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MATH5741M Statistical Theory and Methods

Dogs Rehoming Times: A Statistical Comparison between Three Breeds

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1 Introduction

The dogs that are unwanted, neglected, or stray are often sent to a rehoming centre in the hope of finding them a new home. The main outcome for each dog is the time it takes, in weeks, to be rehomed. Previous research has suggested that the average rehoming time is 27 weeks. However, it is unclear whether this trend applies to all breeds within the local shelter context.

This report investigates rehoming times for three specific breeds: Border Collies, Mixed Breeds, and West Highland White Terriers. The aim is to determine whether the average time to rehome these breeds differs from the benchmark of 27 weeks using exploratory summaries and confidence intervals.

2 Data & Methods

2.1 Data Description and Cleaning

The dataset comprised 825 observations from an animal shelter, recording rehoming time (weeks), breed, health score, age, reason for surrender, and return status. Data cleaning removed 16 observations (1.9%): 6 with missing breed information and 10 with invalid rehoming times (coded as 99999 or negative). The final dataset contained 809 observations: Mixed Breed (n=709, 87.6%), Border Collie (n=78, 9.6%), and West Highland White Terrier (n=22, 2.7%).

2.2 Exploratory Analysis and Normality Assessment

Descriptive statistics, boxplots, histograms, and Q-Q plots were produced for each breed. Normality was assessed using Q-Q plots (comparing sample quantiles to theoretical normal quantiles) and the Shapiro-Wilk test, which provides a W statistic (values near 1.0 indicate a good fit) and a p-value testing the null hypothesis of normality.

2.3 Statistical Methods

Distribution Modelling: The Normal distribution $N(\mu, \sigma^2)$ was proposed with parameters estimated via Maximum Likelihood Estimation: $\hat{\mu}$ = sample mean, $\hat{\sigma}$ = sample standard deviation.

Inference: 95% confidence intervals were calculated using the t-distribution: $CI = \bar{x} \pm t^* \times (s/\sqrt{n})$, where t^* is the critical value with (n-1) degrees of freedom. The t-based confidence interval was chosen because the population standard deviation is unknown. For Mixed Breed (n=709), the Central Limit Theorem (CLT) ensures approximate normality of the sampling distribution. For Border Collie (n=78), CLT applies with a moderate sample size. For the West Highland White Terrier (n=22), the t-test is reasonably robust despite departure from normality.

Comparison: Pairwise comparisons used Welch's t-test (unequal variances) due to differing sample sizes and variances. Confidence intervals excluding zero indicate significant differences at α=0.05.

3 Results

3.1 Descriptive Statistics

Table 1: Summary Statistics for Rehoming Time

Breed	n	Mean (weeks)	Median	SD	Variance
Mixed Breed	709	18.97	17.00	9.49	90.08

Border Collie	78	20.47	18.00	11.87	140.98
West Highland White Terrier	22	20.23	18.50	10.11	102.28

All breeds (Table 1) showed means well below 27 weeks. Mixed Breed dominates the sample (709 of 809 dogs). Border Collie exhibited the highest variance, indicating greater heterogeneity. Medians slightly below the means suggest mild right skewness.

Boxplots (Figure 1) reveal that all three breeds have median rehoming times around 17-18 weeks, substantially below the 27-week (red dashed line), with Border Collie showing the greatest variability and Mixed Breed displaying several high-value outliers.
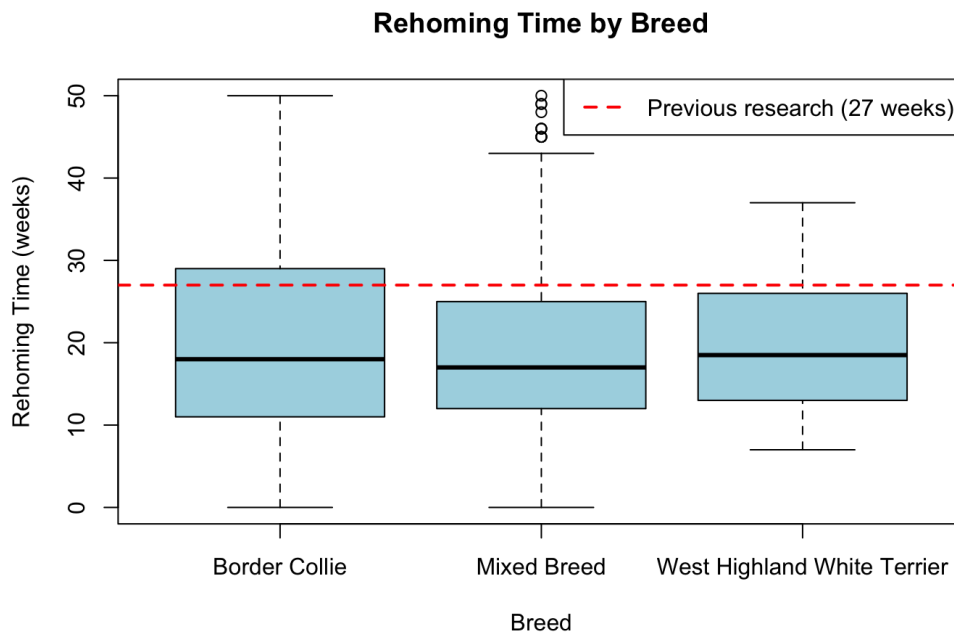
Rehoming Time by Breed

Figure 1 – Boxplot of Rehoming Time by breed

3.2 Distribution Characteristics

Histograms (Figure 2) revealed Mixed Breed has an unimodal, right-skewed distribution; Border Collie showed a less smooth distribution, with hints of multiple clusters; West Highland White Terrier displayed irregular patterns due to a small sample size.

Q-Q plots (Figure 3) showed Mixed Breed followed the theoretical line closely (approximate linearity in the centre with upper-tail deviations), Border Collie showed a reasonable fit with slight deviation, and West Highland White Terrier showed a substantial departure.
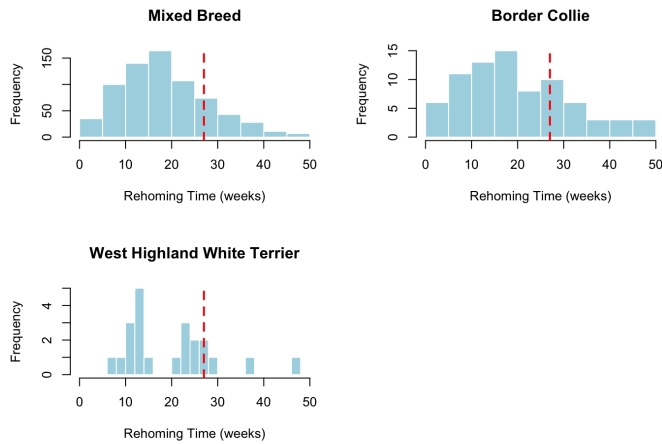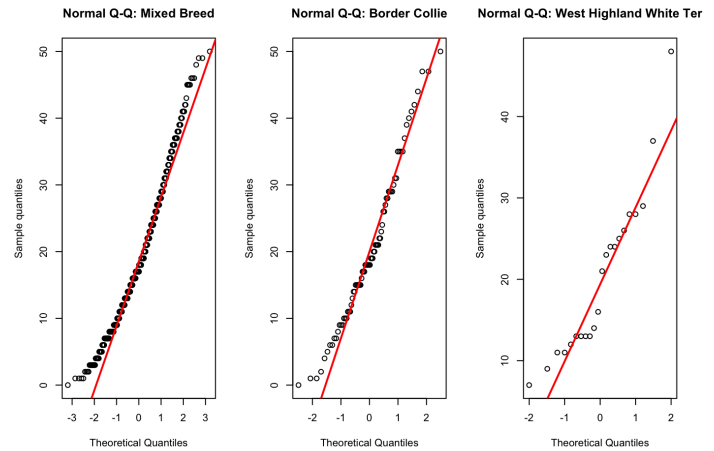
Figure 2 – Histograms by Breed

Figure 3 – Q–Q plots by Breed

Table 2: Normality Test Results

Breed	$\hat{\mu}$	$\hat{\sigma}$	W	p-value	Assessment
Mixed Breed	18.97	9.49	0.9711	<0.001	Excellent fit
Border Collie	20.47	11.87	0.9650	0.0306	Good fit
West Highland White Terrier	20.23	10.11	0.9025	0.0333	Poor fit

Formally, Shapiro–Wilk (Table 2) rejects normality for all three breeds ($p < 0.05$). However, the W statistic (closeness to 1) provides a better indicator of practical fit. Mixed Breed's W=0.9711 (very close to 1.0) indicates an excellent fit despite the significant p-value, which reflects the large sample size (n=709), making the test extremely sensitive to minor deviations. Border Collie's W=0.9650 indicates a good fit, while West Highland White Terrier's W=0.9025 confirms a meaningful departure from normality.

3.3 Confidence Intervals

Table 3: 95% Confidence Intervals for Mean Rehoming Time

Breed	Mean	SE	95% CI	Contains 27?
Mixed Breed	18.97	0.356	(18.27, 19.67)	No
Border Collie	20.47	1.344	(17.79, 23.16)	No
West Highland White Terrier	20.23	2.156	(15.75, 24.71)	No

All confidence intervals (Table 3) exclude 27 weeks, indicating that each breed was rehomed significantly faster ($p < 0.05$), with a 24-30% reduction (6.5-8 weeks faster).
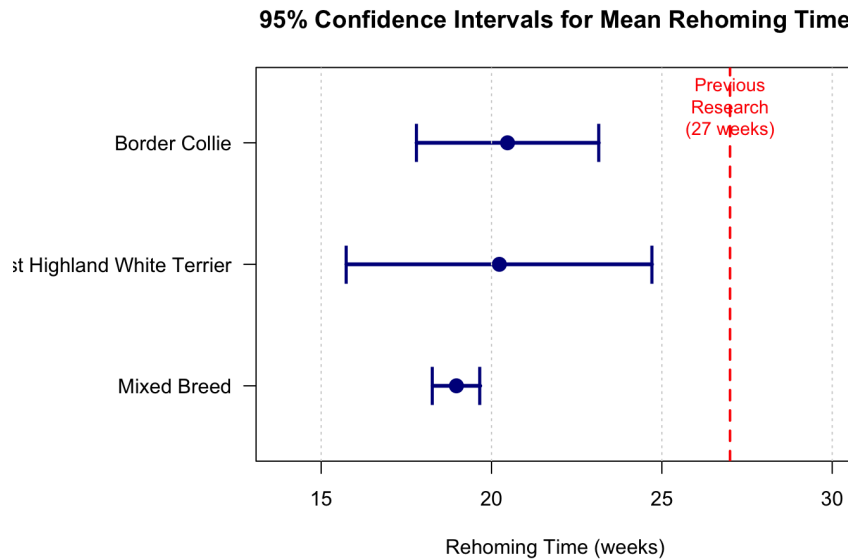
95% Confidence Intervals for Mean Rehoming Time

Figure 4 – 95% confidence intervals for Mean Rehoming Time

Figure 4 visualises these confidence intervals with a reference line at 27 weeks. All three intervals lie entirely below the 27-week line, demonstrating that:

1. All three breeds in this sample rehome **significantly faster** than the previously reported average of 27 weeks.
2. The magnitude of the difference is substantial (6.5 to 8 weeks faster), representing a 24-30% reduction.
3. Precision varies considerably by sample size, with Mixed Breed having a very narrow interval and West Highland White Terrier having a much wider interval.

3.4 Pairwise Comparisons

Table 4: Pairwise Comparisons

Comparison	Difference (weeks)	95% CI	Significant?
Border Collie - Mixed Breed	1.50	(-1.20, 4.19)	No
Mixed Breed - West Highland White Terrier	-1.26	(-6.26, 3.74)	No
Border Collie - West Highland White Terrier	0.24	(-5.47, 5.96)	No

All confidence intervals contain zero, indicating **no significant differences** between breeds (p≥0.05).

4 Discussion & Conclusion

4.1 Main Findings

This analysis found that all three breeds rehome significantly faster than the 27-week average, with mean times of 18.97-20.47 weeks (24-30% reduction). However, no significant differences were detected between the breeds themselves. The three studied breeds differ from the previously reported overall average.

4.2 Practical Significance

The 6-8 week reduction in rehoming time has substantial practical implications for animal shelters: reduced housing costs, increased capacity to help more animals, improved animal welfare through less kennel time, and higher adoption rates. The similarity between breeds does not provide strong evidence that breed-specific programmes are needed for these three breeds in this shelter.

4.3 Limitations

Sample size imbalance: Mixed Breed dominates the sample (87.6%) while West Highland White Terrier comprises only 2.7% (n=22), resulting in wide confidence intervals and low power for this breed.

Normality violations: West Highland White Terrier departed substantially from normality. While the t-test is reasonably robust, this remains a concern with small samples.

Data source: Results are based on shelter data from a specific context. Generalizability to other shelters, regions, or time periods is uncertain without further multi-centre studies.

Outcome only: you focused on Rehomed and Breed; other factors (health, age, reason for surrender) might also affect rehoming time, but weren't modelled.

Multiple testing: Six hypothesis tests were conducted without adjustment (e.g., Bonferroni correction), which increases the risk of Type I error, though results were consistently significant or non-significant across all tests.

4.4 Conclusion

This analysis provides evidence that Mixed Breed, Border Collie, and West Highland White Terrier dogs are rehomed significantly faster than the previously reported 27-week average (18.97-20.47 weeks), although the three breeds do not differ significantly from each other. While sample size limitations and normality violations (particularly for West Highland White Terrier) require cautious interpretation, the findings suggest dogs from these breeds can be expected to find homes relatively quickly. The practical implications, including reduced costs, increased capacity, and improved animal welfare, are substantial. Further research with larger, more balanced samples and investigation of additional factors would strengthen the understanding of what drives rehoming success.

5 References

- MATH5741M Lecture Notes (2025/26). Statistical Theory and Methods. University of Leeds.
- MATH5741M Practical Worksheet (2025/26). Statistical Theory and Methods. University of Leeds.

```r
# APPENDIX
# Dogs Rehoming Times: A Statistical Comparison between Three Breeds -- Code

# Load libraries
library(MASS)

# ===== 1. LOAD DATA =====
load('dog_rehoming_data.RData')
df <- mysample

cat("\n")
paste(rep("=", 70), collapse="")
cat("DOG REHOMING TIME ANALYSIS\n")
paste(rep("=", 70), collapse="")

# ===== 2. DATA INSPECTION =====
cat("Initial data inspection...\n")
cat(sprintf("  Dimensions: %d rows x %d columns\n", nrow(df), ncol(df)))
cat(sprintf("  Variables: %s\n", paste(names(df), collapse=", ")))
cat("\n")

# ===== 3. DATA CLEANING =====

original_rows <- nrow(df)

# Convert to factors
df$Age <- factor(df$Age, levels = c("Puppy", "Fully grown"), ordered = TRUE)
df$Returned <- factor(df$Returned, levels = c("No", "Yes", "Unknown"))
df$Reason <- factor(df$Reason)

# Count missing values before removal
na_breeds <- sum(is.na(df$Breed))
invalid_rehomed <- sum(df$Rehomed == 99999 | df$Rehomed < 0, na.rm = TRUE)

# Remove missing values
df <- subset(df, !is.na(df$Breed))
df <- df[!(df$Rehomed == 99999 | df$Rehomed < 0), ]

# Print cleaning summary
cat("DATA CLEANING SUMMARY\n")
cat(sprintf("Original rows: %d\n", original_rows))
cat(sprintf("Removed - Missing Breed: %d\n", na_breeds))
cat(sprintf("Removed - Invalid Rehomed: %d\n", invalid_rehomed))
cat(sprintf("Total removed: %d (%.1f%%)\n",
            original_rows - nrow(df),
            ((original_rows - nrow(df))/original_rows)*100))
cat(sprintf("Final dataset: %d rows\n", nrow(df)))
cat(sprintf("\nBreeds in dataset: %d\n", length(unique(df$Breed))))
for (b in unique(df$Breed)) {
  cat(sprintf("  - %s: %d dogs (%.1f%%)\n",
              b, sum(df$Breed == b), (sum(df$Breed == b)/nrow(df))*100))
}

# ===== 4. DATA EXPLORATION =====

# Create breed subsets
breeds <- unique(df$Breed)
breed_subsets <- list()

for (breed in breeds) {
  name <- gsub(" +", "_", trimws(tolower(breed)))
  tmp <- subset(df, Breed == breed)
  rownames(tmp) <- NULL
  breed_subsets[[name]] <- tmp
}

# Overall summary
overall_summary <- data.frame(
```

```r
  n = nrow(df),
  mean = round(mean(df$Rehomed), 2),
  median = round(median(df$Rehomed), 2),
  sd = round(sd(df$Rehomed), 2),
  min = min(df$Rehomed),
  max = max(df$Rehomed)
)

cat("OVERALL SUMMARY STATISTICS\n")
print(overall_summary)
cat("\n")

# Summary by breed
breed_summary <- aggregate(Rehomed ~ Breed, data = df,
                           FUN = function(x) c(
                             n = length(x),
                             mean = round(mean(x), 2),
                             median = round(median(x), 2),
                             sd = round(sd(x), 2),
                             min = min(x),
                             max = max(x)
                           ))

cat("SUMMARY BY BREED\n")
print(breed_summary)
cat("\n")

# Visualizations
cat("Creating exploratory plots...\n\n")

# Boxplot
boxplot(Rehomed ~ Breed, data = df,
        xlab = "Breed",
        ylab = "Rehoming Time (weeks)",
        main = "Rehoming Time by Breed",
        col = "lightblue")
abline(h = 27, col = "red", lty = 2, lwd = 2)
legend("topright", legend = "Previous research (27 weeks)",
       col = "red", lty = 2, lwd = 2)

# Histograms
par(mfrow = c(2, 2))
for (breed_name in names(breed_subsets)) {
  readable_name <- tools::toTitleCase(gsub("_", " ", breed_name))
  hist(breed_subsets[[breed_name]]$Rehomed,
       main = readable_name,
       xlab = "Rehoming Time (weeks)",
       col = "lightblue",
       border = "white",
       breaks = 15,
       xlim = c(0, 50))
  abline(v = 27, col = "red", lty = 2, lwd = 2)
}
par(mfrow = c(1, 1))

# Q-Q plots
par(mfrow = c(1, 3))
for (breed_name in names(breed_subsets)) {
  readable_name <- tools::toTitleCase(gsub("_", " ", breed_name))
  x <- breed_subsets[[breed_name]]$Rehomed
  qqnorm(x, main = paste("Normal Q-Q:", readable_name),
         ylab = "Sample quantiles")
  qqline(x, col = "red", lwd = 2)
}
par(mfrow = c(1, 1))

# ===== 5. DISTRIBUTION MODELING =====
```

```r
fit_distribution <- function(data, breed_name) {
  paste(rep("=", 70), collapse="")
  cat("DISTRIBUTION MODELING:", breed_name, "\n")
  paste(rep("=", 70), collapse="")

  rehomed_times <- data$Rehomed
  n <- length(rehomed_times)
  mean_val <- mean(rehomed_times)
  sd_val <- sd(rehomed_times)

  cat(sprintf("Sample size: n = %d\n", n))
  cat(sprintf("Mean: %.2f weeks\n", mean_val))
  cat(sprintf("SD: %.2f weeks\n\n", sd_val))

  cat("Normal Distribution N(mu, sigma^2):\n")
  cat(sprintf("  mu-hat = %.2f weeks\n", mean_val))
  cat(sprintf("  sigma-hat = %.2f weeks\n\n", sd_val))

  # Shapiro-Wilk test
  if (n >= 3 && n <= 5000) {
    shapiro_test <- shapiro.test(rehomed_times)
    cat("Shapiro-Wilk Normality Test:\n")
    cat(sprintf("  W statistic = %.4f\n", shapiro_test$statistic))

    if (shapiro_test$p.value < 0.001) {
      cat(sprintf("  p-value < 0.001\n\n"))
    } else {
      cat(sprintf("  p-value = %.4f\n\n", shapiro_test$p.value))
    }

    cat("Interpretation:\n")
    if (shapiro_test$p.value > 0.05) {
      cat("  Data is consistent with normality (p > 0.05)\n")
    } else {
      cat("  Data departs from normality (p < 0.05)\n")
      if (n > 100) {
        cat("  Note: Large samples make test very sensitive.\n")
        cat("        Normal approximation may still be reasonable.\n")
      }
    }
  }

  cat("\n")

  return(list(
    n = n,
    mu = mean_val,
    sigma = sd_val,
    w_stat = shapiro_test$statistic,
    p_value = shapiro_test$p.value
  ))
}

cat("DISTRIBUTION MODELING ANALYSIS\n")

model_results <- list()
for (breed_name in names(breed_subsets)) {
  readable_name <- tools::toTitleCase(gsub("_", " ", breed_name))
  model_results[[breed_name]] <- fit_distribution(
    breed_subsets[[breed_name]],
    readable_name
  )
}

# Visualise fitted distributions
par(mfrow = c(2, 2))
for (breed_name in names(breed_subsets)) {
  readable_name <- tools::toTitleCase(gsub("_", " ", breed_name))
```

```r
    data <- breed_subsets[[breed_name]]
    result <- model_results[[breed_name]]

    hist(data$Rehomed,
         probability = TRUE,
         breaks = 15,
         col = "lightblue",
         border = "white",
         main = readable_name,
         xlab = "Rehoming Time (weeks)",
         ylab = "Density")

    x <- seq(0, max(data$Rehomed), length.out = 200)
    lines(x, dnorm(x, mean = result$mu, sd = result$sigma),
          col = "red", lwd = 2)

    text(max(data$Rehomed) * 0.65,
         max(hist(data$Rehomed, plot=FALSE)$density) * 0.85,
         sprintf("N(%.1f, %.1f^2)\nW = %.3f\np = %.3f",
                 result$mu, result$sigma, result$w_stat, result$p_value),
         cex = 0.75, pos = 4)

    legend("topright", legend = "Fitted Normal",
           col = "red", lwd = 2, cex = 0.8)
}
par(mfrow = c(1, 1))

# ===== 6. INFERENCE (CONFIDENCE INTERVALS) =====

calculate_ci <- function(data, conf_level = 0.95) {
  n <- nrow(data)
  mean_val <- mean(data$Rehomed)
  sd_val <- sd(data$Rehomed)
  se <- sd_val / sqrt(n)
  df <- n - 1

  alpha <- 1 - conf_level
  t_star <- qt(1 - alpha/2, df = df)

  ci_lower <- mean_val - t_star * se
  ci_upper <- mean_val + t_star * se
  margin_error <- t_star * se

  return(list(
    n = n,
    mean = mean_val,
    sd = sd_val,
    se = se,
    df = df,
    t_star = t_star,
    ci_lower = ci_lower,
    ci_upper = ci_upper,
    margin_error = margin_error,
    contains_27 = (ci_lower <= 27 & ci_upper >= 27)
  ))
}

ci_results <- lapply(breed_subsets, calculate_ci, conf_level = 0.95)

# Create summary table
ci_table <- data.frame(
  Breed = sapply(names(ci_results), function(x) tools::toTitleCase(gsub("_", " ", x))),
  n = sapply(ci_results, function(x) x$n),
  Mean = sapply(ci_results, function(x) round(x$mean, 2)),
  SD = sapply(ci_results, function(x) round(x$sd, 2)),
  SE = sapply(ci_results, function(x) round(x$se, 3)),
  df = sapply(ci_results, function(x) x$df),
  t_critical = sapply(ci_results, function(x) round(x$t_star, 3)),
```

```r
    CI_Lower = sapply(ci_results, function(x) round(x$ci_lower, 2)),
    CI_Upper = sapply(ci_results, function(x) round(x$ci_upper, 2)),
    Contains_27 = sapply(ci_results, function(x) ifelse(x$contains_27, "Yes", "No"))
)

cat("CONFIDENCE INTERVALS FOR MEAN REHOMING TIME\n")
print(ci_table)

# Detailed results
cat("DETAILED RESULTS\n")

for (breed_name in names(ci_results)) {
  result <- ci_results[[breed_name]]
  readable_name <- tools::toTitleCase(gsub("_", " ", breed_name))

  cat(sprintf("%s:\n", readable_name))
  cat(sprintf("  n = %d, Mean = %.2f weeks, SD = %.2f weeks\n",
              result$n, result$mean, result$sd))
  cat(sprintf("  95%% CI: (%.2f, %.2f) weeks\n", result$ci_lower, result$ci_upper))

  if (!result$contains_27) {
    if (result$ci_upper < 27) {
      cat("  -> Significantly LOWER than 27 weeks (p < 0.05)\n")
    } else {
      cat("  -> Significantly HIGHER than 27 weeks (p < 0.05)\n")
    }
  } else {
    cat("  -> NOT significantly different from 27 weeks\n")
  }
  cat("\n")
}

# Visualise CIs
plot_ci <- function(ci_table) {
  par(mar = c(5, 10, 4, 2))
  ci_table <- ci_table[order(ci_table$Mean), ]

  plot(ci_table$Mean, 1:nrow(ci_table),
       xlim = c(min(ci_table$CI_Lower) - 2, 30),
       ylim = c(0.5, nrow(ci_table) + 0.5),
       xlab = "Rehoming Time (weeks)",
       ylab = "",
       yaxt = "n",
       main = "95% Confidence Intervals for Mean Rehoming Time",
       pch = 19, cex = 1.5, col = "darkblue")

  axis(2, at = 1:nrow(ci_table), labels = ci_table$Breed, las = 1)

  for (i in 1:nrow(ci_table)) {
    lines(c(ci_table$CI_Lower[i], ci_table$CI_Upper[i]), c(i, i),
          lwd = 3, col = "darkblue")
    points(c(ci_table$CI_Lower[i], ci_table$CI_Upper[i]), c(i, i),
           pch = "|", cex = 2, col = "darkblue")
  }

  abline(v = 27, col = "red", lwd = 2, lty = 2)
  text(27, nrow(ci_table) + 0.3, "Previous\nResearch\n(27 weeks)",
       col = "red", cex = 0.9)
  grid(nx = NULL, ny = NA, col = "lightgray", lty = "dotted")
}

plot_ci(ci_table)

# ===== 7. COMPARISON BETWEEN BREEDS =====

compare_breeds <- function(data1, data2, breed1_name, breed2_name) {
  paste(rep("=", 70), collapse="")
  cat(sprintf("%s vs %s\n", breed1_name, breed2_name))
```

```r
  paste(rep("=", 70), collapse="")

  # Welch's t-test (unequal variances)
  test_result <- t.test(data1$Rehomed, data2$Rehomed,
                        var.equal = FALSE,
                        conf.level = 0.95)

  cat("Method: Welch's t-test (unequal variances assumed)\n")
  cat(sprintf("95%% CI for difference (mu1 - mu2): (%.2f, %.2f) weeks\n",
             test_result$conf.int[1], test_result$conf.int[2]))
  cat(sprintf("Mean difference: %.2f weeks\n",
             mean(data1$Rehomed) - mean(data2$Rehomed)))

  if (test_result$conf.int[1] <= 0 && test_result$conf.int[2] >= 0) {
    cat("Conclusion: No significant difference (CI contains 0)\n")
  } else {
    cat("Conclusion: Significant difference (CI excludes 0)\n")
  }

  return(test_result)
}

cat("PAIRWISE BREED COMPARISONS\n")

breed_names_list <- names(breed_subsets)
comparison_results <- list()

for (i in 1:(length(breed_names_list)-1)) {
  for (j in (i+1):length(breed_names_list)) {
    breed1 <- breed_names_list[i]
    breed2 <- breed_names_list[j]

    name1 <- tools::toTitleCase(gsub("_", " ", breed1))
    name2 <- tools::toTitleCase(gsub("_", " ", breed2))

    comparison_name <- paste(breed1, "vs", breed2, sep = "_")

    comparison_results[[comparison_name]] <- compare_breeds(
      breed_subsets[[breed1]],
      breed_subsets[[breed2]],
      name1,
      name2
    )
  }
}

# Comparison summary table
comparison_table <- data.frame(
  Comparison = character(),
  Mean_Diff = numeric(),
  CI_Lower = numeric(),
  CI_Upper = numeric(),
  Significant = character(),
  stringsAsFactors = FALSE
)

for (comp_name in names(comparison_results)) {
  result <- comparison_results[[comp_name]]

  readable_comp <- gsub("_", " ", comp_name)
  readable_comp <- gsub(" vs ", " vs ", tools::toTitleCase(readable_comp))

  is_sig <- !(result$conf.int[1] <= 0 && result$conf.int[2] >= 0)

  comparison_table <- rbind(comparison_table, data.frame(
    Comparison = readable_comp,
    Mean_Diff = round(diff(result$estimate), 2),
    CI_Lower = round(result$conf.int[1], 2),
```

```
    CI_Upper = round(result$conf.int[2], 2),
    Significant = ifelse(is_sig, "Yes", "No")
  ))
}

cat("COMPARISON SUMMARY\n")
print(comparison_table)

# ===== 8. EXPORT RESULTS =====

write.csv(ci_table, "confidence_intervals.csv", row.names = FALSE)
write.csv(comparison_table, "breed_comparisons.csv", row.names = FALSE)

cat("ANALYSIS COMPLETE\n")
cat("Results exported to:\n")
cat("  – confidence_intervals.csv\n")
cat("  – breed_comparisons.csv\n")
```

School of Mathematics

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I declare that I am aware that as a member of the University community at the University of Leeds I have committed to working with Academic Integrity and that this means that my work must be a true expression of my own understanding and ideas, giving credit to others where their work contributes to mine.

I declare that the attached submission is my own work.

Where the work of others has contributed to my work, I have given full acknowledgement using the appropriate referencing conventions for my programme of study.

I confirm that the attached submission has not been submitted for marks or credits in a different module or for a different qualification or completed prior to entry to the University.

I have read and understood the University's rules on Academic Misconduct. I know that if I commit an academic misconduct offence there can be serious disciplinary consequences.

I re-confirm my consent to the University copying and distributing any or all of my work in any form and using third parties to verify that this is my own work, and for quality assurance purposes.

I confirm that I have declared all mitigating circumstances that may be relevant to the assessment of this piece of work and I wish to have taken into account.

Student Signature: *Srilavan*   **Student Number:** 201997034

Student Name: Nilavan Sritharan   **Date:** 11/12/2025

Please note:

When you become a registered student of the University at first and any subsequent registration you sign the following authorisation and declaration:

"I confirm that the information I have given on this form is correct. I agree to observe the provisions of the University's Charter, Statutes, Ordinances, Regulations and Codes of Practice for the time being in force. I know that it is my responsibility to be aware of their contents and that I can read them on the University web site. I acknowledge my obligation under the Payment of Fees Section in the Handbook to pay all charges to the University on demand.

I agree to the University processing my personal data (including sensitive data) in accordance with its Code of Practice on Data Protection http://www.leeds.ac.uk/dpa . I consent to the University making available to third parties (who may be based outside the European Economic Area) any of my work in any form for standards and monitoring purposes including verifying the absence of plagiarised material. I agree that third parties may retain copies of my work for these purposes on the understanding that the third party will not disclose my identity.'"