Modeling Plant Functional Traits and Elevation in the Cairngorm Mountains of Scotland

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Abstract. Alpine plants are sensitive to climate change and their functional traits influence their abilities to live in specific habitats on mountain slopes. In the RAPT (Researching Alpine Plant Traits) project, we collected in-situ data that was used to develop a model of existing plant functional traits along a gradient of elevation and climatic variables on Sgòran Dubh Mòr, a summit of the GLORIA (Global Observational Research Initiative in Alpine Environments) target region in the Cairngorm Mountains of Scotland. The MATLAB function polyfit(), for polynomial curve-fitting linear regression and the numerical model approach to the collected trait data were used to obtain representations of species models that corresponded well with the data on existing plant functional trait distribution. This model may be used to predict changes in the distribution of plant functional traits, and possibly species, with climate change in mountainous regions of the Earth.

Keywords: modeling, plants, climate, traits, alpine

1 Introduction

Plants are inextricably linked with environmental constraints and thus have evolved to respond to abiotic and biotic factors in the environment [1], and characteristics of plants that influence their interactions with the environment are called plant functional traits. Examples of plant functional traits include but are not limited to: 1) overall growth form; 2) types of flowers and diasporas produced; 3) formation of clones; 4) photosynthetic pathways; 5) possession of evergreen or deciduous leaves; and 6) morphometric characteristics of leaves such as thickness, area, and complexity of shape. Particular functional traits may prove advantageous to plants that are subjected to different climatic conditions, and may then prove instrumental in determining which species are lost, become newly established in, or remain in plant communities that are subjected to climate change. Alpine plants are sensitive to climate change [2, 3] and analysis of their distributions and functional traits is an important tool in determining species-specific and functional type-specific responses of alpine plants to climate change [1, 4].

The Global Observational Research Initiative in Alpine Environments (GLORIA) program is an international network of long-term monitoring target regions established on summits of many of the world’s mountain ranges [1, 2, 3, 4] with the purpose of understanding the responses of alpine plants to climate change. As functional traits are found in every plant, and as alpine plants are sensitive to climate change, and as climatic conditions change with elevation, we investigated plant functional traits along an elevational gradient downslope from the Scottish GLORIA target region. The goals of the investigation were to develop a knowledge base of the current distribution of alpine plant species with particular functional traits and to develop predictive models of species responses and plant functional type responses to alpine climate change.

Table 1: List of Plant Functional Traits and Properties

<table>
<thead>
<tr>
<th>Plant Functional Traits</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Avg. Leaf Thickness</td>
<td>mm</td>
</tr>
<tr>
<td>Avg. Leaf Length</td>
<td>mm</td>
</tr>
<tr>
<td>Avg. Leaf Width</td>
<td>mm</td>
</tr>
<tr>
<td>Leaf Dry Weight</td>
<td>grams</td>
</tr>
<tr>
<td>Plant Height</td>
<td>mm</td>
</tr>
<tr>
<td>Plant Lateral Spread</td>
<td>mm</td>
</tr>
<tr>
<td>Leaf Area</td>
<td>cm²</td>
</tr>
<tr>
<td>SLA (Specific Leaf Area)</td>
<td>cm²/g</td>
</tr>
</tbody>
</table>

The software tool MATLAB was utilized to develop the models of each species through the data recorded from eight distinct functional traits. Table 1 shows the list of the plant functional traits, and the units in which each trait was measured. Once models are made of each trait for each species, they are used to derive overall species model functions. The MATLAB function polyfit() is the polynomial curve-fitting function that finds the coefficients of a polynomial \( P(x) \) of degree \( N \) that fits the data best in a least-squares sense. \( P \) is a row vector of length \( N+1 \) containing the polynomial coefficients in descending powers [7].

\[
P(1) \times x^N + P(2) \times x^{N-1} + \cdots + P(N) \times x + P(N + 1) \tag{1}
\]
The approach in modeling each plant species is to accurately determine the mathematical functions that describe the functional traits of each species. The data points recorded for each functional trait only describe unique characteristics of each species, but the data does not represent any certain order that can yield to a definitive model function. Therefore, the data of each functional trait is randomly positioned within its own set of values. Each function’s coefficient values were collected and averaged to determine the overall coefficient values that produce each species’ function model. In order to evaluate and validate the model functions, the functions were compared to the changes of functional traits with the elevation changes. It is hypothesized that by using polynomial curve-fitting linear regression MATLAB function polyfit() as the numerical model approach to the data collected for plant functional traits, all species model representations can be obtained.

2 RAPT Project Overview

The Researching Alpine Plant Traits (RAPT) project is an investigation of the responses of alpine plants and their functional traits to climate change in the Cairngorm Mountains of Scotland. RAPT was developed in order to investigate plant functional traits along an elevational gradient on Sgòran Dubh Mòr, a peak in the Cairngorm Mountains of Scotland. The RAPT project was established at Sgòran Dubh Mòr because it is the highest sub-summit of the Scottish GLORIA target region and because information gained on plant functional traits from Sgòran Dubh Mòr can be linked with plant functional trait data from the Scottish GLORIA target region.

2.1 Site Description

Sgòran Dubh Mòr (57°04’49.76”N, 3°48’28.85”W) is a mountain that rises steeply and continuously to 1111m from the Allt a’ Mharcaidh stream within the Allt a’ Mharcaidh catchment of the Cairngorms National Park of eastern Scotland [5]. Soils of Sgòran Dubh Mòr are acidic and are derived from granitic parent material. While trees exist lower in the Allt a’ Mharcaidh catchment, none were present at the Sgòran Dubh Mòr site.

2.2 Species

Species of Sgòran Dubh Mòr represented in the RAPT sampling regime included vascular plants, bryophytes, and lichens. Their scientific names were abbreviated for brevity in equations and models by using the first letter of the genus name followed by a period and the first two letters of the species name. The scientific names, abbreviations in bold, and common names are as follows: Blechnum spicant (L.) Sm., B. sp, the deer fern; Calluna vulgaris (L.) Hull, C.vu, heather; Carex bigelowii Torr. ex Schwein, C.bi, Bigelow’s sedge; Deschampsia flexuosa (L.) Trin., D.fl, wavy hairgrass; Diphasiastrum alpinum L., D.al, alpine clubmoss; Empetrum nigrum L., E.ni, crowberry; Eriophorum angustifolium Honck., E.an, cottongrass; Galium saxatile L., G.sa, heath bedstraw; Huperzia selago L., H.se, fir clubmoss; Juncus trifidus L., J.tr, highland rush; Lycopodium annotinum L., L.an, stiff clubmoss; Nardus stricta L., N.st, mat grass; Rubus chamaemorus L., R.ch, cloudberry; Trichophorum cespitosum (L.) Hartm., T.ce, deergrass; Vaccinium myrtillus L., V.my, bilberry; and Vaccinium vitis-idaea L., V.vi, lingonberry. The bryophytes included Racotritum lanuginosum (Hedw.) Brid, R.la, woolly fringe moss; Sphagnum sp., S.sp, peat moss. Lichens included Cetraria islandica (L.) Ach. C.is and Cladonia sp., C.sp.

2.3 Sampling

Groups of four 1m² vegetation plots with 10cm² grids were randomly placed at the lower (750m), middle (940m), and upper slope (1105m) along an elevational gradient ascending the western slopes of Sgòran Dubh Mòr in the summer of 2013. The upper plots were positioned 6m below the Sgòran Dubh Mòr GLORIA summit to avoid trampling plants. Plots were placed inside and outside of the late snowfield areas which are found at mid-elevation (940 m). The presence and percentage surface cover of all vascular plant species, lichens, and bryophytes within each of the 1m² plots were recorded along with frequency counts of all species in each plot subdivision per elevation. Plant height and lateral spread were recorded in situ and lateral spread of clonal plants was measured as the maximum width of the above ground patch of a tussock.

The leaves of ten plants per species per elevation and from inside and outside of the mid-elevation snowfields were measured for shape, margins, length, width and thickness within 15 hours of collection. Length: width ratios were calculated and leaf area was measured from photographs with Image-J [6]. Specific leaf area (SLA, cm²/g), was calculated from leaf dry weights. Plant trait information collated from taxonomic texts included overall morphology; life history strategies (longevity; clonality and the presence of rhizomes, stolons, adventitious roots or other clonal structures; phenology and type of flowering; pollination; seed or spore production, morphology, persistence, and dispersal); leaf longevity and whether the leaves were evergreen or deciduous; and rooting architecture and depth. Traits not included in this initial model are mentioned here to provide a context for the overall goals of this project, which are to develop predictive models based on large suites of trait data and biotic and abiotic drivers.

Abiotic factors measured at Sgòran Dubh Mòr included slope, aspect, and proximity to late snowfield areas for each plot at each elevation. Values for soil bulk density (g/cm³), volumetric water content (g/cm³), water content (g/g), porosity (%); water filled pore space (%), wet and dry weights (g), and the weight (g) and volume (ml) of stones were obtained at each elevation and inside and outside of late snowfield areas.

3 Numerical Modeling

The data collected for each functional trait consists of data sets containing ten data points. An initial approach of modeling was to utilize the data arranged in the order each fundamental trait was recorded. The data presents itself in a linear form in which
an \( n \)-th-order polynomial accomplishes a best-fit. As an example of \textit{D. flexuosa}'s (D.fl) lateral spread functional trait data, Figure 1 below shows the different results of increasing the order of \texttt{polyfit()} function from 4-th-order to 9-th-order fit.

Figure 1. \textit{D. flexuosa} – Plot 1: Lateral Spread Data, Initial Modeling Approach

This initial approach helped to evaluate the approximation of each polynomial, and its coefficient of determination R-square values. In each case of the functional traits for each species, the R-square value increases with the order of each polynomial. However, the leading coefficients of the polynomial kept approaching zero, and the functions become ill-conditioned. In containing the ill-conditioned polynomials and very small leading coefficients, each function was reduced in order by calculating the error estimation of the polynomials. The approach to the error estimation of an \( n \)-th-order polynomial in order to reduce the order of each function is to check when the error (\( e_n \)) is added to the \( n \)-th-order polynomial (\( f_n \)) case and generates (\( n+1 \))th-order polynomial (\( f_{n+1} \)) case [8]. That is,

\[
f_{n+1}(x) = f_n(x) + e_n
\]

(2)

, in which yields to identify the order of the polynomials in where the functions will not be ill-conditioned.

3.1 Determining the Order of Polynomials

In obtaining best-order for each polynomial, each functional trait was modeled. As mentioned earlier, the data points for each functional trait describe the characteristic measurement value obtained, but the order in which the data was recorded does not represent a certain order in which the data follows. Therefore, the data was randomized for each trait at each run, the coefficient values are stored and then re-run for extra iterations of random positions of the data. In order words, we take the array of the ten data points of a function trait such as:

\[
Data_{\text{Func.Trait}} = [d_0, d_1, d_2, d_3, ..., d_{10}]
\]

(3)

Then, the random permutation \texttt{randperm(N)} function was utilized which returns a vector containing a random permutation of the integers 1 to \( N \) [9], in where one possible outcome of the permutations changes to (3) can represent the data to:

\[
Data_{\text{Func.Trait}} = [d_6, d_3, d_7, d_4, ..., d_7]
\]

(4)

The randomization approached helped in evaluating each functional trait in different ways. In utilizing the \texttt{polyfit()} function, the coefficients of each randomized iteration were obtained. As in examples, Figure 2 and Figure 3 show the 9-th-order and 7-th-order polynomial coefficients values of \textit{D. alpinium} (D.al) for the 40-iterations that were performed respectively.

Figure 2. \textit{D. alpinium} - Leaf-Thickness (9-th-order Model): Coefficient Values Through 40-Iterations

In the case of Figure 2, it can be observed that the leading coefficients are so small that it can be assumed that they are zero, and the range of coefficient values is larger than the range found in Figure 3. In reducing the order of the model from a 9-th-order to a 7-th-order, the model of each iteration went from an ill-condition to a stable model, and the values of each coefficient are more concentrated as the order of the model was reduced. Therefore, the functional trait models will be represented in a 7-th-order polynomial function, and the number of iterations will be increased in order to obtain more converged coefficient values.

3.2 Trait Data at Different Elevations

The form in which the function models will be compared is in how well the elevation changes are represented through different functional trait models. These elevation changes will help to evaluate and validate the approach described in the following section. However, the benchmark window is small.
since only four plant species exist at different elevations within the sampling 1m\(^2\) plots. The four plant species are: C.bi (Carex bigelowii), D.fl (Deschampsia flexuosa), V.my (Vaccinium myrtillus) and E.ni (Empetrum nigrum).

The elevation changes are represented in three levels: high- (H), mid- and low-elevations (L). Within the mid-elevation, there are the internal-snowfield (Mi) and external-snowfield (Me) areas, but they will be regarded as part of the mid-elevation for benchmark purposes. Figure 4 displays an example of how the functional trait leaf area of plant species E.ni changes from low to mid-elevations by using two sets of values: 1) the average-value of the set of leaf area data at each elevation, and 2) the maximum-value of the set of leaf area data at each elevation. For this case, the functional trait leaf area increases for E.ni as the elevation increases. Therefore, the model for the functional trait leaf area for E.ni must represent the increase as well.

4 Procedures

As mentioned before, the data points recorded for each functional trait are the description of the characteristics of each plant species, but they do not represent any certain order of position or priority within the plants. Therefore, as mentioned in the last section, the data placement within the functional trait array was randomized in order to produce different permutations of the coefficient values in a 7th-order polynomial. The number of iterations of the randomized data can also vary, in which turn, the number of coefficient values from the polyfit() function can expand the range of values for each of the coefficients. Then, the number of iterations must be increased in order to: 1) utilize more of the possible existent permutations for data in every functional trait, 2) obtain a mean-value that is more accurate for each coefficient value, and 3) revise if, as the number of iterations will converge to more stable coefficient mean values.

In developing the model for the functional traits, the workflow is shown in Figure 5. Individual functional trait data array were randomized, data\(_{FT}[10]\), using the randperm() function that produces a new random data array data\(_{r}[10]\). The new data array is then evaluated with the polyfit() function to produce the 7th-order curve-fitted polynomial with eight coefficient values. These coefficient values are then placed within a coefficient array, C\([10]_i\), and then added to the previous coefficient values C\([10]_{i-1}\). The workflow then repeats itself for the next iteration to determine the next set of coefficient values. The iterations values are 40, 4000, and 40,000. Once all iterations have been performed, the average value of each coefficient is obtained and used as the coefficient value for each functional trait model. The average value are used in order to avoid using coefficient values in spikes to a very high positive or very low negative values, and represent the coefficients values that are grouped more closely together.

In the case for developing the models for the plant species, the workflow is shown in Figure 6. Each individual functional trait data array is denoted as: data\(_{FT\langle 1:8 \rangle}[10]\); m-number of functional traits, and each is randomized using the randperm() function that produces a new random data array, data\(_{r\langle FT\langle 1:8 \rangle \rangle}[10]\). The new data arrays are then evaluated with the polyfit() function individually and added as aggregates to all of the eight coefficient values. The aggregated coefficient values are then placed within a coefficient array C\([10]_m\]. The workflow then repeats itself for the next iteration to determine the next aggregated set of coefficient values. Once all iterations have been performed, the average values are obtained of each
coefficient, and they’re used as the coefficient values for each plant species model.

\[
f(x)_{FT} = C_9x^9 + C_8x^8 + \ldots + C_1x + C_0
\]

(5)

In other words, each functional trait model, \( f(x)_{FT} \), is combined by aggregate with the other functional trait models of the same plant species;

\[
f(x)_{plant} = \sum_{j=1}^{m} f_{FT_j}(x)
\]

(6)

where the process is then iterated \( i \)-times with new randomized position of the data for each trait and taken the mean of each coefficient in which yields;

\[
f(x)_{plant} = \frac{1}{i} \sum_{j=1}^{m} [C_j]x^9 + \ldots + [C_1]x + [C_0]
\]

(7)

\[C_{10}]_{AVG} = \frac{1}{i} [C[10]_1]
\]

\[f(x)_{plant} = C_9x^9 + C_8x^8 + \ldots + C_1x + C_0
\]

\[f(x)_{plant} = \frac{1}{i} \sum_{j=1}^{m} f_{FT_j}(x)
\]

5 Results

The workflows from Figure 5 and Figure 6 each develop functional trait and plant species models in a 7th-order polynomial respectively. In order to benchmark the model functions, the functional trait models are compared in how the functional trait data changes on average when elevation changes on average. As mentioned earlier, elevation changes are described in three levels: high-elevation (H), mid-elevations (Mi & Me) and low-elevation (L). In the mid-elevation, there are the internal-snowfield (Mi) and external-snowfield (Me) areas, and also, the small number of plant species existing in multiple elevations are mentioned in section 3.2.

To display a resultant case of the functional trait workflow, Figure 7 shows the height functional trait for C.bi. (Carex bigelowii) as it changes elevation on average illustrating: a) the average of the height functional trait of C.bi using the recorded data, and b) by using each height functional trait model at each elevation. In this case, there are three models that represent C.bi at each plot elevation. Each of the models is evaluated from \( x = 1 \) to \( x = 5 \) or \( x = (1:5) \). As it can be observed in Figure 7 b), the mean representation for each plot retains the mean values from part a) as \( x \) increases. However at \( x = 5 \), the three models for C.bi height functional trait begin to fail in representing the correct behavior. Meaning, as \( x \) increases for each height model, then the leading coefficients begin to grow the effect of the much larger tailing coefficients in which distort each of the three models. However, the data is still well represented with the three resultant height functional trait models by using (5) at \( x = (1:4) \) as the number of iterations.
increases that provides proper coefficient mean values for each model.

In a separate case, Figure 8 shows the leaf area functional trait for D.fl (Deschampsia flexuosa) as it changes with elevation on average by illustrating a) the leaf area functional trait of D.fl using the recorded data, and b) by using each leaf area functional trait model at each elevation. In this case, there are four models that represent D.fl at each plot elevation. Each of the models is evaluated from the same x range as Figure 7. As it can be observed in Figure 8 b), the mean representation for each plot struggles to reproduce the mean values from part a) as x increases. Although the four models do not provide the exact behavior of the elevation changes, the models are contained within the correct average value ranges. Also, as x increases for each leaf area model, the elevation changes to leaf area are rectified. Similar results were obtained from the other functional traits due to elevation changes as seen in Figure 7 and 8. The trait models showed that the workflow described on Figure 5 (which determines 7th-order polynomials), such as in (5), helped to generated proper reproduction of the traits in changes of elevation from the same plant species.

In a similar manner, the plant models were obtained as described in the workflow from Figure 6. The resultant plant models are also in a 7th-order polynomial from the aggregate of all of the individual functional traits. Table 2 shows the resultant coefficient values of all plant species. From Table 2, it can be seen that the leading coefficients are very small values in most cases, and as x increases, it can cause the models to be disrupted and misrepresent each plant species. Therefore, the models will be also restricted at in the same manner as the functional trait models. In another observation, the trailing coefficients are similar in value range for the same plant species at different elevations. This projects that each overall plant model will have similar properties and elevation characteristics that describe the functional traits in the aggregate. Overall, the approach procedure in obtaining the coefficient values for individual functional trait models for the 7th-order do show reproduction of data and changes of elevation concurrent with the recorded data which helped to obtained the overall plant model coefficient values.

### 6 Conclusions

The data collected from the RAPT Project were utilized in order to develop models of the functional traits of the plant species, and of the overall plant models through the aggregated functional trait models. The recorded data that were collected are in sets of ten entries for each of the functional traits in which the order of the recorded data does not represent any biological or organizational order. This is important because the sample number does not have biological significance per se. The numerical modeling approach was to utilize the data collected and randomize the position of the data within its vector-form in repetitive iterations. Each of the iterations generated a different outcome of coefficient values of the same data set for each functional trait by using the polyfit() function in MATLAB, the curve-fitting function. It determined the order to the polynomials by starting in the maximum 9th-order representation down to 7th-order polynomial.

The functional trait models were developed by using the same iterative approach in determining the order of the polynomials. However, the average of each coefficient was obtained in order to determine the coefficient values of each model. Then, the models of C.bi (Carex bigelowii), D.fl (Deschampsia flexuosa), V.my (Vaccinium myrtillus) and E.ni (Empetrum nigrum) were compared according to how the data change with elevation: high- elevation (Plot 1), mid-internal-snowfield (Plot 3), mid-external-snowfield (Plot 4) and low-elevation (Plot 2). The models show consistency with the changes of elevation when the models are evaluated at x = (1:4). However, the other models display inconsistencies in one instance in where x ≥ 5. Therefore, each of the model functional trait functions are defined as x = (1:4).

The overall plant species models were generated by using each functional trait in the aggregate by iterative workflow. The average of the coefficient values were again taken to determine
each model as seen in Table 2. As with the resultant models of the functional traits, the plant species models also are defined at \( x = (1:4) \).

These models will be utilized in future representations that integrate a suite of plant functional traits [10] with biotic and abiotic environmental variables of Sgòran Dubh Mòr and the GLORIA target region in Scotland, and that place greater emphasis on the distribution of functional traits than on the distribution of species, as particular functional traits are not necessarily confined to individual species but can reflect responses to environmental conditions along elevational gradients and with distance from snowfields.

### 7 Acknowledgements

We acknowledge the Interact Transnational Access program; (HPC) Montana Tech of the University of Montana; (HPC) Wake Forest University; the Center for Ecology and Hydrology, Edinburgh, Scotland, and the GLORIA program.

### 8 References


