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Calculating landscape diversity with information-theory based indices: A GRASS GIS solution

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ABSTRACT

The assessment of species diversity in relatively large areas has always been a challenging task for ecologists, mainly because of the intrinsic difficulty to judge the completeness of species lists and to undertake sufficient and appropriate sampling. Since the variability of remotely sensed signal is expected to be related to land-scape diversity, it could be used as a good proxy of diversity at species level.

It has been demonstrated that the relation between species and landscape diversity measured from remotely sensed data or land use maps varies with scale. However, Free and Open Source tools (allowing an access to the source code) for assessing landscape diversity at different spatial scales are still lacking today. In this paper, we aim at: i) providing a theoretical background of the mostly used diversity indices stemmed from information theory that are commonly applied to quantify landscape diversity from remotely sensed data and ii) proposing a free and robust Open Source tool (*r.diversity*) with its source code for calculating diversity indices (and allowing an easy potential implementation of new metrics by multiple contributors globally) at different spatial scales from remotely-sensed imagery or land use maps, running under the widely used Open Source program GRASS GIS.

r.diversity can be a valuable tool for calculating landscape diversity in an Open Source space given the availability of multiple indices at multiple spatial scales with the possibility to create new indices directly reusing the code. We expect that the subject of this paper will stimulate discussions on the opportunities offered by Free and Open Source Software to calculate landscape diversity indices.

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"Diversity per se does not exist" (Hurlbert, 1971)

1. Introduction

Measuring the diversity of a landscape is important since it is closely related to its ecological diversity resulting from the interactions between biotic components and their underlying environmental factors (Gillespie et al., 2008; Nagendra and Gadgil, 1999). Further, landscape diversity often relates to species diversity at a range of ecological levels like species community diversity (e.g. Feilhauer and Schmidtlein, 2009;

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Abbreviations: FOSS, Free Open Source Software; GPL, General Public License; GRASS, Geographical Resources Analysis Support System; OSGeo, Open Source Geospatial Foundation.

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Foody and Cutler, 2003; He and Zhang, 2009; Rocchini et al., 2005; St-Louis et al., 2009) and genetic diversity (Balkenhol et al., 2009; Currat et al., 2004; Manel et al., 2003; Storfer et al., 2007). Depending on the study objectives, species diversity can thus be modeled at appropriate scales in time and space (Balkenhol et al., 2009; Osborne et al., 2007).

To date, species-based measures of diversity like species richness (alpha-diversity) or species turnover (beta-diversity) are the most commonly used metrics for quantifying the diversity of an area. Nonetheless, the assessment of species richness in relatively large areas has always been a challenging task for ecologists, mainly because of the intrinsic difficulty in judging the completeness of species lists and in undertaking sufficient appropriate sampling (e.g., Bacaro et al., 2009; Palmer, 1995). Inventorying species over large regions is hampered by the effort required for field sampling and complications resulting from changes in species composition through time (e.g., Kirby and Thomas, 2000; Palmer et al., 2002). Therefore, different methods have been proposed to overcome these issues. These methods include: the use of habitats as a proxy for estimating species diversity (e.g. Cushman et al., 2008; Koellner et al., 2004; Nagendra and Utkarsh, 2003), an improvement of sampling efficiency by developing new site allocation criteria (e.g., Gillison and Brewer, 1985; Hortal and Lobo, 2005), the examination of remotely-sensed proxies for richness (e.g., Rocchini, 2007), and the development of robust methods for an extrapolation of total richness at a larger area or time span (e.g., Shen and He, 2008).

Objective methods for inventorying species are also strongly encouraged for: i) improving statistical estimates of species richness (Chiarucci and Bonini, 2005; D'Alessandro and Fattorini, 2002), ii) comparing biodiversity of different areas over large scales (Koellner et al., 2004), iii) developing multi-year monitoring plans (Ferretti and Chiarucci, 2003; Kalkhan et al., 2007), and iv) avoiding artifacts (Palmer et al., 2008). The use of remote sensing tools for estimating diversity has been widely recognized as one promising approach since it is efficient and can be applied in an objective sampling design (see Rocchini et al., 2010, for a review).

Given the difficulties of field-based data collection, the use of remote sensing for estimating environmental heterogeneity and (subsequently) species diversity represents a powerful tool since it allows for a synoptic view of an area with a high temporal resolution (Kark et al., 2008). As an example, the availability of satellite-derived data like those achieved by the Landsat program makes it feasible to study all parts of the globe up to a resolution of 30 m (Pettorelli et al., 2005; readers are referred to Tucker et al. (2004) for a complete description of the Global Land Cover Facility which provides data access in a public repository). This is particularly relevant in view of the availability of recent Open Source systems for the analysis of remotely-sensed imagery (Neteler and Mitasova, 2008; Neteler et al., 2005, 2008).

Since the variability in the remotely sensed signal is expected to be related to environmental heterogeneity, it could be used as a good proxy of diversity at species level (e.g. Levin et al., 2007). The Spectral Variation Hypothesis posits that the higher the habitat heterogeneity, the higher will be the species diversity therein (Palmer et al., 2002). Even if some case studies could not establish a simple relation between these two measures (Nagendra et al., 2010; Schmidtlein and Sassin, 2004), depending on the scale and the habitat being considered, the Spectral Variation Hypothesis can be expected to hold true in many cases. This is true regardless the taxonomic group being considered because it is expected that, besides random dispersal of species (Hubbell, 2001), a higher heterogeneity of habitats (e.g. number or relative abundances of habitats) will host a higher number of species each of which occupies a particular niche (niche difference model, see Nekola and White, 1999).

The study by Oldeland et al. (2010) demonstrates that the relation between species diversity and landscape diversity measured from remotely sensed data or land use maps varies with scale (grain of sampling units, *sensu* Scheiner et al., 2000; e.g. Fig. 1). For this reason, multi-scale species inventories with smaller sampling units nested within bigger ones have been strongly encouraged and are now common practice (Kalkhan et al., 2007). However, Free and Open Source tools (allowing an access to the source code) for assessing landscape diversity at different spatial scales (e.g. different moving windows) are still lacking today. Such tools may help to develop regression models between species and spectral variability at different spatial scales in a straightforward manner. Further, they allow the application of best-fit-based regression parameters at an appropriate spatial window of analysis, for predicting species diversity over a large region.

The aim of this paper is: i) to provide a theoretical background of the mostly used diversity indices developed in information theory that are commonly applied to quantify landscape diversity from remotely sensed data and ii) to propose a free and robust Open Source tool (*r.diversity*) with its source code for calculating diversity indices (and allowing an easy potential implementation of new metrics by multiple contributors

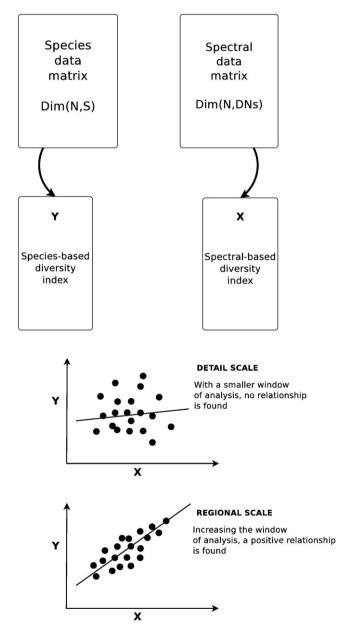


Fig. 1. Starting from species and spectral data, the relation between species (Y) and landscape diversity (spectral variability, X) is a function of spatial scale. Such relation may be hidden at some spatial scales (such as local scales) while it becomes apparent at larger ones. Refer to the main text for major explanations.

globally) from remotely-sensed imagery or land use maps, running under the widely used open source program GRASS GIS.

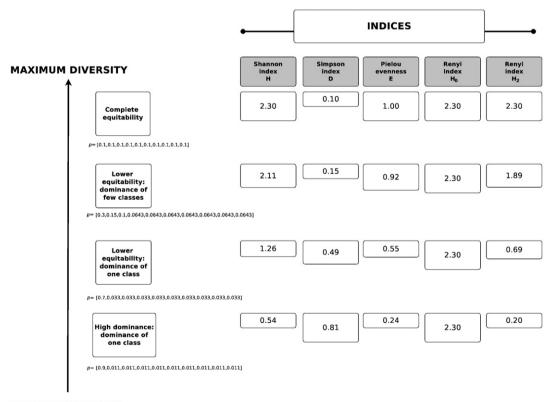
2. On the use of information theory for quantifying landscape diversity

The most popular metrics of biodiversity are derived from information theory which tries to measure the amount of disorder contained in a system (Margalef, 1958). In our case, let *u* be a set of basic units (pixels or patches) composing an image or a map, each of which can be represented as a tuple {z(u),s(u)}, where z(u) = property of the *u*th entity related to its s(u) spatial geometric component (Goodchild et al., 1999). In this paper we will explicitly consider z(u) as either i) the raw Digital Number (DN, e.g., the value on the 0–255 scale in a 8-bit image) or pre-processed (e.g., with sensor calibration and atmospheric correction) reflectance value of pixels composing a remotely sensed image, or ii) the class of each polygon composing a land use (or vegetation) map. In the following paragraphs we will rely on DNs in a remotely sensed image but the same reasoning holds for classes in a land use map.

Assume an 8-bit band of a remotely-sensed image composed of *N* DN values, i.e., with a richness $N = 2^8 = 256$ possible grey levels perpixel, with the relative abundance p_i of the *i*th DN (i = 1, 2, ..., N) such that $0 \le p_i \le 1$ and $\sum p_i = 1$. For simplicity we will refer to such relative abundance simply as p.

Most measures of spectral variability have been proposed based on i) entropy, e.g. the Shannon entropy index (Shannon, 1948; see also Bolliger, 2005; Ricotta, 2005) $H = -\sum p \times \ln(p)$ with $0 \le H \le$ $\ln(N)$, where *p* is the relative abundance of each spectral reflectance value (DN) or on ii) reversed dominance, derived from the Simpson Dominance index $D = \sum p^2$ with $0 \le D \le 1$ (Simpson, 1949), as 1-*D* (i.e., the Simpson Diversity index, Fig. 2). Notice that, while in Shannon's original definition the base 2 logarithm is used to measure information content in bits, in ecological applications the natural logarithm is traditionally used (e.g. MacArthur et al., 1966). However, since entropies with any base are linearly related, different logarithm bases have no effects on final results; it is comparable to measuring distances in kilometers or miles, which does not make any difference in the conclusions. In order to avoid confusion we will explicitly refer to the Simpson Dominance index as D and to the Simpson Diversity index as 1-D. From a practical point of view, distinct diversity measures are aimed to summarize a large multivariate data set into one single value based on distinct objectives and approaches. Therefore, as this operation will always result in a loss of information, it is generally understood that there is no ideal summary statistics capable of unequivocally characterizing all aspects of diversity (Patil and Taillie, 1982). Both H and 1-D will increase if the DN values are equally distributed with no DN value being dominant with respect to the others. Rocchini and Neteler (2012) recently found apparent problems when relying only on entropy based metrics, e.g. i) the impossibility to distinguish different ecological situations using one single index of diversity, ii) the impossibility to discern differences in richness or relative abundance. For instance, they provide a theoretical example in which areas differing in richness or relative abundances of reflectance values (DNs) may show a similar Shannon index value. In this view, coupling such entropy- or reversed-dominance based metrics with indices taking into account evenness would dramatically increase the information content of such metrics. Among them, the mostly used index is the Pielou evenness index $J = \frac{-\sum p \times \ln p}{\ln(N)}$ $< \ln(p)$ (Pielou, 1969) with $0 \le J \le 1$, which takes into account the maximum diversity with the same number of DNs N and thus can be rewritten as $J = \frac{H}{H_{max}}$.

Ricotta and Avena (2003) provided a mathematical work on the Pielou evenness index in species community ecology and landscape ecology, stating that:



MINIMUM DIVERSITY

Fig. 2. Trend of different diversity indices attained by varying the array of relative abundance values (*p*), given the same richness *N* = 10. From top to bottom: higher equitability situations towards higher dominance of few DN values or classes. The size of the boxes is related to the value of each index (with respect to its maximum value, vertical viewing) for each array of relative abundance values (*p*).

"normalisation of *H* with respect to maximum entropy $(J = H/H_{max})$ is termed 'evenness' because it measures deviation from an even distribution of individuals amongst the *N* species". In spectral variability, individuals are represented by pixels while species are represented by DN values.

Rényi (1970) proposed a generalized entropy, $H_{\alpha} = \frac{1}{1-\alpha} \ln \sum p^{\alpha}$ which is extremely flexible and powerful since many popular diversity indices are simply special cases of H_{α} . As an example, for $\alpha = 0$, $H_0 = \ln(N)$ namely the logarithm of richness (N = number of DN values) maximum Shannon entropy index (H_{max}) which is used as the denominator of the Pielou index, while for $\alpha = 2$, $H_2 = \ln(1/D)$ where D is the Simpson Dominance index (Fig. 2). For $\alpha = 1$ the Rényi entropy is defined in the limiting sense using l'Hospital's rule of calculus, and H_1 = Shannon's entropy H.

While traditional metrics supply point descriptions of diversity, Rényi's framework offers a continuum of possible diversity measures, which differ in their sensitivity to rare and abundant DNs, becoming increasingly regulated by the commonest DNs when increasing the values of α . In this view, changing α can be considered as a scaling operation that takes place not in the real but in the data space (Podani, 1992). That is why Rényi generalized entropy has been referred to as a "continuum of diversity measures" (Ricotta et al., 2003).

Fig. 2 provides an example of the trend of the aforementioned indices while changing the relative abundance array from complete evenness to almost complete dominance. As stressed by Nagendra (2002) it is difficult to separate the conflicting influence of richness and evenness on the different diversity indices. For this reason, in the following example we will maintain the same value of richness N = 10 by varying the relative abundance of image DN values or map land cover classes.

Let *p* be the array $[p_1,p_2,p_3,...,p_{10}]$ of relative abundances of a satellite image composed by 10 DN values or a land use map composed of 10 land cover classes (richness N = 10). In case of maximum equitability each DN value or class occupies a proportion equalling 0.1 of the total available area. The array of relative abundance values (*p*) turns out to be:

In this case the Shannon index *H* would reach its maximum value equalling $\ln(N)$ where N = number of DN values or classes, i.e. $\ln(10) =$ 2.30, thus leading to a Pielou evenness equalling $H/\ln(N) = 2.30/2.30 = 1$. The same holds for the Rényi entropy (e.g. $H_0 = H_{max}$ and $H_2 = \ln(1/D)$) which turns out to be $\ln(N)$. Obviously, the Simpson index *D* which is based on dominance, holds a very low value (Fig. 2).

Instead, once the equitability of $p[p_1,p_2,p_3,...,p_{10}]$ decreases with the dominance of few classes, such that e.g.:

p = [0.3, 0.15, 0.1, 0.0643, 0.0643, 0.0643, 0.0643, 0.0643, 0.0643, 0.0643]

the Shannon *H*, the Pielou *J* and the Rényi entropy H_2 indices decrease, while the Simpson D index increases on the strength of the decrease and increase of relative evenness and dominance, respectively (Fig. 2). Notice that Rényi entropy H_0 remains constant despite the structure of the array *p*, since, as previously stated, for $\alpha = 0$, Rényi entropy is only related to richness *N* equaling $\ln(N)$.

Each index increases/decreases in a different manner depending on the relative array of abundances being considered. As an example, passing from the highest possible equitability to the dominance of only one class (from top to bottom of Fig. 2) the Shannon *H* and the Pielou *E* indices decrease up to four times their maximum value gathered with complete evenness, while Rényi entropy H_2 decreases up to eleven times. For this reason, reducing diversity to only one index may be dangerous if the structure of the abundance array *p* is not explicit *a-priori*.

As far as we know, while examples of Free and Open Source Software (FOSS) to calculate landscape metrics exist (e.g. the *r.le* module in GRASS GIS, Baker and Cai, 1992), no FOSS has been developed to calculate diversity in a combined way considering both i) single diversity metrics (such as Shannon, Simpson, Pielou indices) and ii) a continuum of diversity measures (such as the Rényi index with different values of α) at different spatial scales with the potential of extending the code to new metrics. We will first introduce the GRASS GIS Open Source Software which incorporates as an add-on a first version of the newly developed *r.diversity* and then describe the *r.diversity* tool in more detail.

3. Open Source software in Geography for a free calculation of landscape diversity metrics: the GRASS GIS project

The idea of Free and Open Source (FOSS) software has been around for almost as long as software has been developed (Neteler and Mitasova, 2008). The famous "four freedoms" paradigm, developed by Richard Stallman (1985; 1997) in his seminal work, proclaims i) the freedom to run the program for any purpose, ii) the freedom to study how the program works and adapt it to one's own needs, iii) the freedom to redistribute copies, and iv) the freedom to improve the program and release such improvements to the public. This guarantees that the whole community benefits from software development (also see Fogel, 2009).

With the aim of calculating landscape metrics in GIS to ensure robust analysis output, particularly where complex algorithms are concerned (Neteler and Mitasova, 2008; Neteler et al., 2012), the full access to the source code is crucial. There are well-known examples of FOSS in research fields such as Statistics (e.g. R Language and Environment for Statistical Computing, R Development Core Team, 2011), while GIS scientists and more generally landscape ecologists may benefit from the powerful GIS named GRASS (Geographical Resources Analysis Support System, http://grass.osgeo.org), which includes more than 350 modules for managing and analyzing geographical data (Neteler and Mitasova, 2008; Neteler et al., 2012). GRASS GIS was originally created in 1982 by the U.S. Army Construction Engineering Research Laboratories, by further adopting the GNU GPL (General Public License, see http://www.gnu.org) in 1999. Currently, it is one of the cutting-edge projects of the Open Source Geospatial Foundation (OSGeo.org, founded in 2006).

Adoption of the FOSS license changed the development process of GRASS with contributions to the source code becoming decentralized. The legal statements declared in the GPL are based on the aforementioned "four freedoms" paradigm (Stallman, 1985, 1997) and allow the user to use the software's full range of capabilities, and to distribute, study and improve it (Rocchini and Neteler, in press).

A number of GRASS modules deals with the analysis of raster matrices, continuous and discrete data. Among them we developed the *r.diversity* tool based on the aforementioned theory on landscape diversity calculation.

4. The *r.diversity* tool for measuring landscape diversity in a robust manner

The new *r.diversity* function, which is based on the *r.li* module for landscape ecology metrics available with GRASS GIS, can be used to produce a diversity map.

First, when using *r.diversity*, the users must be aware of the spatial dimension of the moving window (i.e. grain, *sensu* Scheiner et al., 2000) that is being used (Fig. 3). Considering all pixels within this window, a diversity measure is calculated. The theoretically smallest window size (1×1) covers a single a pixel (where diversity would equal zero); the window size can be increased (to 3×3 , 5×5 , 7×7 , $n \times n$ pixels) until the whole spatial extent is covered and the value of the calculated diversity index is attached to the central pixel of each moving window of 3×3 pixels, will return the value of each diversity index attached to the central pixel of the window derived using a neighborhood of 3×3 pixels.

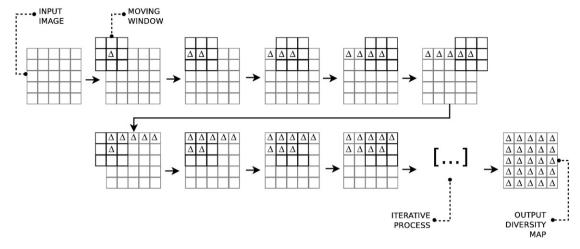


Fig. 3. Starting from an input such as a remotely sensed image or a raster land use map (top left) and setting a moving window size (in this case 3×3 pixels), *r.diversity* will return the value of each diversity index (Δ), which may vary in magnitude from pixel to pixel, attached to the central pixel of the window, calculated using a neighborhood of 3×3 pixels.

This straightforward method to define the grain allows researchers to explicitly account for scaling factor when performing spatial analysis, thus avoiding confounding effects due to scale in calculating diversity measures.

After starting GRASS GIS, a remotely sensed band or a raster land use map in raster format can be imported or via graphical user interface or by the *r.in.gdal* command as:

r.in.gdal in=/path/raster.tif out=raster grass

This command creates a raster file named <code>raster_grass</code> in the GRASS database on which *r.diversity* will calculate the aforementioned diversity measures. r.info <code>raster_grass</code> will prompt the user with metadata about the raster map being used.

The command to be used to calculate diversity is straightforward:

r.diversity input=raster_grass out=diversity size=7
alpha=2

This command will create an output for each index (Shannon *H*, Pielou *J*, Simpson *D*, Rényi H_{α}). In this case, a moving window of 7×7 pixels is used while alpha for the Rényi entropy calculation is explicitly stated. If a particular metric is of interest, an optional parameter method (e.g., method=shannon|pielou|simpson|renyi) can be used.

Moreover, several grains can be considered at a time invoking the scale range by means of the parameter size as:

r.diversityinput=raster_grassout=diversitysize=3-7
alpha=2

thus creating a total of 12 maps (four indices at three grain sizes 3×3 , 5×5 , 7×7), or

r.diversity input=raster_grass out=diversity size=3,7
alpha=2

thus creating a total of 8 maps (four indices at two grain sizes 3×3 and 7×7). In case the input raster file contains NULL value cells, *r.diversity* returns a value of -1 for these cells. If the user wants to keep NULL values instead, they can be restored with a subsequent command use of r.null on the resulting map:

r.null setnull = -1 map = my map

Appendix A reports the complete code of the *r.diversity* command which has been written in Python language. Different window sizes are strongly encouraged in order to test the relationship between species and landscape diversity (Fig. 1). Fig. 4 shows an example of the calculation using different window sizes. Notice that the Simpson diversity index results in an emphasis on small differences of low-

diversity areas (e.g. in homogeneous zones) since its formula contains a squared *p*, while logarithm-based indices (Shannon entropy, Pielou evenness, Rényi generalized entropy) enhance differences of sites with higher evenness (Nagendra, 2002). Since the observed variability is expected to increase with increasing the window size, the differences between the indices increase with grain size.

5. Discussion

In this paper we presented a GRASS GIS-based tool for calculating landscape diversity to be potentially related to biodiversity studies at different spatial scales (moving window sizes). Transitioning the theoretical concept of "scale" to an empirical – and overall explicit – "window size" is a crucial conceptual solution (already introduced by, e.g., FRAGSTATS) since the diversity of any types of attributes has been proven to change as a function of scale (Whittaker, 1972). The proposed automatic and freely available tool for calculating landscape diversity has the potential towards, e.g., i) the generation of species-diversity proxies or indicators (e.g., Chang et al., 2004; Feilhauer and Schmidtlein, 2009), ii) an increase of species-inventory efficiency (e.g., Rocchini et al., 2005), iii) quantitative comparison of different areas with different degrees of diversity at multiple scales (e.g., Oldeland et al., 2010). Remotely sensed information can function as a driver for developing field sampling design strategies.

As previously stated, sampling species in the field has a number of drawbacks such as i) observer bias (Bacaro et al., 2009; Cayuela et al., 2011; McKenzie, 2005), ii) the definition of statistical population when developing sampling designs (Chiarucci, 2007), iii) reproducibility (Ferretti and Chiarucci, 2003), iv) spatial errors (Graham et al., 2008), v) historical bias about species distribution records (Hortal et al., 2008; Rocchini et al., 2011). Refer to Foody (2011) for a complete dissertation about imperfectness of species field data considering both quality (data labelling) and quantity (sample size).

Hence, although we are unable to directly detect organisms remotely (Turner et al., 2003), proxies for community properties provide a valuable data source for the study of species diversity. Therefore, the use of indirect remote sensing techniques for estimating diversity of landscapes shows promise to forecast species diversity over different spatial scales. In this view, *r.diversity* allows measuring landscape diversity and relating it to species diversity at multiple moving window sizes the analysis process, from fine scale field sampling units to the entire study area.

While a number of tailored software tools exist for calculating landscape diversity metrics like FRAGSTATS (McGarigal and Marks, 1995) or Patch Analyst (Elkie et al., 1999) they do not allow users to access and/or review directly the source code, thus hampering the straightforward development of new metrics by several researchers at

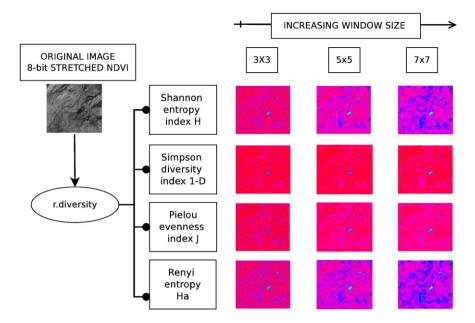


Fig. 4. An example of the output of *r.diversity*, applied to a Normalized Difference Vegetation Index (NDVI) map derived from a Landsat image, using the following command: r.diversity input=raster grass out=diversity size=3-7 alpha=2.

a time. In this view, the introduction of a concurrent versioning system of GRASS GIS in 1999 enabled different institutions and individuals to contribute to the code base simultaneously from different countries around the world, along with real time peer review of the submitted changes (Mitasova and Neteler, 2004). The modular software design of GRASS facilitates the introduction of new functionalities without affecting the overall performance of the system. Moreover, recent improvements also allow GRASS users and developers to make use of the Python programming language (van Rossum, 1995) to introduce new features.

As previously stated, diversity cannot be reduced to single index information, since one can never capture all aspects of diversity in a single statistic (Gorelick, 2006). As an example, Nagendra (2002), dealing with the Shannon H index and the Simpson diversity index 1-D, reports the case of discordant diversity patterns obtained by considering different indices. Such information may remain hidden once only one index is considered. Hence, following O'Neill et al. (1988) in a pioneer study on the landscape indices, a restricted set of non redundant indices could reach significant aspects on the spatial patterns. For this reason, future work will be devoted to the development of a continuum of diversity measures such as the Rényi entropy presented in this paper. Such measures are particularly important since they are not redundant and they allow to consider several measures at a time, by varying one parameter therein, like the α parameter in the generalized Rényi entropy. The very aim of using the Rényi entropy in ecology does not consist in selecting the most appropriate parameter (if any) that best explains the problem under study, but rather in constructing a 'diversity profile' (Patil and Taillie, 1982) of H_{α} vs. α showing how parametric diversity responds to changes in the parameter sensitivity to rare and abundant DNs. As far as we know, this is the first example in which Rényi entropy is provided in an Open Source framework after the first Free (but not Open Source) example by Ricotta et al. (2003). Hence r.diversity's code is available from the GRASS GIS source code repository (http://svn. osgeo.org/grass/grass-addons/raster/r.diversity/) for further modifications, improvements, if needed, bug fixing, and the re-use for a development of new indices based on new or still underused mathematical theory (see also Appendix A).

Understanding the ecological processes which shape diversity over space at different spatial scales may be done by the quantification of surface gradients (gradient maps; e.g. Schmidtlein and Sassin, 2004; Feilhauer et al., 2011; surface gradient model; e.g. Mondal, 2011; Digital Elevation Models derivatives, e.g. Teillet et al., 1982). Spatial gradients may be quantified by relying on the variability – or diversity – of a surface over space, being such surface for instance a remotely sensed image. In this view, *r.diversity* in GRASS GIS can be a valuable tool, on the strength of its major advantages like: i) the availability of multiple indices at a time, ii) the possibility to create new indices directly reusing the code, iii) the possibility to calculate landscape diversity at multiple spatial scales in an explicit way based on varying moving windows, and thus iv) reducing the problems of hidden patterns of the relation between field- and landscape-based diversity due to scale mismatch.

6. Conclusion

We expect that the subject of this paper will stimulate discussions on the opportunities offered by Free and Open Source Software to quantify landscape diversity. Ecological informatics needs the development of both the theoretical mechanisms and the computer based programs for supporting it. For instance, besides the Rényi formula, many other parametric entropies with different mathematical properties have been proposed to generalize the Shannon work (see e.g. Aczél and Daróczy, 1975; Patil and Taillie, 1982; Ricotta and Anand, 2006; Ricotta and Szeidl, 2006; Tsallis, 2002). Nonetheless, rather than being a disadvantage, this multitude of approaches is mostly an advantage; as suggested by Aczél and Daróczy (1975, p. 185): "In practice, of course, one uses that kind of entropy which best fits the given problems of application". Therefore, we hope that researchers involved with complexity/diversity/heterogeneity issues will contribute to the *r.diversity* code with new diversity metrics derived from mathematical theories.

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Appendix A. Source code of r.diversity

```
#
# MODULE: r.diversity
#
 AUTHOR(S): Luca Delucchi
# PURPOSE: It calculates the mostly used indices of diversity based on
#
          information theory. Also available from
#
          http://svn.osgeo.org/grass/grass-addons/raster/r.diversity/
#
# COPYRIGHT: (C) 2010-2012 by Luca Delucchi
#
#
              This program is free software under the GNU General Public
#
              License (>=v2). Read the file COPYING that comes with GRASS
#
              for details.
#
#%module
#% description: Calculate diversity indices based on a moving window using r.li
packages
#% keywords: raster
#%end
#%option
#% key: input
#% type: string
#% gisprompt: input raster
#% key_desc: name
#% description: Name of input raster map
#% required: yes
#%end
#%option
#% key: output
#% type: string
#% gisprompt: output raster
#% key desc: name
#% description: Name of output raster map
#% required: yes
#%end
#%option
#% key: alpha
#% type: double
#% gisprompt: alpha value
#% key desc: alpha value for Renyi entropy
#% description: Order of generalized entropy (>0.0; undefined for 1.0)
#% multiple: yes
#% required: no
#%end
#%option
#% key: size
#% type: integer
#% gisprompt: resolution
#% key_desc: moving window
#% multiple: yes
#% description: Size of processing window(odd number only)
#% answer: 3
#% required: no
#%end
#%option
#% key: method
#% type: string
#% gisprompt: method to use
#% key desc: method
#% options: simpson, shannon, pielou, renyi
```

```
#% multiple: yes
#% description: Name of methods to use
#% required: no
#%end
#%option
#% key: exclude
#% type: string
#% gisprompt: excludemethod
#% key desc: excludemethod
#% options: simpson, shannon, pielou, renyi
#% multiple: yes
#% description: Exclude methods
#% required: no
#%end
# import library
import os, sys, re
import grass.script as grass
# main function
def main():
     # set the home path
     home=os.path.expanduser('~')
      # check if GISBASE is set
      if "GISBASE" not in os.environ:
        # return an error advice
        print "You must be in GRASS GIS to run this program."
        sys.exit(1)
      # input raster map
     map_in = options['input']
      # output raster map
     map out = options['output']
      # resolution of moving windows
     res = options['size']
      # alpha value for r.renyi
     alpha = options['alpha']
      #method to use
     methods = options['method']
      # excluded method
     excludes = options['exclude']
     resolution = checkValues(res)
     if alpha != '':
        alpha_value = checkValues (alpha,True)
        print alpha_value
      # check if~/.r.li path exists
     if not os.path.exists(home+'/.r.li/'):
        # create ~/.r.li
        os.path.mkdir(home+'/.r.li/')
        # create ~/.r.li/history
        os.path.mkdir(home+'/.r.li/history')
      else:
        if not os.path.exists(home+'/.r.li/history'):
              # create ~/.r.li/history
              os.path.mkdir(home+'/.r.li/history')
      # set overwrite
      if grass.overwrite():
           env['GRASS_OVERWRITE'] ='1'
      # if method and exclude option are not null return an error
```

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```
print "You can use method or exclude option not both"
        sys.exit(1)
     # if method and exclude option are null calculate all module
     elif methods == '' and excludes == '':
        # check if alpha value is set,else return an error
        if alpha value == '':
              print "Please you must set alpha value for Renyi entropy"
              svs.exit(1)
        calculateAll(home, map in, map out, resolution, alpha value)
     # calculate method
     elif methods != '':
        methods = methods.split(',')
        checkAlpha(methods, alpha value)
        calculateM(home, map_in, map_out, resolution, alpha_value, methods)
     # calculate not excluded index
     elif excludes!= '':
        excludes = excludes.split(',')
        checkAlpha(excludes,alpha value,True)
        calculateE(home, map_in, map_out, resolution, alpha_value, excludes)
     # remove configuration files
     removeConfFile(resolution, home)
     print 'All works are terminated'
# calculate all indices
def calculateAll(home, map_in, map_out, res, alpha):
      # for each resolution create the config file and calculate all index
     for r in res:
       createConfFile(r,map_in,home)
        r = str(r)
        grass.run command('r.li.simpson', map = map in, out = map out +
        '_simpson_size_' + r,conf = 'conf_diversity_' + r)
        grass.run command('r.li.shannon', map = map in, out = map out +
        ' shannon size ' + r, conf = 'conf diversity ' + r)
        grass.run_command('r.li.pielou', map = map_in, out = map_out +
        ' pielou size ' + r,conf = 'conf diversity ' + r)
        for alp in alpha:
              grass.run_command('r.li.renyi', map = map_in, out = map_out +
              '_renyi_size_' + r + '_alpha_' + str(alp), conf =
              'conf_diversity_' + r, alpha = alp)
# calculate only method included in method option
def calculate M(home, map_in, map_out, res, alpha, method):
     # for each resolution create the config file
     for r in res:
        createConfFile(r,map_in,home)
        r = str(r)
        # for each method in method option calculate index
        for i in method:
              if i == 'renyi':
                for alp in alpha:
                      grass.run_command('r.li.renyi', map = map_in, out =
                      map_out + '_renyi_size_' + r + '_alpha_' + str(alp),
                      conf = 'conf diversity ' + r, alpha = alp)
              else:
                 grass.run command('r.li.' + i,map=map in, out = map out +
                 '_' + i + '_size_' + r, conf = 'conf_diversity_' + r)
# calculate only method excluded with exclude option
def calculate E(home, map_in, map_out, res, alpha, method):
     # set a tuple with all index
     methods = ('simpson', 'shannon', 'pielou', 'renyi')
     # for each resolution create the config file
     for r in res:
        createConfFile(r,map in,home)
```

```
r = str(r)
        # for each method
        for i in methods:
              # if method it isn't in exclude option it is possible to calculate
              if method.count(i) == 0:
                if i == 'renyi':
                      for alp in alpha:
                         grass.run_command('r.li.renyi', map=map_in, out =
                         map out + ' renyi size ' + r + ' alpha ' + str(alp),
                         conf = 'conf diversity ' + r, alpha = alp)
                 else
                      grass.run command('r.li.' + i,map = map in, out = map out +
                       ' ' + i + ' size ' + r, conf = 'conf diversity ' + r)
# check if alph avalue is set when renyi entropy must be calculated
def check Alpha(method, alpha_val, negative =False):
     for alpha in alpha val:
        # it's used when we check the exclude option
        if negative:
           if method.count('renyi') != 1 and alpha == '':
                print "Please set alpha value for Renyi entropy"
                sys.exit(1)
        # it's used when we check the method option
        else:
           if method.count('renyi') == 1 and alpha == '':
                print "Please set alpha value for Renyi entropy"
                sys.exit(1)
#create configuration file instead using r.li.setup
def createConfFile(res, inpumap, home):
      # set the name of conffile
     confilename = home + '/.r.li/history/conf_diversity_' + str(res)
     # start the text for the conf file
     outputLine = ['SAMPLINGFRAME0|0|1|1\n']
     # return r.info about input file
     rinfo = grass.raster info(inpumap)
     # calculate number of lines
     rows = (rinfo["north"]-rinfo["south"])/rinfo['nsres']
     # calculate number of columns
     columns = (rinfo['east']-rinfo['west'])/rinfo['ewres']
     # value for row
     rV = int(res)/rows
     # value for column
     cV = int(res)/columns
     # append the text for the conf file
     outputLine.append('SAMPLEAREA -1|-1|'+str(rV)+'|'+str(cV)+'\n')
     outputLine.append('MOVINGWINDOW\n')
     # open configuration file
     fileConf=open(confilename,'w')
      # write file
     fileConf.writelines(outputLine)
     # close file
     fileConf.close()
# return a list of resolution
def check Values(res,alpha=False):
     # check if more values are passed
     if res.count(',') == 1:
        typ = 'values'
        reso = res.split(',')
     # check if arange of values are passed
     elif res.count('-') == 1:
        typ = 'range'
        reso = res.split('-')
     # else only a value ispassed
```

```
else·
        typ = 'value'
        reso = [res]
      # trasforn string to int and check if is a odd number
     for i in range(len(reso)):
        # check if is a odd number
        reso[i] = float(reso[i])
        if reso[i]%2 == 0:
              # return the error advice
              print "Your size option could not contain odd number"
              svs.exit(1)
     # create a range
     if typ == 'range':
              if alpha:
                 print "Range for alpha values it isn't supported"
                 sys.exit(1)
              else:
                reso = range(reso[0], reso[1]+1, 2)
     return reso
de removeConfFile(res,home):
     for r in res:
        confilename = home + '/.r.li/history/conf diversity '+str(r)
        os.remove(confilename)
if name ==" main ":
     options, flags = grass.parser()
     sys.exit(main())
```

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