

## Article

# Assessing forest biodiversity: A novel index to consider ecosystem, species, and genetic diversity (Electronic Supplementary Material (ESM))

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## 1. Ecosystem diversity indication

Ecosystem diversity indication with BCI considers three biodiversity indicators (*BI*) and one bonus indicator (*Bonus*). If at least two out of four (> 50%) indicators are rated, AFI sub plots are included in the BCI ecosystem diversity assessment. The indication of 100% is always adapted to the maximum number of points possible under the current number of indicators at the AFI sub plot (100% = 27.0 points if *three ecosystem diversity indicators* could be rated with up to 9.0 points; **or** 100% = 18.0 points, if *two ecosystem diversity indicators* could be rated with up to 9.0 points).

$$\text{ecosystem diversity indication} = BI_{\text{layer}} + BI_{\text{devel. level}} + BI_{\text{dead wood}} + Bonus_{\text{structure}}$$

### 1.1. Tree layer structure ( $BI_{\text{layer}}$ )

$BI_{\text{layer}}$  assesses the deviation of the actual tree layer structure (AFI) from an expected, site-specific layer structure (forest typing). Firstly, missing tree layers are rated with zero, tree layers below 30% crown cover with 0.5, and layers with more than 30% crown cover with 1.0 points in the AFI data set. Secondly, tree layer classification (mono, weakly double, double, and multiple layered stand) is performed by summing up the layer ratings on the sub plot level (Tab. S1).

**Table S1.** Rating of tree layer structure. Summing up single tree layers ratings on the sub plot level to classify actual tree layer structure.

| Classification | Sum of ratings | Shrub layer cover    | Tree layer cover I    | Tree layer cover II    |
|----------------|----------------|----------------------|-----------------------|------------------------|
|                |                | (0-33% stand height) | (34-66% stand height) | (67-100% stand height) |
| mono           | 1              | 0                    | 1                     | 0                      |
| weakly double  | 1              | 0.5                  | 0.5                   | 0                      |
|                | 1.5            | 0.5                  | 0.5                   | 0.5                    |
|                | 1.5            | 1                    | 0.5                   | 0                      |
| double         | 2              | 0                    | 1                     | 1                      |
|                | 2              | 1                    | 0.5                   | 0.5                    |
| multiple       | 2.5            | 0.5                  | 1                     | 1                      |
|                | 3              | 1                    | 1                     | 1                      |

For each forest type, Grabherr et al. [50] provided an indicator value for mono, weakly double, double, and multiple layered forest stands respectively. Indicator values range from  $BI_{\text{layer}} = 9.0$  points (natural tree layer structure for a certain forest type) to  $BI_{\text{layer}} = 0$  points (very artificial structure, not possibly accomplished under natural

conditions for a certain forest type). In case forest types cannot be evaluated by the lists in Grabherr et al. [50], the mean of the forest type group the forest type belongs to (appendix A. 2) is used as a reference.

### 1.2. Developmental level ( $BI_{\text{devel. level}}$ )

The biodiversity indicator ‘developmental level’ rewards high successional differentiation on small scales and late successional phases. Sub plots with mountain pine or green alder are not considered in  $BI_{\text{devel. level}}$  as these forest types do not follow the same successional paths. Seven classes of developmental phases are assessed on the sub plot level in the AFI [54]. In a first step, these phases are rated with  $DL_{\text{age I}}$  for AFI plots with one subplot and  $DL_{\text{age II}}$  for  $\geq 2$  subplots covered with forest (Tab. S2).

**Table S2.** Rating of forest successional age. Developmental phases surveyed in the AFI and their successional age rating (DLage). BI (devel. level) distinguishes between AFI plots with = 1 (DL (age I)) and  $\geq 2$  DL(age II) AFI subplots with forest cover.

| Phase number | Developmental phase       | $DL_{\text{age I}}$<br>(1 sub plot rated) | $DL_{\text{age II}}$<br>( $\geq 2$ sub plots rated) |
|--------------|---------------------------|---|---|
| 1            | formative phase           | 3   | -5  |
| 2            | juvenile or initial phase | 4   | -4  |
| 3            | maturing phase            | 5   | -3  |
| 4            | flowering phase           | 9   | 0   |
| 5            | terminal phase            | 9   | 0   |
| 6            | early senescent phase     | 9   | 0   |
| 7            | late senescent phase      | 7   | -2  |

If there is only one out of four sub plots covered with forest,  $DL_{\text{age I}}$  is already equivalent to  $BI_{\text{devel. level}}$ . Otherwise,  $BI_{\text{devel. level}}$  additionally considers the maximum difference between the developmental phases on the AFI plot using  $DL_{\text{mosaic}}$  in a second step (Tab. S3).

**Table S3.** Rating of successional age differentiation. For AFI plots with more than one sub plot with forest cover,  $BI_{\text{devel. level}}$  additionally considers the maximum difference between the developmental phase numbers on the AFI plot by using  $DL_{\text{mosaic}}$ .

| Max. difference between phase numbers<br>(See Tab. S4) | Successional age differentiation on the<br>AFI plot level<br>( $DL_{\text{mosaic}}$ ) |
|--|---|
| 0  | -4  |
| 1  | -3.2  |
| 2  | -2.4  |
| 3  | -1.6  |
| 4  | -0.8  |
| > 5  | 0   |

$BI_{\text{devel. level}}$  can be calculated as:

$$BI_{\text{devel. level}} = DL_{\text{age I}} \quad (\text{for AFI plots with one sub plot with forest cover})$$

or

$$BI_{\text{devel. level}} = 9 + \frac{\sum DL_{\text{age II}}}{\text{nr. sub plots}} + DL_{\text{mosaic}} \quad (\text{for AFI plots with } \geq 2 \text{ sub plots with forest cover})$$

To reward high successional age differentiation, the phase number of the subplot with the respectively lowest developmental phase (e.g., formative phase = phase number

1, see Tab. S2) is subtracted from the phase number of the subplot with the respectively highest developmental phase (e.g., terminal phase = phase number 5) on the AFI plot level. In this example, the maximum difference would be four ( $5 - 1 = 4$ ), resulting in  $DL_{mosaic}$  value of  $-0.8$  (See Tab. S3).

### 1.3. Dead wood ( $BI_{dead\ wood}$ )

Dead wood quantity is assessed by comparing actual AFI sub plot levels with the maximum dead wood amount of a forest type in the AFI data set. If the AFI maximum is exceeded by reference values in protected areas (National parks 'Hohe Tauern' and 'Berchtesgaden', Nature parks and forest nature reserves), the respectively higher value is considered. In case there is no reference data for a forest type, the reference quantity is assumed to be  $28.8\text{ m}^3/\text{ha}$  which is the average of all maxima found in the forest types under study.

$BI_{dead\ wood}$  considers dead wood quantity ( $DW_{quantity}$ ) and quality ( $DW_{quality}$ ).

$$BI_{dead\ wood} = DW_{quantity} + \sum DW_{quality}$$

$DW_{quantity}$  ratings are rising linearly with the share of maximum deadwood level on the sub plot (Tab. S4).

**Table S4.** Rating of dead wood quantity. Values for quantitative dead wood evaluation are derived from comparing actual AFI sub plot data with the highest dead wood level found for the forest type in reference data sets.

| Dead wood quantity<br>(share of DW maximum) | $DW_{quantity}$ |
|---|-----------------|
| 75-100%                                     | 9               |
| 50-75%                                      | 6               |
| 25-50%                                      | 3               |
| < 25%                                       | 0               |

Following Grabherr et al. [50], quantitative dead wood ratings are corrected by adding the sum of awards and reductions according to six dead wood quality proxies (Tab. S5). In seldom cases of negative values or values exceeding 9.0 points after applying correction factors,  $BI_{dead\ wood}$  is set to zero or a maximum of nine points, respectively. If 100% of the dead wood quantity consists of standing harvesting residues,  $BI_{dead\ wood}$  is set to one.

**Table S5.** Rating of dead wood quality. Correcting dead wood quantity ratings (see Tab. S6) by considering proxies for dead wood quality. ( $DW_{quality}$ ).

| Criteria              | Proxies  | Correction factors<br>( $DW_{quality}$ ) |
|-----------------------|--|--|
| management legacies   | > 50% $DW_{quantity}$ are harvesting residues (stocks)                       | $DW_{quantity} * 0.5$                    |
|                       | > 50% $DW_{quantity}$ is standing or lying dead wood of anthropogenic origin | $DW_{quantity} - 0.5$                    |
| diameter distribution | Large diameter logs (> 20 cm) are present                                    | $DW_{quantity} + 1$                      |
|                       | > 50% dead wood displays mean diameter < 10 cm                               | $DW_{quantity} - 0.5$                    |
| standing dead wood    | > 50% $DW_{quantity}$ is standing dead wood                                  | $DW_{quantity} + 1$                      |
| habitat quality       | > 50% of $DW_{quantity}$ is undecomposed                                     | $DW_{quantity} - 0.5$                    |

#### 1.4. Bonus indicator – Structural features ( $Bonus_{structure}$ )

For extraordinary features, a bonus for high forest structural diversity is rewarded. In line with Grabherr et al. [50], the  $Bonus_{structure}$  contains three features which are having a zero to three points rating, respectively.

$$Bonus_{structure} = Bonus_{shrub} + Bonus_{stand\ age} + Bonus_{dbh}$$

- Shrub cover ( $Bonus_{shrub}$ )

A bonus of 3.0 points is awarded to forest types forming a shrub cover under natural conditions if an actual shrub layer can be observed on the sub plot level. Shrubs are defined as being above 1 m in height, while the shrub layer cover needs to exceed 15% crown cover to be considered.

- Stand age ( $Bonus_{stand\ age}$ )

Late stand ages occur seldom in intensively managed forests. For sub plots belonging to the early senescent phase, a bonus of 1.5 points is awarded. For those of the late senescent phase, the bonus accounts for 3.0 points.

- Diameter breast height ( $Bonus_{dbh}$ )

If at least one tree individual exceeds a diameter breast height (dbh) threshold of 30 cm, a bonus of 3.0 points is awarded to the sub plot.

## 2. Species diversity indication

Species diversity indication with BCI considers three biodiversity indicators ( $BI$ ) and one bonus indicator ( $Bonus$ ). Indicator ratings (0–9.0 points) are aggregated without weighing. If at least two out of four (> 50%) indicators are rated, AFI sub plots are included in the BCI species diversity assessment. The indication of 100% is always adapted to the maximum amount of points possible under the current number of indicators at the AFI sub plot (100% = 27.0 points if *three species diversity indicators* could be rated with up to 9.0 points; **or** 100% = 18.0 points, if *two species diversity indicators* could be rated with up to 9.0 points).

$$species\ diversity\ indication = BI_{tree\ species} + BI_{vegetation} + BI_{soil} + Bonus_{game}$$

### 2.1. Tree species diversity ( $BI_{tree\ species}$ )

In line with Grabherr et al. [50], assessment of naturalness of the tree species composition ( $BI_{tree\ species}$ ) is based on a target-performance comparison between actual (AFI) and potential (forest typing data) tree species composition. Firstly, all tree species in the Angle Count sampling [64] are rated according to their relative occurrence (s.s., sum of stems represented) in dominant, subdominant, blended, disseminated and pioneer species (Tab. S6).

**Table S6.** Classification of the potential tree species composition per forest type in the Bitterlich sample [50].

| Rel. Frequency | Classification  | Crown Cover (%) |
|----------------|---|-----------------|
| 1p             | Dominant Species  | > 50            |
| 2p             | Subdominant Species   | 25-50           |
| 3p             | Blended Species   | 6-25            |
| 4p             | Disseminated Species  | 1-5             |
| 5p             | Species occurring in sample area but not potentially possible | > 5             |

|    |   |     |
|----|---|-----|
| 6p | Species is potentially possible pioneer species | > 1 |
|----|---|-----|

The tree species matrix in Grabherr et al. [50] transforms classes of occurrence frequencies from Braun-Blanquet scale into relative values (Tab. S7).

**Table S7.** Tree species matrix to transform classes of occurrence frequencies in relative values  $\beta_{BA}$  (With **a**, the actual species composition and **p**, the potential species composition of the forest type).

|    | 1p | 2p | 3p   | 4p   | 5p   | 6p |
|----|----|----|------|------|------|----|
| 1a | 0  | -1 | -2   | -3   | -4   | +2 |
| 2a | -1 | 0  | -1   | -2   | -4   | +1 |
| 3a | -2 | -1 | 0    | -0.5 | -1   | 0  |
| 4a | -3 | -2 | -0.5 | 0    | -0.5 | 0  |
| 0a | -3 | -2 | -1   | 0    | 0    | 0  |

Secondly, the deviation of the actual status (AFI) from a potential status [53] is depicted and tree species which are over-, or sub represented in the forest type obtain commission. Tree species, which by their nature occur rarely in certain forest types and are missing by chance, do not affect this rating negatively. The commissions add up on the sub plot level and are subtracted from the maximum indicator rating possible (9.0 points) to assess  $BI_{tree\ species}$ .

## 2.2. Ground vegetation ( $BI_{vegetation}$ )

$BI_{vegetation}$  evaluates the naturalness of species composition of the ground vegetation. Firstly, all forest types of Tyrol [53] are allocated into the forest type groups of Grabherr et al. [50], which is precondition to use the plant species reference lists (appendix A.2). For the case study, we additionally invent the two forest type groups 'block forest, rubble, and rock sites on carbonate and silicate. Afterwards, all plant and mosses species found on the 1.521 vegetation plots can be checked for their disturbance indicating value in the forest type group assigned.

All plant species and mosses are checked for their cultivation or disturbance indicating value in forest type groups. According to Grabherr et al. [50], the probability of disturbance indication (SW) can be computed per species as

$$SW = N_{(dist.)} / N_{sum}$$

$N_{(dist.)}$  = Frequency of plant species being a disturbance indication in the forest group.

$N_{sum}$  = Frequency of plant species occurring in the forest group

Next to the value of disturbance indication, the frequency of a plant species occurring typically for the forest group was calculated. SW shows, how likely one plant species is indicating disturbance or cultivation in a forest type group. Species lists of disturbance indicating plants per forest type group can be found in Grabherr et al. [50].

A plant community disturbance index can be calculated by multiplying the disturbance probability with the ratio of the layer cover from all disturbance indicating plants to the whole layer cover of all plants. Extensive method description can be found in Grabherr et al. [50]. If  $BI_{tree\ species}$  on a sub plot was already rated below six points,  $BI_{vegetation}$  is rated with zero.

## 2.3. Surface soil quality ( $BI_{soil}$ )

The biodiversity indicator  $BI_{soil}$  assesses if the actual humus form on the AFI sub plot deviates from the expected one(s) according to forest typing [53]. Divergence from the expected humus form(s) is rated with zero, accordance is rated with nine points.

#### 2.4. Bonus indicator – Game ( $Bonus_{game}$ )

The bonus indicator  $Bonus_{game}$  rewards extensive game impact on forest regeneration for its beneficial effect on tree species diversity and rare tree species occurrence probabilities. Per tree species, the amount of browsed last year's terminal branches for plant heights from 10 - 130 cm is recorded in the AFI. Firstly, the browsing intensity is classified (0%, 1-50%, 51-90%, 91-100% terminal branches damaged). Secondly, average on the sub plot level is combined with the total number of tree species in an evaluation matrix to assess  $Bonus_{game}$  (Tab. S8).

**Table S8.** Rating of game impact. The valuation matrix for Bonus (game) combines average browsing intensity with the number of tree species affected by browsing on the sub plot level.

| Nr. of tree species affected | Mean browsing intensity on sub plot |       |        |       |
|------------------------------|-------------------------------------|-------|--------|-------|
|                              | 0%                                  | 1-50% | 51-90% | > 91% |
| 0                            | 9                                   | -     | -      | -     |
| 1                            | -                                   | 7     | 5      | 0     |
| 2                            | -                                   | 5     | 0      | 0     |
| 3                            | -                                   | 0     | 0      | 0     |
| 4                            | -                                   | 0     | 0      | 0     |
| 5                            | -                                   | 0     | 0      | 0     |

### 3. Genetic diversity indication

Genetic diversity indication with BCI considers three biodiversity indicators ( $BI$ ) and one bonus indicator ( $Bonus$ ). If at least two out of four (> 50%) indicators are rated, AFI sub plots are included in the BCI genetic diversity assessment. The indication of 100% is always adapted to the maximum amount of points possible under the current number of indicators at the AFI sub plot (100% = 27.0 points if *three genetic diversity indicators* could be rated with up to 9.0 points; or 100% = 18.0 points, if *two genetic diversity indicators* could be rated with up to 9.0 points).

$$genetic\ diversity\ indication = BI_{gap} + BI_{autochthony} + BI_{management} + Bonus_{genetic}$$

#### 3.1. Forest gap structure ( $BI_{gap}$ )

Forest fragmentation is serious threat to genetic diversity of inner-forest species [132-135]. To assess  $BI_{gap}$ , a square with side length 150 m (225,000 m<sup>2</sup>) is drawn around each AFI sub plot and overlaid with the TIRIS forest cover. Then, a surface balance between forest and non-forest area is computed in QGIS on the AFI plot level on 900,000 m<sup>2</sup>. Large forest gaps may limit the populations' capabilities to retain rare genetic information and enhance the risk of losing genetic variation and adaptive capacity through genetic drift processes [137-139]. Consequently, small gaps are rated favorable compared to large canopy openings, (Tab S9).

**Table S9.** Assessment of surface balance and rating of forest gaps.  $BI_{gap}$  ratings reflecting forest and non-forest area surface balance on the AFI plot level (90,000 m<sup>2</sup>).

| Forest cover | $BI_{gap}$ |
|--------------|------------|
| 0 – 20 %     | 0          |
| 24 – 40 %    | 2.25       |

|            |      |
|------------|------|
| 41 – 60 %  | 4.5  |
| 61 – 80 %  | 6.75 |
| 80 – 100 % | 9    |

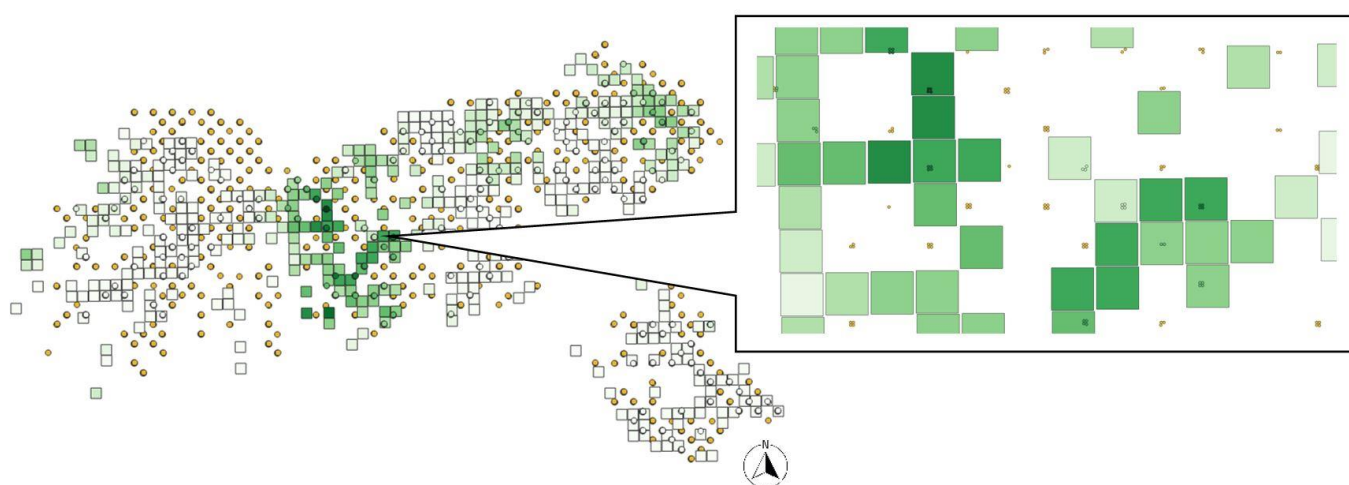
### 3.2. Autochthony ( $BI_{autochthony}$ )

Outcomes of AUPICMAP are used to assess autochthony of *Picea abies* populations of Tyrol. During the forest inventory period 2007-2009 genetic samples of all Norway spruce individuals in the Bitterlich samples have been taken and genotyped. As reference gene pools, unmanaged protective forests sampled in 2000-2002 were defined as being probably equivalent to the local autochthonous gene pool. The objective of BCI is to promote beta-diversity. Hence, the intraspecific genetic distance from haplotypes on AFI plots to the reference gene pool is calculated in the python-based simulation model 'Aupicmap.py' [52]. The sum of the genetic divergences between probably autochthonous (reference areas) and potentially allochthonous (AFI sub plots) haplotypes amounts between zero and one. The intraspecific haplotype distance is rescaled to relative values between 0 – 9.0 points.  $BI_{autochthony}$  can be calculated by averaging the genetic distances of all Norway spruce individuals on the AFI plot level.

$$BI_{autochthony} = \frac{\sum(rv_{autochthony})}{n_{spruce}},$$

with  $n_{spruce}$ , the number of spruce individuals on a plot.

The AUPICMAP results are uploaded in QGIS and merged with inventory data by affine data transformation, establishing a regular grid over Tyrol and blend it with AFI data. Next, squares without AFI data or Norway spruce are deleted (ESM Fig. S1).



**Figure S1.** Mapping autochthony of Norway spruce in Tyrol. Assessment of autochthony of Norway spruce on 440 AFI plots (green dots with squares) and AFI plots without evaluation (orange dots, no squares). Darker shades of green indicate higher probability of autochthony ( $BI_{autochthony}$ ).

### 3.3. Management constraints ( $BI_{management}$ )

Some of the major constraints for alpine harvesting and forest technology are inclination ( $m.constraint_{inclination}$ ) and distance to forest road systems ( $m.constraint_{distance}$ ).  $BI_{management}$  considers both site conditions to estimate probability of high forest management intensity. The underlying assumption is that intense forest management is less likely if management constraints and harvesting costs rise.

$$BI_{management} = m.constraint_{inclination} + m.constraint_{distance}$$

Firstly, inclination on AFI sub plots is classified (0 - 30%, 30 - 60%, 60 - 140%, > 140%) in QGIS. The classes reflect the harvesting technologies used most economical for a terrain [51]. The inclination is rated between 0 (no constraints) to 5 (very high constraints) points by  $m.constraint_{inclination}$  (Tab. S10).

**Table S10.** Rating of the management constraint inclination. Magement constraints caused by inclination are rated between zero (no constraints) and five (highest constraints) by  $m.constraint_{inclination}$ .

| Inclination [%] | Harvesting machines & technology     | $m.constraint_{inclination}$ |
|-----------------|--------------------------------------|------------------------------|
| 0 - 30          | Harvester, Forwarder, Lumber tractor | 0                            |
| 30 - 60         | Caterpillar Harvester, Cable Yarder  | 1.0                          |
| 60 - 140        | Cable Crane                          | 2.5                          |
| > 140           | Helicopter                           | 5.0                          |

Secondly, closest distance to forest roads is measured using the QGIS buffer function with 1000 m around the forest road network of TIRIS. The  $m.constraint_{distance}$  is assigned to the AFI sub plots in two cases:

1. For sites with < 35% inclination,  $m.constraint_{distance}$  is always set to zero, as these forest sites are exhaustive accessible with harvesting machines.
2. For sites with > 35% inclination,  $m.constraint_{distance}$  is rated with 1.0, if closest distance to road is  $\leq 1000$  m (= in reach of long-distance cable cranes) and with 4.0, if closest distance to road is > 1000 m (= out of reach of long-distance cable cranes).

### 3.4. Bonus indicator – Genetic features ( $Bonus_{genetic}$ )

$Bonus_{genetic}$  is calculated as the sum of three surrogates for high genetic diversity in forests:

$$Bonus_{genetic} = Bonus_{regeneration} + Bonus_{phenology} + Bonus_{gene\ flow}$$

### 3.5 Tree planting intensity ( $Bonus_{regeneration}$ )

Artificial transfer of genetic information e.g., using forest reproductive material, tends to degrade forest genetic structures [149]. Tree species, which are planted in high quantities, show a higher risk of showing a disturbed natural gene pool. With  $Bonus_{regeneration}$ , the probability of tree species to contain a native gene pool is evaluated.

The Tyrolean tree species share barely differs from the Austrian one apart from *Pinus cembra* which can be found regularly in high alpine areas of Tyrol but is considered a rare species in overall Austria [48]. We consider the 'Austrian Planting Statistics' which documents the forest reproductive material transfer on the national level from 2003 – 2011 for sixteen common forest tree species and an average value for rare broadleaved and coniferous admixed tree species.

Planting intensity per tree species is assessed by dividing tree species share in Tyrol by the number of young trees planted in average between 2003 – 2011 in Austria (Tab. S11). To transform planting intensities into relative values ( $rv_{planting\ intensity}$ ), seven classes with class width 0.5 are established.

**Table S11.** Rating of tree planting intensity. 'Planting intensity' per tree species is assessed by dividing species share in Tyrol with the number of trees planted in average between 2003 – 2011 in Austria. To transform calculated 'planting intensity' to  $rv$  (planting intensity), seven classes of planting intensity are established.



| Tree species            | Species share in Tyrol [%] | Nr. of trees planted yearly in Austria [100,000 pcs.] | Planting intensity (= species share/ Nr. of trees planted) | $rv_{planting\ intensity}$ |
|-------------------------|----------------------------|---|--|----------------------------|
| <i>Picea abies</i>      | 57.4                       | 218.387   | 0.26   | 0                          |
| <i>Larix decidua</i>    | 5.2                        | 53.628  | 0.10   | 0                          |
| <i>Fagus sylvatica</i>  | 11.9                       | 5.263   | 2.26   | 2.0                        |
| <i>Pinus sylvestris</i> | 4.8                        | 3.979   | 1.21   | 1.0                        |
| <i>Abies alba</i>       | 2.9                        | 10.572  | 0.25   | 0                          |
| <i>Pinus cembra</i>     | 3.0                        | 2.446   | 1.23   | 1.0                        |
| <i>Other species</i>    | 17.5                       | 5.326   | 3.29   | 3.0                        |

| Classes of planting intensity | $rv_{planting\ intensity}$ |
|-------------------------------|----------------------------|
| 0 – 0.5                       | 0                          |
| 0.5 – 1.0                     | 0.5                        |
| 1.0 – 1.5                     | 1.0                        |
| 1.5 – 2.0                     | 1.5                        |
| 2.0 – 2.5                     | 2.0                        |
| 2.5 – 3.0                     | 2.5                        |
| > 3                           | 3                          |

The indicator  $Bonus_{regeneration}$  is assessed by the weighted average of  $rv_{planting\ intensity}$  per tree species in the Bitterlich sample as:

$$Bonus_{regeneration} = \frac{\sum(rv_{planting\ intensity} * n_{trees})}{n_{trees}}$$

with  $n_{trees}$ , the number of trees represented.

Tree species with high species share [%] and low amount of reproductive material planted are showing highest bonus indicator ratings ( $Bonus_{regeneration} = 3.0$ ).

### 3.6. Spruce phenology ( $Bonus_{phenology}$ )

Crown types of spruce are varying naturally according to altitude, temperature, precipitation, and orientation [163]. Historically, spruce reproductive material was often planted without regarding site conditions. Hence, branching types of Norway spruce can be used as a proxy for detecting genetically allochthonous plant material.

During the AFI period 2000/2002, all *Picea abies* individuals in the Bitterlich sample were analyzed for branching architecture in comb, comb-brush, brush, brush-plate, and plate type [163]. Actually, no model predicting natural branching types reliably is available to compare field results with. As a proxy of a natural gene pool,  $Bonus_{phenology}$  evaluates if more than one branching type can be found on AFI sub plots with >1 Norway spruce individuals in the Bitterlich sample. A bonus of 3.0 is rewarded, if all Norway spruces display identical branching types.

### 3.7. Crown structure ( $Bonus_{gene\ flow}$ )

Low crown density is a surrogate for the enhanced long-distance gene flow and pollen densities in tree species (Tab. S12). Definitions of crown density classes can be found in Hauk & Schadauer [54].

**Table S12.** Rating of crown density. Crown density classes [54] rated with Bonus (gene flow).

| Crown density    | $Bonus_{gene\ flow}$ |
|------------------|----------------------|
| Sparse - Clotted | 3.00                 |

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|        |      |
|--------|------|
| Sparse | 2.25 |
| Casual | 1.50 |
| Closed | 0.75 |
| Dense  | 0    |

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All references can be found in the original manuscript.