Niche hypervolume community vulnerability index

26/06/2020

Initial definitions

For calculating the NHCVI the following formula is applied to each species i considering either its binary output (i.e., 0,1) or its habitat suitability both obtained from Species Distribution Models:

(i) the binary case:

$$NHCVI_i = \begin{cases} 0 \text{ if } SDM = 0 \\ 2N_{b,i} - N_{p,i} \text{ if } SDM = 1 \end{cases} \tag{1}$$

Where $N_{b,i}$ and $N_{p,i}$ are, respectively, the Niche Breadth and the Niche Position for a given species i.
In this case, $N_{b,i}$ is given by the SVM-based hypervolume size, and, $N_{p,i}$ is based on the average Euclidean distance between the i-th species centroid and the global community centroid.
In a nutshell, this index intends to maximize vulnerability for species with smaller niche breadth and higher marginality in the community environmental suitable/niche space.

(ii) the habitat suitability case:

$$NHCVI_i = H_{s,i} \times (2N_{b,i} - N_{p,i}) \tag{2}$$

Where $H_{s,i}$ is the habitat suitability value (rescaled by biomod2 between 0-1000) for a given species i.

For obtaining a spatial representation of the index for all species in the community, we can calculate the sum as:

$$NHCVI_i = \sum_{i=1}^{N} H_{s,i} \times (2N_{b,i} - N_{p,i}) \tag{3}$$

With N equal to the total number of species in the community.

Because higher species richness will result in greater vulnerability, we may need to normalize this as:

(i) the binary case:

$$NHCVI_{bin} = \frac{1}{N} \sum_{i=1}^{N} 2N_{b,i} - N_{p,i} \tag{4}$$

(ii) the habitat suitability case:

$$NHCVI_{HS} = \frac{\sum_{i=1}^{N} H_{s,i} \times (2N_{b,i} - N_{p,i})}{\sum_{i=1}^{N} H_{s,i}} \tag{5}$$

Because large values for both $NHCVI_{bin}$ and $NHCVI_{HS}$ relate to low vulnerability it may be useful and more intuitive to use the reciprocal (or the multiplicative inverse) of these indices as:

$$NHCVI'_{bin} = \frac{1}{NHCVI_{bin}} \qquad (6)$$

Or:

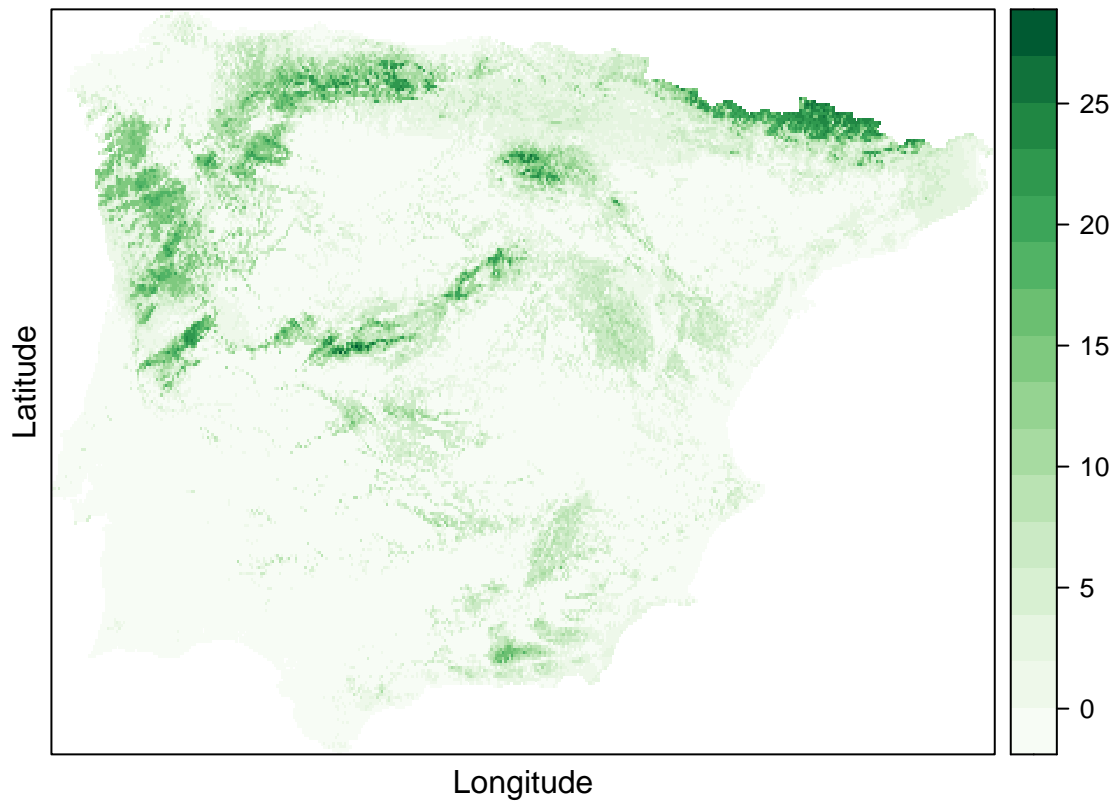$$NHCVI'_{HS} = \frac{1}{NHCVI_{HS}} \qquad (7)$$

Results

Species ranking in terms of vulnerability

The table is sorted by $NHCVI$ (1) from the highest vulnerable species to the least vulnerable one:

Species	NHCVI	NHCVI_inv
RACFAS	-4.014	-0.249
ANDALP	-3.340	-0.299
GRIALP	-3.241	-0.309
GRIELA	-2.605	-0.384
GRICAE	-2.532	-0.395
GRIFUN	-2.315	-0.432
ANDNIV	-2.228	-0.449
GRICRI	-2.123	-0.471
GRIMER	-1.797	-0.556
ANDHEI	-1.524	-0.656
ANDMEG	-1.365	-0.733
ANDCRA	-0.724	-1.380
RACOBT	0.123	8.145
GRIHAR	0.218	4.582
GRITER	1.353	0.739
GRIREF	1.504	0.665
GRIANO	2.150	0.465
GRITOR	2.939	0.340
ANDFRI	4.676	0.214
ANDROT	7.331	0.136
GRILIS	10.115	0.099
GRIDIS	10.278	0.097
GRIOVA	12.432	0.080
GRIORB	16.710	0.060
RACSUD	17.878	0.056
RACMAC	18.930	0.053
RACHET	21.040	0.048
RACAFF	21.451	0.047
GRIMON	32.412	0.031
GRIDEC	33.072	0.030
GRILAE	37.114	0.027
RACLAN	41.143	0.024
RACCAN	42.624	0.023
ANDRUP	52.351	0.019
GRIRAM	55.724	0.018
GRIPUL	63.954	0.016
RACAQU	71.314	0.014
GRITRI	78.970	0.013
RACELO	156.716	0.006

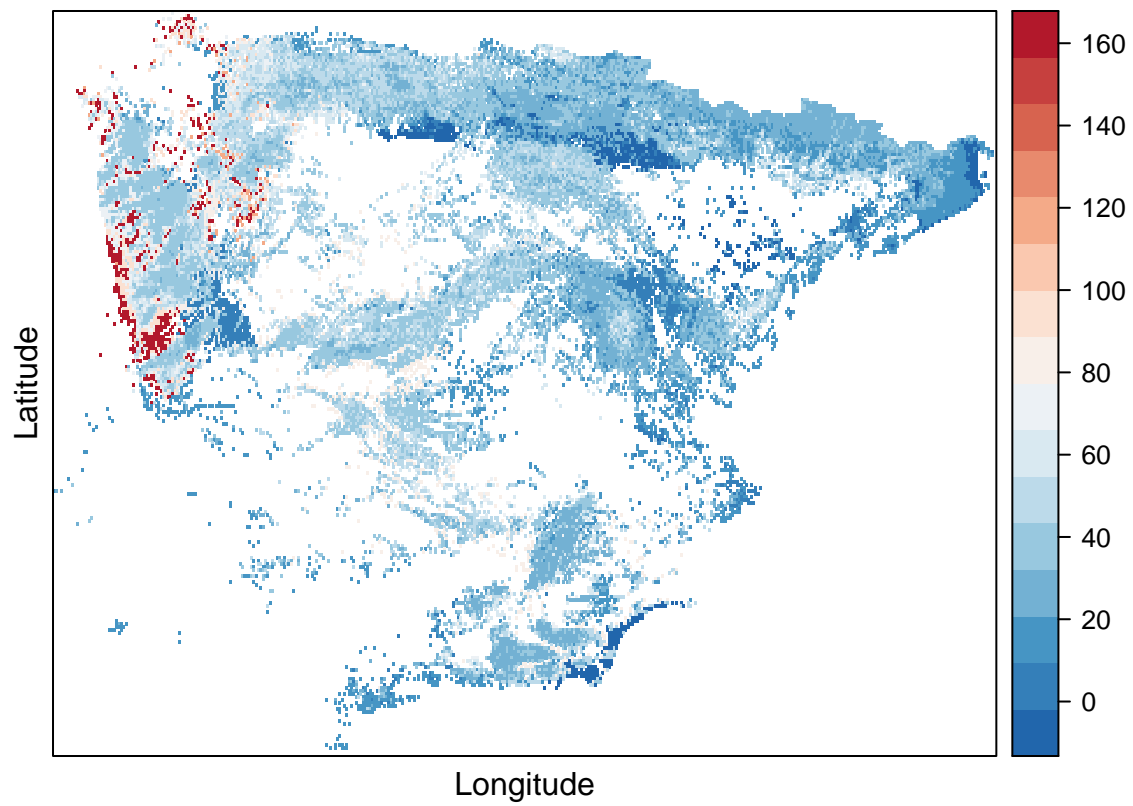**Species Richness**

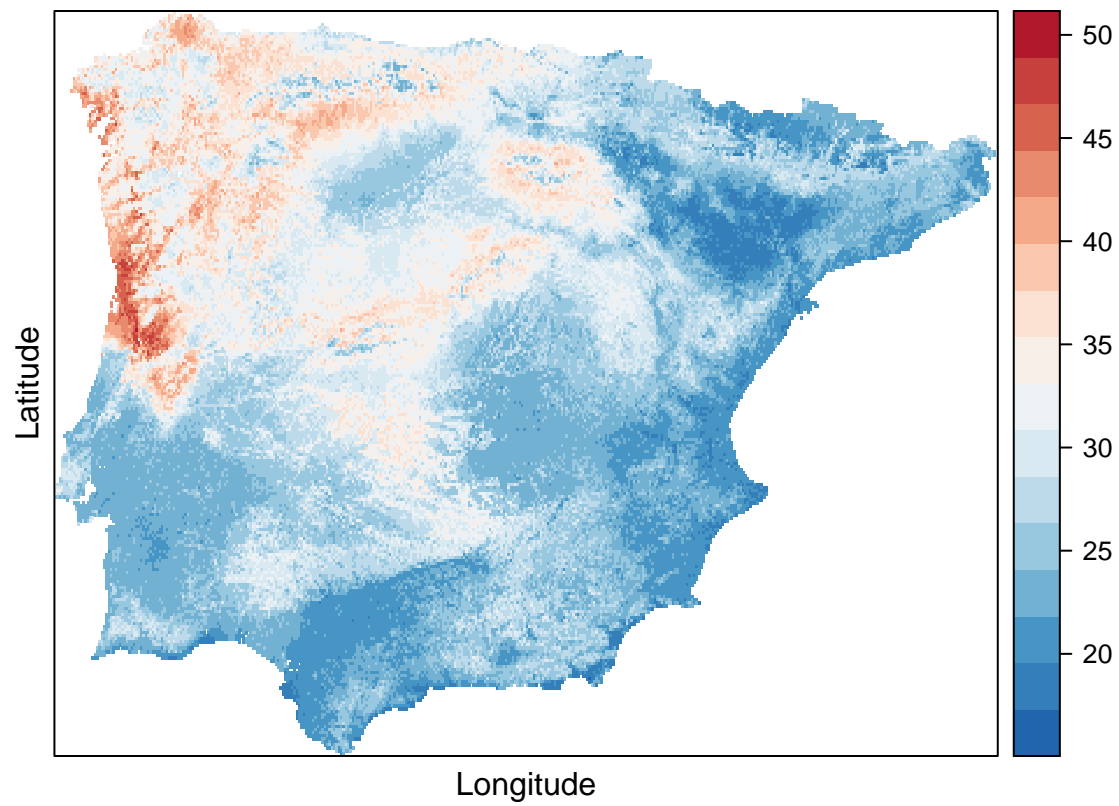Darker green tones depict highest levels of species richness in the map:

NHCVI_bin (binary version, normalized by species richness)

The following map shows the application of (4) with red tones showing less vulnerable areas in contrast to blue tones highlighting more vulnerable areas.
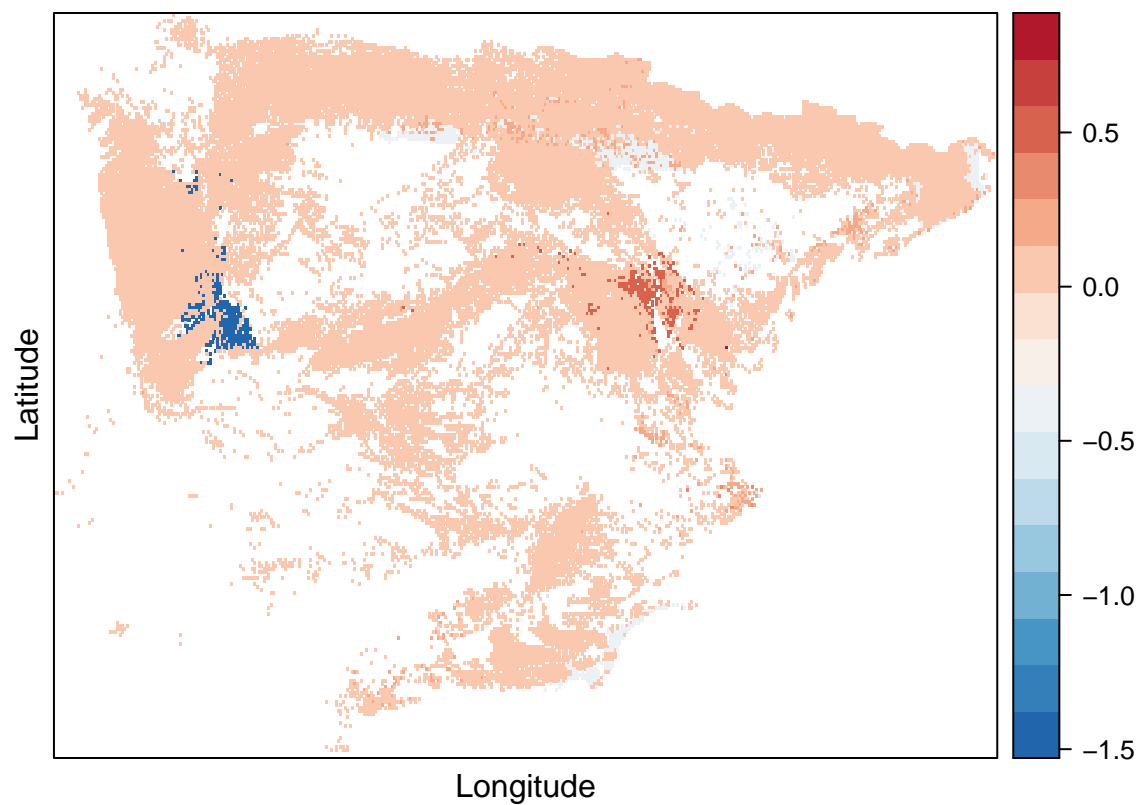
NHCVI_HS (Hab. suit., normalized by habitat suitability sum across all species)

The following map shows the application of (5) with red tones showing less vulnerable areas in contrast to blue tones highlighting more vulnerable areas.

NHCVI_bin' (binary version, normalized by species richness)

The following map shows the application of (6) with blue tones showing less vulnerable areas in contrast to red tones highlighting more vulnerable areas.

NHCVI_HS' (Hab. suitb., normalized by HS sum across all species)

The following map shows the application of (7) with blue tones showing less vulnerable areas in contrast to red tones highlighting more vulnerable areas.
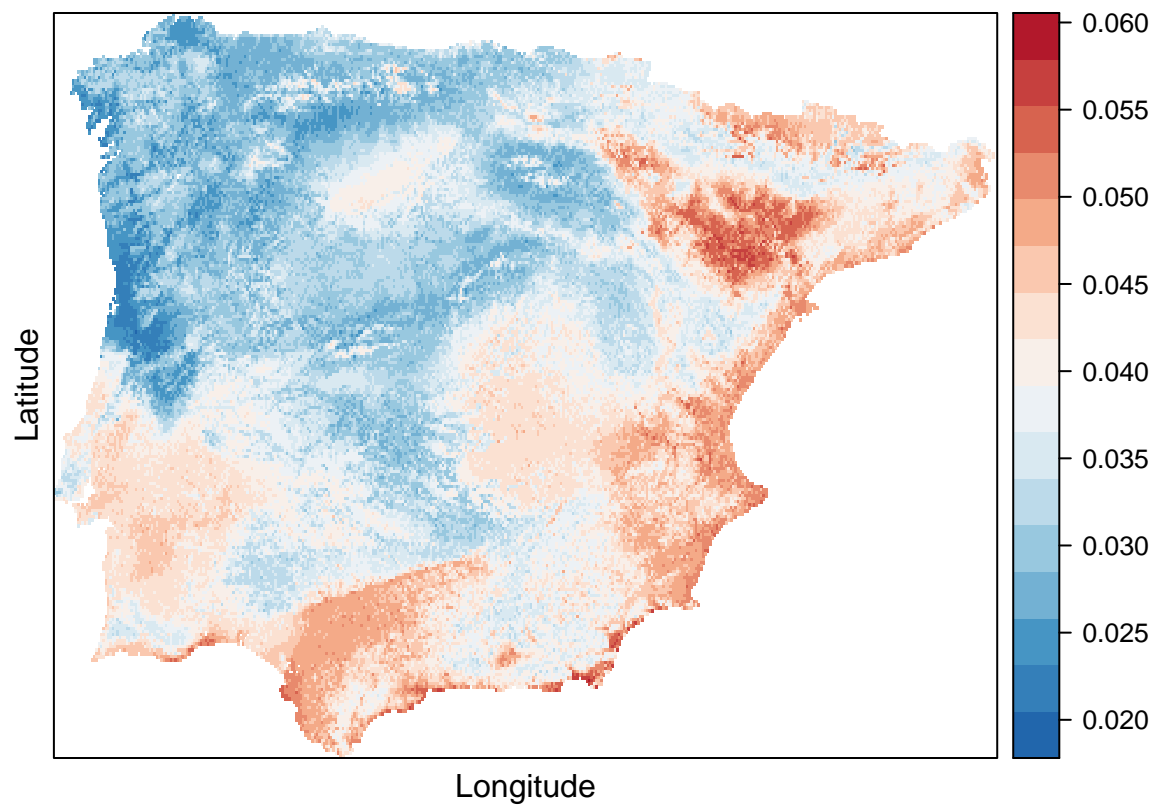
Spearman correlation between NHCVI and Species Richness