

Assignment 9

Decision analysis

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General information

AI was used in b and c.

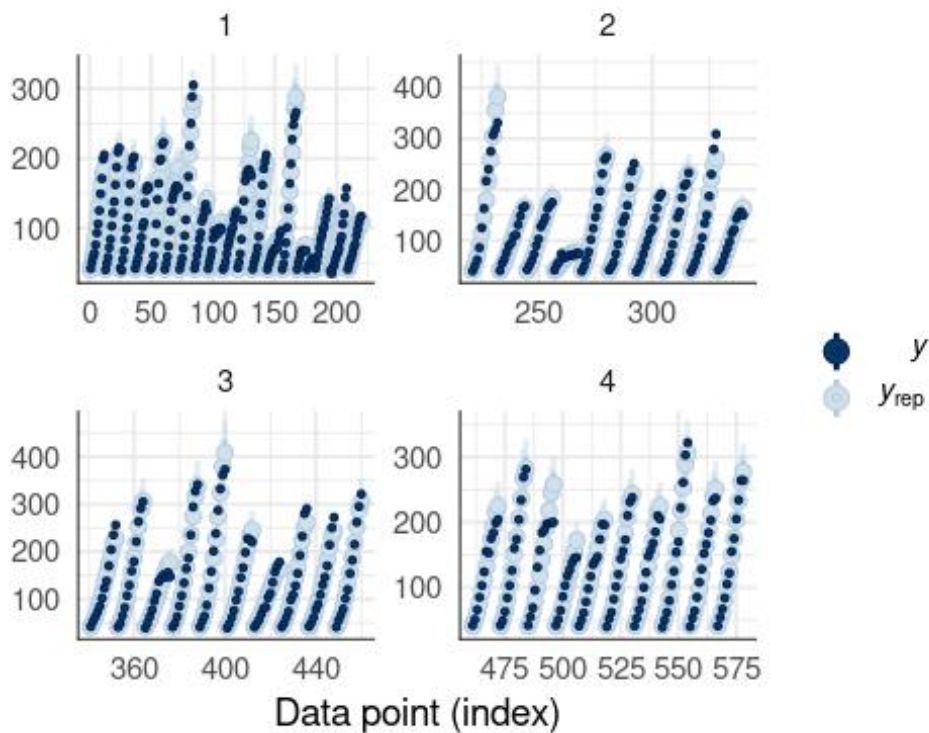
Escaping from the chicken coop

(a)

A simple GP model

```
brms::pp_check(fit, type = "intervals_grouped", group = "Diet")
```

Using all posterior draws for ppc type 'intervals_grouped' by default.



```

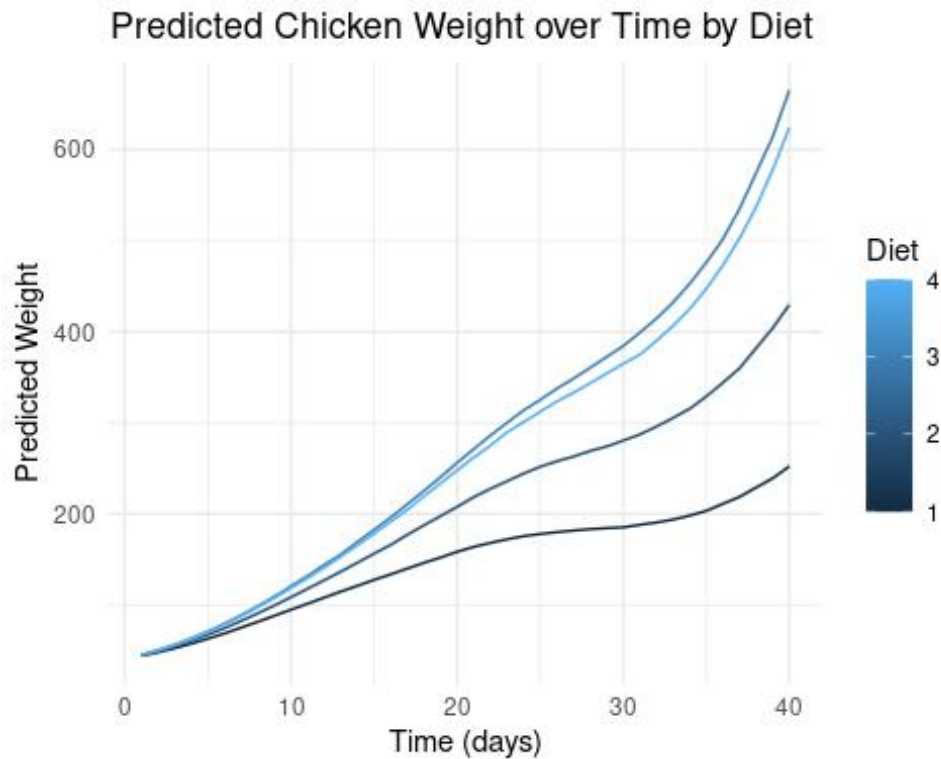
# Useful r functions:
#   rep(..., each=...), cbind, colMeans,
#   posterior_predict(..., newdata=..., allow_new_levels=TRUE, sample_n
#   ew_levels="gaussian")
#   ggplot, geom_line, aes(..., group=..., color=...)
new_data <- expand.grid(Time = 1:40, Diet = unique(ChickWeight$Diet))
new_data$Chick <- 1 # Dummy variable for Chick, needed for prediction
Time = rep(1:40, time=4)
Diet = rep(1:4, each=40)
new_data = data.frame(Time, Chick=51, Diet)

# Predicting weights
predictions <- posterior_predict(fit, newdata = new_data, allow_new_levels = TRUE, sample_new_levels = "gaussian")

# Summarize predictions
new_data$PredictedWeight <- apply(predictions, 2, mean) # Assuming you want the mean

# Visualization
ggplot(new_data, aes(x = Time, y = PredictedWeight, group = Diet, color = Diet)) +
  geom_line() +
  labs(title = "Predicted Chicken Weight over Time by Diet",
       x = "Time (days)",
       y = "Predicted Weight") +
  theme_minimal()

```



Considering chicken growth, the predictions are reasonable in context, as the weight gain is smooth and continuous, and the expected growth rate varies due to dietary differences.

Nonetheless, there is a lack of data on chicken weights from days 22 to 40, resulting in a predictive period from day 22 to day 40 that is unsupported by a sufficient number of observations to affirm the reliability of the forecasts.

Chickenwise probability of escape function

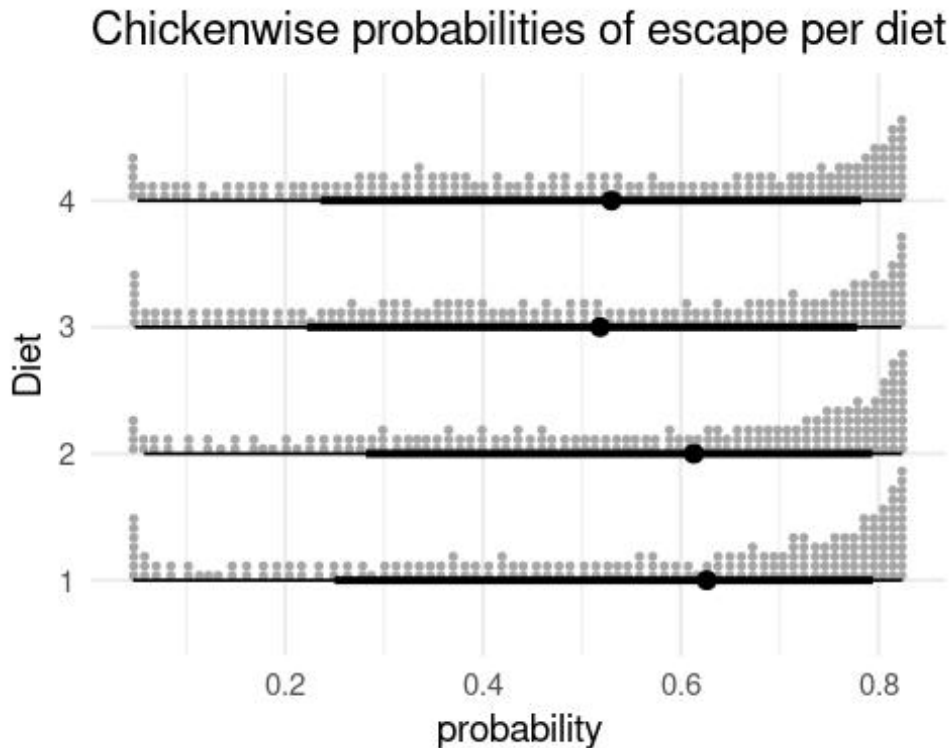
(b)

```
# Useful r functions: chickenwise_probability_of_escape (see above)
# rep(..., each=...), apply,
# ggplot, stat_dotsinterval
# Splitting the predictions into separate variables for each diet
diet1_predictions = predictions[, 1:40]
diet2_predictions = predictions[, 41:80]
diet3_predictions = predictions[, 81:120]
diet4_predictions = predictions[, 121:160]

# Applying the chickenwise_probability_of_escape function to calculate
probabilities for each diet
diet1_escape_probs = apply(diet1_predictions, 1,
  chickenwise_probability_of_escape)
diet2_escape_probs = apply(diet2_predictions, 1,
  chickenwise_probability_of_escape)
diet3_escape_probs = apply(diet3_predictions, 1,
  chickenwise_probability_of_escape)
diet4_escape_probs = apply(diet4_predictions, 1,
  chickenwise_probability_of_escape)

# Combining the calculated probabilities into a single data frame
diet_escape_probabilities = data.frame(
  Diet = rep(c("1", "2", "3", "4"), each = 4000),
  EscapeProbability = c(diet1_escape_probs, diet2_escape_probs,
    diet3_escape_probs, diet4_escape_probs)
)

# Plotting the probabilities using ggplot2
ggplot(diet_escape_probabilities, aes(x = EscapeProbability, y = Diet))
+
  stat_dotsinterval(quantiles = 200, scale = .9) +
  labs(title = "The Probabilities of Escape per Diet", x = "Probability
of Escape", y = "Diet") +
  theme_minimal()
```



From this boxplot, we can infer that the diet has an influence on the probability of escape, with Diet 1 resulting in a lower probability compared to the other diets. Additionally, the presence of an outlier for Diet 2 could indicate an individual chicken's characteristics or conditions not typical of the group. Overall, while most chickens across diets have a moderate chance of escape, there is some variability.

(c)

```
library(dplyr)
```

```
# Calculate predicted weights
```

```
predicted_weights <- posterior_predict(fit, newdata = new_data, allow_new_levels = TRUE, sample_new_levels = "gaussian")
mean_predicted_weights <- apply(predicted_weights, 2, mean)
```

```
# Add the predicted weights to the new data
```

```
new_data$PredictedWeight <- mean_predicted_weights
```

```
# Compute the chickenwise probability of escape for each chicken
```

```
# Assuming new_data is already ordered by Chick and then by Time
```

```
grouped_data <- new_data %>%
```

```
  group_by(Chick) %>%
```

```
  summarise(ProbabilityOfEscape = chickenwise_probability_of_escape(PredictedWeight))
```

```
# Compute wrongProbability using mean predicted weights for each chicken
```

```

grouped_data$wrongProbability <- chickenwise_probability_of_escape(mean
_predicted_weights)

# Aggregate these probabilities by diet
# Joining the diet information to the grouped data
grouped_data <- grouped_data %>%
  left_join(unique(ChickWeight[, c("Chick", "Diet")]), by = "Chick")

final_probabilities <- grouped_data %>%
  group_by(Diet) %>%
  summarise(ExpectedProbabilityOfEscape = mean(ProbabilityOfEscape),
            IncorrectProbabilityOfEscape = mean(wrongProbability))

# Print the final expected probabilities by diet
print(final_probabilities)

```

	Diet	TrueProbability	WrongProbability
1	0.5357926	0.8253136	
2	0.5486213	0.6692241	
3	0.5071666	0.1212868	
4	0.5147546	0.1694232	

The valid expected probability is derived by first determining the escape probability for each individual instance and then computing the mean of these probabilities. Conversely, the flawed method erroneously computes the escape likelihood using the sequence of average weights, which does not align with the intended definition.

Regarding diets 1 and 2, the anticipated probability derived from the accurate method turns out to be lesser. In contrast, for diets 3 and 4, the probability estimated by the inaccurate approach is significantly reduced.