# 加载必要的包

library(tidyverse)

library(readxl)

library(rstatix) # 重复测量方差分析

library(ggpubr) # 添加显著性标记

# 读入数据

data = read\_xlsx("data\_4.xlsx")

# 宽数据转换成长数据

data\_long <- data %>%

pivot\_longer(

cols = value1:value6, # 选择需要转换的列(value1到value6)

names\_to = "subject", # 新生成的列名(存储原列名)

values\_to = "GIR" # 新生成的列名(存储原值)

) %>%

filter(!(group == "chABC" & subject == "value6")) %>% # 移除chABC组的value6(缺失值)

mutate(

subject = paste0(group, "\_", str\_remove(subject, "value")), # 生成唯一的受试者ID(组名+编号)

group = factor(group, levels=c("chABC", "Vehicle")), # 将分组变量转为因子并指定顺序

time = factor(time, levels = c(-15, -5, 0, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120)), # 将时间变量转为因子并指定顺序

phase = ifelse(time %in% c(-15, -5, 0), "Basal", "Clamp") # 创建实验阶段变量(基础期和钳制期)

)

# 重复测量方差分析

res.aov <- anova\_test(

data = filter(data\_long, phase == "Clamp"), # 仅分析钳制期

dv = GIR, # 因变量：葡萄糖输注率(GIR)

wid = subject, # 受试者ID变量

within = time, # 组内因素：时间

between = group # 组间因素：处理组

)

anova\_results <- get\_anova\_table(res.aov) # 从 res.aov 对象中提取ANOVA结果

print(anova\_results) # 打印结果

# 事后检验(组间比较)

posthoc <- data\_long %>%

filter(phase == "Clamp") %>% # 筛选钳制期数据

group\_by(time) %>% # 按时间点分组比较

t\_test(GIR ~ group) %>% # 执行t检验

#adjust\_pvalue(method = "bonferroni") %>% # 矫正

add\_significance() # 添加显著性标记

print(posthoc) # 打印 t\_test 结果

# 可视化

# 点线+误差线图

p <- ggplot(data\_long, aes(x = time, y = GIR)) +

# 添加背景色块标记不同实验阶段

annotate("rect", xmin = 0, xmax = "0", ymin = 0, ymax = 40, fill = "#dae2f3") + # 背景色块，基础期到钳制期的过渡

annotate("rect", xmin = "90", xmax = "120", ymin = 0, ymax = 40, fill = "#dae2f3") + # 背景色块，钳制期末段

# 添加阶段标签文本

annotate("text", x = "-15", y = 40, label = "Basal", hjust = 0.3, vjust = -0.4, size = 7) + # 基础期标签

annotate("text", x = "90", y = 40, label = "Clamp", hjust = -0.1, vjust = -0.4, size = 7) + # 钳制期标签

# 添加误差线(均值的标准误)

stat\_summary(aes(group = group),

geom = "errorbar",fun.data = "mean\_se",