

## **Plant size and allocation to reproduction for plant demography**

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## Abstract

Stage-based population models are an important tool for quantifying the influence of biotic and abiotic factors on populations. Within studies of plant demography and life history, measuring and predicting biomass is an essential tool used to better understand a plant's health and reproductive success. However, measuring biomass is inherently destructive. This study assessed multiple nondestructive measures of plant size to determine which best predicted plant biomass for four species of subalpine wildflowers. We also examined whether allocation to reproductive biomass varied across these species. The four species, *Delphinium nuttallianum*, *Hydrophyllum fendleri*, *Potentilla pulcherrima*, and *Erigeron speciosus*, each chosen for their different life history strategies, were used to study possible predictors of plant biomass in subalpine meadows around the Rocky Mountain Biological Laboratory in Gothic, Colorado. As each plant has a slightly different morphology, different measures of plant size were used across species, such as leaf number or stalk length. Randomly selected individuals of each species were measured, excavated, and dried and weighed for biomass. Most measures of plant size predicted all types of biomass. However, for three of the four species, the best predictor of above-ground biomass differed from total biomass, suggesting that researchers may not be able to depend on just above-ground biomass to represent plant size. Simultaneously, because almost all measures of plant size predicted biomass to some degree, there is a trade-off between accuracy and having a general representation of biomass. The proportion of biomass allocated to reproduction varied across species and was highest in the earliest flowering species, *D. nuttallianum*, perhaps because it had little time to grow before reproducing. The findings of this study can inform future research on the relationship between different plant characteristics and the biomass of different wildflower species, as well as future investigations into the life history of these subalpine plants.

## Introduction

Understanding population dynamics in natural environments and how populations are affected by environmental variation is a central question in ecology. Stage-based population models, using either age or size, are a powerful method for examining how populations respond to variation in the abiotic and biotic environment. These models require accurate measures of age or size that are predictive of vital rates: survival, vegetative growth, and reproduction. With more accurate indicators of vital rates, population models can more effectively link population changes with environmental influences. Evaluating the effects of abiotic factors on plant population growth rates, as well as understanding species' life history strategies, is essential for predicting future population changes, and, consequently, for designing management plans for those communities (Salguero-Gómez et al. 2016; Ehrlén et al. 2016).

To quantify the population growth rates of plants, it is important to be able to estimate plant size in an accurate and efficient manner. Biomass measures often require destroying the plant, which is counterproductive for studies tracking plant populations over multiple years. The ability to non-destructively measure plant biomass is essential for studies of population dynamics and plant life-history and could serve as the basis for more complex and comprehensive research. A current, multi-year experimental demography project at the Rocky Mountain Biological Laboratory in Gothic, Colorado, is examining the effects of pollinator declines on the population growth rates of several perennial subalpine wildflower species with different life history strategies. *Delphinium nuttallianum* flowers early in the spring, grows more slowly than wildflowers native to lower elevation, and is often found growing in sparse, rocky areas (Inouye 2008). *Hydrophyllum fendleri* is quite long-lived and mesophytic, flowering late spring into early summer (Beckmann 1979). *Potentilla pulcherrima* flowers early to mid-summer in meadows and sunny areas (Stinson 2004). Lastly, *Erigeron speciosus* is the latest to flower of the four species, and is often found in habitats similar to those favored by *H. fendleri* (Gucker and Shaw 2019).

In this study, we aim to understand what measure of plant size is most strongly related to biomass (total, above, and belowground) for each species (H1), and whether the best predictor of plant size differs for above-ground vs. total biomass (H2). We expect that the length of the longest leaf will be the best predictor of biomass for *D. nuttallianum* and *P. pulcherrima* species because there is not a lot of variation in leaf number within these plant species (Iler, unpublished data). In contrast, we anticipated that leaf count would be the best predictor of biomass for *H. fendleri* because there is a lot of variation in leaf number across individuals (Iler, unpublished data). Finally, for *E. speciosus*, we expected that stalk count would be the most accurate predictor, because plants with more stalks appear to have more above-ground biomass. Since above-ground biomass will likely be correlated with below-ground biomass, we anticipated no difference between the best predictors of above-ground and total biomass for each species. Finally, this study also investigated whether the percentage of biomass allocated to reproduction varies across species (H3); we predicted that earlier-flowering species would allocate a higher percentage of biomass to reproduction than later flowering species, because early-flowering species do not have as much time to grow vegetatively before reproduction. Alternatively, because all of the study species are long-lived perennials, the percentage of biomass allocated to reproduction may not vary across species.

## Methods

### *Study Area and Plant Identification for Extraction*

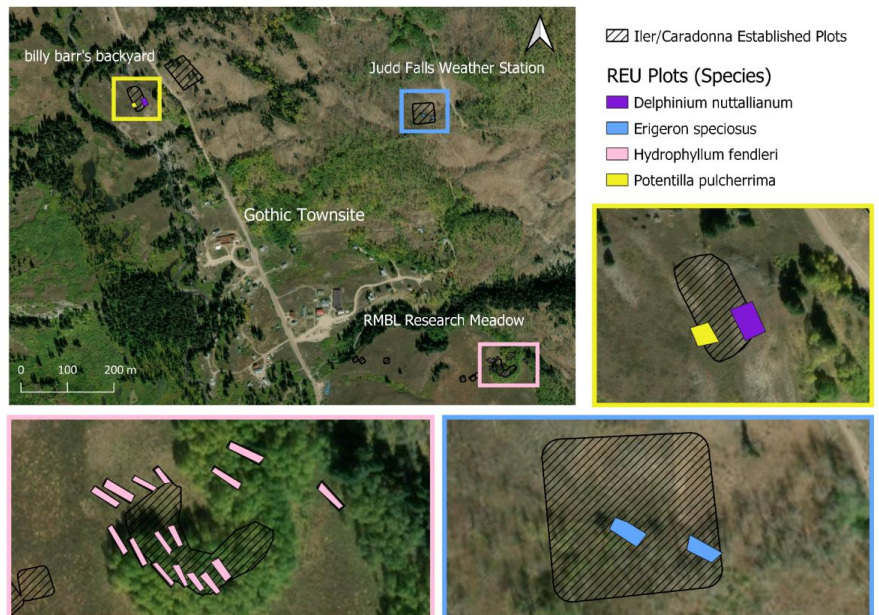
Size and biomass measurements of four species (*Delphinium nuttallianum*, *Hydrophyllum fendleri*, *Potentilla pulcherrima*, and *Erigeron speciosus*) were taken around established research plots at the Rocky Mountain Biological Laboratory in Gothic, Colorado. Our plots were outside, but adjacent to the plots established within Amy Iler and Paul CaraDonna's demography sites.

For *D. nuttallianum*, *P. pulcherrima*, and *E. speciosus*, one or two plots (depending on terrain, abundance of plants, and space constraints), were roughly 10 m x 10 m or 5 m x 10 m and were set up near the aforementioned established plots (however, due to terrain constraints, the plots were sometimes uneven: *D. nuttallianum* was 13 m x 17 m, *P. pulcherrima* was 5 m x 17 m, and *E. speciosus* were 5 m x 9 m and 5 m x 10 m. A random number generator was used to generate 20 coordinates within each plot. The closest, non-herbivorized flowering and non-flowering plant to those coordinates were excavated and removed from the ground. The nearest flowering and non-flowering individual were selected for each coordinate so that environmental differences could be minimized. For *E. speciosus*, there were very few truly non-flowering plants, so these could not be randomly selected. Instead, the plots were searched for plants without any fully-developed flowers (small, aborted flowers were not considered full flowers), and the identified plants were dug up; the flowering *E. speciosus* plants were still randomly selected according to the standard method.

For *H. fendleri*, the extracted plants were located around each of 16 demography plots (Figure 1). Four randomly chosen plots were assigned two ID numbers so that the sample size would be consistent with the other species (20 flowering, 20 nonflowering). Coordinates 1-22 were assigned with the random number generator around the perimeter of each 1 m x 10 m plot, and the nearest flowering and nonflowering plants to that coordinate were extracted. In some cases, plants farther from the plot were chosen in order to avoid digging up rosettes that could be potentially attached to plants inside the demography plots.

All plants were assigned a number and letter ID: the letter designated flowering (F) or nonflowering (N); the number (1-20) referred either to the order in which the coordinate was drawn or to the established plot to which the plant was closest (as mentioned above for *H. fendleri*).

Figure 1. The sites near Gothic, CO, USA, from which samples of four species of subalpine wildflower were extracted.



## Size and Biomass Measurements

Plant size measurements were taken for the 20 flowering and 20 nonflowering individuals extracted for biomass. Different parts of each plant, those most commonly used in plant demography studies, were measured before extraction (Table 1). Each individual was dug up either at peak fruiting time (*D. nuttallianum* and *H. fendleri*) or peak flowering time (*P. pulcherrima* and *E. speciosus*). Due to time constraints in the field, we were unable to wait for *P. pulcherrima* and *E. speciosus* to flower. The plants were dried in a drying oven for 48–72 hours (or longer if necessary; Table 1), and weighed for total biomass, above-ground biomass (AGB), below-ground biomass (BGB), and reproductive biomass (including stalks, fruits, and flowers, where present).

Additionally, 20 flowers from each species (one flower from 20 different individuals other than those dug up) were collected to determine the mean flower biomass, which can be used to calculate total reproductive biomass if flowers are missing from the extracted plant (i.e., for plants collected when fruiting).

Table 1. Nondestructive measurements taken for each species, the date they were collected, and the number of hours dried in the drying oven (60°C).

| Species                | Rosette Number | Leaf Number | Longest Leaf Length (cm) | Leaf Area (cm <sup>2</sup> ) | Stalk Number | Stalk Length (cm) | Date collected | Hours dried (hrs) |
|------------------------|----------------|-------------|--------------------------|------------------------------|--------------|-------------------|----------------|-------------------|
| <i>D. nuttallianum</i> |                | ✓           | ✓                        | ✓                            |              |                   | June 29        | 48                |
| <i>H. fendleri</i>     | ✓              | ✓           | ✓                        |                              |              |                   | July 2-16      | 72                |
| <i>P. pulcherrima</i>  | ✓              | ✓           | ✓                        |                              |              |                   | July 9-21      | 72                |
| <i>E. speciosus</i>    |                |             |                          |                              | ✓            | ✓                 | July 22-27     | 72                |

## Statistical Analysis

A linear regression analysis was used to determine the relationship of each plant size measurement to AGB, BGB, and total biomass, separately, for each species (H1). We used model selection based on AIC values to determine the best predictor of biomass, for each species and response variable. The model with the lowest AIC value was considered the best predictor of biomass. For each species, we compared the best predictor of AGB and TB to see if it is the same or different; we also used correlation analysis to determine the strength of the relationship between AGB and BGB and AGB and total biomass (H2). An ANOVA and post-hoc pairwise t-test (or Kruskal Wallis and Dunn's post-hoc test) were used to compare the percent allocation of biomass to reproduction among the four species (H3; one model for reproductive structures and a separate one for flowers). Microsoft Excel was used for data compilation and organization, and R/RStudio (RStudio Team 2018) was used for statistical analysis and data visualization.

## Results

The three types of biomass were correlated for all species at  $p < 0.001$  (Table 2). The Pearson's  $r$  value was greatest for the relationship between total biomass and below-ground biomass in all species. The metric of plant size most strongly correlated with total biomass was different for most species, but the same characteristic predicted both total biomass and below-ground biomass for all four species (Figure 2; Table 3). Additionally, the best predictor of total biomass differed from the best predictor of above ground biomass for all species except *E. speciosus* (Table 3).

For *D. nuttallianum*, leaf area best predicted total biomass and below-ground biomass, while leaf number best predicted above-ground biomass. Leaf number was the best predictor for *H. fendleri* total and below-ground biomass, with leaf length as the best predictor of above-ground biomass.

*Potentilla pulcherrima* total and below-ground biomass were best predicted by rosette number, and above-ground biomass by leaf length. All biomass types for *E. speciosus* were best predicted by stalk number. All regressions of plant characteristic against biomass type were significant, excepting rosette number for *P. pulcherrima*.

The proportion of total biomass devoted to reproduction varied significantly across all species ( $F_{1,3} = 62.81$ ,  $p < 0.05$ ; Figure 3, Table 4).

*Delphinium nuttallianum* had the highest proportion of reproductive biomass to total biomass (28%), followed by *E. speciosus* (5%) and *P. pulcherrima* (3%), while *H. fendleri* devoted the least (1%).

Table 2. Pearson's  $r$  values for Pearson's product-moment correlations between the three biomass types (total biomass, above-ground biomass, and below-ground biomass) for each of four subalpine wildflower species. All correlation tests significant at  $p < 0.001$ .  $n = 40$ .

| Species                | Total-Above | Total-Below | Above-Below |
|------------------------|-------------|-------------|-------------|
| <i>D. nuttallianum</i> | 0.921       | 0.935       | 0.727       |
| <i>H. fendleri</i>     | 0.922       | 0.995       | 0.892       |
| <i>P. pulcherrima</i>  | 0.781       | 0.999       | 0.748       |
| <i>E. speciosus</i>    | 0.929       | 0.955       | 0.777       |

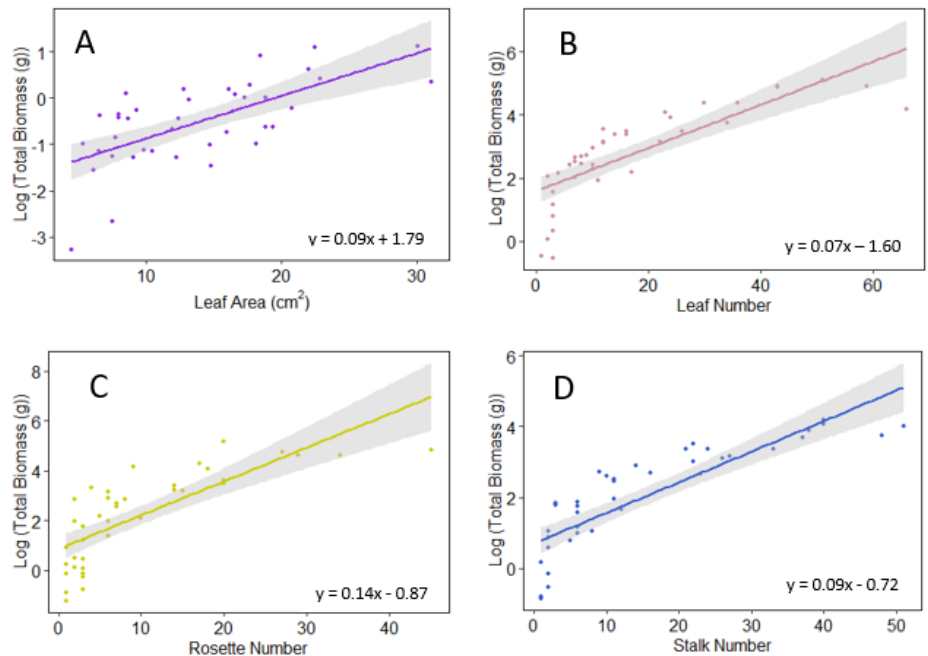


Figure 2. Linear regression of the plant characteristics which best predicted total biomass for each of four subalpine wildflower species sampled June-July 2020 near Gothic, Colorado: (A) *Delphinium nuttallianum*, (B) *Hydrophyllum fendleri*, (C) *Potentilla pulcherrima*, and (D) *Erigeron speciosus*. All data log transformed.  $p < 0.001$  for all species.  $n = 40$ .

The proportion of above-ground biomass (AGB) allocated to reproduction was different between most species, but not between *E. speciosus* and *H. fendleri* (Figure 4, Table 5). Following the pattern previously established, *D. nuttallianum* allocated the most AGB to reproduction (77%), followed by *P. pulcherrima* (29%), *E. speciosus* (14%), and *H. fendleri* (8%).

Table 3. Linear regression statistics of all measured plant characteristics and all biomass types for each species sampled. Bolded rows indicate the plant characteristic which best predicted the corresponding biomass type. dAIC values are the difference in Akaike Information Criterion values for linear models for each plant trait (df = 3). n = 40.

| Species                | Plant trait    | Total Biomass  |              |                  |            | Above-Ground Biomass |              |                  |            | Below-Ground Biomass |              |                  |            |
|------------------------|----------------|----------------|--------------|------------------|------------|----------------------|--------------|------------------|------------|----------------------|--------------|------------------|------------|
|                        |                | R <sup>2</sup> | F(1,38)      | p                | dAIC       | R <sup>2</sup>       | F(1,38)      | p                | dAIC       | R <sup>2</sup>       | F(1,38)      | p                | dAIC       |
| <i>D. nuttallianum</i> | Leaf number    | 0.38           | 23.26        | <0.001           | 4.3        | <b>0.43</b>          | <b>28.42</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.26                 | 13.17        | <0.001           | 8.2        |
|                        | Leaf area      | <b>0.44</b>    | <b>30.26</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.38                 | 23.56        | <0.001           | 3.0        | <b>0.39</b>          | <b>24.77</b> | <b>&lt;0.001</b> | <b>0.0</b> |
|                        | Leaf length    | 0.40           | 24.85        | <0.001           | 3.3        | 0.31                 | 16.70        | <0.001           | 7.8        | 0.37                 | 22.37        | <0.001           | 1.6        |
| <i>H. fendleri</i>     | Leaf number    | <b>0.62</b>    | <b>62.37</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.65                 | 71.43        | <0.001           | 3.8        | <b>0.59</b>          | <b>54.65</b> | <b>&lt;0.001</b> | <b>0.0</b> |
|                        | Rosette number | 0.03           | 1.19         | 0.289            | 37.6       | 0.01                 | 0.36         | 0.55             | 45.7       | 0.03                 | 1.23         | 0.27             | 34.4       |
|                        | Leaf length    | 0.52           | 41.75        | <0.001           | 9.2        | <b>0.68</b>          | <b>82.30</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.47                 | 33.59        | <0.001           | 10.3       |
| <i>P. pulcherrima</i>  | Leaf number    | 0.57           | 51.28        | <0.001           | 2.0        | 0.63                 | 63.77        | <0.001           | 5.4        | 0.55                 | 46.31        | <0.001           | 2.3        |
|                        | Rosette number | <b>0.60</b>    | <b>55.87</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.61                 | 60.57        | <0.001           | 6.7        | <b>0.58</b>          | <b>51.41</b> | <b>&lt;0.001</b> | <b>0.0</b> |
|                        | Leaf length    | 0.59           | 53.65        | <0.001           | 1.0        | <b>0.67</b>          | <b>78.49</b> | <b>&lt;0.001</b> | <b>0.0</b> | 0.56                 | 48.92        | <0.001           | 1.1        |
| <i>E. speciosus</i>    | Stalk number   | <b>0.72</b>    | <b>95.33</b> | <b>&lt;0.001</b> | <b>0.0</b> | <b>0.65</b>          | <b>71.65</b> | <b>&lt;0.001</b> | <b>0.0</b> | <b>0.67</b>          | <b>86.41</b> | <b>&lt;0.001</b> | <b>0.0</b> |
|                        | Stalk length   | 0.51           | 42.43        | <0.001           | 20.2       | 0.60                 | 56.54        | <0.001           | 5.9        | 0.45                 | 32.49        | <0.001           | 22.7       |

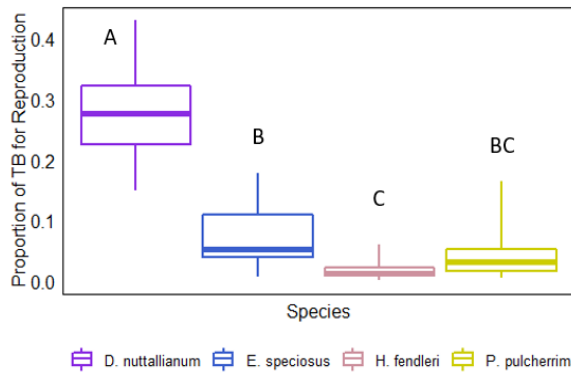


Figure 3. The proportion of total biomass devoted to reproduction (mean) in four subalpine wildflower species. Box = 25<sup>th</sup> and 75<sup>th</sup> percentiles; bars = min and max values. Different letters indicate significantly different means at  $p < 0.001$ , though species with shared letters are still significantly different at  $p < 0.05$ . One-way ANOVA ( $p < 0.001$ ) and post-hoc pairwise t-test.  $n=20$ .

Table 4. Test statistics for mean proportion of total biomass allocated to reproduction between four subalpine wildflower species. One-way ANOVA and Tukey's post-hoc test.  $n = 20$ .

| Species                | <i>H. fendleri</i> |        | <i>P. pulcherrima</i> |        | <i>E. speciosus</i> |        |
|------------------------|--------------------|--------|-----------------------|--------|---------------------|--------|
|                        | t                  | p      | t                     | p      | t                   | p      |
| <i>D. nuttallianum</i> | -13.21             | <0.001 | -9.70                 | <0.001 | -6.74               | <0.001 |
| <i>H. fendleri</i>     |                    |        | 3.51                  | <0.05  | -6.47               | <0.001 |
| <i>P. pulcherrima</i>  |                    |        |                       |        | -2.96               | <0.05  |

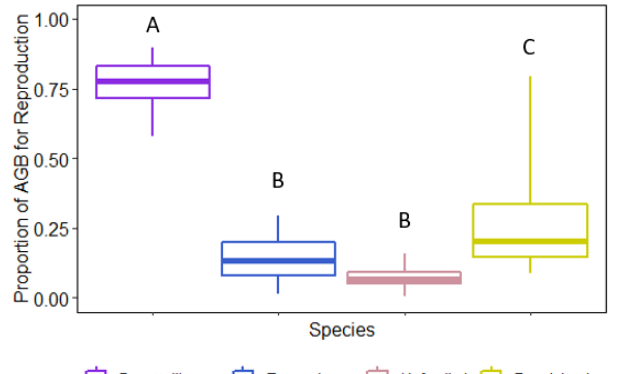


Figure 4. The proportion of above-ground biomass devoted to reproduction (mean) in four subalpine wildflower species. Box = 25<sup>th</sup> and 75<sup>th</sup> percentiles; bars = min and max values. Different letters indicate significantly different means at  $p < 0.001$ . One-way ANOVA ( $p < 0.001$ ) and post-hoc pairwise t-test.  $n=20$ .

Table 5. Test statistics for mean proportion of above-ground biomass allocated to reproduction between four subalpine wildflower species. One-way ANOVA and Tukey's post-hoc test.  $n = 20$ .

| Species                | <i>H. fendleri</i> |        | <i>P. pulcherrima</i> |        | <i>E. speciosus</i> |        |
|------------------------|--------------------|--------|-----------------------|--------|---------------------|--------|
|                        | t                  | p      | t                     | p      | t                   | p      |
| <i>D. nuttallianum</i> | -17.72             | <0.001 | -12.29                | <0.001 | -15.98              | <0.001 |
| <i>H. fendleri</i>     |                    |        | 5.43                  | <0.001 | -1.74               | 0.311  |
| <i>P. pulcherrima</i>  |                    |        |                       |        | 3.69                | <0.05  |

Median individual flower biomass was different between most species (Kruskal-Wallis and Dunn's post-hoc test,  $\chi^2 = 70.4$ ,  $df = 3$ ,  $p < 0.001$ ; Figure 5, Table 6). *Erigeron speciosus* flowers were, on average, the largest, but also the most varied, with *H. fendleri* flowers averaging smallest and least varied.

A comparison between the mean vegetative biomass between flowering and nonflowering plants within species revealed significantly higher vegetative biomass in flowering plants across all species (Welch's t-test (log transformed): *D. nuttallianum* ( $t = -3.56$ ,  $p < 0.05$ ), *H. fendleri* ( $t = -8.11$ ,  $p < 0.001$ ), *P. pulcherrima* ( $t = -5.10$ ,  $p < 0.001$ ), and *E. speciosus* ( $t = -6.14$ ,  $p < 0.001$ );  $n=40$ ). The difference in flower biomass means ranged from 8.7 g (*E. speciosus*) to 0.06 g (*D. nuttallianum*).

## Discussion

The purpose of this study was to determine the best predictors and non-destructive measurements of plant biomass for four species of subalpine perennial wildflowers. By investigating the best ways to predict biomass, researchers can better study different facets of plant demography, such as the relationship between plant population growth rate and changes in the abiotic and biotic environment. The key findings in this study are, briefly: almost all measures of plant size predicted biomass; total biomass is not predicted by the same plant characteristic as above-ground biomass; and the species do not devote the same amount of biomass to reproduction.

Preliminary correlation tests showed that all three types of biomass were correlated with each other for all species (Table 2). The relationship between total biomass and below-ground biomass was strongest in all cases, which confirms the observations that below-ground biomass was usually greater than above-ground biomass, even for *D. nuttallianum*, which had the shallowest root system of the four species. This relationship was further solidified by the finding that the same plant characteristic was the best predictor for both total and below-ground biomass, but not necessarily for above-ground biomass (Table 3). These size measures were not always what we anticipated to be the best predictors, but each species was best predicted by a different size measure. Some predictors were fairly similar: *D. nuttallianum* total biomass was best predicted by leaf area, rather than leaf length, but the difference in their predictive power was not great (Table 3). In *Hydrophyllum fendleri*, total biomass was best predicted by leaf number, as was hypothesized. The measures of plant size for *P. pulcherrima* were all fairly good predictors of total biomass, but rosette number was slightly better than leaf length and leaf number. Stalk number best predicted all three biomass types for *E. speciosus*. In all cases but one, each size

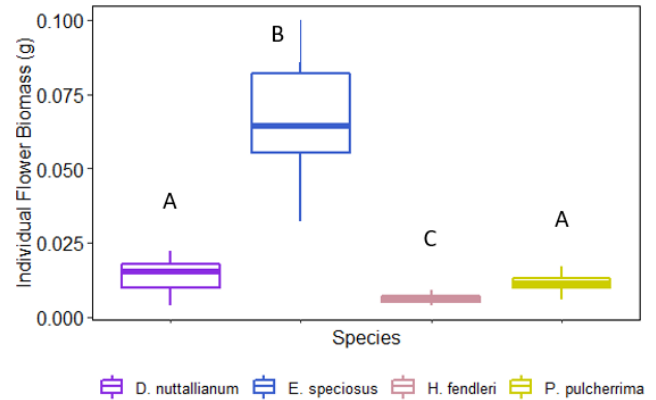


Figure 5. The biomass of individual flowers (median) from four subalpine wildflower species. Box = 25<sup>th</sup> and 75<sup>th</sup> percentiles; bars = 1.5 x interquartile range; outliers included. Different letters indicate significantly different medians at  $p < 0.001$ . Kruskal Wallis test ( $p < 0.001$ ) and Dunn's post-hoc test.  $n=22$ .

Table 6. Test statistics for the comparison of median individual flower biomass between four species of subalpine wildflower. Kruskal Wallis and Dunn's post-hoc test.  $n = 22$ .

| Species                | <i>H. fendleri</i> |         | <i>P. pulcherrima</i> |         | <i>E. speciosus</i> |         |
|------------------------|--------------------|---------|-----------------------|---------|---------------------|---------|
|                        | Z                  | p       | Z                     | p       | Z                   | p       |
| <i>D. nuttallianum</i> | 4.34               | < 0.001 | 0.79                  | 0.429   | -4.01               | < 0.001 |
| <i>H. fendleri</i>     |                    |         | -3.55                 | < 0.001 | 8.35                | < 0.001 |
| <i>P. pulcherrima</i>  |                    |         |                       |         | 4.80                | < 0.001 |

measure was able to predict each type of biomass fairly well. That said, for three of the species, the size measures that best predicted both total biomass and belowground biomass were not the best predictors for above-ground biomass. Estimations for above-ground biomass alone are therefore not sufficient for estimating the total biomass of some species, though the fact that the two biomass types are correlated could allow for approximations of one based on the other.

For our third question, concerning the proportion of total biomass allocated to reproduction, complications with the timing of digging and the stage of reproduction caused inconsistencies in the way reproductive biomass was measured. *Delphinium nuttallianum* and *H. fendleri* were fruiting at the time of collection, while the other two species were collected when flowering. These inconsistencies may have contributed to our finding that *D. nuttallianum* devoted the most biomass to reproduction; this could be due to its earliest flowering time of the four species, or, again, it could be due to the reproductive biomass being largely composed of fruits. *Hydrophyllum fendleri* devoted the least biomass to reproduction, even though it has the second earliest flowering time, and a portion of the reproductive biomass was fruits. The low proportion of biomass allocated to reproduction in *H. fendleri* could also be because of a late season frost on 1 July that damaged the vegetative and reproductive structures of the plant (personal observations). It should also be noted that biomass classified as reproductive for *D. nuttallianum* and *P. pulcherrima* included the stalks to which the flowers were attached, not just the flowers themselves, which perhaps also influenced both the proportion of reproductive biomass to total biomass and the range of those values. In contrast, *E. speciosus* produces smaller stalks but larger flowers, and non-reproductive plants also consists of multiple, non-reproductive stalks, or meristems, which is why only flowers were considered as reproductive biomass.

Interestingly, the same sequence of largest to smallest proportion of reproductive biomass did not hold when the reproductive allocation was taken as a proportion of the above-ground biomass only (Figure 4). *Delphinium nuttallianum* still allocated the most, with more than three-quarters of its above-ground biomass involved in reproduction (again, including flowering stalks), but here *P. pulcherrima* had the second largest allocation, followed by *E. speciosus* and *H. fendleri* with relatively similar allocations to each other. This again suggests that only relying on above ground biomass can provide a different picture of resource allocation than total biomass.

Our key findings suggest that it is possible to estimate most types of biomass using nondestructive measurements for these four wildflower species. A study similar to ours, conducted by Ludwig et al. (1975), but focused on a very different collection of species, observed the size-biomass relationship of a few different Chihuahuan desert shrubs. They found that dimension analysis, in which a relationship between plant measurements and plant biomass is established, could be used to establish regression relationships between plant biomass and plant metrics. Volume and canopy area were overall accurate estimators of plant biomass in desert shrubs. This suggests that plants with different life-history strategies may differ in accurate predictors of plant size, and that predictors should be tailored to a plant's environment

and their life-history strategy. However, it supports our findings that a variety of plant size metrics can be used to non-destructively calculate biomass, and that these methods have potential to show results across a wide range of plant species. In another biomass study, McGraw and Garbutt (1990) present demographic growth analysis, the primary concept of which is that a surrogate is chosen for plant dry mass, taking into account the idea that a plant is constructed of a population of parts, and that a metapopulation size can effectively substitute for destructive measures of plant dry mass in growth analysis. They noted that leaves, stems, buds, shoots are all potential plant parts that could be used for this analysis. This study and this method rely on an accurate surrogate being used for plant dry mass; the results of our study similarly show that different metrics of plant size can be used to predict biomass. The ability to non-destructively determine biomass of a singular plant can aid demographic growth analysis, as the ability to estimate one plant's size is necessary in estimating metapopulation size. Larger metapopulation studies can use metapopulation size estimates as opposed to destructive measures of plant dry mass in growth analysis. Finally, the results of our study could have further implications in plant demography studies. A study conducted by Niklas and Enquist (2001) investigated the relationships between biomass production rates, different measures of body size (dry weight and length), and photosynthetic biomass (or pigment concentration) per plant. They concluded that there is a relationship between the annualized rates of biomass production and body mass. This study examines biomass dynamics on a much wider scale and provides a pathway for a potential next step in the examination of plant size metrics and total biomass. Understanding the best predictors of plant biomass and being able to obtain that information in a nondestructive manner could greatly benefit studies of biomass production in plant populations as a whole.

Estimating total plant size is necessary for quantifying population growth rates in plants and therefore for understanding how plant populations respond to environmental changes, a central question in ecology. The ability to non-destructively measure plant size is essential for long-term studies of population dynamics and plant life-history. This study shows that many intuitive measures of plant size in the field are able to predict plant biomass, whether measured as above ground, below ground, or total biomass. Conversely, although most measures of plant size performed well, the best measures of plant size differed for above vs. total biomass in three of the four species. Researchers therefore face trade-offs between determining the most accurate predictor of biomass vs. time and resources available to assess plant biomass-size relationships.

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