Scottish Seed Stand Project
Appendix A. Local Clustering Methodology

Suitability Assessment

The suitability of each species for clustering was assessed on a number of criteria:

1. Contiguity of populations (approximating gene flow)
2. The number of native seed zones (NSZ) records occur within.
3. The extent to which the number of clusters are feasible for seed stand creation.
4. Species conservation value.

The approach taken for each species are shown in **Table A.1** and resulting maps are shown in **Appendix B** and **Appendix C**.

Table A.1. Clustering method by species.

Species	DBSCAN	NSZ	Notes
Betula nana		X	Populations relatively contiguous across most of Scotland – too few clusters would be generated.
Juniperus communis ssp. *communis* (>400m)		X	Most records isolated outside of NSZ 201 and 202.
Juniperus communis ssp. *nana* (>400m)		X	Natural clusters conform closely to NSZ. Cairngorms population better treated as cluster than using NSZ.
Salix arbuscula	X		Specialist montane willow restricted to central Highlands. NSZ too broad.
Salix aurita (>600m)		X	Populations relatively contiguous across most of Scotland – too few clusters would be generated.
Salix caprea ssp. *sphacelata*		X	Records scattered resulting in too many clusters; conform well to NSZ.
Salix lanata	X		Specialist montane willow restricted to central Highlands. NSZ too broad.
Salix lapponum	X		Specialist montane willow with many populations occurring near the boundary of FRM NSZ. Large clusters SAP 1 and SAP 2 require further subdivision.
Salix myrsinifolia (>400m)	X		Submontane willow with majority of records occurring in single NSZ.
Salix myrsinites	X		Specialist montane willow, FRM boundaries may be suitable in some areas – e.g, NSZ 105
Salix phylicifolia (>400m)	X		Submontane willow with high-altitude distribution captured well by six clusters.
Salix repens (>600m)		X	Fairly contiguous populations across Central Highlands. N.B. 600m threshold likely too high outside of Cairngorms.
Salix reticulata	X		Specialist montane willow almost entirely restricted to Central Highlands. NSZ too broad.
Sorbus rupicola		X	Scattered populations too disjunct, resulting in very large number of clusters for which establishing seed stands would not be feasible.

Method

Clusters were created using Density Based Spatial Clustering Analysis with Noise (DBSCAN)[1] in QGIS[2], using records compiled in the Habitat Map of Scotland dataset[3].

The minimum number of records for a cluster was set as 5. This threshold was selected because montane willows are under-recorded, and a single record often represents numerous individuals. However, this means some clusters may not have sufficient genetic material present and may need to be combined with other populations.

The maximum distance between points in each cluster was set as 10 km. This threshold has been used to approximate similarity in conditions, and the likelihood of historic gene flow between remnant populations.

Limitations

There are of course a number of limitations to this approach, which should be recognised when using the outputs of this project to inform seed stand creation:

1. The use of clusters to guide the seed stand creation framework is based on the assumption that spatial relationships are representative of similarity in conditions. However, individual populations may be adapted to different conditions which are not related to geographical proximity:

    For example, cluster SMR3 in Breadalbane includes *Salix myrsinites* growing on calcareous schist in the West, and dolomite at Schiehallion.

2. The use of 10km to indicate historic gene flow is a broad approximation. Work based on genetic analysis of diversity, adaptive potential and gene flow would be superior to the approach taken here.

Therefore, the clusters mapped in Appendix B and employed in the seed stand database are intended only to guide seed stand creation through the identification of gaps in supply and the location of source populations. These will (and already have been) subdivided and aggregated in many areas.

For example, SAP1 encompasses the majority of mountain woodland restoration sites in the Highlands and therefore multiple stands have already been created. As these stands all have sufficient genetic diversity due to the comparative abundance of source populations, the approach that has already been taken by restoration practitioners is far superior to if only a single stand had been created.

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[1] Ester, M., Kriegel, H. P., Sander, J., & Xu, X. (1996). A density-based algorithm for discovering clusters in large spatial databases with noise. In *Data Clustering: Algorithms and Applications* (Vol. 96, No. 34, pp. 226-231).
[2] QGIS.org, %%Y. QGIS Geographic Information System. QGIS Association. http://www.qgis.org
[3] NatureScot (2023). Habitat Map of Scotland – Mountain Woodland 2023 – Wild, relict or remnant. Available at:
https://opendata.nature.scot/datasets/snh::habmos-mountain-woodland-2023-wild-relict-or-remnant/about