



# The assembly of a plant network in alpine vegetation

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**The assembly of a plant network in alpine vegetation**

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Appendix S3 Methodological details of plant functional traits, soil analysis and spatial point-pattern analysis.

**Methods S1** Plant functional traits.

**Methods S2** Soil analysis.

**Methods S3** Spatial point-pattern analysis.

### **Methods S1** Soil analysis.

We measured the following plant traits for each individual plant (i.e., ramet for clonal plants): diameter, height, number of leaves, leaf mass per area. Plant diameter and height was measured for vegetative parts, excluding flowering stems, with 0.1 cm accuracy. Number of leaves was visually counted. Leaf mass per area was measured as the ratio between leaf dry weight and leaf area. Leaf dry weight was measured after drying a leaf at 80°C for 48h. Leaves were weighted with 0.01mg. Leaf area was measured scanning fresh leaves and measuring their surface (accuracy 16 mm<sup>2</sup>).

### **Methods S2** Soil analysis.

To quantify small-scale spatial heterogeneity in soil conditions, soil gravel content was measured in composite samples of three subsamples per 1 m<sup>2</sup> by sieving with a 2 mm mesh. From the same soil samples, we also determined gravimetric soil water content by mass loss after drying at 105°C for at least 72 h and the soil C:N ratio with a CHN analyzer (Leco TruSpec Micro CHN, Leco Corporation, St. Joseph, MI).

### **Methods S3** Spatial point-pattern analysis.

First, we carried out univariate analyses for each single species distribution. We created maps of species occurrence and covariate maps of environmental variables using plant functional traits and soil properties (Supporting Information Fig. S4). Local surface smoothing and ordinary kriging were used as interpolation methods across space. Then, we fitted three different null models of spatial distributions exploring which environmental variables underlie species distribution and assessing the spatial structure of species distribution, specifically whether species were clumped or not. These three null models were modelled using covariate maps (Fig. S4), stochastic processes resembling dispersal (Fig. S5) or combining both (see Supporting Information Methods S2 for more details). To

predict and simulate the distribution of each species the model with the best goodness-of-fit was selected as the null model of independence (Supporting Information Fig. S6, Table S3). This null model was then used for inference when testing spatial associations among species.

We employed the Ripley K function (Ripley, 1981; Wiegand & Moloney, 2014; Baddeley *et al.*, 2015) to test each species' spatial pattern against a complete spatial randomness model (CSR), also known as homogeneous Poisson process (HPP). The CSR model is defined by the intensity function  $\lambda$ , which is approximated as  $\lambda = n/A$ , where  $n$  is the number of points, i.e., the number of individuals of the same species, and  $A$  is the observational window. For a CSR model with intensity  $\lambda$ , the expected number of points within a circle of radius  $r$  around an arbitrary point  $i$  is equal to  $\lambda K(r)$ .

The empirical K function for a HPP is estimated as

$$\hat{K}(r) = \frac{1}{A} \sum_{i=1}^n \sum_{j \neq i} \frac{w_{ij}}{\lambda^2} I(d_{ij} \leq r)$$

where  $A$  is the area of the window,  $n$  is the number of points in the plot,  $w_{ij}$  is an edge correction factor (translation correction),  $I$  is the indicator function that equals 1 if the distance  $d$  between points  $i$  and  $j$  is less than or equal to the radius of the circle  $r$  and 0 elsewhere. Theoretical CSR model has constant intensity throughout the study area and assumes independent point distribution  $K(r) = \pi r^2$  (Illian *et al.*, 2008).

To test if each species distribution can be explained by this random model, we performed Monte Carlo tests based on simulation envelopes for the  $K(r)$  function (Baddeley *et al.*, 2015) for each  $r = 1$  cm along 75 cm (i.e., one fourth of the shortest side length of the plot, according with Shen *et al.* (2013)). The empirical  $\hat{K}(r)$  function of each species was compared with the theoretical envelope, built with 95% CI (i.e., the fifth lowest and the fifth highest simulated values of 199 simulations). All plant species significantly differed from a CSR model (Supporting Information Fig. S5).

Consequently, we fitted three different point pattern process models : i) Poisson cluster, ii) inhomogeneous Poisson, and iii) inhomogeneous Poisson cluster. Then, we evaluated which process best described the spatial pattern of each species.

### *Poisson cluster*

A Poisson cluster process (PC) generates non-independent (clustered) points in a two-step process. First, a homogeneous Poisson process (HPP) of “parent” points is generated with an intensity  $\rho$ . Then, each parent point  $i$  produces “offsprings”  $j$  according to a Poisson distribution. The locations of offsprings is independent and isotropically normally distributed around the parent point  $i$ , with mean 0 and standard deviation  $\delta$ . The theoretical  $K$  function for a PC is

$$K(r; \rho; \delta) = \pi r^2 + \frac{1 - e^{-\frac{r^2}{4\delta^2}}}{\rho}$$

The empirical  $K$  function is the same as for HPP.

Model fitting involves iteratively choosing the parameters  $\rho$  and  $\delta$  that minimise the discrepancy measure  $D(\theta)$ :

$$D(\theta) = \int_0^{r_0} w(r) [\{\widehat{K}(r)\}^c - \{K(r; \delta)\}^c]^2 dr$$

where  $r$  is the vector of  $r$  values at which the  $K$  function is estimated,  $\widehat{K}(r)$  and  $K(r; \delta)$  are the empirical and the theoretical  $K$  functions, respectively,  $r_0$  is the maximum radius  $r$  for which the  $K$  function has been computed, the weighting function  $w(r)$  and the constant  $c$  are used to control for sampling fluctuations in  $\widehat{K}(r)$ . According with Diggle (2003) we set  $w(r) = 1$  and  $c = 0.25$ .

### *Inhomogeneous Poisson*

An inhomogeneous Poisson process (IPP) shares with CSR the independence of points but in contrast to CSR its intensity  $\lambda$  is not constant. In IPP,  $\lambda$  varies from place to place in the study area according to an intensity function  $\lambda(u)$  assumed to be caused by environmental heterogeneity (Baddeley *et al.*, 2000; Wiegand *et al.*, 2007; Getzin *et al.*, 2008; Wiegand & Moloney, 2014). Hence, IPP is considered as a generalisation of a deterministic niche process.

The inhomogeneous  $K$  function is  $K_I(r) = \pi r^2$  (Baddeley *et al.*, 2000) and its estimate is:

$$\widehat{K}(r) = \frac{1}{A} \sum_{i=1}^n \sum_{j \neq i} \frac{w_{ij}}{\lambda(x_i)\lambda(x_j)} I(d_{ij} \leq r)$$

The intensity function  $\lambda$  of each species was estimated as a log-linear function of the measured environmental covariates using the *ppm* function of *spatstat* (Baddeley *et al.*, 2015). These spatial covariates were both biotic and abiotic ecological factors with a known role in species distribution (Lauber & Wagner, 1996; Silvertown, 2004; Shipley *et al.*, 2012; Fortunel *et al.*, 2016): soil gravel content, soil water content, soil C/N ratio, plant height, plant biomass (measured as the leaf dry mass [g] x number of leaves), distance [cm] to nearest *Dryas octopetala* patch (i.e., the ecosystem engineer of our study system), moss diameter (i.e., indicator of surface runoff), *Saxifraga aizoides* biomass (i.e., indicator of surface), *Anthyllis vulneraria* biomass (legume, indicator of rich soil nutrient content), *Oxytropis jacquini* biomass (legume, indicator of rich soil nutrient content). For producing covariate maps, soil gravel content, soil water content and soil C/N ratio maps were produced with ordinary kriging, while the other covariate maps were produced with kernel smoothing (Fig. S4). A stepwise-selected model procedure by AIC was carried out for the best log-linear model for each species.

#### *Inhomogeneous Poisson cluster*

An inhomogeneous Poisson cluster process (IPC) is an extension of the PC with, in addition, the distribution of points is assumed to be heterogeneous. The null expectation of the inhomogeneous  $K$  function of an IPC is:

$$K_I(r) = \pi r^2 + \frac{1 - e^{-\frac{r^2}{4\delta^2}}}{\rho}$$

The empirical  $\hat{K}(r)$  function is computed as for an inhomogeneous point pattern IPP. Model fitting involves iteratively choosing the parameters  $\theta$  that minimise the discrepancy measure  $D(\theta)$  but based on the inhomogeneous  $K$  function (Waagepetersen, 2007).

#### *Null model selection*

The overall fit of each process was evaluated with the goodness-of-fit  $u$  statistic (Diggle, 2003; Loosmore & Ford, 2006):

$$\nu = \int_{r=0}^{r_{max}} \{\hat{K}(r) - \bar{K}(r)\}^2 dr$$

where  $\hat{K}(r)$  is the estimation of Ripley's function  $K$  of each null model for each plant species,  $\bar{K}(r)$  is the mean of the theoretical  $K$  functions of each null model over the 199 simulated patterns,  $r$  is the range of spatial scales at which the functions are estimated (from 1–75cm with 1 cm steps). After adjusting and evaluating all the three models,

the null model with the smallest  $\nu$  was selected as the best null model to predict the distribution of each species (Supporting Information Fig. S7, Table S2).

All analyses were conducted in R 3.3.0 (R Core Team, 2017), using *spatstat* (Baddeley *et al.*, 2015) and *ecespa* (De la Cruz, 2008).

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