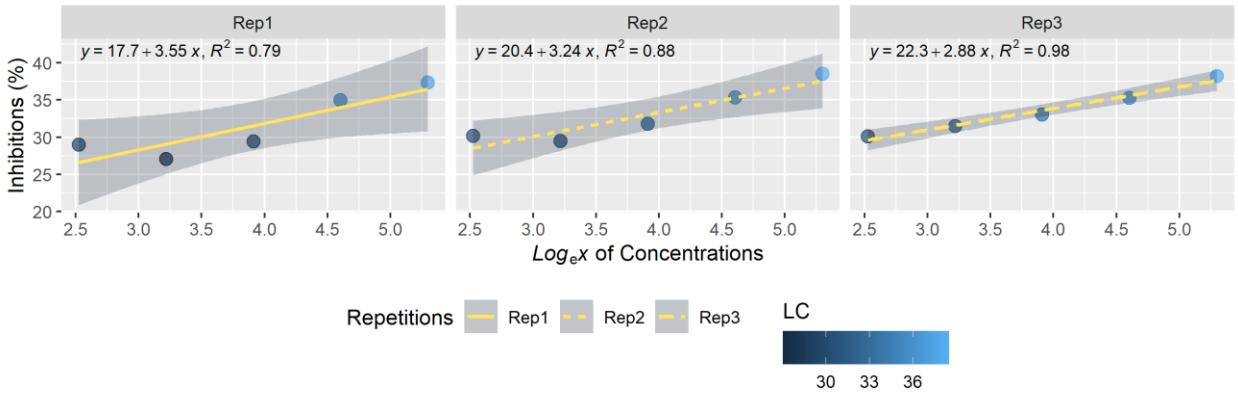
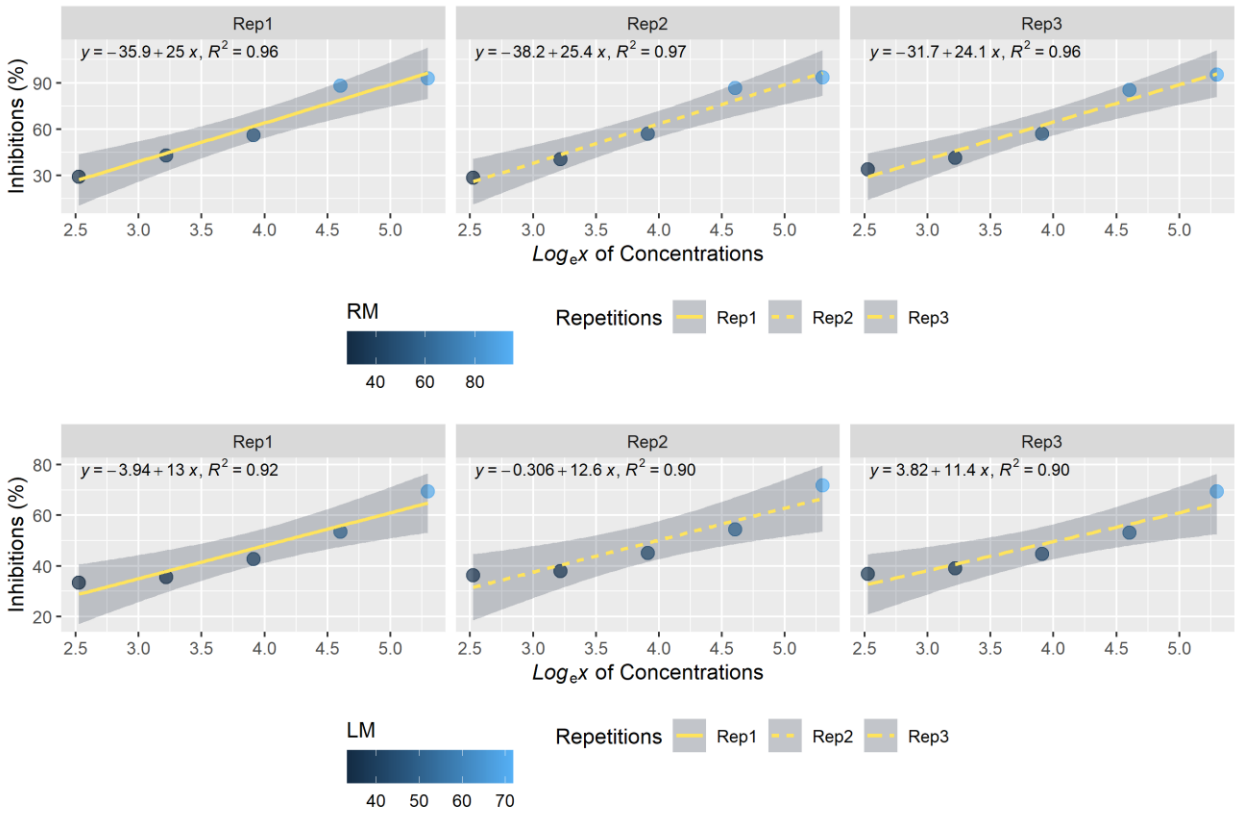

Absorbance (T = 30 mins, λ = 517nm)
Concentrations (ppm)
Absorbance
0.75
0.70
0.65
0.60
0.55
12.5
25
50
100
200
LC LE LM RC RM
Extracts
Absorbance
0.2 0.4 0.6 0.8
Rep1
Rep2
Rep3
y = 13.1 + 13.7 x, R² = 0.96
y = 14.5 + 14.1 x, R² = 0.97
y = 16.4 + 13.2 x, R² = 0.93
Inhibitions (%)
Log_e x of Concentrations
Repetitions
Rep1
Rep2
Rep3
AA
25 30 35 40 45


Rep1
y = 10.5 + 5.67 x, R² = 0.97
Rep2
y = 13.6 + 5.11 x, R² = 0.92
Rep3
y = 12.7 + 5.21 x, R² = 0.96
Inhibitions (%)
Log_e x of Concentrations
Repetitions
Rep1
Rep2
Rep3
LE
30
35
40


Rep1
y = 23.6 + 2.03 x, R² = 0.96
Rep2
y = 10.5 + 2.86 x, R² = 0.98
Rep3
y = 9.08 + 3.04 x, R² = 0.96
Inhibitions (%)
Log_e x of Concentrations
Repetitions
Rep1
Rep2
Rep3
RC
20
25
30


Rep1
y = 17.7 + 3.55 x, R² = 0.79
Rep2
y = 20.4 + 3.24 x, R² = 0.88
Rep3
y = 22.3 + 2.88 x, R² = 0.98
Inhibitions (%)
Log_e x of Concentrations
Repetitions
Rep1
Rep2
Rep3
LC
30
33
36



Supplemental File

RStudio/2023.03.1+446 © 2009-2023 Posit Software, PBC.
"Cherry Blossom" Release (6e31ffc3, 2023-05-09) for windows

The following algorithm was used to produce the figures from raw data material of IC50 spectrophotometry analysis.

```
library(gcookbook)
library(viridis)
library(ggpmisc)
#Absorbance_Extracts2.0
ggplot(data=IC50_R_Studio, mapping = aes(x = E, y = Absorbance, color = Absorbance))+
 # geom_point()
 #str(IC50_R_Studio)
 #IC50_R_Studio %>% ggplot(aes(x = E, y = Absorbance, color = Absorbance))+
 geom_point(size = 3, alpha = 0.7)+
 facet_wrap(~ Conc, nrow = 1, scales = "free")+
 #facet_grid()+
 #gradient_color("RdYlBu")+
 #scale_fill_viridis(discrete = FALSE, option = "C")+
 xlab("Extracts") +
```

```
  ylab("Absorbance (T = 30 mins, ʎ = 517nm)") +
  #theme_minimal() +
  theme(legend.position = "bottom")+
  theme(axis.title.x=element_text(size=13))+
  theme(axis.title.y=element_text(size=13))+
  guides(colour = guide_colorbar(title.position = "top"))+
  theme(axis.title.x = element_text(vjust=-1.5))
  #theme(legend.title = element_text(size=13))
ggsave("Absorbance_Extracts.tiff", width = 9, height = 5)

#Absorbance_Ascorbic Acid
ggplot(data=IC50_R_Studio_AA, mapping = aes(x = Concentrations.ppm, y = Absorbance, color
= Absorbance))+
  #geom_point()
  #str(IC50_R_Studio_AA)
  #IC50_R_Studio_AA %>% ggplot(aes(x = Concentrations.ppm, y = Absorbance, color =
Absorbance))+
  geom_point(size = 3, alpha = 0.7)+
  #facet_wrap(~ Concentrations.ppm, nrow = 1, scales = "free")+
  #labs(fill = "Absorbance")+
  #theme(legend.title = element_text ("Absorbance")) +
  xlab("Concentrations (ppm)") +
  ylab("Absorbance (T = 30 mins, ʎ = 517nm)")
ggsave("Absorbance_AA.tiff", width = 9, height = 3)

#Linear_regression_KA
ggplot(IC50_R_Studio_IN, aes(ConcEx, RC, linetype = Repetitions, grp.label = Repetitions))+
  geom_point(aes(color = RC), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_KA.tiff", width = 9, height = 3)

#Linear_regression_MA
ggplot(IC50_R_Studio_IN, aes(ConcEx, RM, linetype = Repetitions, grp.label = Repetitions))+
```

```
  geom_point(aes(color = RM), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_MA.tiff", width = 9, height = 3)

#Linear_regression_KD
ggplot(IC50_R_Studio_IN, aes(ConcEx, LC, linetype = Repetitions, grp.label = Repetitions))+
  geom_point(aes(color = LC), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_KD.tiff", width = 9, height = 3)

#Linear_regression_MD
ggplot(IC50_R_Studio_IN, aes(ConcEx, LM, linetype = Repetitions, grp.label = Repetitions))+
  geom_point(aes(color = LM), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
```

```
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_MD.tiff", width = 9, height = 3)

#Linear_regression_ED
ggplot(IC50_R_Studio_IN, aes(ConcEx, LE, linetype = Repetitions, grp.label = Repetitions))+
  geom_point(aes(color = LE), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_ED.tiff", width = 9, height = 3)

#Linear_regression_AA
ggplot(IC50_R_Studio_INA, aes(ConcExAA, AA, linetype = Repetitions, grp.label = Repetitions))+
  geom_point(aes(color = AA), size = 3, alpha = 0.7) +
  stat_poly_line(fill= "#001128", color = "#FFE45C", alpha = 0.2) +
  stat_poly_eq(use_label(c("eq", "r2")), size = 3, label.y = 40) +
  #scale_color_viridis(discrete = TRUE, option = "D")+
  #scale_fill_viridis(discrete = TRUE, option = "D") +
  facet_wrap(~ Repetitions)+
  #theme_minimal() +
  theme(legend.position = "bottom") +
  theme(legend.box = "horizontal")+
  guides(colour = guide_colorbar(order = 1))+
  guides(colour = guide_colorbar(title.position = "top"))+
  labs(x=expression(paste(italic("Log")["e"], italic("x")," of Concentrations"))) +
  ylab("Inhibitions (%)")
ggsave("Inhibitions_AA.tiff", width = 9, height = 3)
```