SILand: an R package for estimating the spatial influence of landscape

Author details

Florence Carpentier[1,2], Olivier Martin[3]

[1]UMR BIOGER, INRA, AgroParisTech, Université Paris-Saclay, 78850, Thiverval-Grignon, France

[2]MaIAGE, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France.

[3]BioSP, INRA, 84914, Avignon, France

Abstract

1. The spatial distributions of species and populations are both influenced by local variables and by characteristics of surrounding landscapes. Understanding how a landscape spatially structures the frequency of a trait in a population, the abundance of a species or the species' richness is difficult since it requires estimating the intensity and the spatial scale effects of the landscape variables.
2. Here, we present 'SILand', an R package for analysing georeferenced point observations associated with landscape characteristics described in a Geographic Information System shapefile format. By modelling the effect of landscape variables using spatial influence functions, 'SILand" simultaneously estimates the intensities and spatial scales of landscape variable effects. Different types of observations (continuous, discrete, proportion) are considered. Local, fixed and random effects are added.
3. 'SILand' allows for testing the significance of local and landscape variables effects and for estimating the significant influence area of a landscape variable to create maps of their effects and to compare models by computing the AIC criteria.

4. We illustrate the main steps of a landscape analysis with a case study about codling moth density in a landscape composed of organic and conventional orchards and vineyards to demonstrate the functionality of SILand.

Keywords : landscape, scale, Kernel smoothing

Introduction

Numerous studies demonstrate that the distribution of species richness and abundance depend on both local and landscape variables (for example, see García et al., 2011; Rusch et al., 2016; Remm et al., 2017). However, studying the relationships between landscape and species distributions remains challenging because the shape and the scale of landscape effects are unknown (Miguet et al., 2016) and can be missed if assessed at an incorrect scale (Smith et al., 2011). The studied data usually contains georeferenced observations at point sites, named response variables hereafter, and the description of several landscape spatial variables, named landscape variables hereafter. Their studies are often referred to as focal patch studies (Thornton et al., 2011). To identify the scale of landscape variable effects, the common approach consists of the following: (i) *a priori* defining a set of scales; (ii) creating summary variables by computing measures of the landscape variables within discs or rings of radii equal to each scale centred on the observation sites (named buffers hereafter); and (iii) applying a regression model to the response variable with the summary variables as the explanatory variables, for example, a linear model or a random forest algorithm (Bradter et al., 2012). For each landscape variable, the scale of effect is then considered to be the size of the buffer best explaining the response variable.

One of the main disadvantages of this classic method is that the number of explanatory variables artificially increases with the number of spatial scales considered. One then faces a complex statistical dilemma, which is dealing with numerous explanatory variables that by their construction are highly correlated. Consequently, the potential scales chosen are often too few and their ranges are too limited (Jackson & Fahrig, 2015). Finally, the effect of a landscape variable is modelled as uniform within

the buffer and as null outside it (Chandler & Hepinstall-Cymerman, 2016), which is unrealistic and biologically unjustified as a continuously decreasing effect is expected (Moilanen & Hanski, 2001). Several new methods based on distance weighting effects have been proposed to model a distance-decreasing effect (Aue et al., 2011; Henry et al., 2012; Serckx et al., 2016), but they explore a limited predefined set of spatial scales for predictors. Other methods quantified the scale of landscape effects without an *a priori* choice of spatial scales (Walsh & Webb, 2014; Chandler & Hepinstall-Cymerman, 2016). However, none of these methods are yet implemented in a ready-to-use software.

Here, we present "SILand", a package for the R statistical computing environment, which is designed to provide a generic tool to estimate landscape effects on a response variable. Using the framework proposed by Chandler & Hepinstall-Cymerman (2016), the main functions of SILand allow the user (i) to estimate the intensity of local and landscape effects and the parameters of the Spatial Influence Function (SIF), thus describing the scale effect of each landscape variable, (ii) to test these effects and (iii) to compare models. Several types of response variables (continuous, discrete, proportion) are handled within the SILand package. The effects of local variables can be treated as fixed or random. In addition, the package allows for plotting landscape effects on maps. We exemplified the package's use by analysing the landscape effects of conventional and organic orchards on the density of codling moth larvae per apple tree.

Model and method

The R package SILand estimates local and landscape effects based on the framework proposed by Chandler & Hepinstall-Cymerman (2016). The response variable is measured at n different sites denoted Y_i (i stands for a site). The L local variables can be continuous or discrete and are denoted as x_i^l (l stands for a local variable and i for a site). The spatial distribution over the entire study area of each of the K landscape variables is rasterized, *i.e.,* represented by pixels in a regular grid, named R_k. The landscape variables can have continuous or discrete values. Each landscape variable is denoted

as z_r^k (k stands for a landscape variable and r for a pixel). For instance, if the landscape variable k is a presence/absence variable, z_r^k will be equal to one or zero.

The SILand model is based on the generalized linear model framework. The expected value of the response variable Y_i is modelled as follows :

$$\mu_i = \mu + \sum_{l \in L} \alpha_l x_i^l + \sum_{k \in K} \beta_k \sum_{r \in R, r \neq i} f_{\delta_k}(d_{i,r})\, z_r^k$$

where μ is the intercept, and α_l and β_k are the parameters respectively associated with the local and landscape variables. $f_{\delta k}(.)$ is the **SIF** associated with the landscape variable k and $d_{i,r}$ is the distance between the centre of pixel r and the observation site i. The SIF is a density function decreasing with the distance. The influence scale of the landscape variable k is calibrated through the parameter δ_k. Two families of SIF are currently implemented in the SILand package, the exponential and Gaussian families. They are respectively defined as $f_\delta(d)=2/(\pi\delta^2)exp(-2d/\delta)$ and $f_\delta(d)=1/(2\delta\sqrt{\pi})exp(-d\pi/2\delta)^2$ (Austerlitz et al., 2004). Notice that δ is equal to the mean distance of f_δ (when f_δ is considered as a probability density function).

The effect of a landscape variable k is then modelled by an intensity parameter β_k describing the strength and direction of this effect and by a scale parameter δ_k, describing how this effect declines with distance. In this model, each pixel where the landscape variable is present, potentially has an effect on the response variable at any observation site. The scale of the effects is only determined during the estimation. All parameters (associated with landscape and local variables) are estimated simultaneously by maximum likelihood estimation by using an iterative procedure based on the conditional linearity of the model to the scale parameters $\{\delta_1,..,\delta_K\}$.

The package can handle a large variety of models, so different types of response variables can be considered. For continuous, counting or presence-absence data, Gaussian, Poisson and Binomial distributions are implemented. Local effects can be modelled as fixed or random (considering repeated measurements, for instance).

Package description

The SILand package is written entirely in the scientific computing language R (R Core Team, 2019). It is available on https://github.com/silandpackage/siland and on CRAN (https://cran.r-project.org/web/packages/SILand/index.html) and can be installed via a standard procedure.

Case study

We illustrate the abilities of SILand on an example previously described and analysed in Ricci et al. (2009) : the study of codling moth densities, an insect pest specialized on apple orchards in the Basse Durance Valley in southeastern France. The data are decomposed into two datasets. The first contains the mean number of codling moth overwinter larvae by tree in a total of 54 orchards observed in 2006 over a 70-km² area, and the second dataset contains the landscape variable maps in this area.

Importing data

The datasets and the associated R script are available on https://github.com/silandpackage/siland in the Materials_MEE directory. Here, we described the general procedure to import datasets from GIS (Geographic Information System) files coded in the shapefile format. Notice that the datasets can be directly extracted from the package using the commands `data(dataCmoth)` and `data(landCmoth)`.

The observations of the response variable and eventually the local variables can be extracted with the `data.gis( )` function:

```
dataCmoth=data.gis(dsn="./GIS",layer="dataCarpo",varname=c("Cmoth","trait"))
```

The argument `dsn` is the name of the folder containing the files describing the response and local variables (here named `GIS and` located in the working directory), `layer` is the name of the shapefile without filename extensions (in the `GIS` folder, there are 3 files describing the response variable: `dataCarpo.shp`, `dataCarpo.dbx` and `dataCarpo.shx`), and `varname` refers to the variable names

in the attribute file (dataCarpo.dbf). The observations of the response variable are described as points. Local variables can be described as points at the locations of the response observations or as polygons over the landscape. dataCmoth is a dataframe with a number of rows equal to the number of observations. Its two first columns are named X and Y and contain the observation locations. The third column is Cmoth, which is the mean number of codling moths in the orchards, and represents the response variable of the study. The following column is trait, which is a local variable describing the number of insecticide treatments applied in the orchard.

Landscape observations can be extracted via the land.gis( ) function:

```
landCmoth1=land.gis(dsn="./GIS",layer="landCarpo",varname="OrgConv",landname =
c("conv","org"),wd=40)
```

where dsn is the name of the folder containing the files describing the landscape, layer is the name of the shapefiles without filename extensions, and varname is the name used in the layer.dbf file to describe the landscape features (only one column can be specified). The landname argument is a vector containing the names of the landscape variables of interest (in landCarpo.dbf, the OrgConv column owned two values of org and conv). The variable varname can be described as polygons, segments or points. The land.gis() function returns a list of dataframes describing each landscape variable along a regular grid of mesh wd wide. Notably, landscape data can be easily extracted from two different columns of the layer.dbf or from two different GIS files with the function land.gis() by combining the two objects as shown below:

```
landCmoth2=land.gis(dsn="./GIS",layer="landCarpo",varname="Vine",landname="vine"
, wd=40)
landCmoth=c(landCmoth1,landCmoth2)
```

We thus obtained landCmoth, a list of 3 dataframes corresponding to the distributions of 3 landscape variables: organic, describing the organic apple orchards, conventional, describing the conventional variables (see Figure 1) and vine, the vineyards.

Fitting models with local and landscape variables

Model estimation is performed with the function `siland()`.

```
>res3G=siland(loc.model= Cmoth~trait, land=landCmoth, data=dataCmoth,
sif="gaussian",test=T, family="gaussian")
```

The argument `loc.model` specifies the local variables. The syntax of the formula `"y ~ model"` is similar as in `the lm()` and `glm()` functions of the `stat` package. In this example, the response variable is `Cmoth` and the local explanatory variable is `trait`. The argument `land` specifies the landscape variables and is a list of dataframes describing each landscape variable (here `conventional, organic and vine`). The argument `test` indicates whether tests for parameters are computed (notice that these likelihood ratio tests can be time consuming if numerous landscape variables are considered). Finally, the argument family gives the assumed distribution of the response variable (here it is `Gaussian`, as `Cmoth` is a continuous variable). In this model, the mean number of codling moths per tree in an orchard is explained by the number of insecticide treatments sprayed in this orchard (local fixed effect) and the spatial influences of organic orchards, conventional orchards and vineyards in the landscape (landscape effects).

The estimated parameters and tests are printed with the function `summary()`.

```
 > summary(res3G)
Coefficients:(Intercept)trait conventional
organic vine SIF.conventional SIF.organic SIF.vine
11.93915 -0.14763 -51.72189 92.55240 -10.43483 1323.21699
150.40262 1721.81616

pvalue (L.R. Test):
        trait conventional      organic         vine
     3.74e-01     1.04e-01     6.15e-09     9.90e-01
```

```
AIC: 327.39    AIC (no landscape): 364.79
(No landscape effect) p-value: 6.211436e-09
```

The effect of the local variable trait on `Cmoth` is not significant (p-value at 3.74e-01) and is negative (estimated at -0.15). Globally, the landscape variable effects are significant, according to the likelihood ratio test testing the complete model vs the model and including only the local variable (p-value at 6e-9 on the "`No landscape effect`" line). The effect of the landscape variable `conventional` (presence of conventional orchard) is slightly significant (p-value= 1.04e-01) and negative (about -51.7). The spatial influence parameter of its SIF is estimated at 1323 m. The effect of the landscape variable `organic` (presence of organic orchard) is significant (p-value=6.15e-09) and positive (approximately 92.5). The spatial influence parameter of its SIF is estimated to be shorter at 150.4 m. The effect of the landscape variable `vine` (presence of vineyards) is not significant (p-value=0.99). We then analyse `res2G` like `res3G` without the third landscape variable `vine`:

```
 >res2G=siland(loc.model=Cmoth~trait,land=landCmoth[c(1,2)],data=dataCmoth,
sif="gaussian",initSIF=c(100,100),test=T, family="gaussian")
> summary(res2G)
Coefficients:
(Intercept) trait  conventional organic SIF.conventional      SIF.organic
11.25      -0.15      -48.85     93.13  1322.14              150.59
pvalue (L.R. Test):
        trait conventional      organic
     3.45e-01     4.99e-04     3.52e-09

AIC: 323.41    AIC (no landscape): 364.79
(No landscape effect) p-value: 4.872222e-10
```

We obtain similar results to `res3G` except for the variable `conventional`, whose spatial effect

becomes more significant (p-value=4.99e-04)

Random effects and a generalized linear model can be evaluated using a syntax similar to the lme4 package. The dataSiland (`data(dataSiland)`) and landSiland (`data(landSiland)`) datasets are available in the package and contain data obtained by simulations (see `help(dataSiland)` and `help(landSiland)` for more information). The example below illustrates how to analyse discrete and repeated measurements using a Poisson model (`family="poisson"`) and a random individual effect (`+(1|Id)`, with `Id` the variable describing individuals).

```
>siland(loc.model= y~varloc+(1|Id), land=landSiland, data=dataSiland,
sif="exponential”,  initSIF=c(100,100), test=T, family="poisson")
```

Interpreting spatial influence functions (SIF)

Different functions' families for the SIF can then be chosen. `res2` is similar to `res2G`, except that the exponential family was chosen instead of the Gaussian one :

```
res2=siland(loc.model= Cmoth~trait, land=landCmoth[c(1,2)],
data=dataCmoth, sif="exponential",initSIF=c(100,100), test=T,
family="gaussian")

 > summary(res2)
Coefficients:
(Intercept)    trait   conventional organic SIF.conventional     SIF.organic
11.08      -0.11       -50.76     86.99            1586.88      184.92

pvalue (L.R. Test):
        trait conventional      organic
     5.05e-01     1.82e-03     2.08e-07
```

```
AIC: 331.28    AIC (no landscape): 364.79
(No landscape effect) p-value: 2.113485e-08
```

For both the Gaussian and the exponential family the parameter δ estimated is the mean distance of the SIF. The larger the parameter δ is, the broader is the spatial effect of the landscape parameter.

The SIF shapes differ according to the chosen function family (see Figures 2). To determine the optimal shape, the AIC can be used. Here, the AIC of the exponential SIF model is 331.28 whereas the Gaussian SIF model AIC is 323.41. Thus, in our case study the Gaussian model is more adapted.

We propose a new indices that is easy to interpret and summarizes both the SIF shape and mean distance. We define the **area of significant influence** of a landscape variable as the disc containing 95% of the influence of its SIF (neglecting 5% of its broader effect). This can be computed with:

```
>siland.quantile(res2G,c(0.5,0.95))
                   0.5      0.95
SIF.conventional 1241.46 2581.68
SIF.organic       141.40 294.05
```

The median (0.5 quantile) and the 0.95 quantile of the conventional orchard SIF are respectively estimated at 1241 m and 2581 m. This means that half of the influence of the conventional orchard is located within a radius of 1241 m and that the area of significant influence has a radius of 2581 m. The spatial influence of organic orchards is more limited as its quantiles are approximately 9 times shorter. The estimated SIF can be graphically represented using the command `plotsiland.sif(res2G)` (see Figure 2).

Graphical representations

The function `plotsiland()` visualizes the spatial distribution of landscape variables and the location of observed data and also compares the estimated scales of the landscape variables' effects (see Figure 1).

```
> plotsiland(res2G,landCmoth[c(1,2)],dataCmoth)
```

The `plotsiland.land()` function maps the predicted effects of the landscape. If `var` is equal to *k*, the effect of the *k*th landscape variable is plotted. Otherwise, if the argument `var` is set to 0, the global effect of the landscape (summing the effects of all landscape variables) is plotted. Figures 3, 4 and 5 represent the maps obtained for `var` equal to 1, 2 and 0, respectively.

```
> plotsiland.land(res2G,land=landCmoth[c(1,2)],data=dataCmoth,var=1)
```

Choice of the mesh

In the SILand package, the computation of the spatial influence of landscape variables is based on an approximation through the description of landscape variables distribution along a regular grid (a raster). The choice of the mesh of this grid can have an impact on the estimation. The finer the grid mesh is, the more accurate the approximation is, but the computation time is also longer. Here, we present two examples with a mesh grid of 200 metres (`res2Gw200`) and 20 metres (`res2Gw20`) instead of the 40 m wide mesh of the previous analysis.

```
 > summary(res2Gw200)
Coefficients:
      (Intercept)  trait conventional organic SIF.conventional SIF.organic
      3.81  0.35  -16.79 102.38      526.27      871.03

AIC: 357.43    AIC (no landscape): 364.79
(No landscape effect) p-value: 0.00400627

 > summary(res2Gw20)
Coefficients:
      (Intercept)            trait     conventional organic
```

```
SIF.conventional      SIF.organic
  11.00      -0.12       -48.99  93.84  1327.21       162.43

AIC: 331.09    AIC (no landscape): 364.79
(No landscape effect) p-value: 1.922918e-08
```

With the large 200 m. mesh, the results highly differ from those previous obtained in res2G, even for the effect of the local variable (trait). For instance, the conventional SIF mean parameter is estimated at 526 m instead of 1322 m. Conversely, the estimation remains stable when the size of the mesh becomes finer from 40 m to 20 m. In our experience, we recommend using a mesh size at least three times smaller than the smallest estimated average distance among the landscape variables SIF. In `res2Gw200`, this recommendation is not satisfied (200>526/3); thus, the mesh size is too wide to permit a reliable estimation.

Conclusion

We demonstrate how the R package SILand can be used for the following: (i) quickly import GIS files in R; (ii) infer easily and directly the spatial influence of landscape variables based on the framework proposed by Chandler et al. (2016); (iii) test different effects and compare SIF shapes; (iv) give the area of significant influence of each landscape variable; and (v) plot the estimated SIF and map the predicted effects of the landscape. SILand is the first user-friendly tool that permits a complete and complex analysis of landscape effects, using few functions based on a “classic” syntax similar to well-known packages (such as stat and lme4). Moreover, as the spatial influence is modelled from the landscape variables and not from the observation locations, the estimated indices can be more easily interpreted in another landscape distribution. For instance, the estimated SIF can be used to produce predictions of landscape effects in other landscape geometries and areas of significant influence can drive management rules. We recommend to carefully check whether the chosen scale for the discretization of the landscape variables is fine enough to permit a consistent

estimation. This technical challenge will be overcome in future versions of the SILand package (with an exact computation of the effect integration over the landscape).

Authors' contributions

F.C. and O.M. conceived the ideas and designed methodology, programmed the r package. All authors contributed critically and equally to the drafts and gave final approval for publication.

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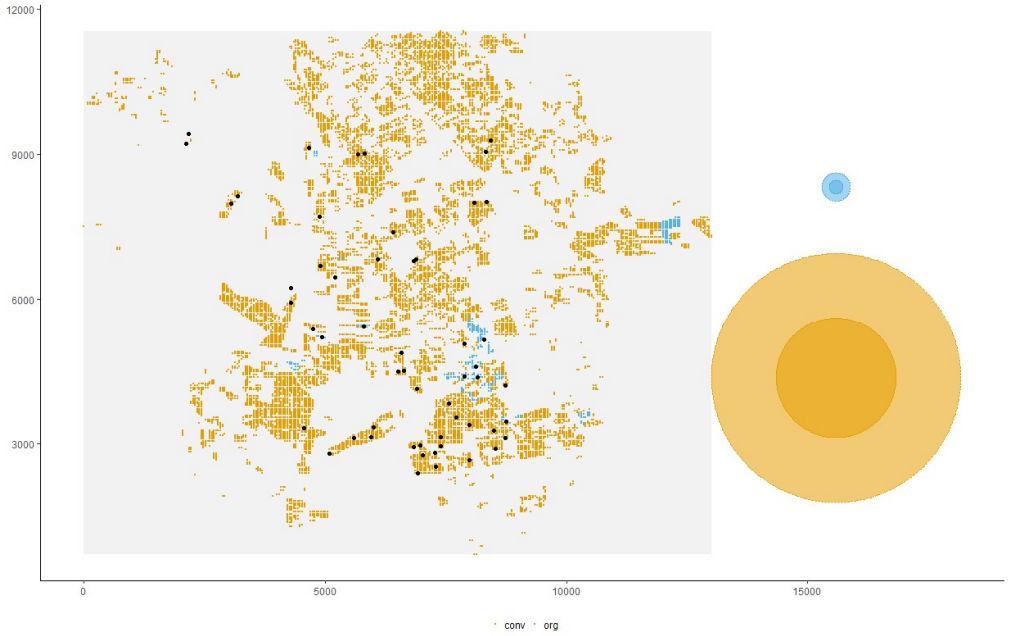

Figure 1: Plot of the data and SIF estimations

The black points represent locations of response variable observations. The yellow squares are the pixels where conventional orchards are present. The blue squares represent the pixels where organic orchards are present. At the margins of the plot, the light and dark discs represent the median distance estimated and the **area of significant influence**, respectively, blue and yellow colors represent conventional and the organic orchards, respectively.

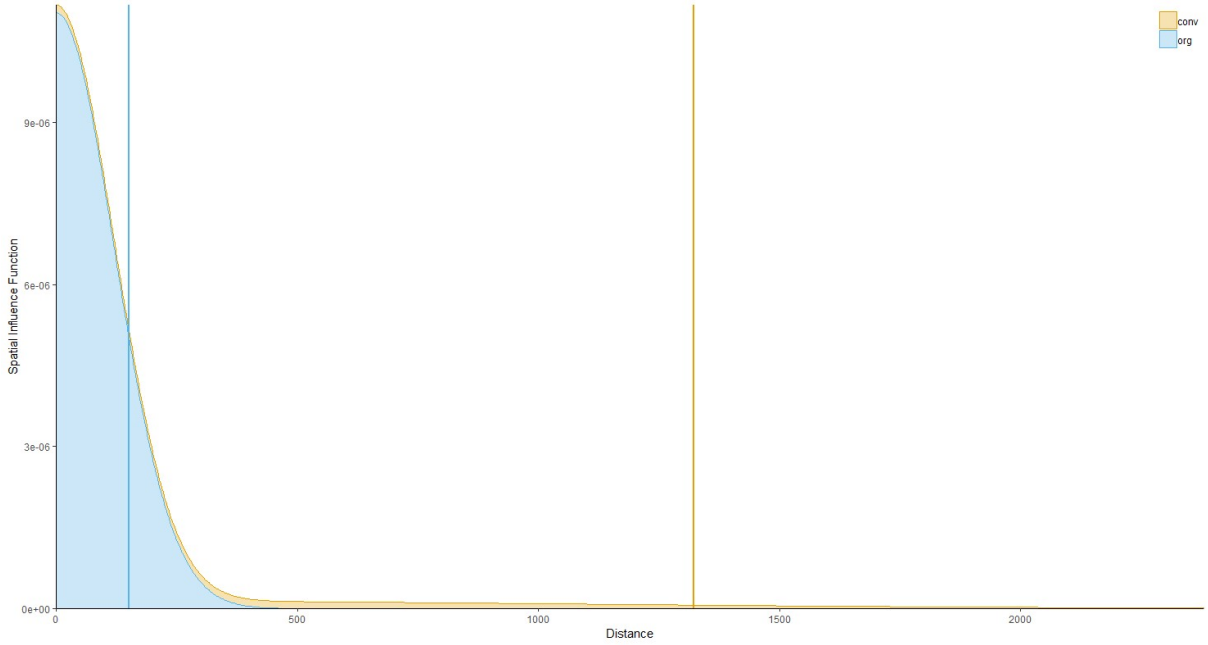

Figure 2: Estimated Spatial Influence Function (SIF) for the conventional and organic orchards landscape variable. The blue and orange lines represent the estimated SIF for the organic and conventional orchards, respectively. The vertical lines represent the SIF mean distance.

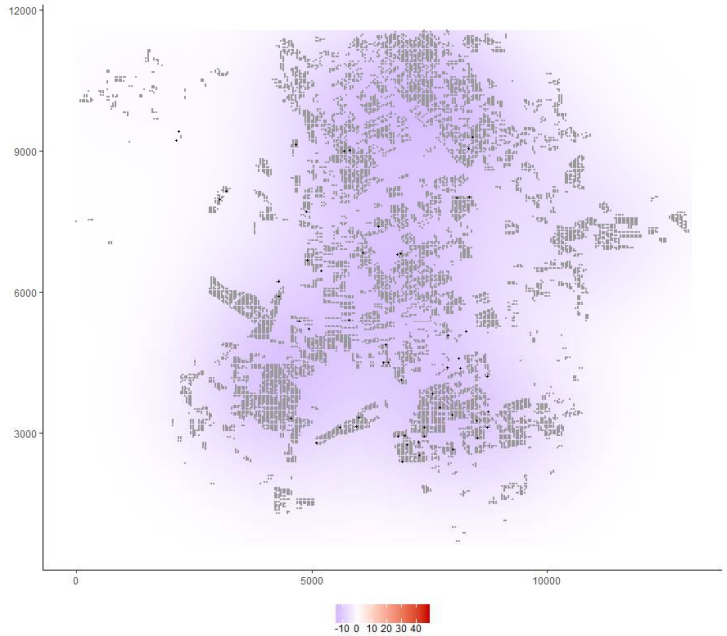

Figure 3: Map of the predicted effect of conventional orchards.

The black points represent locations of response variable observations, i.e., the mean density of codling moth by tree. The gray points are the pixels where conventional orchards are present. The response surface represents the cumulative effect for the conventional landscape variable. At the bottom margin, the bar color gives the scale of the effect. In this example, conventional variable has a negative effect.

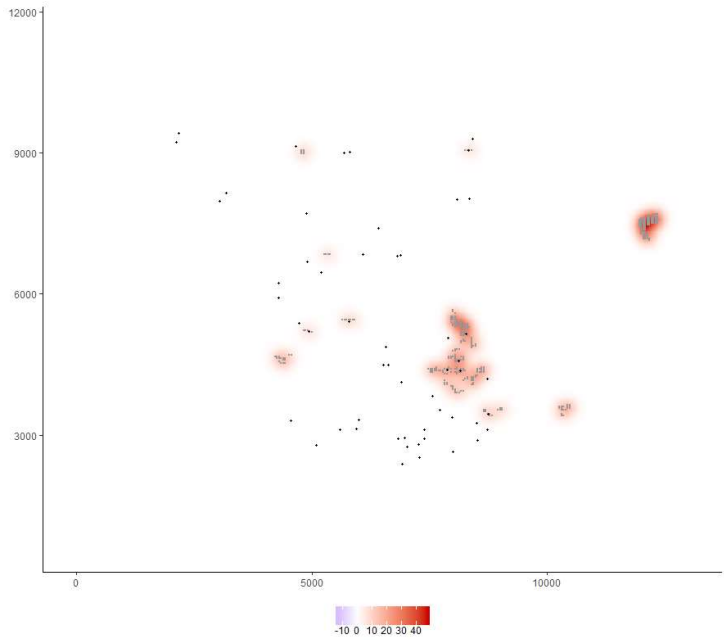

Figure 4: Map of the predicted effect of organic orchards

The black points represent locations of response variable observations. The gray points are the pixels where conventional orchards are present. The response surface represents the cumulative effect for the organic landscape variable. At the bottom margin, the bar color gives the scale of the effect. Here organic variable has a positive effect.

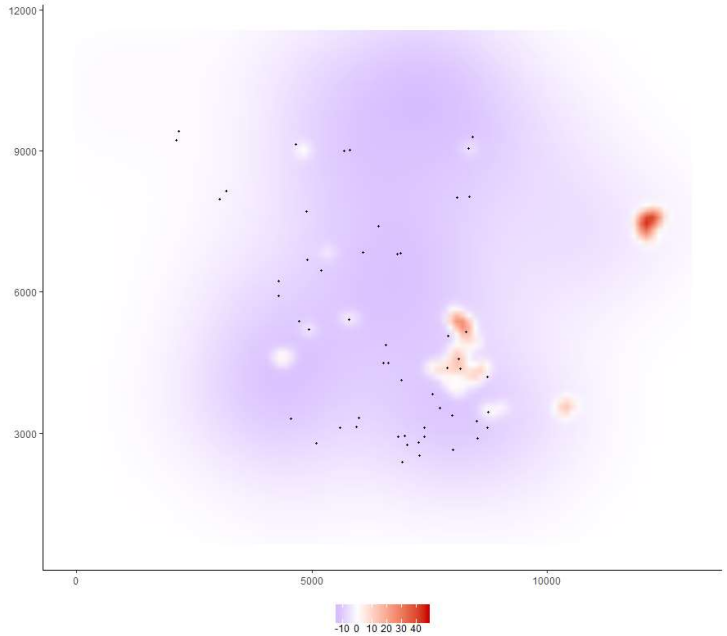

Figure 5: Map of the predicted global effects of the landscape

The black points represent locations of response variable observations. The response surface represents the cumulative effect for all landscape variables. At the bottom margin, the bar color gives the scale for cumulative effects.