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ARMA

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```
X123 <- read.csv("NoEvoData=SE=Feb14 2012.csv")

# Prepare log-transformed orange panel data
orange_data <- data.frame(
    day = X123$day,
    algae = log(X123$Algae.orange1),
    flagellates = log(X123$Flag.orange1),
    rotifers = log(X123$Rot.orange1)
)

# Subset data between day 41 and 107
orange_data <- orange_data[orange_data$day >= 41 & orange_data$day <= 107, ]

# Handle infinite values in rotifers
orange_data$rotifers[!is.finite(orange_data$rotifers)] <-
    min(orange_data$rotifers[is.finite(orange_data$rotifers)]) - 1

summary(orange_data)</pre>
```

```
##
         day
                        algae
                                     flagellates
                                                       rotifers
                   Min.
##
   Min.
        : 41.0
                         : 7.013
                                    Min.
                                           :3.932
                                                    Min.
                                                           :-3.4849
   1st Qu.: 57.5
                    1st Ou.: 9.856
                                    1st Qu.:5.366
                                                    1st Qu.:-0.6360
##
##
   Median : 74.0
                   Median :11.283
                                    Median :6.209
                                                    Median : 0.3011
         : 74.0
   Mean
                   Mean
                         :11.215
                                    Mean :6.180
                                                    Mean : 0.2567
##
   3rd Qu.: 90.5
                    3rd Ou.:12.589
                                    3rd Ou.:7.056
##
                                                    3rd Qu.: 1.4142
##
   Max.
          :107.0
                   Max.
                          :13.892
                                    Max.
                                           :8.114
                                                    Max.
                                                           : 2.2357
```

```
species_names <- c("algae", "flagellates", "rotifers")
arima_models <- list()

for(species in species_names) {
   ts_data <- ts(orange_data[[species]], frequency = 1)

# Auto ARIMA
   auto_model <- auto.arima(ts_data, seasonal = FALSE, stepwise = FALSE)
   arima_models[[species]] <- auto_model</pre>
```

```
}
n_total <- nrow(orange_data)</pre>
h forecast <- 8 # Forecast horizon
n train <- n total - h forecast
train data <- orange data[1:n train, ]</pre>
test_data <- orange_data[(n_train + 1):n_total, ]</pre>
forecast_performance <- data.frame()</pre>
for(species in species names) {
  # Refit model on training data
  train_ts <- ts(train_data[[species]], frequency = 1)</pre>
  # Get ARIMA order from full model
  full model <- arima models[[species]]</pre>
  arima order <- arimaorder(full model)</pre>
  # Refit on training data
  train model <- Arima(train ts, order = arima order)</pre>
  # Generate forecasts
  forecasts <- forecast(train_model, h = h_forecast)</pre>
  # Calculate performance metrics
  actual <- test_data[[species]]</pre>
  predicted <- as.numeric(forecasts$mean)</pre>
  mae <- mean(abs(actual - predicted))</pre>
  rmse <- sqrt(mean((actual - predicted)^2))</pre>
  mape <- mean(abs((actual - predicted) / actual)) * 100</pre>
  # Naive forecast (random walk)
  naive_forecast <- rep(tail(train_data[[species]], 1), h_forecast)</pre>
  mae naive <- mean(abs(actual - naive forecast))</pre>
  rmse naive <- sqrt(mean((actual - naive forecast)^2))</pre>
  forecast performance <- rbind(forecast performance, data.frame(</pre>
    species = species,
    mae arima = mae,
    rmse arima = rmse,
    mape_arima = mape,
    mae_naive = mae_naive,
    rmse_naive = rmse_naive,
    improvement = (rmse naive - rmse) / rmse naive * 100
  ))
}
```

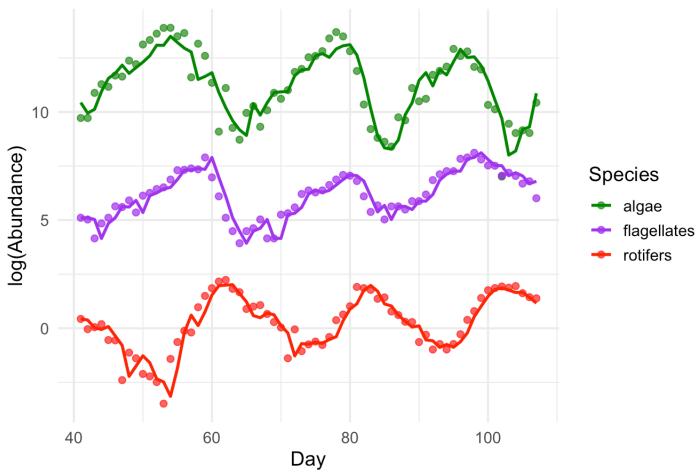
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```
# Combine all fitted values into one long dataframe
fitted_all <- data.frame()</pre>
for(species in species names) {
  model <- arima models[[species]]</pre>
  fitted vals <- fitted(model)</pre>
  df <- data.frame(</pre>
    day = orange data$day,
    observed = orange_data[[species]],
    fitted = as.numeric(fitted vals),
    species = species
  )
  fitted all <- bind rows(fitted all, df)</pre>
}
# Pivot longer for ggplot
fitted long <- fitted all %>%
  pivot_longer(cols = c(observed, fitted), names_to = "type", values_to = "log_abunda
nce")
# Unified plot: points for observed, dashed lines for fitted
ggplot(fitted long, aes(x = day, y = log abundance, color = species)) +
  geom_point(data = filter(fitted_long, type == "observed"), size = 2, alpha = 0.7) +
  geom line(data = filter(fitted long, type == "fitted"), linewidth = 1) +
  scale color manual(values = c(
    algae = "green4",
    flagellates = "purple",
    rotifers = "red"
  scale_linetype_manual(values = c(fitted = "dashed")) +
  labs(
    title = "ARIMA Fitted vs. Observed (Log-Transformed)",
    x = "Day",
    y = "log(Abundance)",
    color = "Species",
    linetype = "Type"
  ) +
  theme minimal(base size = 14) +
  theme(plot.title = element_text(hjust = 0.5))
```

```
## Warning: No shared levels found between `names(values)` of the manual scale and th
e
## data's linetype values.
```

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total_loglik <- sum(sapply(arima_models, function(model) logLik(model)))
total_loglik</pre>

[1] -176.4332