Flower Shrinkage Analysis

Data Loading and Preparation

```
# Load the data
data <- read_csv("../data/raw/fl_shrinkage2.csv")
```

```
Rows: 33 Columns: 6
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (1): site
dbl (5): plant, flower, time, weight, area

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# Clean the data - remove rows with missing flower or area data
data_clean <- data %>%
  filter(!is.na(flower), !is.na(area), !is.na(weight)) %>%
  # Create a unique identifier for each individual flower (plant)
  mutate(flower_id = paste("Plant", plant, sep = " "))

# Display data structure
glimpse(data_clean)
```

```
Rows: 32
Columns: 7
$ site      <chr> "cojo", "cojo", "cojo", "cojo", "cojo", "cojo", "cojo", "coj~
$ plant     <dbl> 1, 1, 1, 2, 2, 2, 3, 3, 4, 4, 4, 5, 5, 5, 6, 6, 6, 7, 7, 7, ~
$ flower    <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
$ time      <dbl> 1, 2, 3, 1, 2, 3, 1, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, ~
```

```
$ weight    <dbl> 0.02591, 0.02155, 0.02023, 0.01555, 0.01175, 0.01077, 0.0079~
$ area      <dbl> 3.084, 3.525, 2.437, 2.326, 1.252, 1.470, 1.335, 1.191, 2.01~
$ flower_id <chr> "Plant 1", "Plant 1", "Plant 1", "Plant 2", "Plant 2", "Plan~
```

Summary Statistics

```r
# Show summary of the cleaned data
cat("Number of individual flowers:", length(unique(data_clean$plant)), "\n")
```

```
Number of individual flowers: 11
```

```r
cat("Number of observations:", nrow(data_clean), "\n")
```

```
Number of observations: 32
```

```r
cat("Weight range:", round(range(data_clean$weight, na.rm = TRUE), 4), "grams\n")
```

```
Weight range: 0.0046 0.0391 grams
```

```r
cat("Area range:", round(range(data_clean$area, na.rm = TRUE), 2), "cm²\n")
```

```
Area range: 0.98 4.96 cm²
```

```r
# Data overview
cat("Individual flowers in dataset:", paste(sort(unique(data_clean$plant)), collapse = ", "))
```

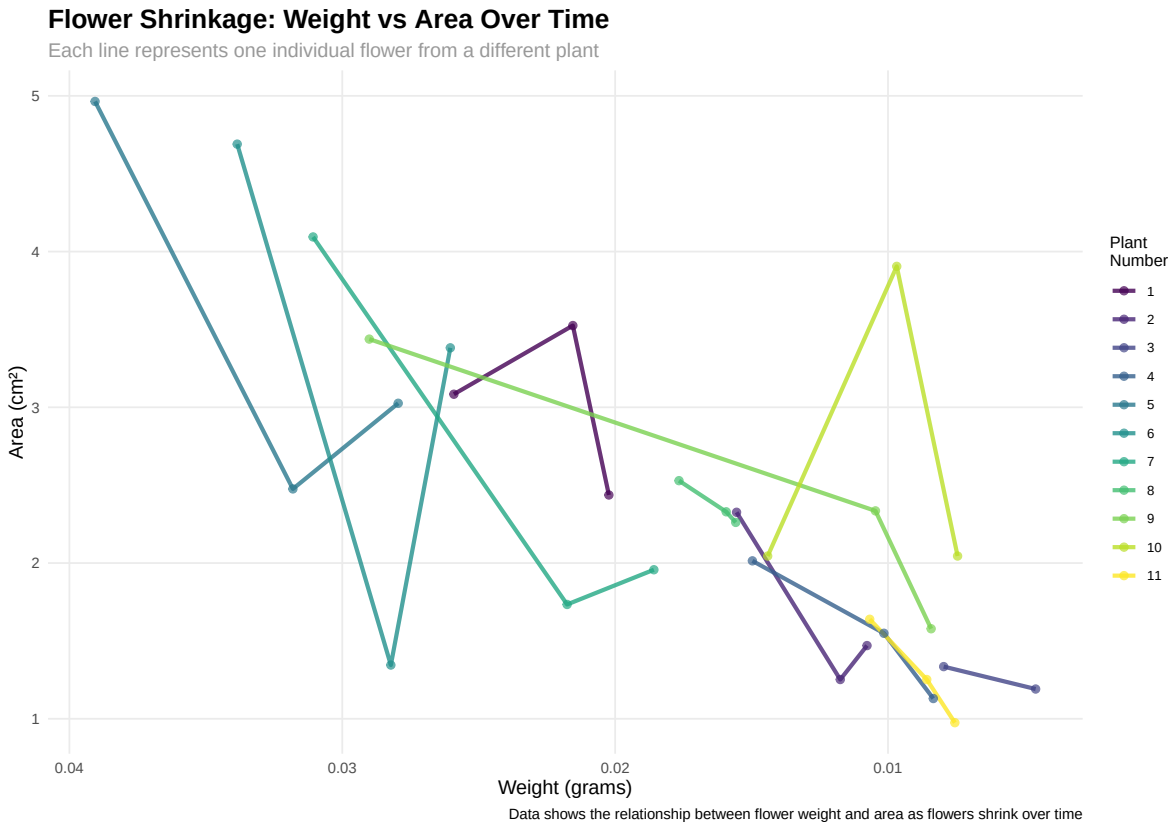
```
Individual flowers in dataset: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11
```

Weight vs Area Plot

```r
# Create the plot with weight on x-axis and area on y-axis
# Each plant (individual flower) gets its own line
p <- ggplot(data_clean, aes(x = weight, y = area, color = factor(plant))) +
  geom_line(size = 1.2, alpha = 0.8) +
  geom_point(size = 2, alpha = 0.7) +
  scale_x_reverse() +
  scale_color_viridis_d(name = "Plant\nNumber") +
  labs(
    title = "Flower Shrinkage: Weight vs Area Over Time",
    subtitle = "Each line represents one individual flower from a different plant",
    x = "Weight (grams)",
    y = "Area (cm²)",
    caption = "Data shows the relationship between flower weight and area as flowers shrink d
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    plot.subtitle = element_text(size = 12, color = "gray60"),
    axis.title = element_text(size = 12),
    legend.title = element_text(size = 10),
    legend.text = element_text(size = 8),
    panel.grid.minor = element_blank()
  )
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

```r
print(p)
```



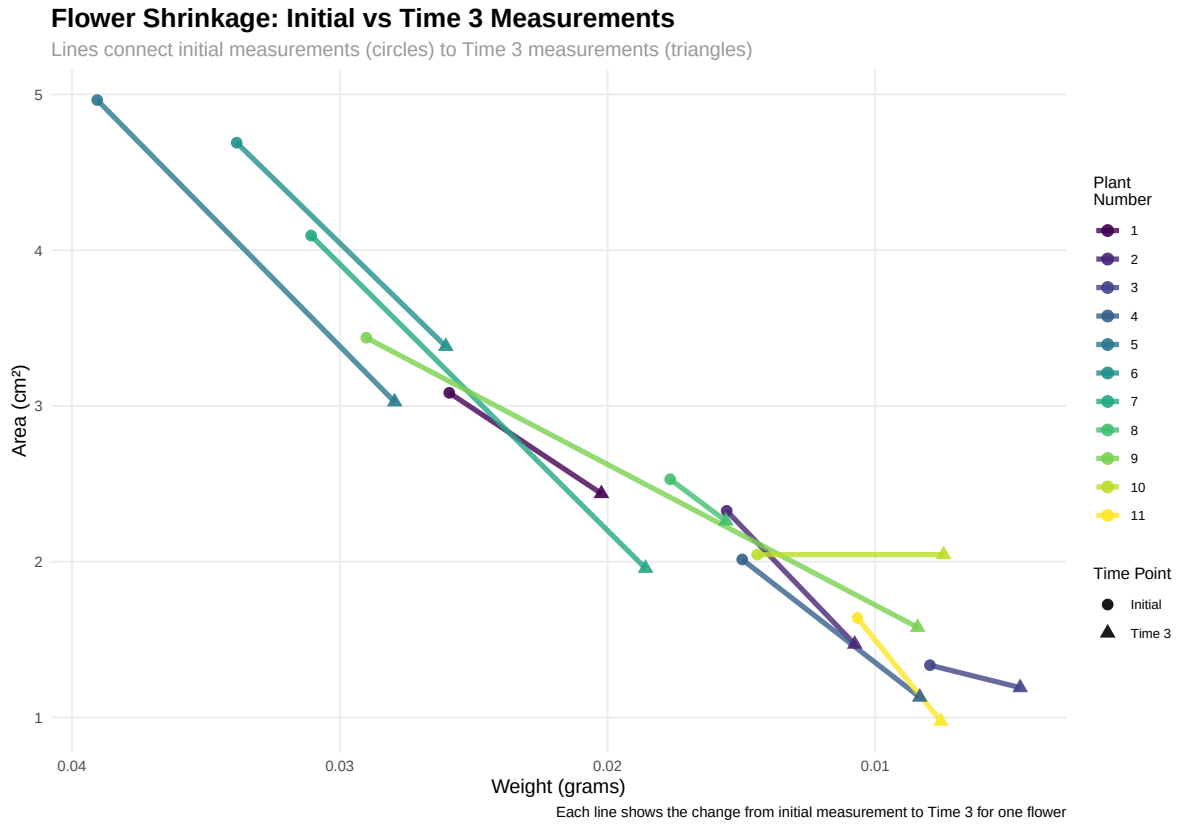
Before and After Comparison Plot (Time 1 vs Time 3)

```
# Filter data for only time points 1 and 3
before_after_data <- data_clean %>%
  filter(time %in% c(1, 3)) %>%
  mutate(time_label = ifelse(time == 1, "Initial", "Time 3"))

# Create plot showing only first and third measurements
p3 <- ggplot(before_after_data, aes(x = weight, y = area, color = factor(plant))) +
  geom_line(aes(group = plant), size = 1.5, alpha = 0.8) +
  geom_point(aes(shape = time_label), size = 3, alpha = 0.9) +
  scale_x_reverse() +
  scale_color_viridis_d(name = "Plant\nNumber") +
  scale_shape_manual(values = c("Initial" = 16, "Time 3" = 17), name = "Time Point") +
  labs(
    title = "Flower Shrinkage: Initial vs Time 3 Measurements",
    subtitle = "Lines connect initial measurements (circles) to Time 3 measurements (triangle
```

```
    x = "Weight (grams)",
    y = "Area (cm²)",
    caption = "Each line shows the change from initial measurement to Time 3 for one flower"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    plot.subtitle = element_text(size = 12, color = "gray60"),
    axis.title = element_text(size = 12),
    legend.title = element_text(size = 10),
    legend.text = element_text(size = 8),
    panel.grid.minor = element_blank()
  )

print(p3)
```



Data Table with Proportional Changes

```
::: {.cell}

```{.r .cell-code}
# Calculate proportional changes in weight and area for each plant
data_with_changes <- data_clean %>%
  arrange(plant, time) %>%
  group_by(plant) %>%
  mutate(
    # Calculate proportional change from first measurement (baseline)
    weight_prop_change = (weight - first(weight)) / first(weight),
    area_prop_change = (area - first(area)) / first(area)
  ) %>%
  ungroup() %>%
  select(plant, time, weight, area, weight_prop_change, area_prop_change)

# Display the complete data table
data_with_changes %>%
  mutate(
    weight = round(weight, 4),
    area = round(area, 2),
    weight_prop_change = round(weight_prop_change, 3),
    area_prop_change = round(area_prop_change, 3)
  ) %>%
  knitr::kable(
    caption = "Complete flower shrinkage data with proportional changes",
    col.names = c("Plant", "Time", "Weight (g)", "Area (cm²)",
                  "Weight Change (%)", "Area Change (%)"),
    align = c("c", "c", "r", "r", "r", "r")
  )
```
```

Table 1: Complete flower shrinkage data with proportional changes

Plant	Time	Weight (g)	Area (cm²)	Weight Change (%)	Area Change (%)
1	1	0.0259	3.08	0.000	0.000
1	2	0.0216	3.52	-0.168	0.143
1	3	0.0202	2.44	-0.219	-0.210
2	1	0.0156	2.33	0.000	0.000
2	2	0.0118	1.25	-0.244	-0.462
2	3	0.0108	1.47	-0.307	-0.368
3	1	0.0080	1.33	0.000	0.000
3	3	0.0046	1.19	-0.423	-0.108

Plant	Time	Weight (g)	Area (cm²)	Weight Change (%)	Area Change (%)
4	1	0.0150	2.01	0.000	0.000
4	2	0.0101	1.55	-0.322	-0.231
4	3	0.0083	1.13	-0.443	-0.439
5	1	0.0391	4.96	0.000	0.000
5	2	0.0318	2.48	-0.186	-0.501
5	3	0.0279	3.03	-0.284	-0.390
6	1	0.0338	4.69	0.000	0.000
6	2	0.0282	1.34	-0.166	-0.713
6	3	0.0260	3.38	-0.231	-0.279
7	1	0.0311	4.09	0.000	0.000
7	2	0.0218	1.73	-0.300	-0.576
7	3	0.0186	1.96	-0.402	-0.522
8	1	0.0177	2.53	0.000	0.000
8	2	0.0159	2.33	-0.098	-0.079
8	3	0.0156	2.26	-0.118	-0.106
9	1	0.0290	3.44	0.000	0.000
9	2	0.0105	2.34	-0.639	-0.321
9	3	0.0084	1.58	-0.710	-0.541
10	1	0.0144	2.04	0.000	0.000
10	2	0.0097	3.90	-0.328	0.910
10	3	0.0074	2.04	-0.483	0.000
11	1	0.0107	1.64	0.000	0.000
11	2	0.0086	1.25	-0.196	-0.236
11	3	0.0076	0.98	-0.292	-0.405

:::