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# Solution of parts a and b by using R:

# y: times to death
y <- c(65, 156, 100, 134, 16, 108, 121, 4, 39, 143, 56, 26, 22, 1, 1, 5, 65)

# x: Log10(initial white blood cell count)
x <- c(3.36, 2.88, 3.63, 3.41, 3.78, 4, 4.02, 4.23, 3.73, 3.85, 3.97, 4.51, 4.54, 5, 5, 4.72, 5
      )

# 1)
# model under H1 (M1):
m1 <- glm(y ~ x, family = Gamma(link = "log"))
summary(m1, dispersion = 1)
# model under H0 (M0):
m0 <- glm(y ~ 1, family = Gamma(link = "log"))
summary(m0, dispersion = 1)

# 2) Find test statistics:  $D_0 \geq D_1$ 
#  $\Delta D = D_0 - D_1 \sim \chi^2(p-q)$ 
#  $D_0$  = Deviance of model  $M_0$ 
#  $D_1$  = Deviance of model  $M_1$ 
#  $p$  = number of parameters in  $M_1 = 2$ 
#  $q$  = number of parameters in  $M_0 = 1$ 
D0 <- deviance(m0)
D0
D1 <- deviance(m1)
D1
delta_D <- D0 - D1
delta_D

# 3) To find table value:
# use chi-square table,  $df = p - q = 2 - 1 = 1$ 
df_diff <- m0$df.residual - m1$df.residual
df_diff
critical_value <- qchisq(1 - 0.05, df_diff)
critical_value

# or by code: anova(m0, m1, test = "Chisq") for step 2 and step 3

# 4) Decision:
if (delta_D > critical_value) {
  print("Reject H0")
} else {
  print("Do not Reject H0")
}

```