Woodland Flora Translocation Tool

Project Proposal

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2023-01-06

Introduction

The majority of vascular plant diversity in temperate woodlands existed in the understory.

Need to . . . biodiversity.

The UK's target of . . . woodland creation

In in the 2021/2022 planting season 6970 hectares of broadleaved woodland were created in the UK (Maxwell 2022).

Legacy of woodland creation without management plans in place to ensure . . .

Our understanding of how the composition of traits within a community of organisms scales to constitute and influence ecosystem functioning (Chacón-Labella et al. 2022) is a developing field, lacking . . . .

Where spatio-temporal barriers to migration exist, the self-assembly of woodland understory communities cannot be relied upon, necessitating a proactive approach must be taken in ecosystem restoration (Smith 2017).

Such a stance, namely the promotion of assisted colonisation to newly planted woodlands with dispersal-limited understory flora is an increasingly recognised management need in woodland creation schemes, with the Woodland Trust making the need to "Establish Richer Communities" explicit in their Woodland Creation Guide (Herbert et al. 2022). Practically, organisations such as Eadha Enterprises now operate woodland understory flora nurseries (Eadha Enterprises 2023b) and offer ecological site survey services for understory species translocation suitability (Eadha Enterprises 2023a). Centralised guidance has also recently been developed in the form of the NatureScot Research Report *Establishing woodland plants in broadleaved woods - interim best practice guidance for conservation translocations* (Worrell et al. 2021). Despite such advancements, there is still a distinct lack of UK-wide guidance.

Aims

In response to this growing need for management advice on woodland flora translocation the development of an R Shiny (R Core Team 2022; Chang et al. 2022) web application is proposed. This application will act as a Decision Support Tool (DSS), aiding users in examining the suitability of woodland under-story flora for translocation to a target woodland site. The application will synthesise the analysis results with additional user inputs to generate a report using a pro-forma which be developed based on the Scottish code for translocations project form (National Species Reintroduction Forum 2014).

A two-stage development strategy is proposed:

1. A functional proof-of-concept tool.
   - Using the current best available data.
   - Developed as part of a scoping exercise by the author.
   - No specific project funding.
2. A comprehensive tool.
   - Using data derived from additional analysis.
   - Developed with a project team.
   - Specific project funding (to be obtained).

The methodologies outlined in the Analysis Process section below correspond to development stage 1, with the additional analyses proposed for development stage 2 described in section A3 - Stage 2 Development.

It is hoped that the development stage 1 application will be opened to user-testing, with the view to collating feedback to inform development priorities for stage 2.

Analysis Process

Following the . . . .

- Decide whether a conservation translocation is appropriate
- Increase the chance of success and wider potential benefits
- Reduce the chance of failure and negative outcomes

The framework laid out in Worrell et al. (2021) will be adopted. . .

Taking inspiration from the restoration diagnostic framework described in (Vitis et al. 2022) the suitability of selected species for assisted migration are assessed against the following criteria:

- Colonisation Sources
    - Are there areas of Ancient Woodland within colonisation distance?
    - Are there areas of other woodland within colonisation distance?
    - If surveyed, is the selected species present in woodlands within colonisation distance?
- Genetic Factors
- Biotic Factors
    - B1 - Does the species require an animal vector for pollination?
- Abiotic Factors * Is the selected species suitable for the environmental niche on site?
- Landscape Features
    - Are there any physical barriers to colonisation?
- Planning and Land Management Factors
    - P6 - Is it likely that the selected species will be out-competed?

Worrell et al. (2021) recommends that a four-step process be undertaken to examine the necessity of woodland flora translocation, namely the examination of:

1. *Which species are already present in the target woodland?*
2. *Which plant species are already present in adjacent woodland and habitats?*
3. *Which species would naturally occur in the wood?*
4. *Which species are missing from the woodland and nearby linked habitats?*

Following this guidance, we define four key criteria which determine translocation suitability:

1. Niche Suitability
2. Community Suitability
3. Migration Probability
4. Distribution Suitability

Niche Suitability

To examine whether a selected species is suitable for the sites specific biogeoclimatic conditions, the multi-MOVE plant species niche models (Henrys, Smart, et al. 2015; Henrys, Butler, et al. 2015; Smart et al. 2019) will be utilised in conjunction with baseline (1961-1990) climate data along with future climate projections obtained from the CHESS-SCAPE dataset (Robinson et al. 2022) for the annual average rainfall, minimum January temperature, and maximum July temperature. The Forest Research ESC soil survey data will be used, with the 'Soil Wetness', 'Substrate Fertility' MultiMOVE niche metrics mapped to the (Soil Nutrient Regime) and SMR (Soil Moisture Regime) values.

Community Suitability

To assess whether the selected species is sociologically suited to the community of flora present, or desired community at the selected woodland, two options will made available to the user:

1. Selection of a target National Vegetation Classification (NVC) community.
2. Assessment of the closest NVC woodland communities already present.

To facilitate option 2, an R implementation of the Modular Analysis of Vegetation Information System (MAVIS) will be utilised, requiring the user to enter NVC survey data for the target woodland.

The presence of the selected species will then be cross-referenced against the closest fitted NVC communities to the survey data for phytosociological suitability.

Migration Probability

To determine the likelihood that the selected species will successfully migrate from a nearby source (if present) to the target woodland, the maximum dispersal distance (MDD) will be calculated by taking the product of the yearly MDD, and user-defined time period (measured in years). This distance will then be compared to the distance between the target woodland, and source populations of the selected species obtained through survey data entry and retrieval of species occurrence data from the NBN Atlas (NBN 2023) application programming interface (API).

Estimations of the yearly MDD will obtained through a literature review and estimation using the {dispeRsal} R package (Tamme et al. 2014).

The user will then select the time period over which to examine dispersal likelihood, with three options available:

1. An estimate for the optimum successional age (in years) for the selected species, measured from the disturbance/establishment time of the target woodland derived from Milan (2021).
2. The difference between the age of the target woodland, and an ecological restoration target age.
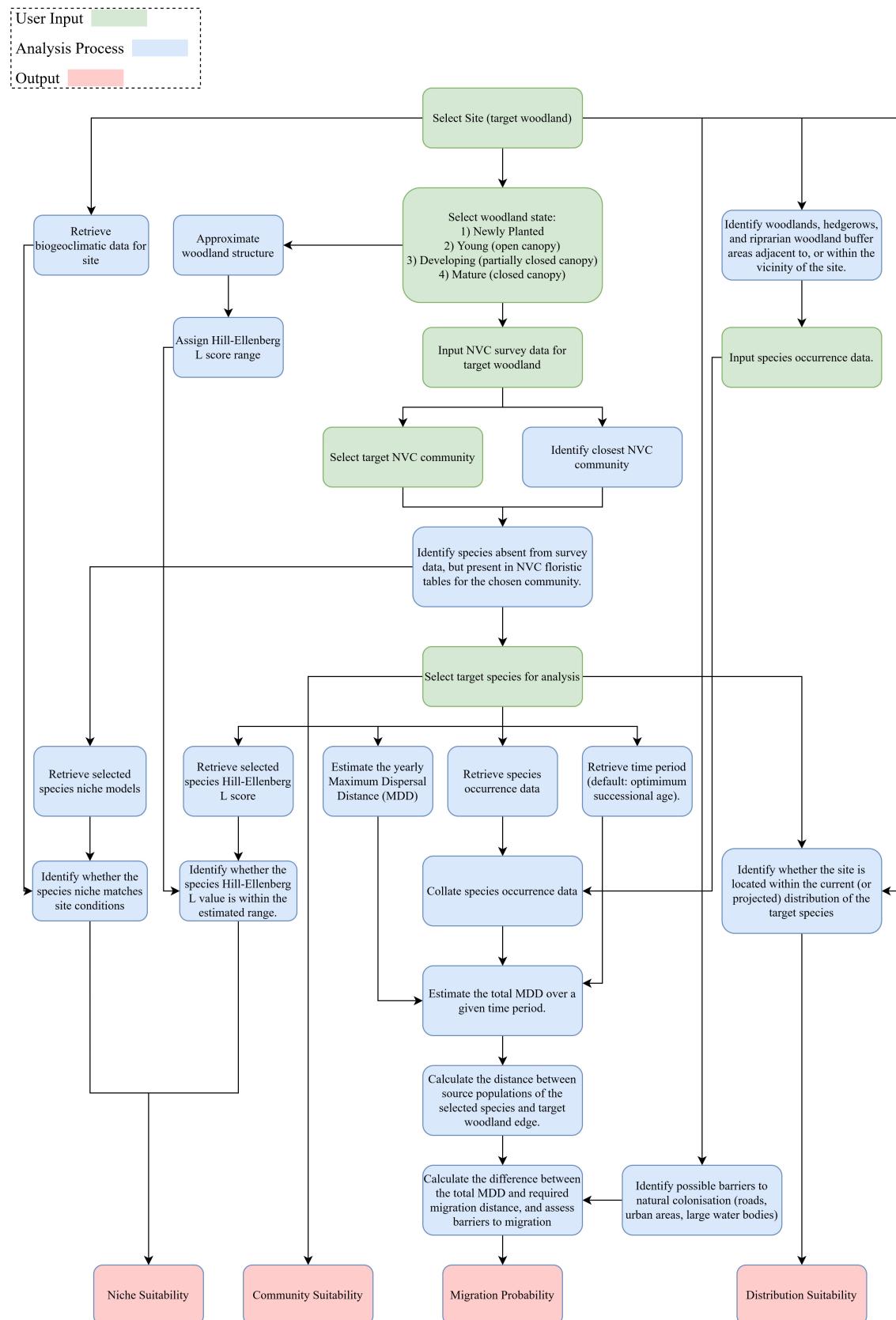3. A custom, user-stipulated value.

Figure 1: A flow diagram representing the proposed analysis workflow.

Barriers to migration such as roads, paths, rivers, trainlines, and urban areas will be assessed as obstacles based on the path of migration and dispersal symdrome. In the case See Figure 2 for a provisional representation of how the migration factors will be communicated to the user.

Distribution Suitability

To determine whether the target woodland is within the distribution of the selected species permission is currently being sought from the Botanical Society of Britain & Ireland for use of their distribution data.

Survey Data

The user will be able to use the tool without inputting any survey data, however the results will be insufficiently rigorous to inform translocation suitability, being reliant on only a user-stipulated target community and NBN occurrence data. For a rigorous assessment, the user will be required to input NVC survey data for the target woodland, and species presence data for ancient woodlands, other woodlands, scrub habitat, and hedgerows in the vicinity.

Selected Species

A limited subset of species will be included in stage 1 of the application. This selection will be determined by the available data, with species selected if they are: 1) present in the NVC floristic tables for communities W1 - W18e; 2) present in the MultiMOVE niche models; and 3) used as Ancient Woodland Indicators, as determined by Glaves et al. (2009). The application of these criteria results in the selection of 158 species. Only 30 of these species are represented in the baseline {dispeRsal} data, necessitating estimation of the MDD by traits at the genus or family level, or manually through a literature review if possible. See Section A2 - Selected Species for a list of proposed species.
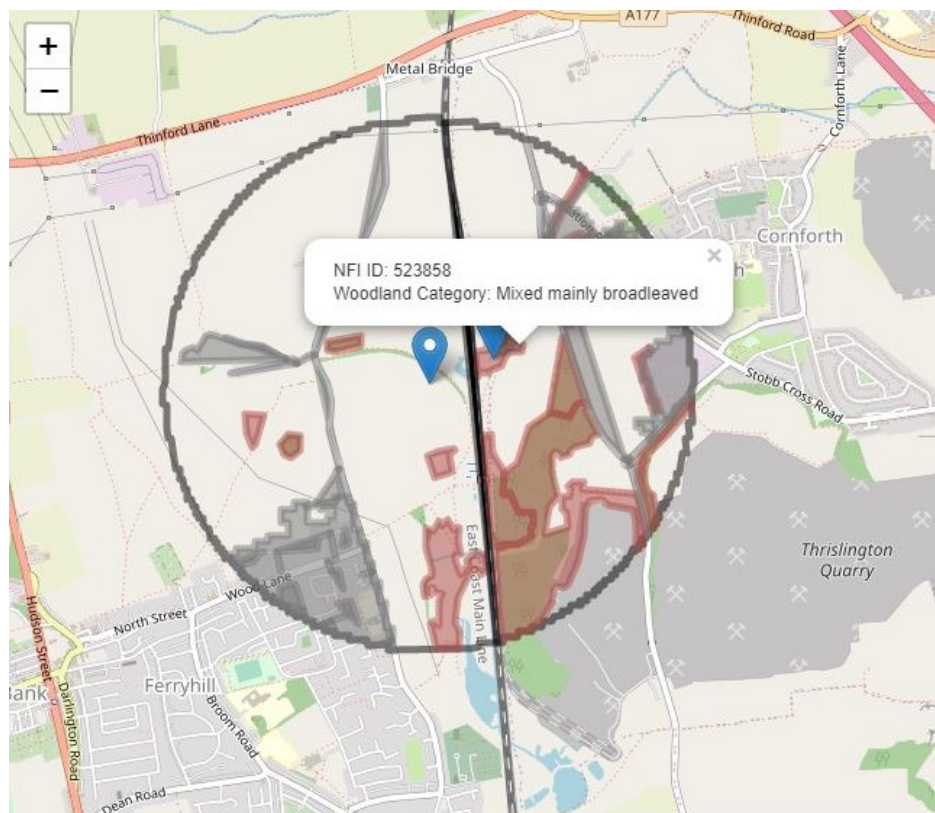

Figure 2: A screenshot of the interactive map interface taken from the prototype application.

Analysis Results

Following assessment against the aforementioned four criteria, it is proposed that the selected species will be recommended for translocation or assisted migration (or conservatively further investigation) if it is:

1. Absent from the target woodland site.
2. Present in the closest, or target community.
3. Suitable to the sites local biogeoclimatic conditions, at a given stage of woodland development.
4. Estimated to be unlikely to naturally migrate to the site within a reasonable time frame.
5. Within the known distribution of the species.

Appendix

A1 - Project Personal

It is proposed that an advisory committee be established to guide stage 1 of the applications development. It is proposed that funding is allocated to cover the time of all project personal for stage 2.

Current participants include:

- Zeke Marshall, Forest Research - Lead developer.
- Simon Smart, UK Centre for Ecology & Hydrology (UKCEH) - Advisor
- Paul Smith, University of Bristol - Advisor

A2 - Selected Species

Table 1: The species selected for stage 1 of the WFTTool.

species	nvcFT	indAW	plantATT	multiMOVE	dispeRsal
Acer campestre	Yes	Yes	Yes	Yes	
Adoxa moschatellina	Yes	Yes	Yes	Yes	
Ajuga reptans	Yes	Yes	Yes	Yes	
Allium ursinum	Yes	Yes	Yes	Yes	Yes
Anemone nemorosa	Yes	Yes	Yes	Yes	
Apium nodiflorum	Yes	Yes	Yes	Yes	
Arum maculatum	Yes	Yes	Yes	Yes	
Athyrium filix-femina	Yes	Yes	Yes	Yes	
Berula erecta	Yes	Yes	Yes	Yes	
Blechnum spicant	Yes	Yes	Yes	Yes	
Brachypodium sylvaticum	Yes	Yes	Yes	Yes	
Calamagrostis canescens	Yes	Yes	Yes	Yes	
Calamagrostis epigejos	Yes	Yes	Yes	Yes	
Calluna vulgaris	Yes	Yes	Yes	Yes	Yes
Campanula latifolia	Yes	Yes	Yes	Yes	
Campanula trachelium	Yes	Yes	Yes	Yes	Yes
Cardamine amara	Yes	Yes	Yes	Yes	
Carex acuta	Yes	Yes	Yes	Yes	
Carex acutiformis	Yes	Yes	Yes	Yes	
Carex binervis	Yes	Yes	Yes	Yes	
Carex elata	Yes	Yes	Yes	Yes	
Carex laevigata	Yes	Yes	Yes	Yes	
Carex nigra	Yes	Yes	Yes	Yes	
Carex pallescens	Yes	Yes	Yes	Yes	
Carex paniculata	Yes	Yes	Yes	Yes	
Carex pendula	Yes	Yes	Yes	Yes	
Carex pseudocyperus	Yes	Yes	Yes	Yes	
Carex remota	Yes	Yes	Yes	Yes	Yes
Carex riparia	Yes	Yes	Yes	Yes	
Carex sylvatica	Yes	Yes	Yes	Yes	
Carpinus betulus	Yes	Yes	Yes	Yes	Yes
Cephalanthera damasonium	Yes	Yes	Yes	Yes	Yes
Chrysosplenium oppositifolium	Yes	Yes	Yes	Yes	
Circaea lutetiana	Yes	Yes	Yes	Yes	

Table 1: The species selected for stage 1 of the WFTTool. *(continued)*

species	nvcFT	indAW	plantATT	multiMOVE	dispeRsal
Clematis vitalba	Yes	Yes	Yes	Yes	Yes
Conopodium majus	Yes	Yes	Yes	Yes	
Convallaria majalis	Yes	Yes	Yes	Yes	
Cornus sanguinea	Yes	Yes	Yes	Yes	
Corylus avellana	Yes	Yes	Yes	Yes	Yes
Crataegus laevigata	Yes	Yes	Yes	Yes	
Crepis paludosa	Yes	Yes	Yes	Yes	Yes
Daphne laureola	Yes	Yes	Yes	Yes	
Dryopteris carthusiana	Yes	Yes	Yes	Yes	
Epilobium montanum	Yes	Yes	Yes	Yes	Yes
Epilobium obscurum	Yes	Yes	Yes	Yes	
Epipactis helleborine	Yes	Yes	Yes	Yes	
Equisetum fluviatile	Yes	Yes	Yes	Yes	
Equisetum sylvaticum	Yes	Yes	Yes	Yes	
Equisetum telmateia	Yes	Yes	Yes	Yes	
Erica tetralix	Yes	Yes	Yes	Yes	
Euonymus europaeus	Yes	Yes	Yes	Yes	
Eupatorium cannabinum	Yes	Yes	Yes	Yes	Yes
Euphorbia amygdaloides	Yes	Yes	Yes	Yes	
Fragaria vesca	Yes	Yes	Yes	Yes	
Frangula alnus	Yes	Yes	Yes	Yes	
Galium odoratum	Yes	Yes	Yes	Yes	
Geranium robertianum	Yes	Yes	Yes	Yes	Yes
Geranium sanguineum	Yes	Yes	Yes	Yes	
Geranium sylvaticum	Yes	Yes	Yes	Yes	Yes
Geum rivale	Yes	Yes	Yes	Yes	Yes
Geum urbanum	Yes	Yes	Yes	Yes	
Glechoma hederacea	Yes	Yes	Yes	Yes	
Goodyera repens	Yes	Yes	Yes	Yes	
Gymnocarpium dryopteris	Yes	Yes	Yes	Yes	
Hedera helix	Yes	Yes	Yes	Yes	
Holcus mollis	Yes	Yes	Yes	Yes	
Humulus lupulus	Yes	Yes	Yes	Yes	
Hyacinthoides non-scripta	Yes	Yes	Yes	Yes	
Hymenophyllum wilsonii	Yes	Yes	Yes	Yes	
Hypericum hirsutum	Yes	Yes	Yes	Yes	
Hypericum humifusum	Yes	Yes	Yes	Yes	
Hypericum pulchrum	Yes	Yes	Yes	Yes	
Hypericum tetrapterum	Yes	Yes	Yes	Yes	Yes
Ilex aquifolium	Yes	Yes	Yes	Yes	
Iris foetidissima	Yes	Yes	Yes	Yes	
Iris pseudacorus	Yes	Yes	Yes	Yes	
Lamiastrum galeobdolon	Yes	Yes	Yes	Yes	
Lonicera periclymenum	Yes	Yes	Yes	Yes	
Luzula pilosa	Yes	Yes	Yes	Yes	
Luzula sylvatica	Yes	Yes	Yes	Yes	

Table 1: The species selected for stage 1 of the WFTTool. *(continued)*

species	nvcFT	indAW	plantATT	multiMOVE	dispeRsal
Lycopus europaeus	Yes	Yes	Yes	Yes	
Lysimachia nemorum	Yes	Yes	Yes	Yes	
Lysimachia nummularia	Yes	Yes	Yes	Yes	
Lysimachia thyrsiflora	Yes	Yes	Yes	Yes	
Lysimachia vulgaris	Yes	Yes	Yes	Yes	
Lythrum portula	Yes	Yes	Yes	Yes	
Melampyrum pratense	Yes	Yes	Yes	Yes	
Melica uniflora	Yes	Yes	Yes	Yes	
Mercurialis perennis	Yes	Yes	Yes	Yes	Yes
Milium effusum	Yes	Yes	Yes	Yes	
Moehringia trinervia	Yes	Yes	Yes	Yes	
Molinia caerulea	Yes	Yes	Yes	Yes	
Myosotis scorpioides	Yes	Yes	Yes	Yes	Yes
Myosotis secunda	Yes	Yes	Yes	Yes	
Myosotis sylvatica	Yes	Yes	Yes	Yes	
Oenanthe crocata	Yes	Yes	Yes	Yes	
Ophioglossum vulgatum	Yes	Yes	Yes	Yes	
Orchis mascula	Yes	Yes	Yes	Yes	
Osmunda regalis	Yes	Yes	Yes	Yes	
Oxalis acetosella	Yes	Yes	Yes	Yes	Yes
Platanthera chlorantha	Yes	Yes	Yes	Yes	
Polygonatum multiflorum	Yes	Yes	Yes	Yes	
Polystichum aculeatum	Yes	Yes	Yes	Yes	
Polystichum setiferum	Yes	Yes	Yes	Yes	
Populus tremula	Yes	Yes	Yes	Yes	
Potentilla sterilis	Yes	Yes	Yes	Yes	
Primula elatior	Yes	Yes	Yes	Yes	Yes
Primula vulgaris	Yes	Yes	Yes	Yes	
Prunus avium	Yes	Yes	Yes	Yes	Yes
Prunus padus	Yes	Yes	Yes	Yes	
Pyrola minor	Yes	Yes	Yes	Yes	
Ranunculus auricomus	Yes	Yes	Yes	Yes	
Ranunculus flammula	Yes	Yes	Yes	Yes	
Ribes nigrum	Yes	Yes	Yes	Yes	
Ribes rubrum	Yes	Yes	Yes	Yes	
Ribes uva-crispa	Yes	Yes	Yes	Yes	
Rosa arvensis	Yes	Yes	Yes	Yes	
Rubus idaeus	Yes	Yes	Yes	Yes	Yes
Rubus saxatilis	Yes	Yes	Yes	Yes	
Rumex sanguineus	Yes	Yes	Yes	Yes	
Ruscus aculeatus	Yes	Yes	Yes	Yes	
Salix aurita	Yes	Yes	Yes	Yes	
Salix caprea	Yes	Yes	Yes	Yes	
Salix cinerea	Yes	Yes	Yes	Yes	
Salix pentandra	Yes	Yes	Yes	Yes	

Table 1: The species selected for stage 1 of the WFTTool. *(continued)*

species	nvcFT	indAW	plantATT	multiMOVE	dispeRsal
Sanicula europaea	Yes	Yes	Yes	Yes	
Scrophularia nodosa	Yes	Yes	Yes	Yes	Yes
Scutellaria minor	Yes	Yes	Yes	Yes	
Sedum telephium	Yes	Yes	Yes	Yes	
Senecio aquaticus	Yes	Yes	Yes	Yes	
Serratula tinctoria	Yes	Yes	Yes	Yes	Yes
Silene dioica	Yes	Yes	Yes	Yes	Yes
Solidago virgaurea	Yes	Yes	Yes	Yes	Yes
Sorbus aucuparia	Yes	Yes	Yes	Yes	
Sorbus torminalis	Yes	Yes	Yes	Yes	
Stachys sylvatica	Yes	Yes	Yes	Yes	
Stellaria alsine	Yes	Yes		Yes	
Stellaria holostea	Yes	Yes	Yes	Yes	
Stellaria neglecta	Yes	Yes	Yes	Yes	
Tamus communis	Yes	Yes	Yes	Yes	
Taxus baccata	Yes	Yes	Yes	Yes	
Teucrium scorodonia	Yes	Yes	Yes	Yes	
Thalictrum flavum	Yes	Yes	Yes	Yes	
Tilia cordata	Yes	Yes	Yes	Yes	Yes
Trientalis europaea	Yes	Yes	Yes	Yes	
Trollius europaeus	Yes	Yes	Yes	Yes	
Ulmus glabra	Yes	Yes	Yes	Yes	Yes
Vaccinium myrtillus	Yes	Yes	Yes	Yes	
Valeriana officinalis	Yes	Yes	Yes	Yes	Yes
Veronica chamaedrys	Yes	Yes	Yes	Yes	
Veronica montana	Yes	Yes	Yes	Yes	
Veronica officinalis	Yes	Yes	Yes	Yes	
Viburnum lantana	Yes	Yes	Yes	Yes	
Viburnum opulus	Yes	Yes	Yes	Yes	
Vicia sepium	Yes	Yes	Yes	Yes	
Viola odorata	Yes	Yes	Yes	Yes	Yes
Viola palustris	Yes	Yes	Yes	Yes	
Viola riviniana	Yes	Yes	Yes	Yes	Yes

A3 - Stage 2 Development

A3i - Niche Suitability

There are a number of potential developments for the niche suitability analysis. Firstly, species absent in MultiMOVE but present in the NVC floristic tables could be examined. Secondly, using Forest Research soil survey data and derived datasets for SMR and SNR, the MultiMOVE niche models could be expanded to assess the 'Soil Wetness' and 'Substrate Fertility' variables independently, rather than as a function of the community-weighted mean Hill-Ellenberg values. Thirdly, a Bayesian approach could be taken to integrate species occurrence and more comprehensive presence-absence survey data following Morera-Pujol et al. (2022), additionally further survey data could be added. Fourthly, the 1km resolution climatic data used to identify the site conditions could be down-scaled using the {microclimc} R package (Maclean and Klinges 2021), with the influence of woodland structure on the microclimate accounted for.

A3ii - Community Suitability

Further development of the community suitability analysis could include examination of species absent from the NVC floristic tables and/or inclusion of a community classification system other than the NVC, e.g. the UK Habitat Classification System.

A3iii - Migration Probability

It is likely that the largest source of uncertainty in the analysis is the examination of the likelihood of migration. There are several avenues which could be explored to improve this methodology. Firstly, the probability of successful migration could be calculated using a probability density function such as the total dispersal kernel (Rogers et al. 2019), Such functions could be estimated using empirical data (Bullock et al. 2016) where available. This approach is necessary for both capturing the uncertainty inherent in estimating dispersal distance, and for correctly representing species with sequential dispersal syndromes such as *Mercurialis perennis*, the seeds of which are first dispersed ballistically as estimated in Tamme et al. (2014), but are then also dispersed by ants (Jefferson 2008).

A3iv - Distribution Suitability

Further development of the distribution suitability analysis could include. . . .

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