

# SHC 798 Assignment 1, 2025

Richard Lubega

2025-07-14

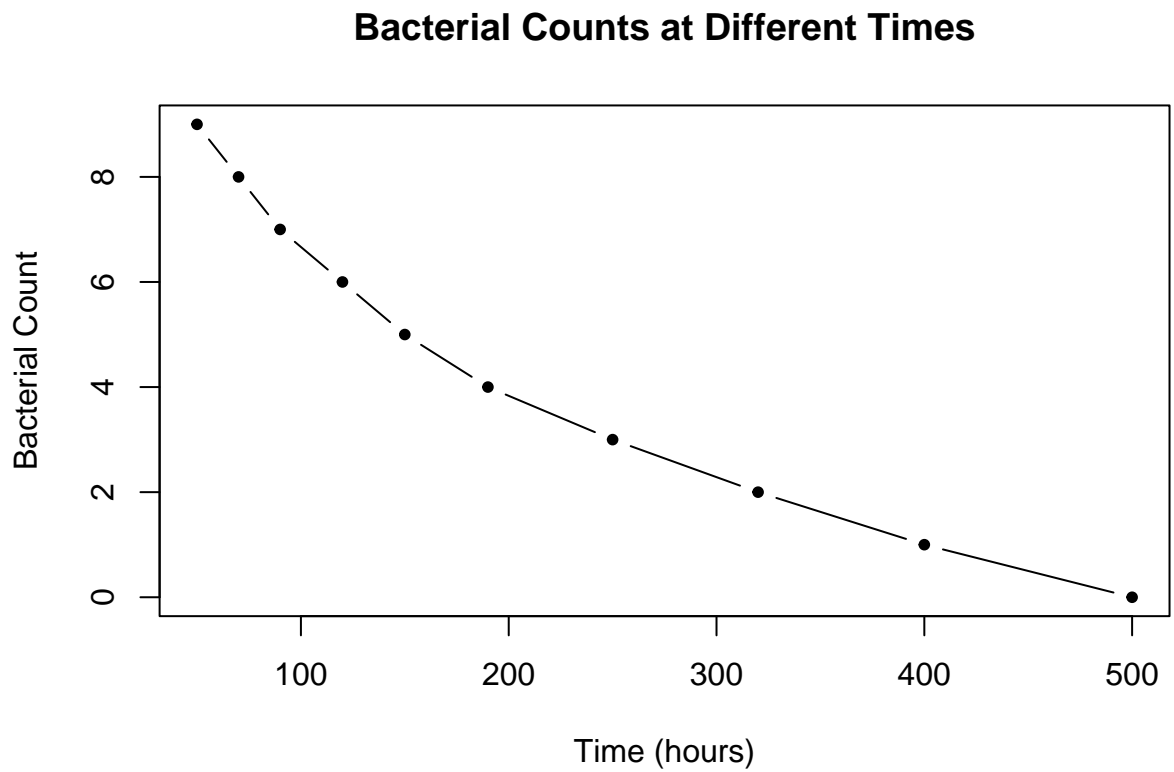
## SHC 798 Assignment 1, 2025

### Part 3: Simple regression

#### Question 3

```
time <- 0:9
count <- c(500, 400, 320, 250, 190, 150, 120, 90, 70, 50)
decay <- data.frame(time, count)

plot(decay$count, decay$time, type = "b", main = "Bacterial Counts at Different Times", pch=20, xlab =
```



(a)

(b) Fit an exponential decay model and determine if this function better explains the data than a simple linear model.

### 1. Simple Linear Model

```
# Simple Linear Model
lm_decay <- lm(count ~ time, data = decay)
summary(lm_decay)

##
## Call:
## lm(formula = count ~ time, data = decay)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -48.06 -32.59  -9.00   22.71   69.45
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  430.545     24.935   17.27 1.29e-07 ***
## time         -48.121       4.671  -10.30 6.79e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 42.42 on 8 degrees of freedom
## Multiple R-squared:  0.9299, Adjusted R-squared:  0.9212
## F-statistic: 106.1 on 1 and 8 DF,  p-value: 6.792e-06
```

### 2. Exponential Model

- The exponential Model is obtained from a logged response model.
- From general decay models,  $C(t) = C_0 \cdot e^{-k \cdot t}$ , where  $C$  implies bacterial count and  $t$ , time (hours).
- We linearise to  $\log[C(t)] = \log[C_0] - k \cdot t$ , which is generally written as  

$$-\log(\text{count}) = \beta_0 + \beta_1 \cdot \text{time} + E_i \dots\dots\dots \text{a logged response model}$$

```
exp_decay <- lm(log(count) ~ time, data = decay)
summary(exp_decay)

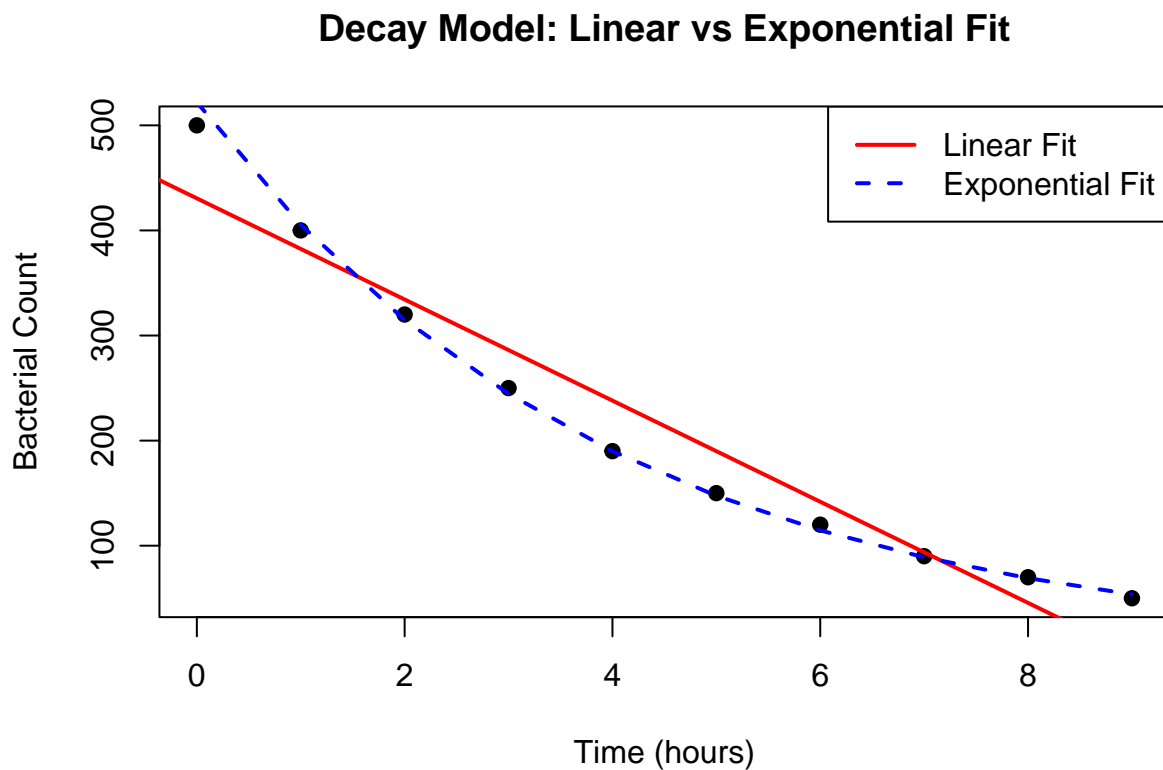
##
## Call:
## lm(formula = log(count) ~ time, data = decay)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.070704 -0.009861  0.012290  0.016734  0.046494
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.257540   0.021321  293.49 < 2e-16 ***
## time        -0.252757   0.003994  -63.29 4.32e-12 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03628 on 8 degrees of freedom
## Multiple R-squared:  0.998, Adjusted R-squared:  0.9978
## F-statistic: 4005 on 1 and 8 DF, p-value: 4.321e-12
```

### Visualising the models

```
plot(time, count, pch = 19, col = "black",
     xlab = "Time (hours)", ylab = "Bacterial Count",
     main = "Decay Model: Linear vs Exponential Fit")
abline(lm_decay, col = "red", lwd = 2)
# abline(exp_decay, col = "red", lwd = 2)

lines(time, exp(predict(exp_decay)), col = "blue", lwd = 2, lty = 2)
legend("topright", legend = c("Linear Fit", "Exponential Fit"),
     col = c("red", "blue"), lwd = 2, lty = c(1, 2))
```



### Comparing Explanatory Power:

The exponential model *fits* (explains) the data **better** because it does have a higher R-Squared value (0.998) compared to the simple linear model (with 0.9299).

(c) Predict the bacterial count at time = 10 hours

```

pred_c <- predict(exp_decay, newdata = data.frame(time = 10))
pred_10 <- exp(pred_c)
cat("the bacterial count at time = 10 hours is:", pred_10, "\n")

```

```
## the bacterial count at time = 10 hours is: 41.67785
```

(d) Compute a 95% confidence interval for the estimated decay rate

```

# The decay rate is the slope
cat("the 95% confidence interval for the estimated decay rate is: \n")

```

```
## the 95% confidence interval for the estimated decay rate is:
```

```
confint(exp_decay, "time")
```

```
##           2.5 %      97.5 %
## time -0.2619668 -0.2435471
```