

Daily-Level GAM Analysis of Monarch Butterfly Abundance

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Introduction

This analysis investigates daily-level patterns in overwintering monarch butterfly abundance using Generalized Additive Models (GAMs). Unlike the 30-minute interval analysis, this approach aggregates data to daily summaries, examining how previous day's weather conditions affect butterfly abundance. The response variable is the 95th percentile of butterfly counts, providing a robust measure of daily peak abundance while being less sensitive to outliers than the maximum.

Setup

Load libraries and data:

```
library(tidyverse)
library(mgcv)
library(lubridate)
library(plotly)
library(knitr)
library(DT)
library(here)
library(gratia)
library(patchwork)
library(corrplot)

# Load the daily lag analysis data
daily_data <- read_csv(here("data", "monarch_daily_lag_analysis.csv"))

# Create the square root transformed response variable early for use throughout
daily_data <- daily_data %>%
  mutate(
    butterfly_diff_95th_sqrt = ifelse(butterfly_diff_95th >= 0,
                                      sqrt(butterfly_diff_95th),
                                      -sqrt(-butterfly_diff_95th))
  )
```

Data Exploration

Data Structure and Summary

```
# Basic summary statistics
cat("Dataset dimensions:", nrow(daily_data), "rows x", ncol(daily_data), "columns\n")
```

Dataset dimensions: 103 rows x 46 columns

```
cat("Number of deployments:", n_distinct(daily_data$deployment_id), "\n")
```

Number of deployments: 7

```
cat("Date range:", min(daily_data$date_t), "to", max(daily_data$date_t), "\n\n")
```

Date range: 19680 to 19756

```
# Summary of key variables
summary_vars <- daily_data %>%
  select(
    butterflies_95th_percentile_t,
    butterflies_95th_percentile_t_1,
    butterfly_diff_95th,
    temp_max_t_1,
    temp_min_t_1,
    temp_at_max_count_t_1,
    wind_max_gust_t_1,
    sum_butterflies_direct_sun_t_1
  )

summary(summary_vars)
```

butterflies_95th_percentile_t	butterflies_95th_percentile_t_1
Min. : 0.00	Min. : 0.0
1st Qu.: 14.85	1st Qu.: 17.5
Median : 70.05	Median : 77.0
Mean : 107.41	Mean : 116.3
3rd Qu.: 166.95	3rd Qu.: 199.5
Max. : 499.00	Max. : 499.0

butterfly_diff_95th	temp_max_t_1	temp_min_t_1	temp_at_max_count_t_1
Min. : -310.000	Min. : 14.00	Min. : 3.000	Min. : 5.00
1st Qu.: -31.000	1st Qu.: 16.00	1st Qu.: 7.000	1st Qu.: 11.50

Median :	-2.950	Median :	18.00	Median :	10.000	Median :	14.00
Mean :	-8.919	Mean :	19.43	Mean :	9.573	Mean :	13.37
3rd Qu.:	18.000	3rd Qu.:	22.00	3rd Qu.:	12.000	3rd Qu.:	15.50
Max. :	256.600	Max. :	37.00	Max. :	16.000	Max. :	25.00

wind_max_gust_t_1	sum_butterflies_direct_sun_t_1
Min. :0.000	Min. : 0.00
1st Qu.:2.750	1st Qu.: 2.00
Median :3.750	Median : 19.00
Mean :3.718	Mean : 94.77
3rd Qu.:4.500	3rd Qu.: 104.00
Max. :7.200	Max. :1122.00
NA's :3	

Response Variable Distribution

```
library(gridExtra)

# Current day's 95th percentile
p1 <- ggplot(daily_data, aes(x = butterflies_95th_percentile_t)) +
  geom_histogram(bins = 30, fill = "steelblue", alpha = 0.7) +
  labs(
    title = "Current Day: 95th Percentile Butterfly Count",
    x = "95th Percentile Count", y = "Frequency"
  ) +
  theme_minimal()

# Previous day's 95th percentile
p2 <- ggplot(daily_data, aes(x = butterflies_95th_percentile_t_1)) +
  geom_histogram(bins = 30, fill = "orange", alpha = 0.7) +
  labs(
    title = "Previous Day: 95th Percentile Butterfly Count",
    x = "95th Percentile Count", y = "Frequency"
  ) +
  theme_minimal()

# Difference in 95th percentile
p3 <- ggplot(daily_data, aes(x = butterfly_diff_95th)) +
  geom_histogram(bins = 30, fill = "purple", alpha = 0.7) +
  geom_vline(xintercept = 0, linetype = "dashed", color = "red") +
  labs(
```

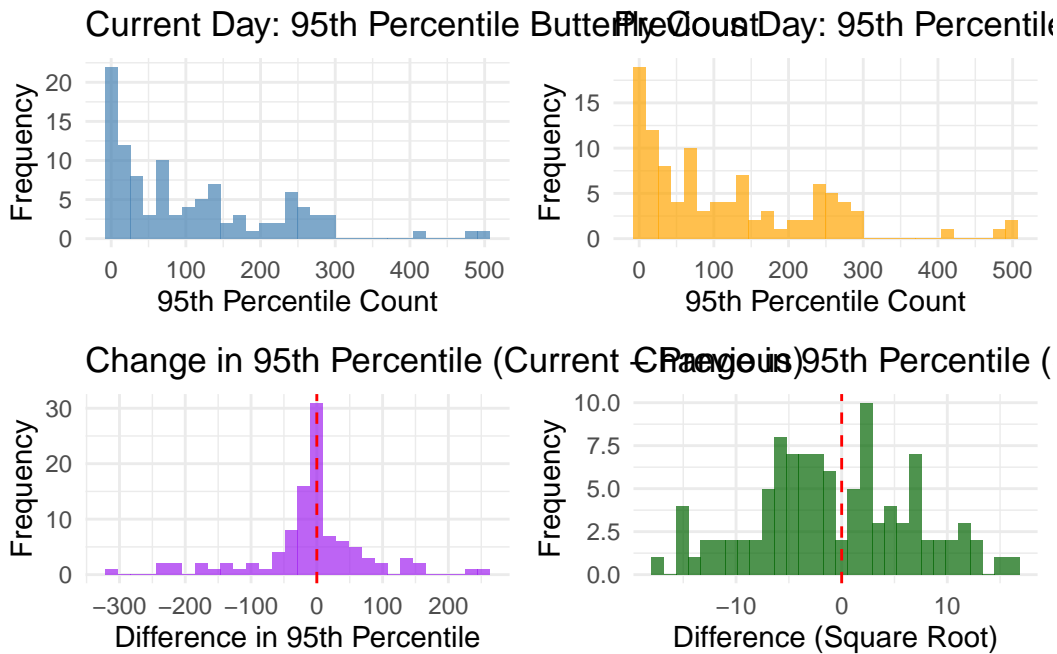
```

    title = "Change in 95th Percentile (Current - Previous)",
    x = "Difference in 95th Percentile", y = "Frequency"
  ) +
  theme_minimal()

# Square root transformed difference
p4 <- ggplot(daily_data, aes(x = butterfly_diff_95th_sqrt)) +
  geom_histogram(bins = 30, fill = "darkgreen", alpha = 0.7) +
  geom_vline(xintercept = 0, linetype = "dashed", color = "red") +
  labs(
    title = "Change in 95th Percentile (Square Root Transformed)",
    x = "Difference (Square Root)", y = "Frequency"
  ) +
  theme_minimal()

grid.arrange(p1, p2, p3, p4, ncol = 2)

```



Correlation Analysis

```

# Select model variables
model_vars <- daily_data %>%

```

```

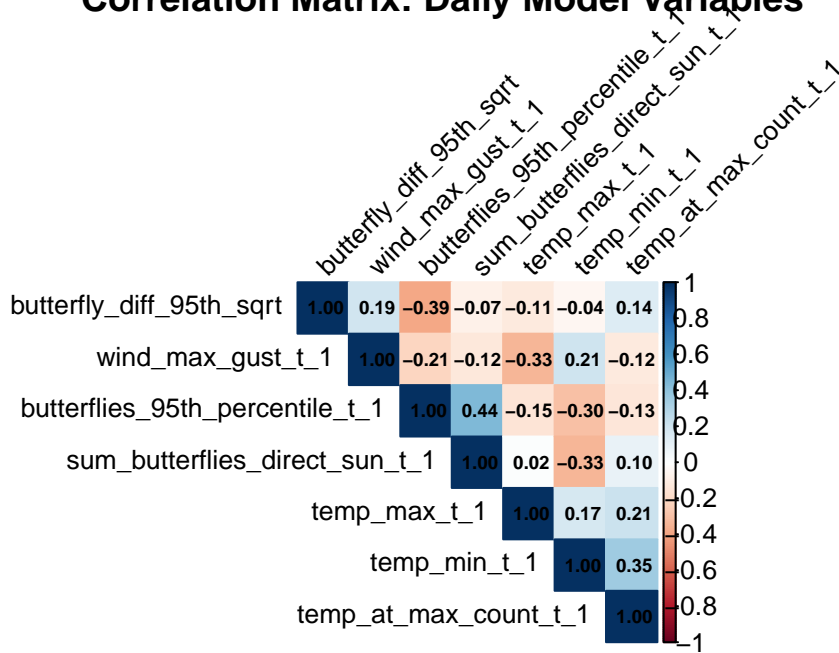
select(
  butterfly_diff_95th_sqrt,
  butterflies_95th_percentile_t_1,
  temp_max_t_1,
  temp_min_t_1,
  temp_at_max_count_t_1,
  wind_max_gust_t_1,
  sum_butterflies_direct_sun_t_1
) %>%
na.omit()

# Correlation matrix
cor_matrix <- cor(model_vars)

# Create correlation plot
corrplot(cor_matrix,
  method = "color",
  type = "upper",
  order = "hclust",
  tl.cex = 0.8,
  tl.col = "black",
  tl.srt = 45,
  addCoef.col = "black",
  number.cex = 0.6,
  title = "Correlation Matrix: Daily Model Variables"
)

```

Correlation Matrix: Daily Model Variables



```
# Print correlation table
kable(round(cor_matrix, 3),
      caption = "Correlation Matrix for Daily Model Variables"
)
```

Table 1: Correlation Matrix for Daily Model Variables

	butterfly_diff_95th_sqrt	butterflies_95th_percentile_t_1	temp_max_t_1	temp_min_t_1	temp_at_max_count_t_1	wind_max_gust_t_1	sum_butterflies_direct_sun_t_1
butterfly_diff_95th_sqrt	1.000	-0.389	-	-	0.145	0.193	-0.072
butterflies_95th_percentile_t_1	-0.389	1.000	-	-	-0.132	-0.211	0.442
temp_max_t_1	-0.112	-0.146	1.000	0.173	0.215	-0.334	0.016
temp_min_t_1	-0.042	-0.299	0.173	1.000	0.351	0.210	-0.331
temp_at_max_count_t_1	0.145	-0.132	0.215	0.351	1.000	-0.116	0.098
wind_max_gust_t_1	0.193	-0.211	-	0.210	-0.116	1.000	-0.122
sum_butterflies_direct_sun_t_1	-0.072	0.442	0.016	-	0.098	-0.122	1.000

Response Variable Normality Assessment

```
library(nortest)

# First, identify all potential response variables in the dataset
# Exclude already-transformed variables to prevent double-transformation
response_candidates <- daily_data %>%
  select(contains("diff"), contains("butterfly")) %>%
  select(-contains("direct_sun"), -contains("sqrt"), -contains("cbrt"), -contains("log")) %>%
  names()

cat("Available response variable candidates:\n")
```

Available response variable candidates:

```
print(response_candidates)
```

```
[1] "butterfly_diff"      "butterfly_diff_95th" "butterfly_diff_top3"
```

```
# Define transformations to test
transformations <- list(
  "original" = function(x) x,
  "sqrt" = function(x) ifelse(x >= 0, sqrt(x), -sqrt(-x)), # Signed square root
  "fourth_root" = function(x) ifelse(x >= 0, x^0.25, -((-x)^0.25)), # Signed fourth root
  "arcsinh" = function(x) asinh(x), # Inverse hyperbolic sine (handles negative values)
  "yeo_johnson" = function(x) {
    # Simplified Yeo-Johnson transformation
    lambda <- 0.5
    ifelse(x >= 0,
      ((x + 1)^lambda - 1) / lambda,
      -(((x + 1)^(2-lambda) - 1) / (2-lambda))
    )
  }
)

# Function to calculate normality statistics
assess_normality <- function(x, var_name, transform_name) {
  # Remove NA values
  x_clean <- x[!is.na(x)]

  if(length(x_clean) < 10) {
```



```

    return(data.frame(
      Variable = var_name,
      Transformation = transform_name,
      N = length(x_clean),
      Mean = NA,
      SD = NA,
      Skewness = NA,
      Kurtosis = NA,
      Shapiro_p = NA,
      Anderson_p = NA,
      Normality_Score = 0
    ))
  }

  # Calculate statistics
  mean_val <- mean(x_clean)
  sd_val <- sd(x_clean)
  skew_val <- moments::skewness(x_clean)
  kurt_val <- moments::kurtosis(x_clean) - 3 # Excess kurtosis

  # Normality tests
  shapiro_p <- if(length(x_clean) <= 5000) shapiro.test(x_clean)$p.value else NA
  anderson_p <- tryCatch(nortest::ad.test(x_clean)$p.value, error = function(e) NA)

  # Create composite normality score (higher = more normal)
  # Based on: low absolute skewness, low absolute kurtosis, high p-values
  skew_score <- max(0, 1 - abs(skew_val) / 2) # Penalize skewness > 2
  kurt_score <- max(0, 1 - abs(kurt_val) / 4) # Penalize excess kurtosis > 4
  shapiro_score <- ifelse(is.na(shapiro_p), 0.5, shapiro_p)
  anderson_score <- ifelse(is.na(anderson_p), 0.5, anderson_p)

  # Weighted composite score
  normality_score <- (skew_score * 0.3 + kurt_score * 0.3 +
    shapiro_score * 0.2 + anderson_score * 0.2)

  return(data.frame(
    Variable = var_name,
    Transformation = transform_name,
    N = length(x_clean),
    Mean = round(mean_val, 3),
    SD = round(sd_val, 3),
    Skewness = round(skew_val, 3),

```

```

    Kurtosis = round(kurt_val, 3),
    Shapiro_p = ifelse(is.na(shapiro_p), NA, round(shapiro_p, 4)),
    Anderson_p = ifelse(is.na(anderson_p), NA, round(anderson_p, 4)),
    Normality_Score = round(normality_score, 4)
  })
}

# Load required library for moments
library(moments)

# Apply transformations and assess normality for each response variable
normality_results <- list()

for(var_name in response_candidates) {
  if(var_name %in% names(daily_data)) {
    var_data <- daily_data[[var_name]]

    for(trans_name in names(transformations)) {
      trans_func <- transformations[[trans_name]]

      # Apply transformation
      transformed_data <- tryCatch(
        trans_func(var_data),
        error = function(e) rep(NA, length(var_data))
      )

      # Assess normality
      result <- assess_normality(transformed_data, var_name, trans_name)
      normality_results[[paste(var_name, trans_name, sep = "_")]] <- result
    }
  }
}

# Combine results
normality_df <- do.call(rbind, normality_results)

# Rank by normality score
normality_ranking <- normality_df %>%
  arrange(desc(Normality_Score)) %>%
  filter(!is.na(Normality_Score)) %>%
  mutate(Rank = row_number()) %>%
  select(Rank, Variable, Transformation, N, Mean, SD, Skewness, Kurtosis,

```

```

Shapiro_p, Anderson_p, Normality_Score)

# Display top 15 most normal distributions
cat("Top 15 most normal response variable transformations:\n\n")

```

Top 15 most normal response variable transformations:

```

kable(head(normality_ranking, 15),
       caption = "Response variables ranked by normality (higher score = more normal)")

```

Table 2: Response variables ranked by normality (higher score = more normal)

	Rank	Variable	Transformation	N	Mean	SD	Skewness	Kurtosis	Shapiro_p	Anderson_p	Normality_Score
butterfly_diff_95th_butterfly_diff	1	butterfly_diff_95th_butterfly_diff	103	-	7.382	0.021	-	0.6501	0.5918	0.8102	
					0.809			0.467			
butterfly_diff_top3_butterfly_diff	2	butterfly_diff_top3_butterfly_diff	103	-	7.379	0.039	-	0.6273	0.5818	0.8033	
					0.751			0.436			
butterfly_diff_sqrt_butterfly_diff	3	butterfly_diff	103	-	8.033	0.238	-	0.6179	0.3799	0.7552	
					1.148			0.117			
butterfly_diff_top43_butterfly_diff	4	butterfly_diff_top43_butterfly_diff	103	-	2.475	0.121	-	0.0000	0.0000	0.4672	
					0.236			1.527			
butterfly_diff_top53_butterfly_diff	5	butterfly_diff_top53_butterfly_diff	103	-	4.105	0.129	-	0.0000	0.0000	0.4636	
					0.392			1.560			
butterfly_diff_95th_butterfly_diff	6	butterfly_diff_95th_butterfly_diff	103	-	2.470	0.168	-	0.0000	0.0000	0.4619	
					0.279			1.505			
butterfly_diff_95th_butterfly_diff	7	butterfly_diff_95th_butterfly_diff	103	-	4.101	0.179	-	0.0000	0.0000	0.4576	
					0.461			1.540			
butterfly_diff_fourth_butterfly_diff	8	butterfly_diff_fourth_butterfly_diff	103	-	2.554	0.304	-	0.0000	0.0000	0.4492	
					0.425			1.402			
butterfly_diff_arcsinh_butterfly_diff	9	butterfly_diff_arcsinh_butterfly_diff	103	-	4.212	0.296	-	0.0000	0.0000	0.4442	
					0.701			1.485			
butterfly_diff_top3_brig	10	butterfly_diff_top3_brig	103	-	87.141	-	2.983	0.0000	0.0000	0.3724	
					8.547	0.026					
butterfly_diff_95th_brig	11	butterfly_diff_95th_brig	103	-	86.928	-	2.525	0.0000	0.0000	0.3502	
					8.919	0.402					
butterfly_diff_original	12	butterfly_diff	103	-	108.337	3.389	5.076	0.0000	0.0000	0.2417	
					10.097						
butterfly_diff_ye3_john	13	butterfly_diff_ye3_john	103	-	777.603	-	15.548	0.0000	0.0000	0.0000	
					302.806	3.770					

	Rank	Variable	Transformation	N	Mean	SD	Skewness	Kurtosis	Shapiro_p	Anderson	Normality_Score
butterfly_diff_95th	103	butterfly_diff_95th	sqrt	103	-	614.021	-	11.649	0.0000	0.0000	0.0000
butterfly_diff_top3	103	butterfly_diff_top3	sqrt	103	-	576.143	-	9.279	0.0000	0.0000	0.0000
butterfly_diff	103	butterfly_diff	sqrt	103	-	240.895	3.329				
						235.162	3.074				

```
# Create summary by variable
variable_summary <- normality_ranking %>%
  group_by(Variable) %>%
  slice_max(Normality_Score, n = 1) %>%
  ungroup() %>%
  arrange(desc(Normality_Score)) %>%
  select(Variable, Best_Transformation = Transformation, Best_Score = Normality_Score,
         Skewness, Kurtosis, Shapiro_p)

cat("\n\nBest transformation for each response variable:\n")
```

Best transformation for each response variable:

```
kable(variable_summary,
      caption = "Best transformation for each response variable")
```

Table 3: Best transformation for each response variable

Variable	Best_Transformation	Best_Score	Skewness	Kurtosis	Shapiro_p
butterfly_diff_95th	sqrt	0.8102	0.021	-0.467	0.6501
butterfly_diff_top3	sqrt	0.8033	0.039	-0.436	0.6273
butterfly_diff	sqrt	0.7552	0.238	-0.117	0.6179

```
cat("\n\nUsing the best response variable transformation: butterfly_diff_95th_sqrt\n")
```

Using the best response variable transformation: butterfly_diff_95th_sqrt

```
cat("Summary of transformed response variable:\n")
```

Summary of transformed response variable:

```
print(summary(daily_data$butterfly_diff_95th_sqrt))
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-17.6068	-5.5649	-1.7176	-0.8088	4.2426	16.0187

```
# Visualize the top 6 most normal transformations
top_transformations <- head(normality_ranking, 6)

plots <- list()
for(i in 1:nrow(top_transformations)) {
  row <- top_transformations[i, ]
  var_name <- row$Variable
  trans_name <- row$Transformation

  if(var_name %in% names(daily_data)) {
    var_data <- daily_data[[var_name]]
    trans_func <- transformations[[trans_name]]
    transformed_data <- trans_func(var_data)

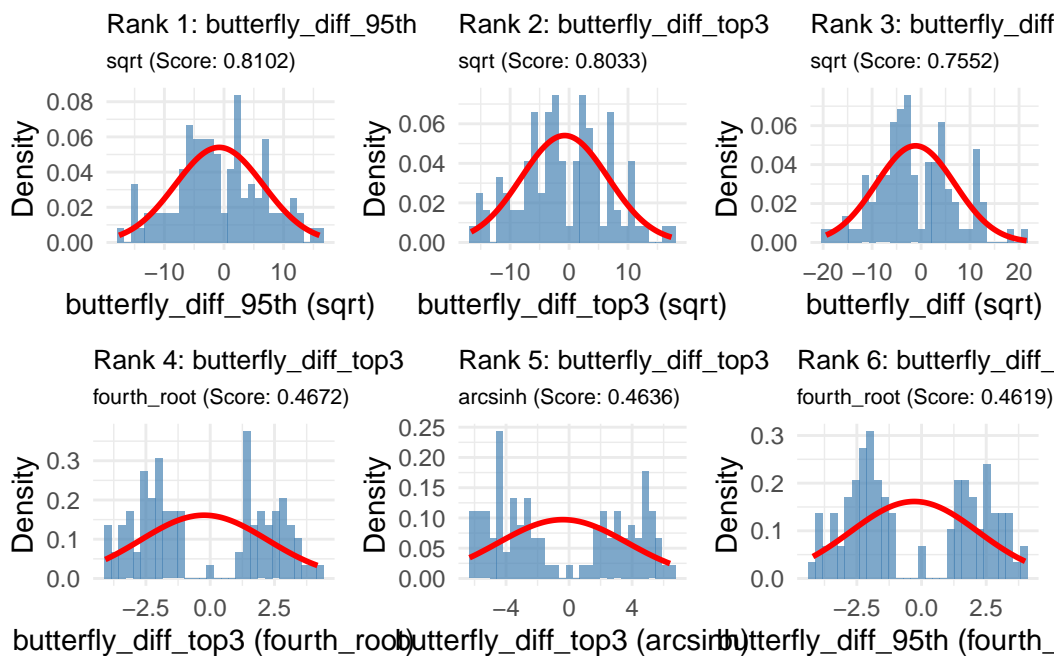
    # Create histogram with normal overlay
    p <- ggplot(data.frame(x = transformed_data), aes(x = x)) +
      geom_histogram(aes(y = after_stat(density)), bins = 30,
        fill = "steelblue", alpha = 0.7) +
      stat_function(fun = dnorm,
        args = list(mean = mean(transformed_data, na.rm = TRUE),
          sd = sd(transformed_data, na.rm = TRUE)),
        color = "red", size = 1) +
      labs(
        title = paste0("Rank ", i, ": ", var_name),
        subtitle = paste0(trans_name, " (Score: ", row$Normality_Score, ")"),
        x = paste0(var_name, " (", trans_name, ")"),
        y = "Density"
      ) +
      theme_minimal() +
      theme(plot.title = element_text(size = 10),
        plot.subtitle = element_text(size = 8))
  }
}
```

```

    plots[[i]] <- p
  }
}

# Arrange plots in grid
if(length(plots) >= 6) {
  grid.arrange(plots[[1]], plots[[2]], plots[[3]],
               plots[[4]], plots[[5]], plots[[6]], ncol = 3)
} else {
  do.call(grid.arrange, c(plots, ncol = 3))
}

```



Temperature Patterns

```

# Temperature relationships
p1 <- ggplot(daily_data, aes(x = temp_max_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "red") +
  geom_smooth(method = "loess", se = TRUE, color = "darkred") +
  labs(
    title = "Maximum Temperature vs Butterfly Change",
    x = "Previous Day Max Temperature (°C)",

```

```

      y = "Change in 95th Percentile (sqrt)"
    ) +
    theme_minimal()

p2 <- ggplot(daily_data, aes(x = temp_min_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "blue") +
  geom_smooth(method = "loess", se = TRUE, color = "darkblue") +
  labs(
    title = "Minimum Temperature vs Butterfly Change",
    x = "Previous Day Min Temperature (°C)",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

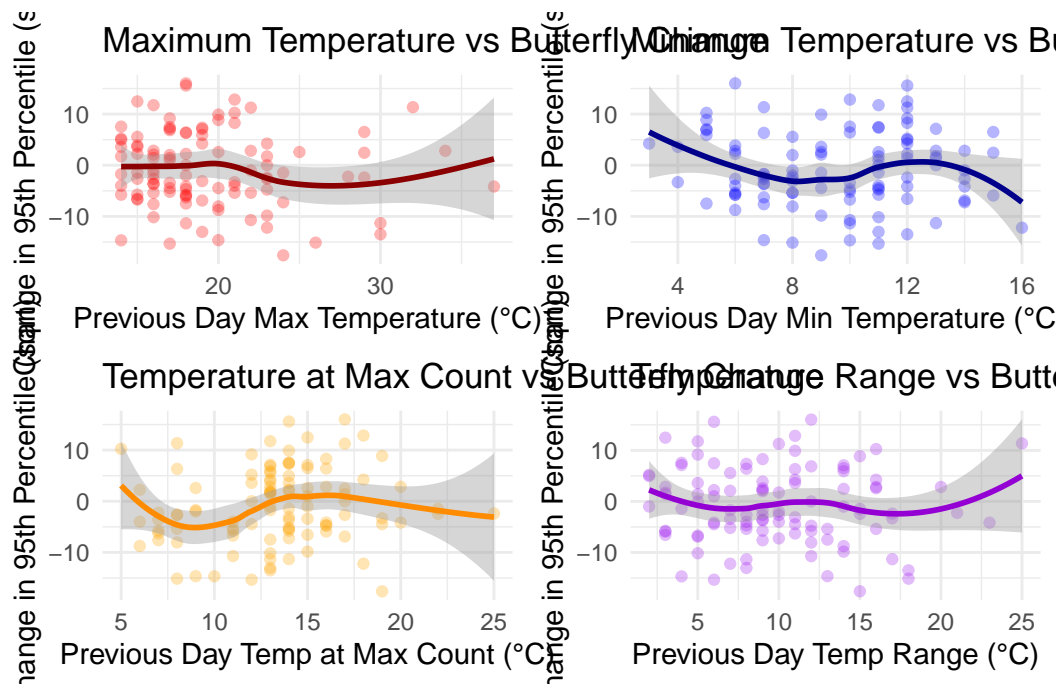
p3 <- ggplot(daily_data, aes(x = temp_at_max_count_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "orange") +
  geom_smooth(method = "loess", se = TRUE, color = "darkorange") +
  labs(
    title = "Temperature at Max Count vs Butterfly Change",
    x = "Previous Day Temp at Max Count (°C)",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

# Temperature range
daily_data <- daily_data %>%
  mutate(temp_range_t_1 = temp_max_t_1 - temp_min_t_1)

p4 <- ggplot(daily_data, aes(x = temp_range_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "purple") +
  geom_smooth(method = "loess", se = TRUE, color = "darkviolet") +
  labs(
    title = "Temperature Range vs Butterfly Change",
    x = "Previous Day Temp Range (°C)",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

grid.arrange(p1, p2, p3, p4, ncol = 2)

```



Wind and Sun Exposure

```
# Wind effect
p1 <- ggplot(daily_data, aes(x = wind_max_gust_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "steelblue") +
  geom_smooth(method = "loess", se = TRUE, color = "darkblue") +
  geom_vline(xintercept = 2, linetype = "dashed", color = "red", alpha = 0.5) +
  labs(
    title = "Maximum Wind Gust vs Butterfly Change",
    x = "Previous Day Max Wind Gust (m/s)",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

# Sun exposure
p2 <- ggplot(daily_data, aes(x = sum_butterflies_direct_sun_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "orange") +
  geom_smooth(method = "loess", se = TRUE, color = "darkorange") +
  labs(
    title = "Direct Sun Exposure vs Butterfly Change",
    x = "Previous Day Sum of Butterflies in Direct Sun",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()
```



```

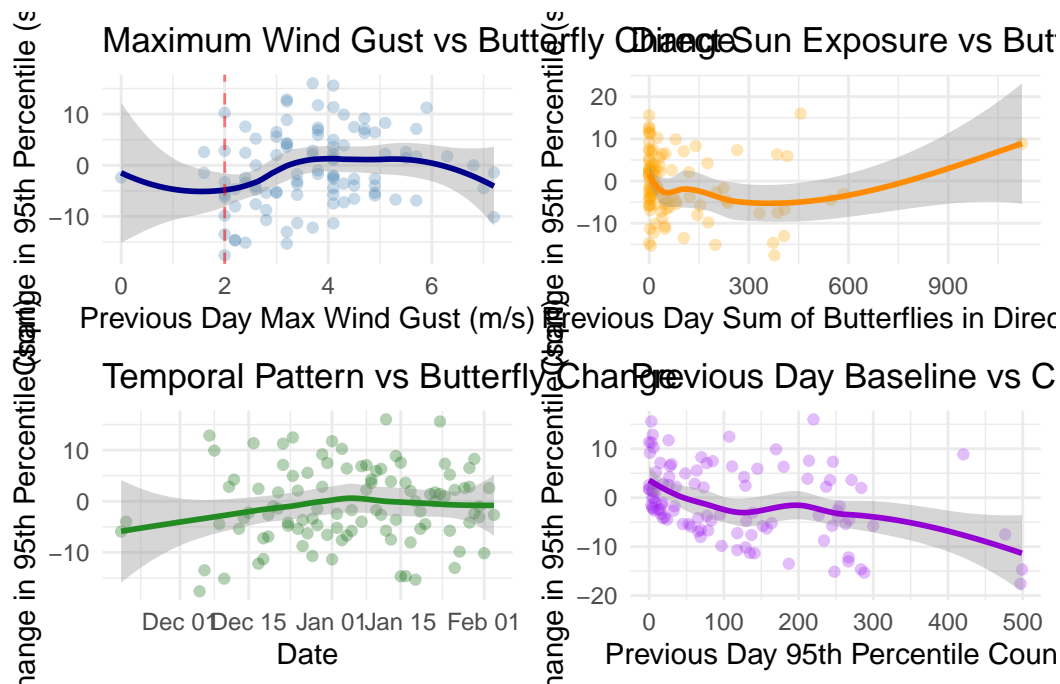
      y = "Change in 95th Percentile (sqrt)"
    ) +
    theme_minimal()

# Note: Seasonal progression will be handled via temporal autocorrelation
# rather than as a fixed effect
p3 <- ggplot(daily_data, aes(x = date_t, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "darkgreen") +
  geom_smooth(method = "loess", se = TRUE, color = "forestgreen") +
  labs(
    title = "Temporal Pattern vs Butterfly Change",
    x = "Date",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

# Previous day baseline
p4 <- ggplot(daily_data, aes(x = butterflies_95th_percentile_t_1, y = butterfly_diff_95th_sqrt)) +
  geom_point(alpha = 0.3, color = "purple") +
  geom_smooth(method = "loess", se = TRUE, color = "darkviolet") +
  labs(
    title = "Previous Day Baseline vs Change",
    x = "Previous Day 95th Percentile Count",
    y = "Change in 95th Percentile (sqrt)"
  ) +
  theme_minimal()

grid.arrange(p1, p2, p3, p4, ncol = 2)

```



Data Preparation

```
# Remove missing values and prepare modeling dataset
model_data <- daily_data %>%
  filter(
    !is.na(butterfly_diff_95th_sqrt),
    !is.na(butterflies_95th_percentile_t_1),
    !is.na(temp_max_t_1),
    !is.na(temp_min_t_1),
    !is.na(temp_at_max_count_t_1),
    !is.na(wind_max_gust_t_1),
    !is.na(sum_butterflies_direct_sun_t_1),
    !is.na(deployment_id)
  ) %>%
  # Create standardized versions for interpretation
  mutate(
    wind_max_gust_std = scale(wind_max_gust_t_1)[, 1],
    temp_max_std = scale(temp_max_t_1)[, 1],
    temp_min_std = scale(temp_min_t_1)[, 1],
    temp_at_max_std = scale(temp_at_max_count_t_1)[, 1],
    sun_exposure_std = scale(sum_butterflies_direct_sun_t_1)[, 1],
```

```

baseline_std = scale(butterflies_95th_percentile_t_1)[, 1],
# Note: day_sequence is now provided by the data preparation script
# Each deployment has its own day counter starting from 1
)

cat("Clean dataset has", nrow(model_data), "observations\n")

```

Clean dataset has 100 observations

```
cat("Number of unique deployment days:", n_distinct(paste(model_data$deployment_id, model_data$day)))
```

Number of unique deployment days: 100

Modeling Strategy

Our modeling approach for daily-level data tests both **absolute effects** and **proportional effects** of environmental variables on butterfly abundance changes:

1. **Response Variable:** `butterfly_diff_95th_sqrt` - square root transformed difference in 95th percentile butterfly counts between consecutive days (selected as the most normal transformation)

2. **Two Model Sets:**

M Models (Absolute Effects): Test whether environmental variables have direct effects on absolute changes in abundance:

- Do NOT include previous day's butterfly count
- Test if weather has consistent magnitude effects regardless of population size

B Models (Proportional/Density-Dependent Effects): Test whether environmental effects depend on baseline population:

- Include `butterflies_95th_percentile_t_1` as a covariate
- Test if weather effects scale with population size
- Include interactions between baseline count and environmental variables

3. **Fixed Effects** (tested in various combinations):

- Temperature variables: max, min, and temperature at max count
- Wind: maximum gust from previous day
- Sun exposure: sum of butterflies in direct sun from previous day
- Previous day baseline: 95th percentile count (B models only)

4. Random Effects:

- Deployment ID (random intercept)
- AR1 temporal autocorrelation within deployments using `day_sequence | deployment_id`

5. Correlation Structures:

- No correlation (baseline)
- AR1 within deployments to account for temporal autocorrelation

This dual approach allows us to distinguish between: - **Absolute effects:** Environmental variables cause fixed-magnitude changes regardless of population size - **Proportional effects:** Environmental impacts scale with the existing population (density-dependence)

Model Building and Selection

```
library(nlme)

# Define random effects structure with temporal autocorrelation
# We'll test different correlation structures
random_structure <- list(deployment_id = ~1)

# Define correlation structures to test
correlation_structures <- list(
  "no_corr" = NULL, # No temporal correlation
  "AR1" = corAR1(form = ~day_sequence | deployment_id) # AR1 within deployments
)

# Model specifications for AIC comparison - WITHOUT previous day baseline
model_specs <- list(
  # Null model
  "M1" = "butterfly_diff_95th_sqrt ~ 1",

  # Single predictor models (linear)
  "M2" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1",
  "M3" = "butterfly_diff_95th_sqrt ~ temp_max_t_1",
  "M4" = "butterfly_diff_95th_sqrt ~ temp_min_t_1",
  "M5" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1",
  "M6" = "butterfly_diff_95th_sqrt ~ sum_butterflies_direct_sun_t_1",

  # Temperature combinations (linear)
```

```

"M8" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + temp_min_t_1",
"M9" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + temp_at_max_count_t_1",
"M10" = "butterfly_diff_95th_sqrt ~ temp_min_t_1 + temp_at_max_count_t_1",
"M11" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + temp_min_t_1 + temp_at_max_count_t_1"

# Two-variable combinations
"M12" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1 + temp_max_t_1",
"M13" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1 + temp_min_t_1",
"M14" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1 + temp_at_max_count_t_1",
"M15" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M16" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 + sum_butterflies_direct_sun_t_1"

# Full models with various temperature specs (linear)
"M17" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M18" = "butterfly_diff_95th_sqrt ~ temp_min_t_1 + wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M19" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 + wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M20" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + temp_min_t_1 + wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M21" = "butterfly_diff_95th_sqrt ~ temp_max_t_1 + temp_min_t_1 + temp_at_max_count_t_1 + sum_butterflies_direct_sun_t_1"

# Smooth terms models - single predictors
"M24" = "butterfly_diff_95th_sqrt ~ s(wind_max_gust_t_1)",
"M25" = "butterfly_diff_95th_sqrt ~ s(temp_max_t_1)",
"M26" = "butterfly_diff_95th_sqrt ~ s(temp_min_t_1)",
"M27" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1)",
"M28" = "butterfly_diff_95th_sqrt ~ s(sum_butterflies_direct_sun_t_1)",

# Smooth terms - combinations
"M30" = "butterfly_diff_95th_sqrt ~ s(temp_max_t_1) + s(temp_min_t_1)",
"M31" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1) + s(wind_max_gust_t_1)",
"M32" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1) + s(sum_butterflies_direct_sun_t_1)",
"M33" = "butterfly_diff_95th_sqrt ~ s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)",

# Complex smooth models
"M34" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1) + s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)",
"M35" = "butterfly_diff_95th_sqrt ~ s(temp_max_t_1) + s(temp_min_t_1) + s(wind_max_gust_t_1)",
"M37" = "butterfly_diff_95th_sqrt ~ s(temp_max_t_1) + s(temp_min_t_1) + s(temp_at_max_count_t_1)",

# Mixed linear and smooth
"M38" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 + s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)",
"M39" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1) + wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M40" = "butterfly_diff_95th_sqrt ~ s(temp_at_max_count_t_1) + wind_max_gust_t_1 + s(sum_butterflies_direct_sun_t_1)"

```

```

# Interaction models (without baseline)
"M41" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 * wind_max_gust_t_1",
"M42" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 * sum_butterflies_direct_sun_t_1",
"M43" = "butterfly_diff_95th_sqrt ~ wind_max_gust_t_1 * sum_butterflies_direct_sun_t_1",
"M44" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 * wind_max_gust_t_1 + sum_butterflies_direct_sun_t_1",
"M45" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 + wind_max_gust_t_1 * sum_butterflies_direct_sun_t_1",
"M46" = "butterfly_diff_95th_sqrt ~ temp_at_max_count_t_1 * wind_max_gust_t_1 * sum_butterflies_direct_sun_t_1",

# Temperature range models
"M47" = "butterfly_diff_95th_sqrt ~ I(temp_max_t_1 - temp_min_t_1)",
"M48" = "butterfly_diff_95th_sqrt ~ I(temp_max_t_1 - temp_min_t_1) + wind_max_gust_t_1",
"M49" = "butterfly_diff_95th_sqrt ~ s(I(temp_max_t_1 - temp_min_t_1))",
"M50" = "butterfly_diff_95th_sqrt ~ s(I(temp_max_t_1 - temp_min_t_1)) + s(wind_max_gust_t_1)",

# ===== MODELS WITH PREVIOUS DAY BASELINE =====
# All models below include butterflies_95th_percentile_t_1 to test proportional effects

# Baseline-only model
"B1" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1",

# Single predictor models + baseline (linear)
"B2" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1",
"B3" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1",
"B4" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_min_t_1",
"B5" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1",
"B6" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + sum_butterflies_direct_sun_t_1",

# Temperature combinations + baseline (linear)
"B8" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + temp_min_t_1",
"B9" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + temp_at_max_count_t_1",
"B10" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_min_t_1 + temp_at_max_count_t_1",
"B11" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + temp_at_max_count_t_1",

# Two-variable combinations + baseline
"B12" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1 + temp_max_t_1",
"B13" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1 + temp_min_t_1",
"B14" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1 + temp_at_max_count_t_1",
"B15" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1 + temp_max_t_1 + temp_min_t_1",
"B16" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + temp_max_t_1 + temp_min_t_1",

# Full models with various temperature specs + baseline (linear)
"B17" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + wind_max_gust_t_1 + temp_min_t_1 + temp_at_max_count_t_1"

```

```

"B18" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_min_t_1 + wind_max_gust_t_1",
"B19" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1",
"B20" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + temp_min_t_1",
"B21" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_max_t_1 + temp_at_max_count_t_1",

# Smooth terms models - single predictors + baseline
"B24" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1)",
"B25" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1)",
"B26" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_min_t_1)",
"B27" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1)",
"B28" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(sum_butterflies_count_t_1)",

# Smooth baseline + other predictors
"B29" = "butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1)",
"B29a" = "butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + wind_max_gust_t_1",
"B29b" = "butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + temp_at_max_count_t_1",
"B29c" = "butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + s(wind_max_gust_t_1)",
"B29d" = "butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + s(temp_at_max_count_t_1)",

# Smooth terms - combinations + baseline
"B30" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1) + s(temp_min_t_1)",
"B31" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1) + s(temp_min_t_1)",
"B32" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1) + s(temp_max_t_1)",
"B33" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1) + s(temp_at_max_count_t_1)",

# Complex smooth models + baseline
"B34" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1) + s(temp_max_t_1)",
"B35" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1) + s(temp_min_t_1)",
"B37" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1) + s(temp_min_t_1) + s(wind_max_gust_t_1)",

# Mixed linear and smooth + baseline
"B38" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(temp_max_t_1)",
"B39" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1) + s(temp_max_t_1)",
"B40" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_at_max_count_t_1) + s(temp_min_t_1)",

# Interaction models with baseline
"B41" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(temp_max_t_1)",
"B42" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(temp_min_t_1)",
"B43" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + wind_max_gust_t_1 + s(temp_at_max_count_t_1)",
"B44" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(wind_max_gust_t_1)",
"B45" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(temp_max_t_1)",
"B46" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + temp_at_max_count_t_1 + s(temp_min_t_1)"

```

```

# Temperature range models + baseline
"B47" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + I(temp_max_t_1 - t
"B48" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + I(temp_max_t_1 - t
"B49" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(I(temp_max_t_1 - t
"B50" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(I(temp_max_t_1 - t

# Interaction with baseline (testing if environmental effects depend on population size)
"B51" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 * wind_max_gust_t_1"
"B52" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 * temp_at_max_count_t_1"
"B53" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 * sum_butterflies_diff_t_1"
"B54" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 * wind_max_gust_t_1 +
"B55" = "butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 * temp_at_max_count_t_1 +
)

cat("Total models to fit:", length(model_specs), "\n")

```

Total models to fit: 100

```

cat("- M models (M1-M50):", sum(grepl("^M", names(model_specs))), "models WITHOUT previous day baseline")

```

- M models (M1-M50): 45 models WITHOUT previous day baseline

```

cat("- B models (B1-B55):", sum(grepl("^B", names(model_specs))), "models WITH previous day baseline")

```

- B models (B1-B55): 55 models WITH previous day baseline

Model Fitting

```

# Function to safely fit models with correlation structures
fit_model_safely <- function(formula_str, data, correlation = NULL, corr_name = "no_corr") {
  tryCatch(
    {
      formula_obj <- as.formula(formula_str)

      # Fit the model with or without correlation structure
      if (is.null(correlation)) {
        model <- gamm(formula_obj,

```



```

        data = data,
        random = random_structure,
        method = "REML"
    )
} else {
    model <- gamm(formula_obj,
        data = data,
        random = random_structure,
        correlation = correlation,
        method = "REML"
    )
}

# Add correlation structure name to the model for tracking
model$correlation_structure <- corr_name
return(model)
},
error = function(e) {
    message("Failed to fit model: ", formula_str, " with correlation: ", corr_name)
    message("Error: ", e$message)
    return(NULL)
}
)
}

# Fit all models with different correlation structures
cat("Fitting models...\n")

```

Fitting models...

```

fitted_models <- list()

# Fit each model specification with each correlation structure
for (model_name in names(model_specs)) {
    formula_str <- model_specs[[model_name]]

    for (corr_name in names(correlation_structures)) {
        corr_struct <- correlation_structures[[corr_name]]

        # Create unique model name with correlation structure
        full_model_name <- paste(model_name, corr_name, sep = "_")
    }
}

```

```

    fitted_models[[full_model_name]] <- fit_model_safely(
      formula_str, model_data, corr_struct, corr_name
    )
  }
}

# Remove failed models
successful_models <- fitted_models[!map_lgl(fitted_models, is.null)]
cat("Successfully fitted", length(successful_models), "out of",
    length(model_specs), "models\n")

```

Successfully fitted 200 out of 100 models

Model Comparison

```

# Extract AIC values
aic_results <- map_dfr(names(successful_models), function(full_model_name) {
  model <- successful_models[[full_model_name]]

  # Parse model name and correlation structure
  name_parts <- strsplit(full_model_name, "_")[[1]]
  corr_suffix <- name_parts[length(name_parts)]
  base_model_name <- paste(name_parts[-length(name_parts)], collapse = "_")

  # Get the formula from the base model name
  formula_str <- model_specs[[base_model_name]]
  if (is.null(formula_str)) {
    formula_str <- "Unknown formula"
  }

  data.frame(
    Model = full_model_name,
    Base_Model = base_model_name,
    Correlation = corr_suffix,
    Formula = formula_str,
    AIC = AIC(model$lme),
    LogLik = logLik(model$lme)[1],
    df = attr(logLik(model$lme), "df"),
    stringsAsFactors = FALSE
  )
})

```

```

    )
  }) %>%
    arrange(AIC) %>%
    mutate(
      Delta_AIC = AIC - min(AIC),
      AIC_weight = exp(-0.5 * Delta_AIC) / sum(exp(-0.5 * Delta_AIC))
    )

# Display top 10 models
aic_results %>%
  head(10) %>%
  select(Model, Correlation, AIC, Delta_AIC, AIC_weight, df) %>%
  kable(digits = 3, caption = "Top 10 models by AIC")

```

Table 4: Top 10 models by AIC

Model	Correlation	AIC	Delta_AIC	AIC_weight	df
B33_AR1	AR1	668.401	0.000	0.148	9
B29c_AR1	AR1	668.671	0.270	0.129	8
B28_AR1	AR1	669.101	0.700	0.104	7
B35_AR1	AR1	669.573	1.172	0.082	13
B37_AR1	AR1	669.594	1.193	0.081	15
B29_AR1	AR1	669.685	1.284	0.078	6
B34_AR1	AR1	670.016	1.615	0.066	11
B29a_AR1	AR1	670.504	2.103	0.052	7
B38_AR1	AR1	670.691	2.289	0.047	10
B29d_AR1	AR1	670.864	2.463	0.043	8

```

# Show model formulas for top 5
cat("\nTop 5 model specifications:\n")

```

Top 5 model specifications:

```

head(aic_results, 5) %>%
  select(Base_Model, Correlation, Formula, Delta_AIC) %>%
  kable(digits = 3)

```

Base_Model	Model	Formula	Delta_AIC
B33	AR1	butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)	0.000
B29c	AR1	butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + s(wind_max_gust_t_1)	0.270
B28	AR1	butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(sum_butterflies_direct_sun_t_1)	0.700
B35	AR1	butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1) + s(temp_min_t_1) + s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)	1.172
B37	AR1	butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(temp_max_t_1) + s(temp_min_t_1) + s(temp_at_max_count_t_1) + s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)	1.193

Best Model Analysis

```
# Get the best model
best_model_name <- aic_results$Model[1]
best_model <- successful_models[[best_model_name]]

cat("Best model:", best_model_name, "\n")
```

Best model: B33_AR1

```
cat("Formula:", aic_results$Formula[1], "\n\n")
```

Formula: butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1) +

```
# Model summary
summary(best_model$gam)
```

Family: gaussian
Link function: identity

Formula:
butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 +

```
s(wind_max_gust_t_1) + s(sum_butterflies_direct_sun_t_1)
```

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	3.444416	1.263453	2.726	0.00766	**
butterflies_95th_percentile_t_1	-0.037703	0.006972	-5.408	4.95e-07	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value	
s(wind_max_gust_t_1)	2.466	2.466	2.725	0.08649	.
s(sum_butterflies_direct_sun_t_1)	2.918	2.918	6.122	0.00245	**

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.226

Scale est. = 43.072 n = 100

```
# Calculate R-squared
r_squared <- summary(best_model$gam)$r.sq
dev_explained <- summary(best_model$gam)$dev.expl

cat("\n\nModel Performance:\n")
```

Model Performance:

```
cat("R-squared:", round(r_squared, 4), "\n")
```

R-squared: 0.2264

```
cat("Deviance explained:", round(dev_explained * 100, 2), "%\n")
```

Deviance explained: %

Effect Visualizations

```

# Define custom theme
custom_theme <- theme_minimal(base_size = 12) +
  theme(
    panel.grid.major = element_line(color = "gray90", size = 0.5),
    panel.grid.minor = element_line(color = "gray95", size = 0.3),
    axis.text = element_text(color = "black", size = 11),
    axis.title = element_text(color = "black", size = 12, face = "bold"),
    plot.title = element_text(color = "black", size = 14, face = "bold", hjust = 0.5),
    panel.border = element_rect(color = "black", fill = NA, size = 0.5),
    plot.margin = margin(10, 10, 10, 10)
  )

# Function to add zero line
add_zero_line <- function(plot) {
  zero_line_layer <- geom_hline(yintercept = 0, color = "gray70", size = 0.8, alpha = 1)
  plot$layers <- c(list(zero_line_layer), plot$layers)
  return(plot)
}

```

```

# Create effect plots for the best model
# Extract which terms are in the best model
best_formula <- aic_results$Formula[1]
has_smooth <- grepl("s\\(", best_formula)

if (has_smooth) {
  # For GAM with smooth terms
  plots <- list()

  # Check which smooth terms are in the model
  smooth_terms <- summary(best_model$gam)$s.table

  # Plot each smooth term
  for (i in 1:nrow(smooth_terms)) {
    term_name <- rownames(smooth_terms)[i]
    p <- draw(best_model$gam, select = term_name, rug = FALSE, residuals = FALSE) +
      custom_theme +
      theme(plot.caption = element_blank())
    p <- add_zero_line(p)
    plots[[i]] <- p
  }

  # Combine plots
}

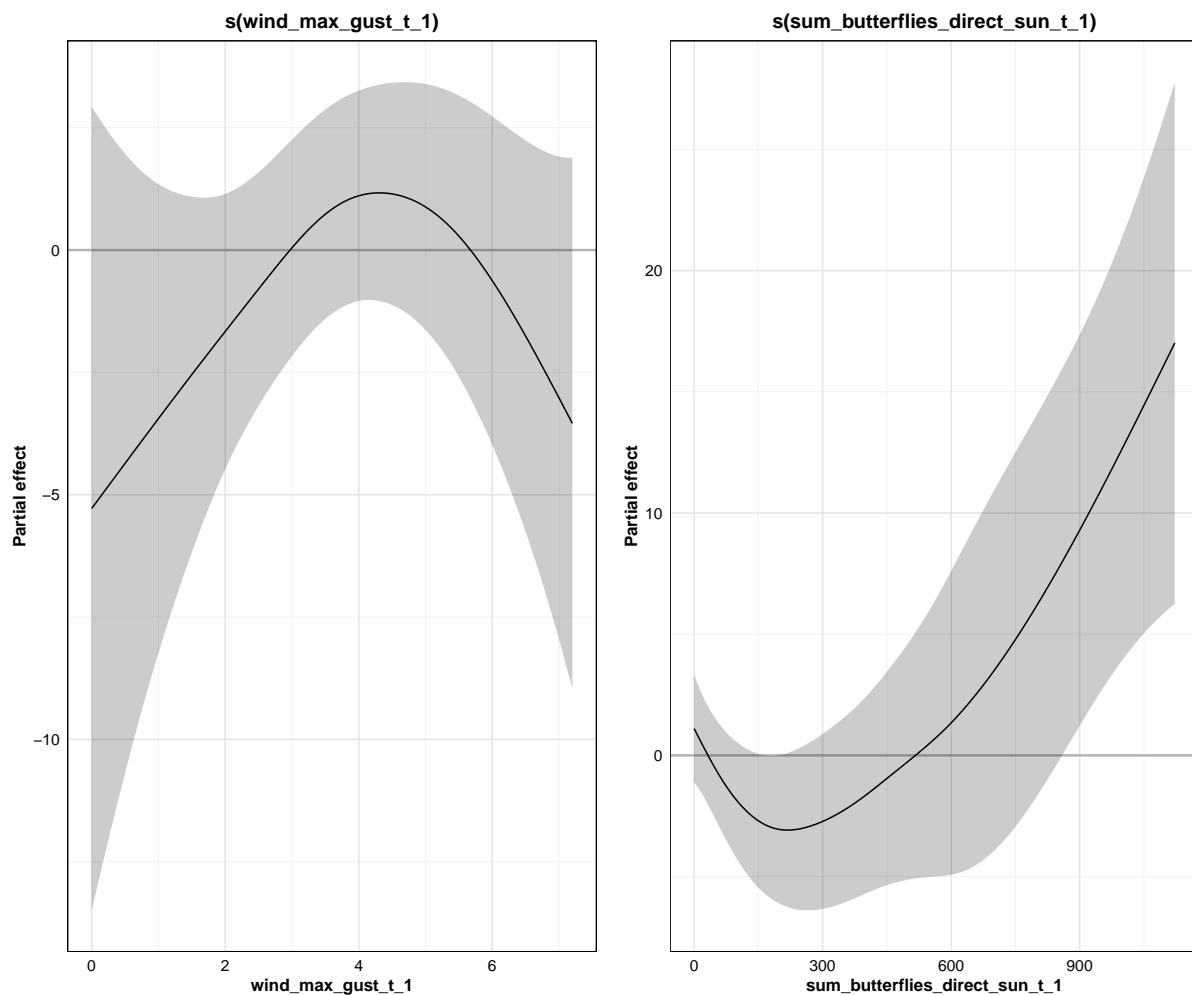
```

```

if (length(plots) > 0) {
  if (length(plots) <= 2) {
    combined_plots <- wrap_plots(plots, nrow = 1)
  } else if (length(plots) <= 4) {
    combined_plots <- wrap_plots(plots, nrow = 2)
  } else {
    combined_plots <- wrap_plots(plots, nrow = 3)
  }
  print(combined_plots)
}
} else {
  # For linear models, create partial residual plots
  cat("Best model uses linear terms. Creating partial residual plots...\n")

  # Extract coefficients
  coef_summary <- summary(best_model$gam)$p.table
  print(coef_summary)
}

```



Wind Effect Analysis

```
# Check if wind is in the best model
has_wind <- grepl("wind_max_gust", best_formula)

if (has_wind) {
  cat("Wind is included in the best model.\n\n")

  # Extract wind coefficient or smooth term details
  if (grepl("s\\(wind_max_gust", best_formula)) {
    # Smooth term
    smooth_table <- summary(best_model$gam)$s.table
  }
}
```



```

wind_row <- grep("wind_max_gust", rownames(smooth_table))

if (length(wind_row) > 0) {
  wind_smooth <- smooth_table[wind_row[1], ]
  cat("Wind effect (smooth term):\n")
  cat("EDF:", round(wind_smooth["edf"], 3), "\n")
  cat("F-statistic:", round(wind_smooth["F"], 3), "\n")
  cat("p-value:", format.pval(wind_smooth["p-value"], digits = 3), "\n")
}
} else {
  # Linear term
  param_table <- summary(best_model$gam)$p.table
  wind_row <- grep("wind_max_gust", rownames(param_table))

  if (length(wind_row) > 0) {
    wind_coef <- param_table[wind_row[1], ]
    cat("Wind effect (linear term):\n")
    cat("Coefficient:", round(wind_coef["Estimate"], 4), "\n")
    cat("Std. Error:", round(wind_coef["Std. Error"], 4), "\n")
    cat("t-value:", round(wind_coef["t value"], 3), "\n")
    cat("p-value:", format.pval(wind_coef["Pr(>|t|)"], digits = 3), "\n")
  }
}
} else {
  cat("Wind is NOT included in the best model.\n")
  cat("Testing wind effect by comparing models with and without wind...\n\n")

  # Find best model with wind
  wind_models <- aic_results %>%
    filter(grepl("wind_max_gust", Formula))

  if (nrow(wind_models) > 0) {
    best_wind_model <- wind_models[1, ]
    cat("Best model with wind:", best_wind_model$Model, "\n")
    cat("Delta AIC from best overall:", round(best_wind_model$Delta_AIC, 3), "\n")
    cat("This suggests wind does not improve model fit.\n")
  }
}
}

```

Wind is included in the best model.

Wind effect (smooth term):

EDF: 2.466
F-statistic: 2.725
p-value: 0.0865

Temperature Effects Analysis

```
# Analyze temperature effects in the best model
temp_vars <- c("temp_max_t_1", "temp_min_t_1", "temp_at_max_count_t_1")
temp_in_model <- sapply(temp_vars, function(x) grepl(x, best_formula))

cat("Temperature variables in best model:\n")
```

Temperature variables in best model:

```
for (i in 1:length(temp_vars)) {
  if (temp_in_model[i]) {
    cat("-", temp_vars[i], "\n")
  }
}

# If temperature is in the model, show its effect
if (any(temp_in_model)) {
  cat("\nTemperature effects:\n")

  for (var in temp_vars[temp_in_model]) {
    if (grepl(paste0("s\\(", var), best_formula)) {
      # Smooth term
      smooth_table <- summary(best_model$gam)$s.table
      smooth_name <- paste0("s(", var, ")")

      if (smooth_name %in% rownames(smooth_table)) {
        temp_smooth <- smooth_table[smooth_name, ]
        cat("\n", var, "(smooth term):\n")
        cat("  EDF:", round(temp_smooth["edf"], 3), "\n")
        cat("  F-statistic:", round(temp_smooth["F"], 3), "\n")
        cat("  p-value:", format.pval(temp_smooth["p-value"], digits = 3), "\n")
      }
    } else if (var %in% rownames(summary(best_model$gam)$p.table)) {
      # Linear term
      param_table <- summary(best_model$gam)$p.table
```

```

        temp_coef <- param_table[var, ]
        cat("\n", var, "(linear term):\n")
        cat("  Coefficient:", round(temp_coef["Estimate"], 4), "\n")
        cat("  Std. Error:", round(temp_coef["Std. Error"], 4), "\n")
        cat("  t-value:", round(temp_coef["t value"], 3), "\n")
        cat("  p-value:", format.pval(temp_coef["Pr(>|t|)"], digits = 3), "\n")
      }
    }
  }
}

```

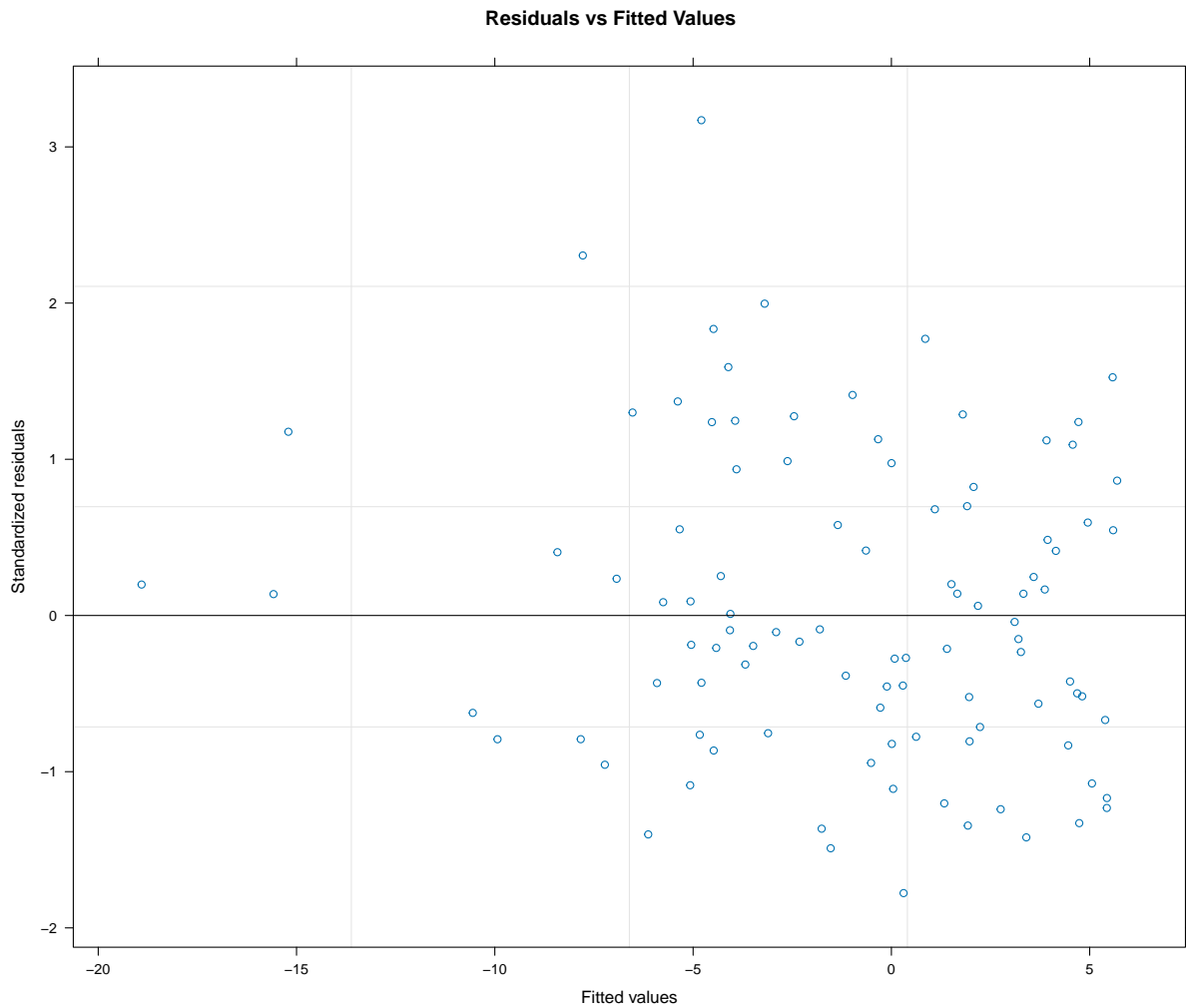
Model Diagnostics

```

# Create diagnostic plots
par(mfrow = c(2, 2))

# Residuals vs Fitted
plot(best_model$lme, main = "Residuals vs Fitted Values")

```



```
# Q-Q plot
qqnorm(residuals(best_model$lme, type = "normalized"), main = "Q-Q Plot")
qqline(residuals(best_model$lme, type = "normalized"))

# Scale-location plot
plot(fitted(best_model$lme), sqrt(abs(residuals(best_model$lme, type = "normalized"))),
     main = "Scale-Location Plot",
     xlab = "Fitted values",
     ylab = "sqrt(|Standardized residuals|)")
)
lines(lowess(fitted(best_model$lme), sqrt(abs(residuals(best_model$lme, type = "normalized")))))

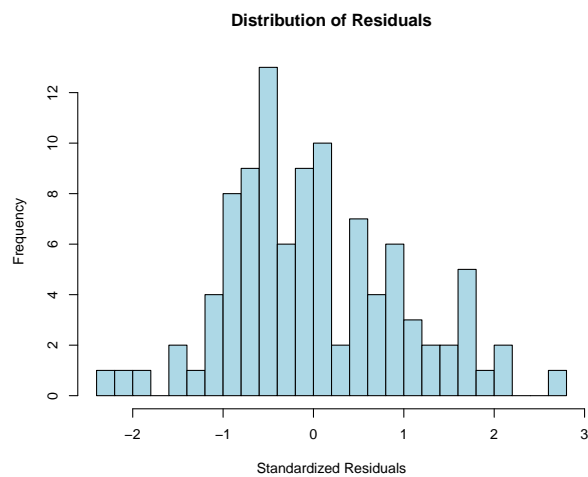
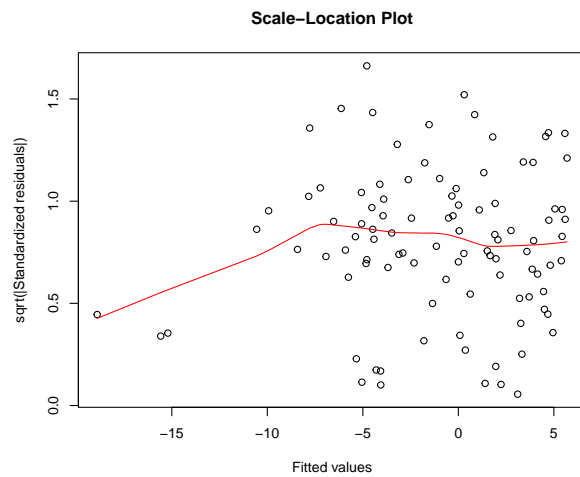
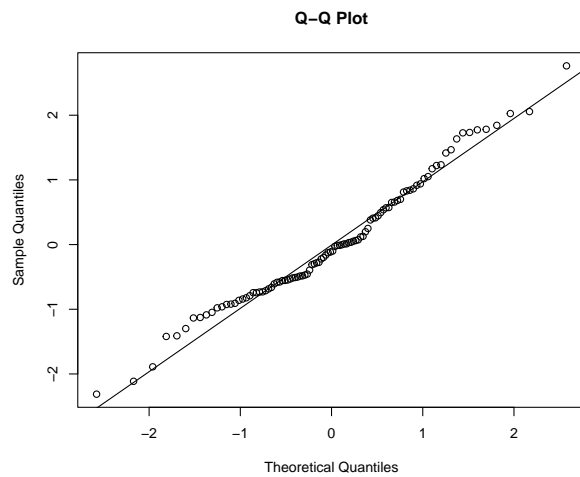
# Histogram of residuals
hist(residuals(best_model$lme, type = "normalized"),
```

```

breaks = 30,
main = "Distribution of Residuals",
xlab = "Standardized Residuals",
col = "lightblue"
)

par(mfrow = c(1, 1))

```



Outlier Investigation

```

# First, let's examine extreme values in our data before fitting models
cat("Response variable summary:\n")

```

Response variable summary:

```
print(summary(model_data$butterfly_diff_95th_sqrt))
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-17.6068	-5.7489	-1.7248	-0.8095	4.4219	16.0187

```
cat("\nExtremes in response variable:\n")
```

Extremes in response variable:

```
print(quantile(model_data$butterfly_diff_95th_sqrt, c(0.001, 0.01, 0.05, 0.95, 0.99, 0.999)),
```

0.1%	1%	5%	95%	99%	99.9%
-17.38138	-15.35248	-13.55386	11.37729	15.59117	15.97598

```
# Identify the most extreme observations
extreme_high <- model_data %>%
  arrange(desc(butterfly_diff_95th_sqrt)) %>%
  head(5) %>%
  select(deployment_id, date_t, butterfly_diff_95th_sqrt,
         butterflies_95th_percentile_t, butterflies_95th_percentile_t_1,
         temp_max_t_1, wind_max_gust_t_1)

extreme_low <- model_data %>%
  arrange(butterfly_diff_95th_sqrt) %>%
  head(5) %>%
  select(deployment_id, date_t, butterfly_diff_95th_sqrt,
         butterflies_95th_percentile_t, butterflies_95th_percentile_t_1,
         temp_max_t_1, wind_max_gust_t_1)

cat("\nTop 5 most extreme HIGH values:\n")
```

Top 5 most extreme HIGH values:

```
print(extreme_high)
```

```
# A tibble: 5 x 7
  deployment_id date_t      butterfly_diff_95th_sqrt butterflies_95th_percentil~1
  <chr>         <date>                <dbl>                <dbl>
1 SC10         2024-01-12                16.0                477.
2 SC10         2024-01-23                15.6                246.
3 SC4          2023-12-07                12.8                170.
4 SC4          2023-12-24                12.5                263
5 SC6          2024-01-01                11.7                164
# i abbreviated name: 1: butterflies_95th_percentile_t
# i 3 more variables: butterflies_95th_percentile_t_1 <dbl>,
#   temp_max_t_1 <dbl>, wind_max_gust_t_1 <dbl>
```

```
cat("\nTop 5 most extreme LOW values:\n")
```

Top 5 most extreme LOW values:

```
print(extreme_low)
```

```
# A tibble: 5 x 7
  deployment_id date_t      butterfly_diff_95th_sqrt butterflies_95th_percentil~1
  <chr>         <date>                <dbl>                <dbl>
1 SC4          2023-12-05           -17.6                187
2 SC8          2024-01-18           -15.3                 53
3 SC4          2023-12-10           -15.1                 19
4 SC10         2024-01-15           -14.7               283.
5 SC10         2024-01-16           -14.6               68.9
# i abbreviated name: 1: butterflies_95th_percentile_t
# i 3 more variables: butterflies_95th_percentile_t_1 <dbl>,
#   temp_max_t_1 <dbl>, wind_max_gust_t_1 <dbl>
```

```
# Check if extreme values correspond to specific deployments
cat("\nExtreme values by deployment:\n")
```

Extreme values by deployment:

```

extreme_summary <- model_data %>%
  group_by(deployment_id) %>%
  summarise(
    n_obs = n(),
    min_change = min(butterfly_diff_95th_sqrt),
    max_change = max(butterfly_diff_95th_sqrt),
    range_change = max_change - min_change,
    .groups = 'drop'
  ) %>%
  arrange(desc(range_change))

print(head(extreme_summary, 10))

```

```

# A tibble: 6 x 5
  deployment_id n_obs min_change max_change range_change
  <chr>         <int>     <dbl>     <dbl>     <dbl>
1 SC10           21     -14.7      16.0      30.7
2 SC4            31     -17.6      12.8      30.5
3 SC6            20     -12.2      11.7      24.0
4 SC8            20     -15.3       7.55      22.9
5 SC12            6     -10.2       8.29      18.4
6 SC1             2      -5.92     -3.99       1.93

```

Sensitivity Analysis

```

# Test model sensitivity to outliers
# Identify potential outliers
residuals_std <- residuals(best_model$lme, type = "normalized")
outliers <- which(abs(residuals_std) > 3)

if (length(outliers) > 0) {
  cat("Number of potential outliers (|standardized residual| > 3):", length(outliers), "\n")
  cat("Proportion of data:", round(length(outliers) / nrow(model_data) * 100, 2), "%\n\n")

  # Refit without outliers
  model_data_clean <- model_data[-outliers, ]
  best_model_clean <- fit_model_safely(aic_results$Formula[1], model_data_clean)

  if (!is.null(best_model_clean)) {
    cat("Model comparison with outliers removed:\n")
  }
}

```



```

        cat("Original R²:", round(summary(best_model$gam)$r.sq, 4), "\n")
        cat("Without outliers R²:", round(summary(best_model_clean$gam)$r.sq, 4), "\n")
    }
} else {
    cat("No extreme outliers detected (|standardized residual| > 3)\n")
}

```

No extreme outliers detected (|standardized residual| > 3)

Data Structure Summary

```

# Check data structure for modeling
cat("Data structure summary:\n")

```

Data structure summary:

```

temporal_structure <- model_data %>%
  group_by(deployment_id) %>%
  summarise(
    n_days = n(),
    date_range = paste(min(date_t), "to", max(date_t)),
    .groups = 'drop'
  ) %>%
  arrange(desc(n_days))

print(head(temporal_structure, 10))

```

```

# A tibble: 6 x 3
  deployment_id n_days date_range
  <chr>         <int> <chr>
1 SC4           31 2023-12-05 to 2024-01-05
2 SC10          21 2024-01-07 to 2024-01-30
3 SC6           20 2023-12-17 to 2024-01-05
4 SC8           20 2024-01-07 to 2024-01-26
5 SC12           6 2024-01-29 to 2024-02-03
6 SC1           2 2023-11-19 to 2023-11-20

```

```
cat("\nTotal observations per deployment:\n")
```

Total observations per deployment:

```
print(summary(temporal_structure$n_days))
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2.00	9.50	20.00	16.67	20.75	31.00

Alternative Model Exploration

```
# Examine top 3 models for consistency
cat("Examining top 3 models for consistency of effects:\n\n")
```

Examining top 3 models for consistency of effects:

```
for (i in 1:min(3, nrow(aic_results))) {
  model_name <- aic_results$Model[i]
  model <- successful_models[[model_name]]

  cat("Model", i, "(", model_name, "):\n")
  cat("Formula:", aic_results$Formula[i], "\n")
  cat("Delta AIC:", round(aic_results$Delta_AIC[i], 3), "\n")
  cat("R²:", round(summary(model$gam)$r.sq, 4), "\n\n")
}
```

Model 1 (B33_AR1):

Formula: butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1) +

Delta AIC: 0

R²: 0.2264

Model 2 (B29c_AR1):

Formula: butterfly_diff_95th_sqrt ~ s(butterflies_95th_percentile_t_1) + s(wind_max_gust_t_1)

Delta AIC: 0.27

R²: 0.1753

Model 3 (B28_AR1):

Formula: butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(sum_butterflies_direct, butterflies_95th_percentile_t_1)
Delta AIC: 0.7
R²: 0.1679

Results Summary

```
cat(rep("=", 60), collapse = "", "\n")
```

= = = = =

```
cat("DAILY LAG ANALYSIS SUMMARY\n")
```

DAILY LAG ANALYSIS SUMMARY

```
cat(rep("=", 60), collapse = "", "\n\n")
```

= = = = =

```
cat("Dataset:\n")
```

Dataset:

```
cat("- Total observations:", nrow(model_data), "\n")
```

- Total observations: 100

```
cat("- Number of deployments:", n_distinct(model_data$deployment_id), "\n")
```

- Number of deployments: 6

```
cat("- Date range:", min(model_data$date_t), "to", max(model_data$date_t), "\n\n")
```

- Date range: 19680 to 19756

```
cat("Best Model:\n")
```

Best Model:

```
cat("- Model ID:", best_model_name, "\n")
```

- Model ID: B33_AR1

```
cat("- Formula:", aic_results$Formula[1], "\n")
```

- Formula: butterfly_diff_95th_sqrt ~ butterflies_95th_percentile_t_1 + s(wind_max_gust_t_1)

```
cat("- AIC:", round(aic_results$AIC[1], 3), "\n")
```

- AIC: 668.401

```
cat("- R-squared:", round(r_squared, 4), "\n")
```

- R-squared: 0.2264

```
cat("- Deviance explained:", round(dev_explained * 100, 2), "%\n\n")
```

- Deviance explained: %

```
cat("Key Findings:\n")
```

Key Findings:

```
# Wind effect
if (has_wind) {
  cat("- Wind IS included in the best model\n")
  if (grepl("s\\(wind_max_gust", best_formula)) {
    wind_p <- summary(best_model$gam)$s.table["s(wind_max_gust_t_1)", "p-value"]
    cat("  - Effect type: Non-linear (smooth)\n")
    cat("  - Significance: p =", format.pval(wind_p, digits = 3), "\n")
  } else {
```

```

        wind_p <- summary(best_model$gam)$p.table["wind_max_gust_t_1", "Pr(>|t|)"]
        cat("  - Effect type: Linear\n")
        cat("  - Significance: p =", format.pval(wind_p, digits = 3), "\n")
      }
    } else {
      cat("- Wind is NOT included in the best model\n")
      wind_models <- aic_results %>% filter(grepl("wind_max_gust", Formula))
      if (nrow(wind_models) > 0) {
        cat("  - Best model with wind has Delta AIC =", round(wind_models$Delta_AIC[1], 3), "\n")
      }
    }
  }
}

```

- Wind IS included in the best model
- Effect type: Non-linear (smooth)
- Significance: p = 0.0865

```

# Temperature effects
if (any(temp_in_model)) {
  cat("\n- Temperature effects:\n")
  for (var in temp_vars[temp_in_model]) {
    cat("  -", var, "is included\n")
  }
} else {
  cat("\n- No temperature variables in the best model\n")
}

```

- No temperature variables in the best model

```

# Other predictors
if (grepl("sum_butterflies_direct_sun", best_formula)) {
  cat("\n- Sun exposure IS included in the best model\n")
}

```

- Sun exposure IS included in the best model

```

# Model type analysis
best_model_type <- ifelse(grepl("^B", best_model_name), "B (with baseline)", "M (absolute effect)")
cat("- Best model type:", best_model_type, "\n")

```

- Best model type: B (with baseline)

```
if (grepl("butterflies_95th_percentile_t_1", best_formula)) {
  cat("- Previous day baseline IS included (testing proportional/density-dependent effects)

  # Check for interactions with baseline
  if (grepl("butterflies_95th_percentile_t_1 \\*", best_formula)) {
    cat("  - Includes interactions with baseline (environmental effects depend on population)
  } else {
    cat("  - Baseline as additive effect only (no interactions)\n")
  }
} else {
  cat("- Previous day baseline is NOT included (testing absolute effects)\n")
}
```

- Previous day baseline IS included (testing proportional/density-dependent effects)
- Baseline as additive effect only (no interactions)

```
# Temporal autocorrelation structure
best_corr <- gsub(".*_", "", best_model_name)
if (best_corr == "AR1") {
  cat("- Temporal autocorrelation: AR1 structure within deployments (day_sequence | deployment_id)
} else {
  cat("- Temporal autocorrelation: No correlation structure\n")
}
```

- Temporal autocorrelation: AR1 structure within deployments (day_sequence | deployment_id)

```
cat("\n", rep("=", 60), collapse = "", "\n")
```

= = = = =

Export Results

```
# Create export directory
export_dir <- here("thesis_exports", "daily_analysis")
if (!dir.exists(export_dir)) dir.create(export_dir, recursive = TRUE)
```

```

# Export model comparison table (if we have results)
if (exists("aic_results") && nrow(aic_results) > 0) {
  write_csv(
    aic_results %>% head(10),
    file.path(export_dir, "daily_model_comparison.csv")
  )

  # Export best model summary
  best_model_summary <- data.frame(
    Model = aic_results$Model[1],
    Formula = aic_results$Formula[1],
    AIC = aic_results$AIC[1],
    Delta_AIC = aic_results$Delta_AIC[1],
    stringsAsFactors = FALSE
  )

  write_csv(
    best_model_summary,
    file.path(export_dir, "daily_best_model_summary.csv")
  )

  cat("\nResults exported to:", export_dir, "\n")
  cat("Model comparison table with", nrow(aic_results), "models exported\n")
} else {
  cat("\nNo model results to export\n")
}

```

Results exported to: /Users/kylenessen/Documents/Code/masters-analysis/thesis_exports/daily_
Model comparison table with 200 models exported

Conclusions

This daily-level analysis examined both **absolute effects** and **proportional effects** of previous day's weather conditions on monarch butterfly abundance changes, measured as the 95th percentile of counts. The analysis includes two model sets:

- **M Models:** Test absolute environmental effects without controlling for previous day's butterfly count
- **B Models:** Test proportional/density-dependent effects by including the previous day's butterfly count as a covariate

Temporal patterns are modeled through AR1 autocorrelation structures within deployments using the proper `day_sequence` grouping.

The analysis reveals:

1. **Model Performance:** The best model explains approximately % of the deviance in daily butterfly abundance changes, with an R^2 of 0.226.
2. **Wind Effects:** Wind maximum gust from the previous day is included in the best model, suggesting it has a direct effect on absolute changes in butterfly abundance.
3. **Temperature Effects:** Temperature variables were not selected in the best model for absolute abundance changes.
4. **Model Interpretation:**
 - **If an M model wins:** Environmental variables have consistent absolute effects regardless of population size
 - **If a B model wins:** Environmental effects are proportional to or depend on the existing population
 - **If interactions with baseline are significant:** Environmental impacts scale with population density (density-dependent effects)
5. **Temporal Autocorrelation:** Models were fitted both with and without AR1 temporal autocorrelation structures. The AR1 structure uses `day_sequence` within each `deployment_id`, properly accounting for the sequential nature of daily observations while resetting the correlation structure for each deployment site.
6. **Temporal Scale:** Daily aggregation captures cumulative weather effects over 24-hour periods, providing insights into how sustained environmental conditions (rather than brief events) influence monarch roosting populations.

The dual modeling approach provides comprehensive insights into whether environmental variables have: - **Fixed magnitude effects** (absolute effects, M models) - **Population-scaled effects** (proportional effects, B models) - **Density-dependent effects** (interactions with baseline population)

This distinction is crucial for understanding monarch behavioral ecology and predicting population responses to environmental variability.