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APPLICATION



NLMR and landscapetools: An integrated environment for simulating and modifying neutral landscape models in R

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rOpenSci Resources

The software package NLMR and landscapetools developed as part of this research effort, was extensively reviewed and approved by the rOpenSci project (https://ropensci.org). A full record of the review is available at Link to package on rOpenSci: https://github.com/ropensci/NLMR and https://github.com/ropensci/landscapetools

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Abstract

- 1. Neutral landscape models (NLMs) simulate landscape patterns based on theoretical distributions and can be used to systematically study the effect of landscape structure on ecological processes. NLMs are commonly used in landscape ecology to enhance the findings of field studies as well as in simulation studies to provide an underlying landscape. However, their creation so far has been limited to software that is platform dependent, does not allow a reproducible workflow or is not embedded in R, the prevailing programming language used by ecologists.
- 2. Here, we present two complementary R packages NLMR and landscapetools, that allow users to generate and manipulate NLMs in a single environment. They grant the simulation of the widest collection of NLMs found in any single piece of software thus far while allowing for easy manipulation in a self-contained and reproducible workflow. The combination of both packages should stimulate a wider usage of NLMs in ecology. NLMR is a comprehensive collection of algorithms with which to simulate NLMs. landscapetools provides a utility toolbox which facilitates an easy workflow with simulated neutral landscapes and other raster data.
- 3. We show two example applications that illustrate potential use cases for NLMR and landscapetools: First, an agent-based simulation study in which the effect of spatial structure on disease persistence was studied. The second example shows how increases in spatial scaling can introduce biases in calculated landscape metrics.
- 4. Simplifying the workflow around generating and handling NLMs should encourage an uptake in the usage of NLMs. NLMR and landscapetools are both generic frameworks that can be used in a variety of applications and are a further step to having a unified simulation environment in R for answering spatial research questions.

KEYWORDS

artificial landscape, landscape generator, spatial patterns, spatial visualisation, virtual landscape

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1 | INTRODUCTION

Neutral landscape models (NLMs) are algorithms which generate landscape patterns in the absence of biotic and abiotic processes (Caswell, 1976; Gardner, Milne, Turnei, & O'Neill, 1987; Li et al., 2004). These models were originally developed as null models to test landscape-scale hypotheses (Gardner & Urban, 2007; With & King, 1997). NLMs are now used in a variety of ways to examine landscape-scale observations and metrics of ecological patterns and processes (With & King, 1997; Turner, Gardner, & O'Neill, 2001). With and King (1997) outlined three uses for NLMs which were further highlighted by Turner and Gardner (2015): (a) coupling ecological models with NLMs to predict changes in ecological processes, (b) analyse the extent of structural deviation between real and neutral landscapes, and (c) development and testing of novel landscape metrics. The large number of applications and their increased uptake has led to the development of a variety of software designed to generate NLMs, using a range of algorithms. Options include standalone software such as RULE (Gardner, 1999), its successor QRULE (Gardner & Urban, 2007) and SIMMAP (Saura & Martínez-Millán, 2000), as well as LG (van Strien, Slager, de Vries, & Grêt-Regamey, 2016). However, arguably the most useful pieces of software are those that offer a collection of different NLM algorithms based in an open-source programming language which allow for reproducible and consistent workflow. Packages developed for common programming languages, such as NLMpy (Etherington, Holland, & O'Sullivan, 2015) for PYTHON, fulfill these criteria. However, currently there is no NLM software package available for R, the programming language most widely used by ecologists (R Core Team, 2017). Examining 150 recent articles in Methods in Ecology and Evolution, we found a clear trend in the community towards R with 106 publications utilising R (see Supporting Information, Figure S1). The lack of a flexible framework in R may limit the overall use of NLMs. We have, therefore, developed two complementary R packages, NLMR and landscapetools, to allow for the easy simulation and manipulation of NLMs and other rasters. These packages are the first to provide a large range of NLM algorithms, along with tools to manipulate them, embedded in a reproducible framework in the $\ensuremath{\mathbb{R}}$ environment. This utility allows for the easier generation and handling of NLMs, while also allowing for these simulations to be tied into the extensive body of geospatial libraries native to R.

Both packages will allow a growing group of scientific R users to make use of NLMs in their research while permitting a streamlined workflow contained in the R environment. Furthermore, the integration of major geographical information system libraries (such as GDAL and GEOS) in R embed our packages in a framework that allows analyses and simulations to be done in R without relying on proprietary software.

2 | FUNCTIONALITY

NLMR and landscapetools both build on the established geospatial environments in R, e.g. the raster (Hijmans, 2017) and sf packages (Pebesma, 2018). The nomenclature of all our functions was designed to facilitate a reproducible workflow while being distinct from the naming conventions of other geospatial packages, thus avoiding namespace conflicts with other functions and packages.

2.1 | NLMR

The NLMR package is a generic numeric framework to generate NLMs using the widest collection of algorithms found in any single piece of software, while also enabling different NLM algorithms to be combined and integrated. Functions in NLMR (Table 1) simulate two-dimensional raster objects. By default, no spatial reference system is applied but can be incorporated, allowing NLMs to be projected to the spatial extent of any study area. Algorithms differ from each other in terms of how spatial autocorrelation is controlled. Some algorithms have no control over spatial autocorrelation ranging from no autocorrelation (i.e. random) to a constant gradient (i.e. planar gradients). Other algorithms allow the user to control the level of spatial autocorrelation through one (nlm_mpd) or many (nlm_gaussian) parameters (Figure 1).

The basic syntax used to simulate an NLM is as follows: nlm _ modeltype(ncol, nrow, resolution, ...)

Raster objects returned from NLMR can readily be transformed and visualised by landscapetools or incorporated into spatially-explicit analyses or simulations.

TABLE 1 List of implemented neutral landscape models in NLMR with a specification of the model and the associated literature for more information

Function	Model specification	Cross- reference	Reference
nlm_curds	Simulates a randomly curdled or wheyed neutral landscape model. Random curdling recursively subdivides the landscape into blocks. At each level of the recursion, a fraction of these blocks is declared as habitat while the remaining stays matrix. When option q is set, it simulates a wheyed curdling model, where previously selected cells that were declared matrix during recursion, can now contain a proportion of habitat cells	Figure 1a,p	O'Neill, Gardner, and Turner (1992); Keitt (2000)

TABLE 1 (Continued)

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Function	Model specification	Cross- reference	Reference
nlm _ distance gradient	Simulates a distance gradient neutral landscape model. The gradient is always measured from a rectangle that one has to specify in the function (parameter <i>origin</i>)	Figure 1b	Etherington et al. (2015)
nlm _edge gradient	Simulates a linear gradient orientated neutral model. The gradient has a specified or random direction that has a central peak, which runs perpendicular to the gradient direction	Figure 1c	Travis and Dytham (2004)
nlm _fbm	Simulates neutral landscapes using fractional Brownian motion (fBm). fBm is an extension of Brownian motion in which the amount of spatial autocorrelation between steps is controlled by the Hurst coefficient H	Figure 1d	Travis and Dytham (2004); Schlather et al. (2015)
nlm_gaussian field	Simulates a spatially correlated random fields (Gaussian random fields) model, where one can control the distance and magnitude of spatial autocorrelation	Figure 1e	Schlather et al. (2015)
nlm _ mosaic field	Simulates a mosaic random field neutral landscape model. The algorithm imitates fault lines by repeatedly bisecting the landscape and lowering the values of cells in one half and increasing the values in the other half. If one sets the parameter <i>infinit</i> to TRUE, the algorithm approaches a fractal pattern	Figure 1f	Schlather et al. (2015)
nlm _ neigh	Simulates a neutral landscape model with land cover classes and clustering based on neighbourhood characteristics. The cluster are based on the surrounding cells. If there is a neighbouring cell of the current value/type, the target cell will more likely turned into a cell of that type/value	Figure 1g	Schlather et al. (2015)
nlm _ percolation	Simulates a binary neutral landscape model based on percolation theory. The probability for a cell to be assigned habitat is drawn from a uniform distribution	Figure 1h	Gardner, O'Neill, Turner, and Dale (1989)
nlm _ planar gradient	Simulates a planar gradient neutral landscape model. The gradient is sloping in a specified or (by default) random direction between 0 and 360 degree	Figure 1i	Palmer (1992)
nlm _ mosaictess	Simulates a patchy mosaic neutral landscape model based on the tessellation of a random point process. The algorithm randomly places points (parameter <i>germs</i>) in the landscape, which are used as the centroid points for a voronoi tessella- tion. A higher number of points therefore leads to a more fragmented landscape	Figure 1k	Gaucherel (2008), Method 1
nlm_mosaic gibbs	Simulates a patchy mosaic neutral landscape model based on the tessellation of an inhibition point process. This inhibition point process starts with a given number of points and uses a minimisation approach to fit a point pattern with a given interaction parameter (0 - hardcore process; 1 - Poisson process) and interaction radius (distance of points/germs being apart)	Figure 1j	Gaucherel (2008), Method 2
nlm _ random	Simulates a spatially random neutral landscape model. The values are drawn a uniform distribution	Figure 1I	With and Crist (1995)
nlm _ random cluster	Simulates a random cluster nearest-neighbour neutral landscape. The parameter ai controls for the number and abundance of land cover classes and p controls for proportion of elements randomly selected to form clusters	Figure 1m	Saura and Martínez-Millán (2000)
nlm _ mpd	Simulates a midpoint displacement neutral landscape model where the parameter <i>roughness</i> controls the level of spatial autocorrelation	Figure 1n	Peitgen and Saupe (1988)
nlm_random rectangular cluster	Simulates a random rectangular cluster neutral landscape model. The algorithm randomly distributes overlapping rectangles until the landscape is filled	Figure 1o	Gustafson and Parker (1992)

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2.2 | landscapetools

The package landscapetools contains a set of utility functions to complete tasks involved in most landscape manipulations and presentation (Figure 2). This includes visualisation, (re-) classification and merging methods, thus providing a workflow to apply NLM algorithms in a broad range of different contexts.

All functions in landscapetools require raster objects as inputs.

The functions util _ classify and util _ binarise (re-) classify raster data into proportions based upon given weightings. util _ classify allows users to factorially encode (classify) landscape data in raster objects, for example, to label different land-use types. util _ binarise returns landscapes with a

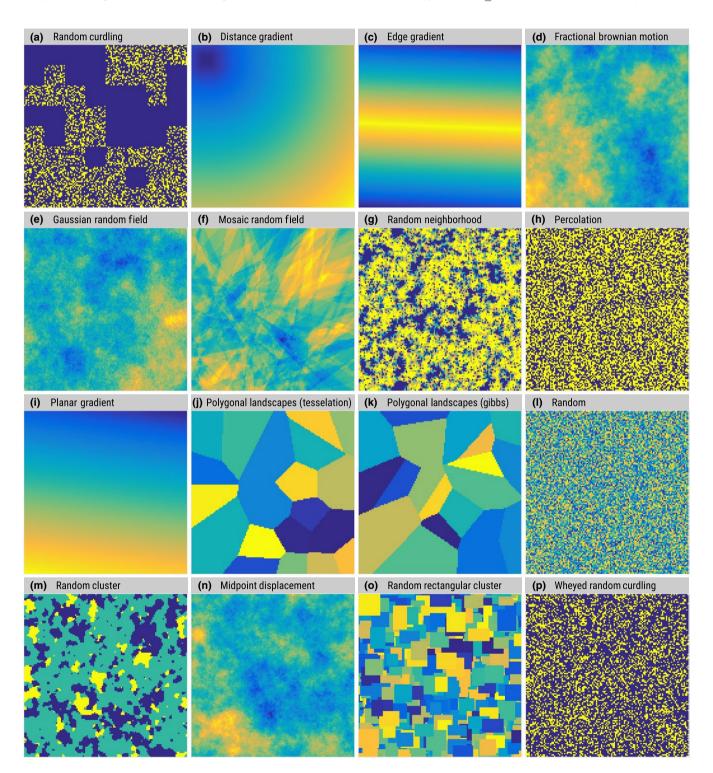


FIGURE 1 Collection of all neutral landscape models (NLM) implemented in the NLMR package (Table 1). See Data accessibility for R code to create each of the NLMs

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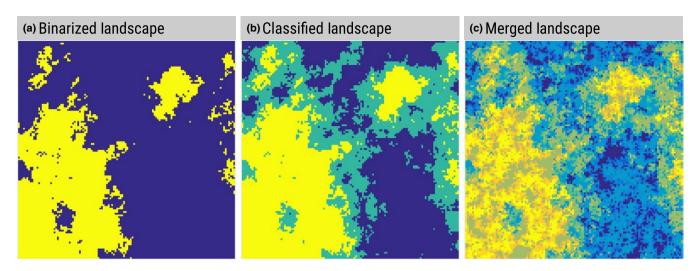


FIGURE 2 Visualisation of the main functionality of landscapetools with an underlying fractional Brownian motion neutral landscape model ($nlm_fbm()$, Figure 1d). (a) shows the util_binarise() function, that classifies landscapes into habitat and matrix (here, the parameter breaks was set to 0.31415). (b) is the same landscape classified (util_classify()) into three landscape categories with equal proportions (parameter weightings = c(0.3, 0.3, 0.3)). (c) shows the the classified landscape from (b) merged (util_merge()) with a random neighbourhood neutral landscape model (Figure 1g). See Data accessibility for R code about how to use landscapetools

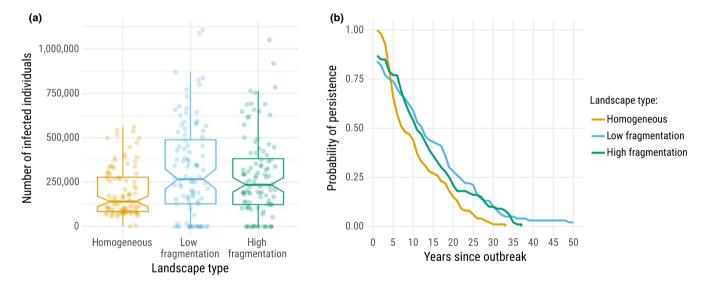


FIGURE 3 Disease outcomes using different landscape types in an epidemiological model. Landscape type "low fragmentation" describes a pattern of some large patches ($nlm_mosaictess(germs = 25)$) while landscapes with "high fragmentation" consist of multiple small patches of varying host capacities ($nlm_mosaictess(germs = 250)$). The landscape dimension was 50×25 cells. (a) Overall number of infected individuals per simulation run and landscape type shown as boxplot and raw data. (b) Probability of the disease being persistent over time, estimated as yearly ratio of simulations with ongoing infections per overall simulations (100 per landscape type)

binary representation of a raster, e.g. matrix/habitat distributions. As simulation experiments often rely on multiple proportions of matrix and habitat, it is possible to define multiple breaks and compute a collection (RasterStack) of binarised landscapes simultaneously. The function util _ merge merges a weighted combination of multiple rasters allowing for even more sophisticated landscape patterns. The merging of NLMs, such as planar gradients with less autocorrelated landscapes, provides an established method for deriving ecotones (Etherington et al., 2015; Travis & Dytham, 2004). util _ rescale is used internally in

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all algorithms implemented in NLMR, but is a public function in landscapetools to linearly rescale raster cell data into a range between zero and one.

landscapetools offers functions and themes for the visual communication of spatial data as ggplot2 objects (Wickham, 2009). The visualisation focuses on achieving outputs that can be used in publications, consequently applying one of the colourblind friendly colour scales (which can be changed with the *scales* parameter in the plot and theme functions) from the viridis package (Garnier, 2018) and typographic elements that support a reproducible workflow.

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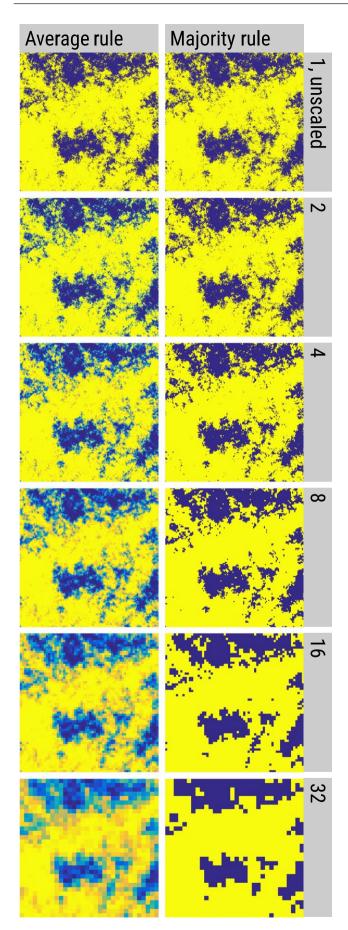


FIGURE 4 Visualisation of the aggregation methods used in case study 2: Aggregation by average rule (left column) and by majority rule (right column). Cell size range from 1 to 32 map units. The landscape example was generated with *roughness* = 0.9 and classified with p = 0.7. The underlying neutral landscape model is the midpoint displacement algorithm (simulated with $nlm _ mpd()$ from NLMR and discretised with util $_ classify()$ from landscapetools)

Auxiliary functions in landscapetools help to coerce raster data in tibbles (Müller & Wickham, 2018), the new standard for rectangular data in R, and vice versa.

3 | EXAMPLE APPLICATIONS

This section describes two example applications of NLMR and land-scapetools (code available in Data accessibility): (i) disease persistence in heterogeneous landscapes and (ii) effects of changing resolution on landscape metrics under different landscape patterns.

3.1 | Case study 1: Disease persistence in heterogeneous landscapes

Simulation models often assume underlying landscapes to be homogeneous or simply suitable habitat distributed in an unsuitable matrix. Given the comprehensive collection of NLMs with differing distribution patterns provided by NLMR, we were able to test the effect of homogeneous versus heterogeneous landscapes on ecological dynamics. We demonstrate the effect of spatial heterogeneity on the dynamics of a directly transmitted disease, Classical Swine Fever, infecting a wild boar population. We used a modified version of an existing agent- and grid-based simulation model (Kramer-Schadt, Fernández, Eisinger, Grimm, & Thulke, 2009; Lange, Kramer-Schadt & Thulke, 2012) with an SIR epidemiological classification (susceptible, infected, recovered). Susceptibility and disease-induced mortality differed between age classes and the processes were simulated stochastically for each individual. Transmission between individuals was calculated based on the health status of individuals in the same and adjacent cells.

Heterogeneous landscapes (50 × 25 cells) were simulated using the nlm _ mosaictess() function with two levels of fragmentation (low with *germs* = 25 and high with *germs* = 250). Total carrying capacities were equal for all simulated landscapes. Patchy, fragmented mosaic NLMs were selected to represent typically fragmented landscape structures in which the boars were located. The algorithm used to create those landscapes allowed to control for different levels of fragmentation in terms of overall number of patches (*germs*). landscapetools allowed for the classification of the generated landscapes into ecologically reasonable breeding capacities per cell (0 to 9 breeding females per home range with a mean of 4.5, resulting in a density of *c*. 5 wild boars per km²; (EFSA Panel on Animal Health and Welfare, 2009; Spitz, 1986)) and analysis of our results, all within

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the R environment. Our results show that disease outcomes were less variable in homogeneous setups compared to heterogeneous, fragmented landscapes (Figure 3). On the one hand, the reason for the differences in invasion success is plausibly the initial conditions the pathogen faces with a lower number of susceptible individuals in some heterogeneous landscapes compared to homogeneous ones (critical invasion threshold, Keeling & Rohani, 2008). The longer outbreak duration on the other hand is most likely the result of the presence of high density patches of hosts and the asynchronous dynamics between patches of different densities leading to recurrent infections (Bolker & Grenfell, 1995; Hess, 1996). Our simulation results underline that the assumption of a well-mixed population in epidemiological models might overestimate the real invasion success while underestimating the possible number of infections within a population (Riley, Eames, Isham, Mollison, & Trapman, 2015).

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3.2 | Case study 2: effects of changing resolution on landscape metrics under different landscape patterns

Altering the resolution of maps (scaling up) can result in a systematic bias of metrics describing any contained spatial patterns (Wu, Shen, Sun, & Tueller, 2002). We utilised NLMRs' functionality to generate differing neutral landscapes as a base for investigating this phenomenon. Initially, we started with landscapes similar to the ones used by Bocedi, Pe'er, Heikkinen, Matsinos, and Travis (2012); these landscapes were essentially discrete fractal landscapes with a varying amount of habitat cells and multiple degrees of spatial autocorrelation. To highlight several possible scaling outcomes we implemented two different aggregation methods.

First, we produced multiple landscapes (70 landscapes per parameter combination, each with $1,024 \times 1,024$ cells) with low to high fragmentation grade (roughness = 0.1, 0.5, 0.9) by

using NLMR's midpoint displacement algorithm ($nlm_mpd()$). Afterwards, we discretised the desired amount of habitat cells (p = 0.1, 0.3, 0.5, 0.7) with landscapetools' classification algorithm (util_classify()). Second, we used (aggregate()) from the raster package with a simple averaging (fun = mean) and majority rule (fun = modal) as aggregation methods to scale up the landscape (Figure 4).

Third, we calculated the desired landscape metric p (proportion of suitable cells; in the case of average rule cells that contain at least some suitable habitat) for each scaling step and visualised possible biases (Figure 5).

This example demonstrates over- and underestimation of the targeted metric which could occur due to scaling methods, depending on the initial landscape. These results confirm that scaling up is most problematic in highly fragmented landscapes. However, this bias drops significantly in specific variable combinations (e.g. p = 0.5, roughness = 0.9, majority rule). Additionally, it is not always clear if a metric is overestimated or underestimated as it can change with differing combinations of scaling method and parameter choice (see majority rule).

4 | CONCLUSION AND OUTLOOK

NLMR is the first software to allow the simulation of NLMs within the self-contained, reproducible framework of R. It can be applied in all landscape analyses in which one wants to test the influence of NLMs on ecological dynamics. Although existing tools are capable of simulating some of the NLMs contained in NLMR (Gardner, 1999; Gardner & Urban, 2007; Saura & Martínez-Millán, 2000; van Strien et al., 2016; Etherington et al., 2015), none of them combine as many different types and none are as well integrated in a native geospatial workflow. Hence, the majority of the limitations that previous

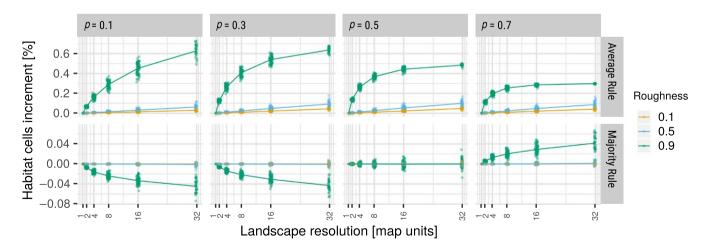


FIGURE 5 Mean increment of detected suitable cells in the landscapes. Each point represents the absolute difference from the scaled up landscape to the original landscape. Lines display the mean at each scaling step. Negative values indicate underestimation and positive values indicate overestimation of suitable cells. Increasing values of *p* indicate an increasing proportion of habitat patches and the higher *roughness* the higher the fragmentation grade of the landscape structure. One can read the figure as follows: If the proportion of suitable cells would be detected correctly during each scaling step for every method, the lines representing the mean would be a flat line at 0. A value higher than 0 indicates systematic overestimation of the proportion of suitable cells and values smaller than 0 would indicate systematic underestimation. Be aware that the upper and lower row of facets are on different scales

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NLM software exhibit, such as developing own methods for spatial operations like masking and extracting, are overcome. The functions in landscapetools provide a variety of established methods to handle raster data, and allow for NLMs to easily be analysed with current R packages and tools. We believe that our functions are complementary to packages like rasterVis (Perpiñán & Hijmans, 2018), which enhance the visualisation of landscape patterns allowing for clearer communication of landscape research.

NLMR and landscapetools are both designed to simplify the workflow of landscape analyses. Thus, it is extensively documented and the implementation of each simulation model was based on published literature. Every function provides examples in its respective help file. A vignette in NLMR combines the information about the functions and the examples into an introduction of a basic workflow for using NLMs. Future extensions of NLMR and landscapetools aim to include all established algorithms that have been used to create NLMs and accompanying utility functions.

We believe that being capable of simulating NLMs natively in R is highly beneficial for the field of landscape ecology. NLMR and landscapetools have been officially released on CRAN (current versions 0.3.0) and peer-reviewed by rOpenSci (https://github.com/ropensci/onboarding/issues/188).

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AUTHORS' CONTRIBUTIONS

M.S. and C.E.S. conceived of the original package concept. M.S. led code development, and all other coauthors were co-developers. M.S. drafted the manuscript, with case studies analysed and drafted by C.S. and M.F. All co-authors contributed critically to the drafts and gave final approval for publication.

DATA ACCESSIBILITY

The NLMR and landscapetools packages and documentation are hosted at https://github.com/ropensci/NLMR as well as at https://github.com/ropensci/landscapetools. Reproducible scripts for the figures and case studies are available from https://zenodo.org/record/1298646.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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