

# Woodland Flora Translocation Tool

## A brief project proposal

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## Introduction

The UK government has set an ambitious target of increasing UK-wide planting rates from 13850 hectares (ha) per year (Maxwell 2022) to 30000 ha per year by 2025 (National Audit Office 2022). In in the 2021/2022 planting season 6970 ha of broadleaved woodland were created in the United Kingdom (UK). However, at present the majority of tree-planting in the UK occurs on former agricultural land, which generally results in the development of species-poor understory flora communities after establishment (Worrell et al. 2021). This represents a significant conservation gap, as woodland understory flora represents the majority of vascular plant diversity in temperate forest ecosystems and is critical to ecosystem functioning.

These outcomes are a consequence of numerous spatio-temporal barriers which inhibit the migration of woodland flora, particularly dispersal-limited, niche-restricted Ancient Woodland Indicator (AWI) plant species. The aggregate effect of these barriers on flora migration to new woodlands and subsequent effect on species composition is an example of ‘colonisation credit’ (Watts et al. 2020). In attempts to reduce colonization credit in newly planted woodlands, woodland creation schemes often aim to establish new woodlands adjacent to ancient semi-natural woodland (ASNW), with the view to reducing migration distance and barriers. This practice has been shown to reduce, but not eliminate colonisation credit relative to isolated newly planted woodlands (Hughes et al., n.d.).

As such, the creation of diverse woodland understory communities cannot be relied upon to occur through self-assembly within the time frames stipulated in the Kunming-Montreal Global Biodiversity Framework (UNEP 2022). Specifically, target 4 states the need to:

*“Ensure urgent management actions to halt human induced extinction of known threatened species and for the recovery and conservation of species, in particular threatened species, to significantly reduce extinction risk, as well as to maintain and restore the genetic diversity within and between populations of native, wild and domesticated species to maintain their adaptive potential, including through in situ and ex situ conservation and sustainable management practices. . . . .”*

As part of achieving such ecosystem restoration targets, a proactive approach must be taken to assist in the colonisation of woodland flora to newly planted woodlands through translocation, accelerating the creation of ancient woodland characteristics (Smith 2017).

This approach is an increasingly recognised management need. Organisations such as the Woodland Trust make the need to *“Establish Richer Communities”* explicit in their 2022 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). Problematically, despite such advances the infrastructure and guidance to facilitate woodland flora translocation at scale is in its infancy.

## Aims

In response to the 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 - the Woodland Flora Translocation Tool (WFTTTool). This application will act as a Decision Support System (DSS), aiding users in examining the suitability of woodland understory 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

Translocations should be planned and managed carefully to reduce risk of failure or negative outcomes (Vitis et al. 2022). The conservation translocation guidance provided by DEFRA (2021) describes how conservation translocations should be ecologically appropriate and conducted with the correct permissions and licences. It is proposed that this tool is constructed in accordance with the frameworks established in the English (DEFRA 2021), Scottish (National Species Reintroduction Forum 2014), and International Union for Conservation of Nature (IUCN) (IUCN/SSC 2013) guidance documents.

In the context of woodland flora translocations Worrell et al. (2021) recommends that a four-step process be undertaken to ascertain translocation suitability, namely:

1. *“Assess the plant communities present in the woodland.”*
2. *“Assess the species present in adjacent woods and habitats that may colonise naturally.”*
3. *“Assess which plant species would occur naturally in the woodland.”*
4. *“Work out which plant species are missing.”*

Following this guidance, we define four key criteria for use in determining translocation suitability:

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

Proposed methods to examine the aforementioned criteria are described below, and represented in Figure 1.

### Niche Suitability

Worrell et al. (2021) recommends that soils conditions are assessed for species suitability using Hill-Ellenberg scores (Hill et al. 1999) or the Forest Research Ecological Site Classification (ESC) tool (Pyatt, Ray, and Fletcher 2001). To examine whether a selected species is suitable for the sites specific biogeoclimatic conditions, it is instead proposed that the MultiMOVE plant species niche models (Henrys, Smart, et al. 2015; Henrys,

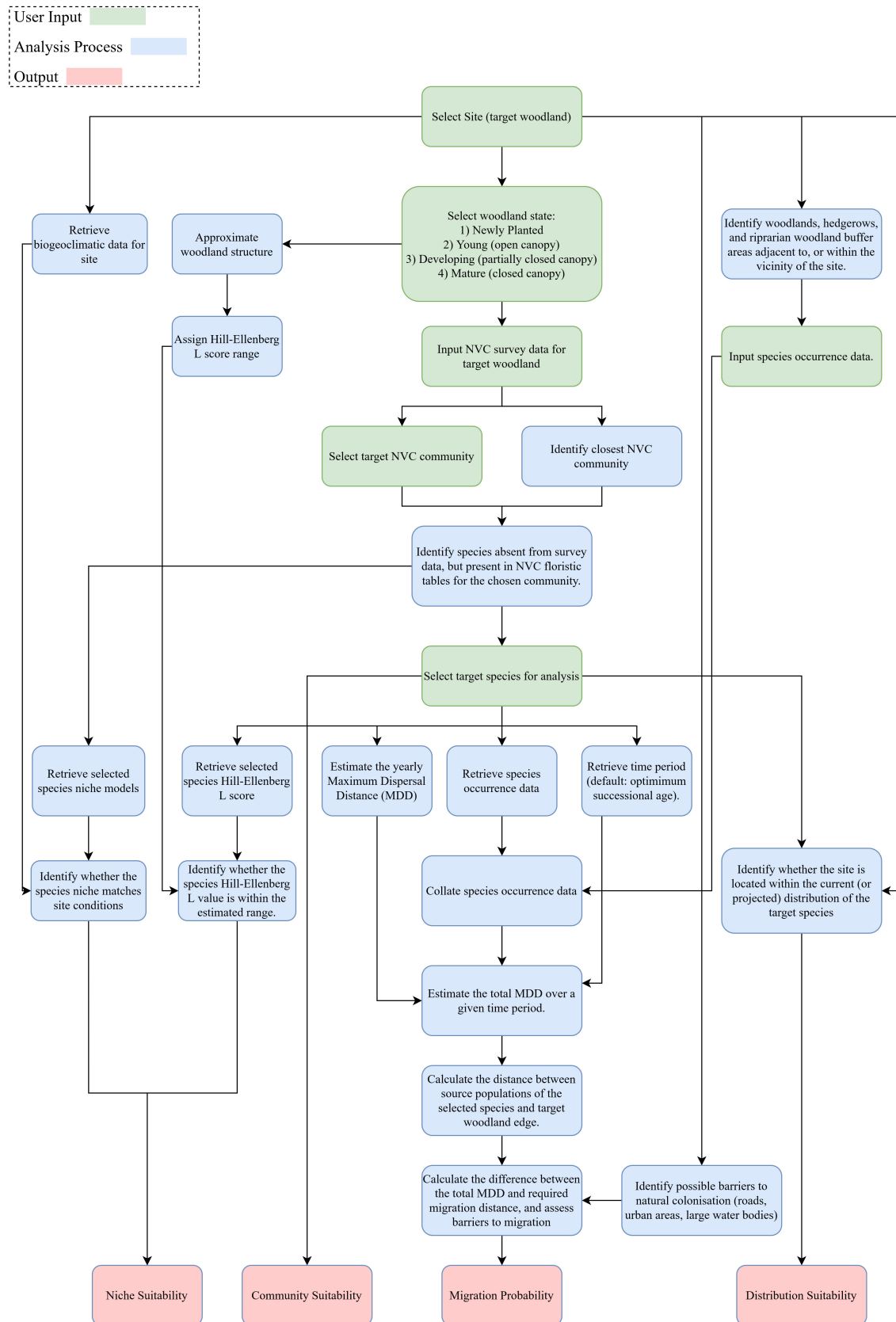


Figure 1: A flow diagram representing the proposed analysis workflow.

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 CHES-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. Lastly, the effect of woodland structure and light availability will be assessed using the Hill-Ellenberg light indicator values (Hill et al. 1999).

## Community Suitability

Our understanding of how the composition of traits within a community of organisms scales to constitute and influence ecosystem functioning is a developing field (Chacón-Labelle et al. 2022). Lacking the understanding to design species compositions which form functioning ecosystems we are reliant on the use of target communities.

As recommended by Worrell et al. (2021), to assess whether the selected species is sociologically suited to the community of flora present, or the desired community at the selected woodland two options will be 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 selected species will then be cross-referenced against its presence/absence in the the closest fitted NVC communities to determine phytosociological suitability.

## Migration Probability

To determine the likelihood that the selected species will successfully migrate from nearby sources (if present) to the target woodland, the maximum dispersal distance (MDD) will be estimated by taking the product of the yearly MDD, and user-selected time period (measured in years). This distance will then be compared to the distance between the target woodland and source populations.

Source populations will be determined through the entry of species presence data for the nearby forest habitat network (adjacent woodlands, hedgerows, and riparian woodland buffer areas) as recommended by Worrell et al. (2021). This data will be supplemented by the retrieval of species occurrence data from the National Biodiversity Network (NBN) Atlas (NBN 2023) application programming interface (API).

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

It is proposed that 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 Chytry et al. (2021).
2. The difference between the age of the target woodland, and an ecological restoration target age.
3. A custom, user-stipulated value.

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 syndrome. See Figure 2 for a provisional representation of how the migration factors will be communicated to the user.

## Distribution Suitability

Worrell et al. (2021) recommends that the site location should be checked to ensure that it is within the native range of the species being assessed for translocation. 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.

## 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 the list of proposed species, which will be subject to change based on further review.

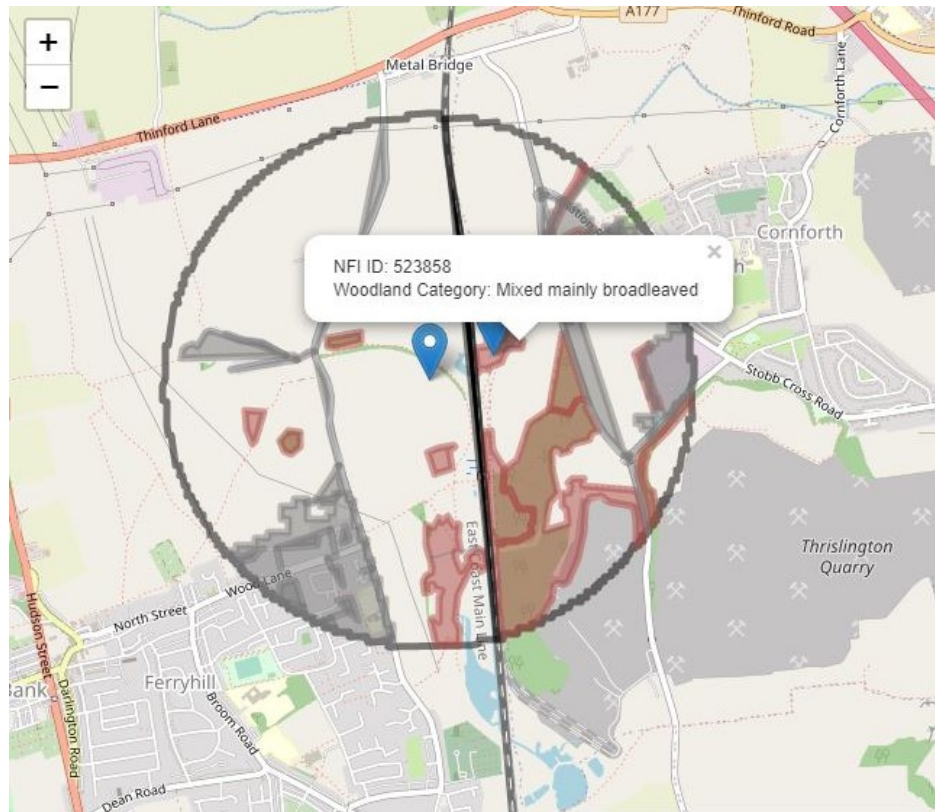


Figure 2: A screenshot of the interactive map interface taken from the prototype application.

# 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
<i>Acer campestre</i>	Yes	Yes	Yes	Yes	
<i>Adoxa moschatellina</i>	Yes	Yes	Yes	Yes	
<i>Ajuga reptans</i>	Yes	Yes	Yes	Yes	
<i>Allium ursinum</i>	Yes	Yes	Yes	Yes	Yes
<i>Anemone nemorosa</i>	Yes	Yes	Yes	Yes	
<i>Apium nodiflorum</i>	Yes	Yes	Yes	Yes	
<i>Arum maculatum</i>	Yes	Yes	Yes	Yes	
<i>Athyrium filix-femina</i>	Yes	Yes	Yes	Yes	
<i>Berula erecta</i>	Yes	Yes	Yes	Yes	
<i>Blechnum spicant</i>	Yes	Yes	Yes	Yes	
<i>Brachypodium sylvaticum</i>	Yes	Yes	Yes	Yes	
<i>Calamagrostis canescens</i>	Yes	Yes	Yes	Yes	
<i>Calamagrostis epigejos</i>	Yes	Yes	Yes	Yes	
<i>Calluna vulgaris</i>	Yes	Yes	Yes	Yes	Yes
<i>Campanula latifolia</i>	Yes	Yes	Yes	Yes	
<i>Campanula trachelium</i>	Yes	Yes	Yes	Yes	Yes
<i>Cardamine amara</i>	Yes	Yes	Yes	Yes	
<i>Carex acuta</i>	Yes	Yes	Yes	Yes	
<i>Carex acutiformis</i>	Yes	Yes	Yes	Yes	
<i>Carex binervis</i>	Yes	Yes	Yes	Yes	
<i>Carex elata</i>	Yes	Yes	Yes	Yes	
<i>Carex laevigata</i>	Yes	Yes	Yes	Yes	
<i>Carex nigra</i>	Yes	Yes	Yes	Yes	
<i>Carex pallescens</i>	Yes	Yes	Yes	Yes	
<i>Carex paniculata</i>	Yes	Yes	Yes	Yes	
<i>Carex pendula</i>	Yes	Yes	Yes	Yes	
<i>Carex pseudocyperus</i>	Yes	Yes	Yes	Yes	
<i>Carex remota</i>	Yes	Yes	Yes	Yes	Yes
<i>Carex riparia</i>	Yes	Yes	Yes	Yes	
<i>Carex sylvatica</i>	Yes	Yes	Yes	Yes	
<i>Carpinus betulus</i>	Yes	Yes	Yes	Yes	Yes
<i>Cephalanthera damasonium</i>	Yes	Yes	Yes	Yes	Yes
<i>Chrysosplenium oppositifolium</i>	Yes	Yes	Yes	Yes	
<i>Circaea lutetiana</i>	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 thyrsoflora	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
<i>Sanicula europaea</i>	Yes	Yes	Yes	Yes	
<i>Scrophularia nodosa</i>	Yes	Yes	Yes	Yes	Yes
<i>Scutellaria minor</i>	Yes	Yes	Yes	Yes	
<i>Sedum telephium</i>	Yes	Yes	Yes	Yes	
<i>Senecio aquaticus</i>	Yes	Yes	Yes	Yes	
<i>Serratula tinctoria</i>	Yes	Yes	Yes	Yes	Yes
<i>Silene dioica</i>	Yes	Yes	Yes	Yes	Yes
<i>Solidago virgaurea</i>	Yes	Yes	Yes	Yes	Yes
<i>Sorbus aucuparia</i>	Yes	Yes	Yes	Yes	
<i>Sorbus torminalis</i>	Yes	Yes	Yes	Yes	
<i>Stachys sylvatica</i>	Yes	Yes	Yes	Yes	
<i>Stellaria alsine</i>	Yes	Yes		Yes	
<i>Stellaria holostea</i>	Yes	Yes	Yes	Yes	
<i>Stellaria neglecta</i>	Yes	Yes	Yes	Yes	
<i>Tamus communis</i>	Yes	Yes	Yes	Yes	
<i>Taxus baccata</i>	Yes	Yes	Yes	Yes	
<i>Teucrium scorodonia</i>	Yes	Yes	Yes	Yes	
<i>Thalictrum flavum</i>	Yes	Yes	Yes	Yes	
<i>Tilia cordata</i>	Yes	Yes	Yes	Yes	Yes
<i>Trientalis europaea</i>	Yes	Yes	Yes	Yes	
<i>Trollius europaeus</i>	Yes	Yes	Yes	Yes	
<i>Ulmus glabra</i>	Yes	Yes	Yes	Yes	Yes
<i>Vaccinium myrtillus</i>	Yes	Yes	Yes	Yes	
<i>Valeriana officinalis</i>	Yes	Yes	Yes	Yes	Yes
<i>Veronica chamaedrys</i>	Yes	Yes	Yes	Yes	
<i>Veronica montana</i>	Yes	Yes	Yes	Yes	
<i>Veronica officinalis</i>	Yes	Yes	Yes	Yes	
<i>Viburnum lantana</i>	Yes	Yes	Yes	Yes	
<i>Viburnum opulus</i>	Yes	Yes	Yes	Yes	
<i>Vicia sepium</i>	Yes	Yes	Yes	Yes	
<i>Viola odorata</i>	Yes	Yes	Yes	Yes	Yes
<i>Viola palustris</i>	Yes	Yes	Yes	Yes	
<i>Viola riviniana</i>	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 Klimes 2021), to account for the influence of woodland structure on microclimate.

### 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 capturing the uncertainty inherent in estimating dispersal distance, particularly for zoochory-mediated dispersal 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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