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:

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

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:

$$NHCVI'_{bin} = \frac{1}{NHCVI_{bin}} \tag{6}$$

Or:

$$NHCVI'_{HS} = \frac{1}{NHCVI_{HS}} \tag{7}$$

Results

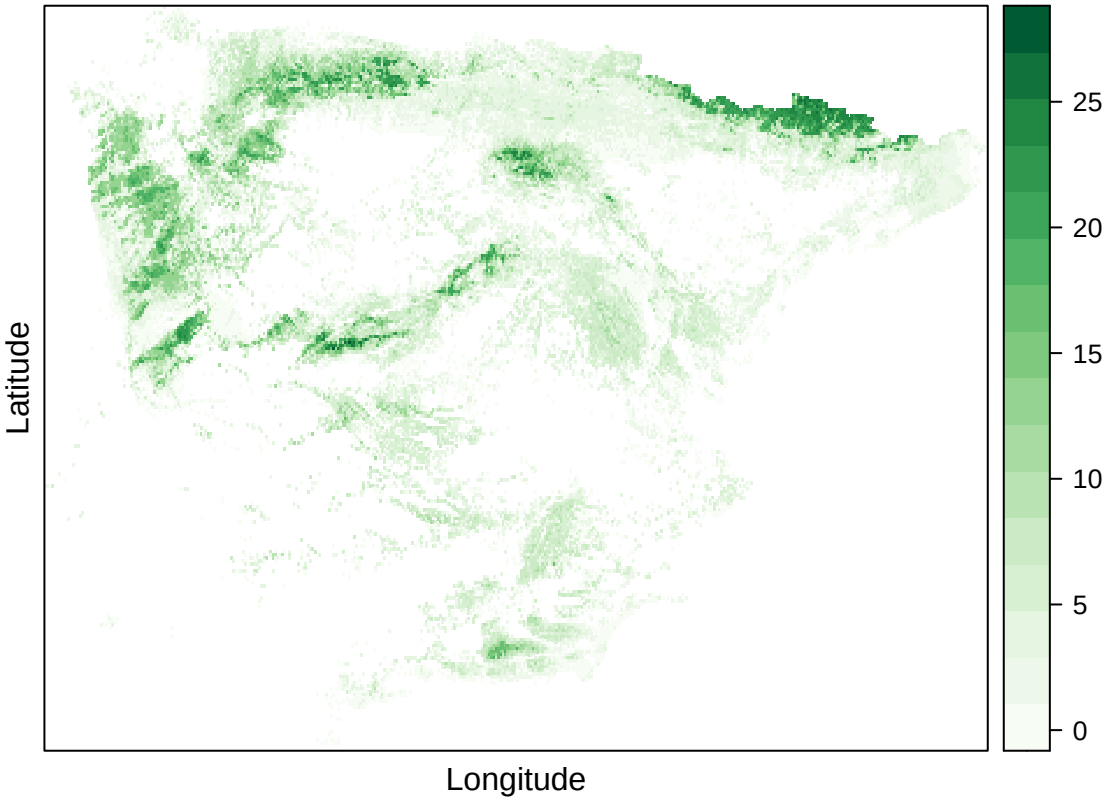
Species ranking in terms of vulnerability

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

Species	NHCVI	NHCVI_norm	NHCVI_n_inv
RACFAS	-4.014	0.000	1.000
ANDALP	-3.340	0.004	0.996
GRIALP	-3.241	0.005	0.995
GRIELA	-2.605	0.009	0.991
GRICAE	-2.532	0.009	0.991
GRIFUN	-2.315	0.011	0.989
ANDNIV	-2.228	0.011	0.989
GRICRI	-2.123	0.012	0.988
GRIMER	-1.797	0.014	0.986
ANDHEI	-1.524	0.015	0.985
ANDMEG	-1.365	0.016	0.984
ANDCRA	-0.724	0.020	0.980
RACOBT	0.123	0.026	0.974
GRIHAR	0.218	0.026	0.974
GRITER	1.353	0.033	0.967
GRIREF	1.504	0.034	0.966
GRIANO	2.150	0.038	0.962
GRITOR	2.939	0.043	0.957
ANDFRI	4.676	0.054	0.946
ANDROT	7.331	0.071	0.929
GRILIS	10.115	0.088	0.912
GRIDIS	10.278	0.089	0.911
GRIOVA	12.432	0.102	0.898
GRIORB	16.710	0.129	0.871
RACSUD	17.878	0.136	0.864
RACMAC	18.930	0.143	0.857
RACHET	21.040	0.156	0.844
RACAFF	21.451	0.158	0.842
GRIMON	32.412	0.227	0.773
GRIDEC	33.072	0.231	0.769
GRILAE	37.114	0.256	0.744
RACLAN	41.143	0.281	0.719
RACCAN	42.624	0.290	0.710
ANDRUP	52.351	0.351	0.649
GRIRAM	55.724	0.372	0.628
GRIPUL	63.954	0.423	0.577
RACAQU	71.314	0.469	0.531
GRITRI	78.970	0.516	0.484
RACELO	156.716	1.000	0.000

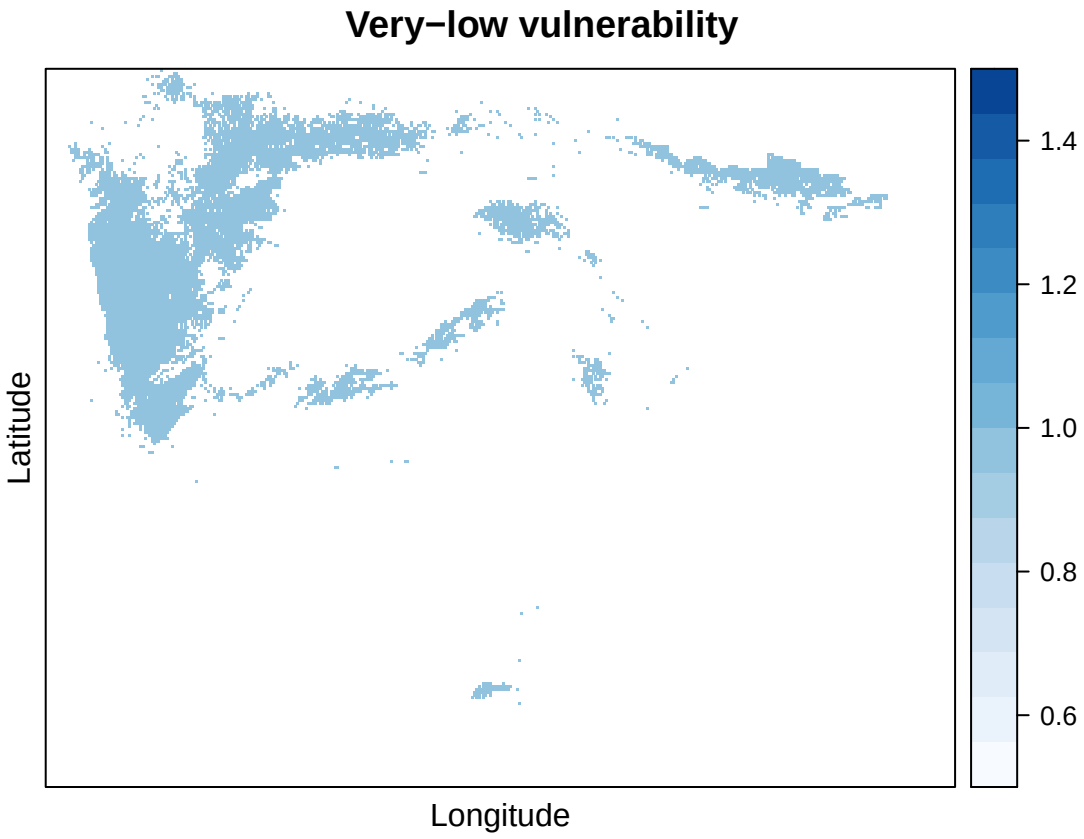
Species Richness

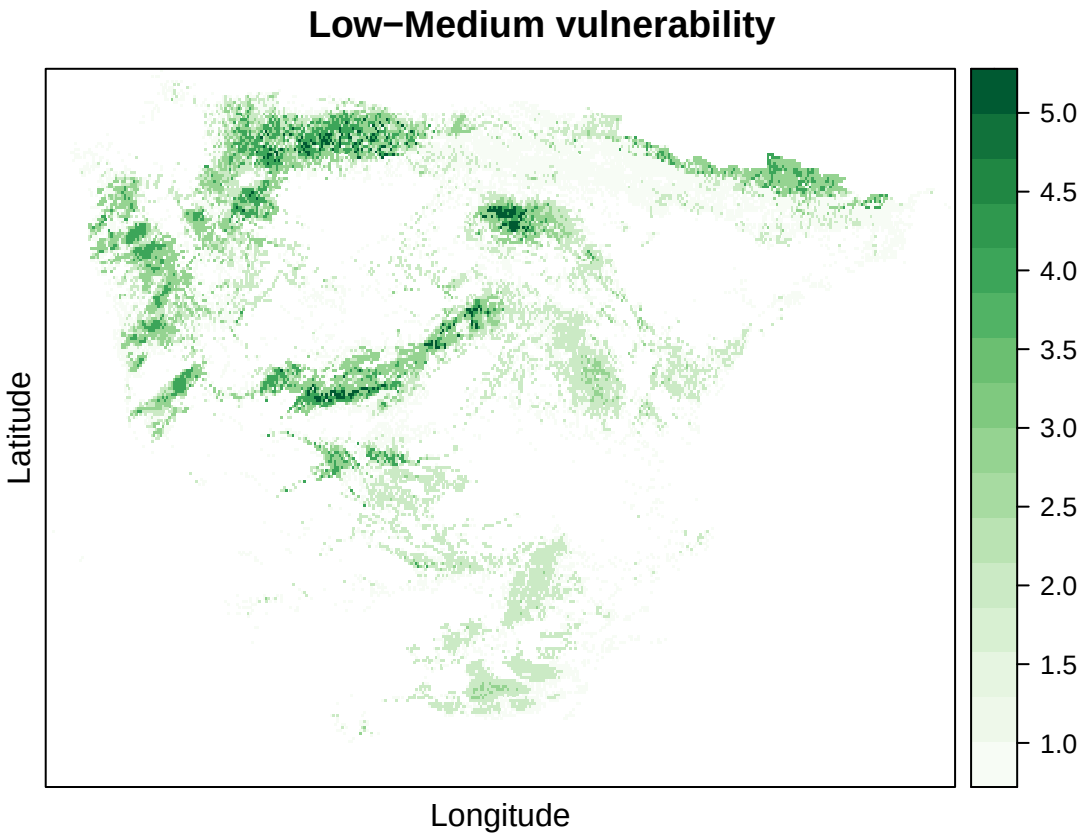
Darker green tones depict highest levels of species richness in the map (pixels with zero species have been converted to NODATA for better visualization):

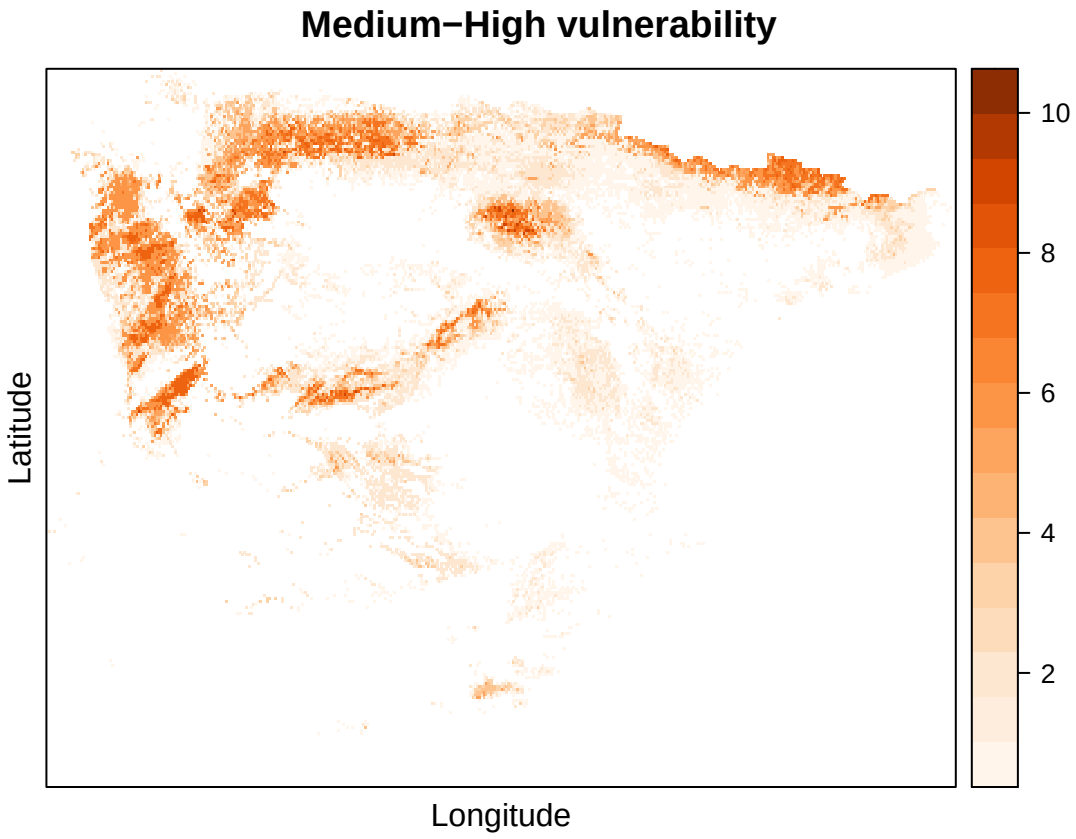


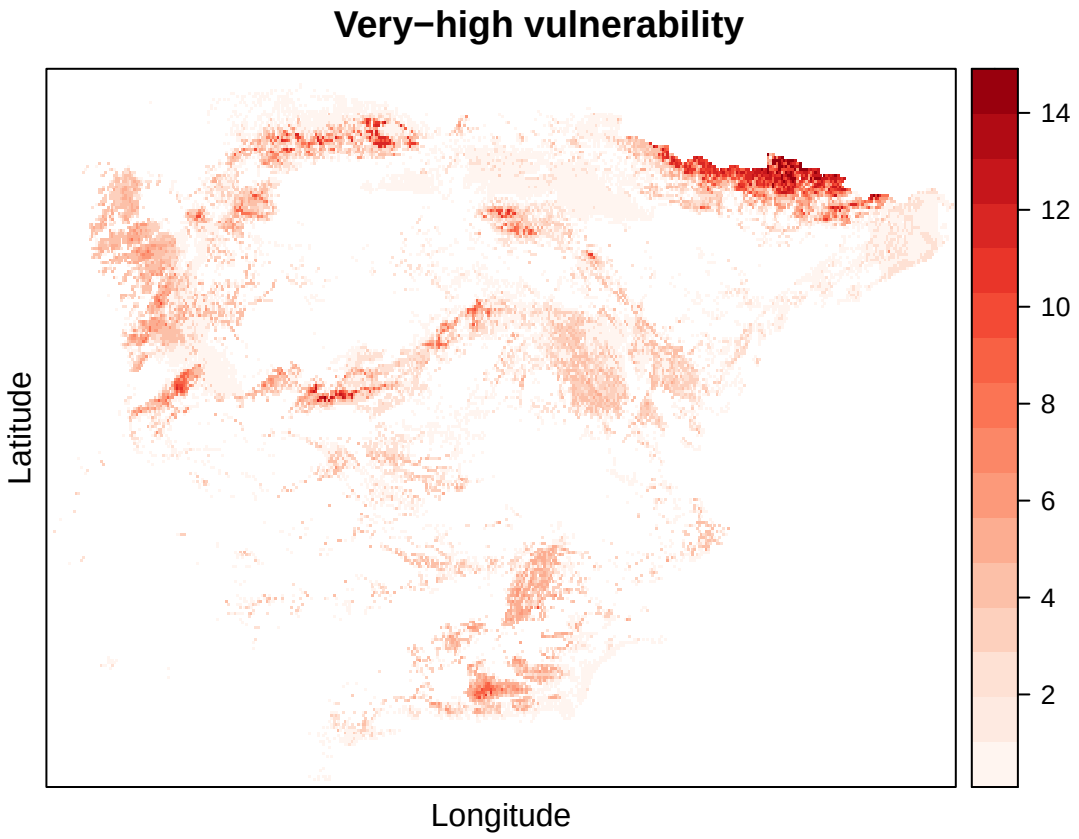
The following maps present species richness across four different levels of species vulnerability:

- Very-low: in blue tones
- Low-Medium: in green tones
- Medium-High: in orange tones
- Very-high: in red.


Very−low vulnerability
Latitude
Longitude
1.4
1.2
1.0
0.8
0.6

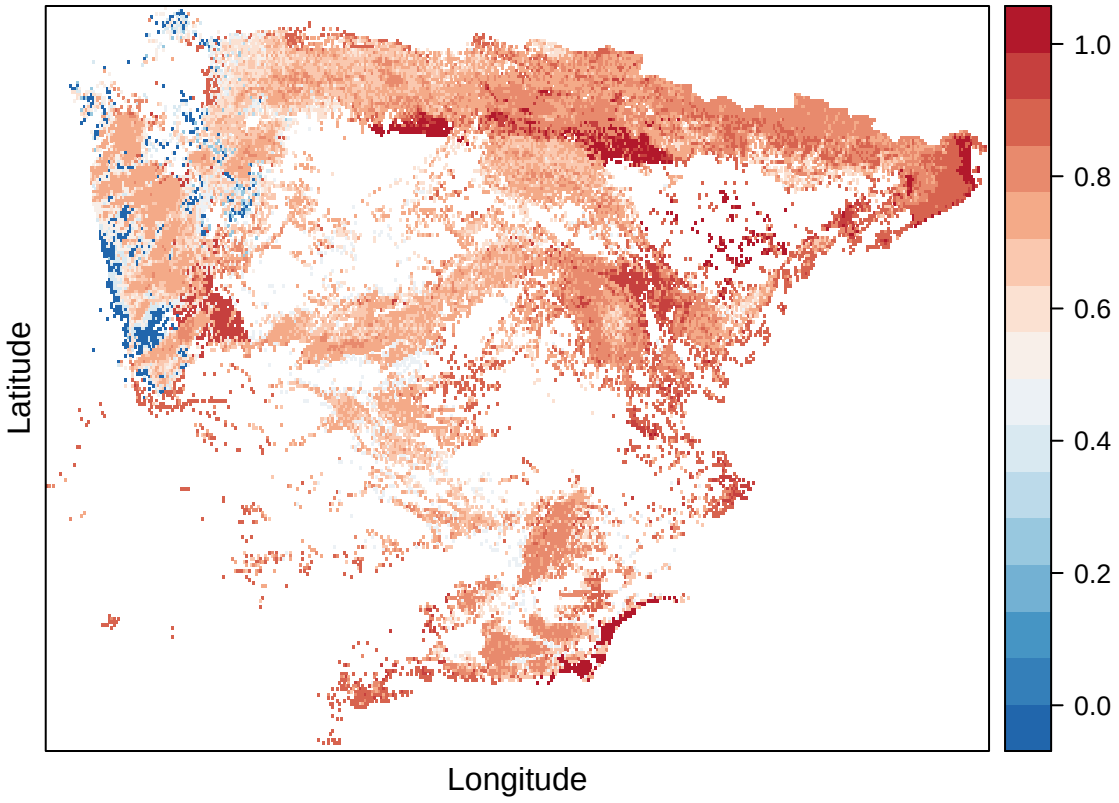

Low−Medium vulnerability
Latitude
Longitude
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0

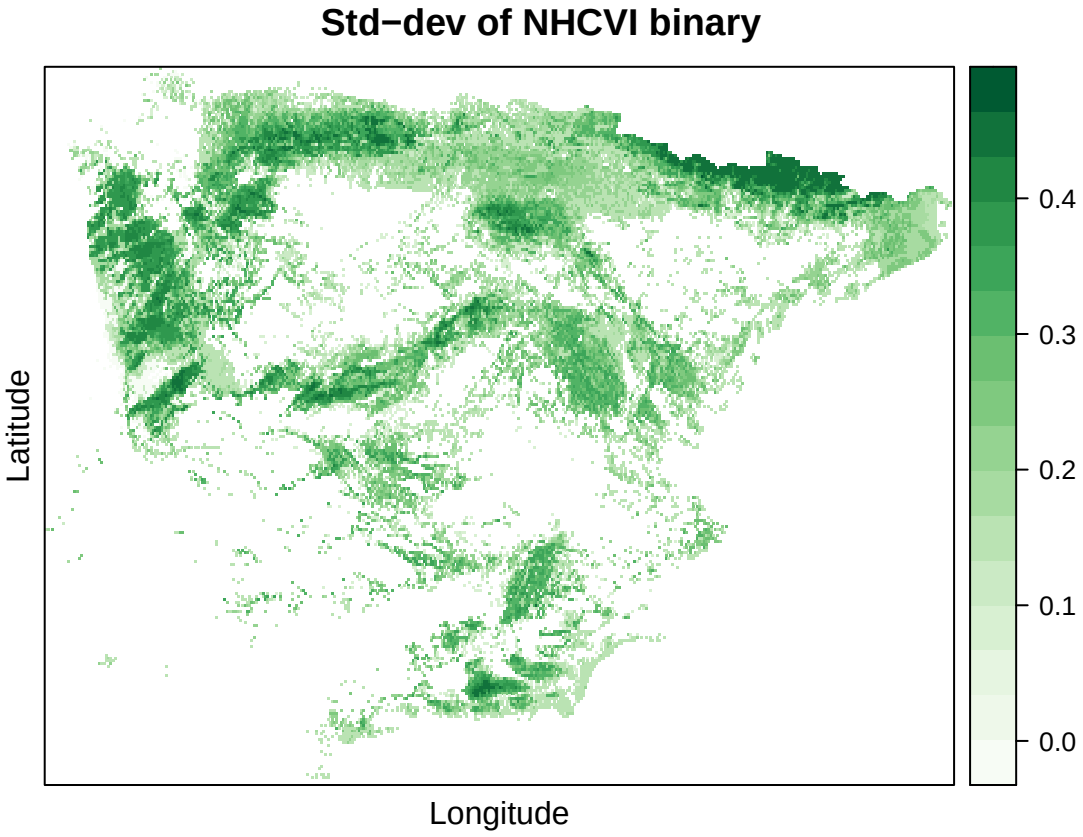

Medium−High vulnerability
Latitude
Longitude
10
8
6
4
2

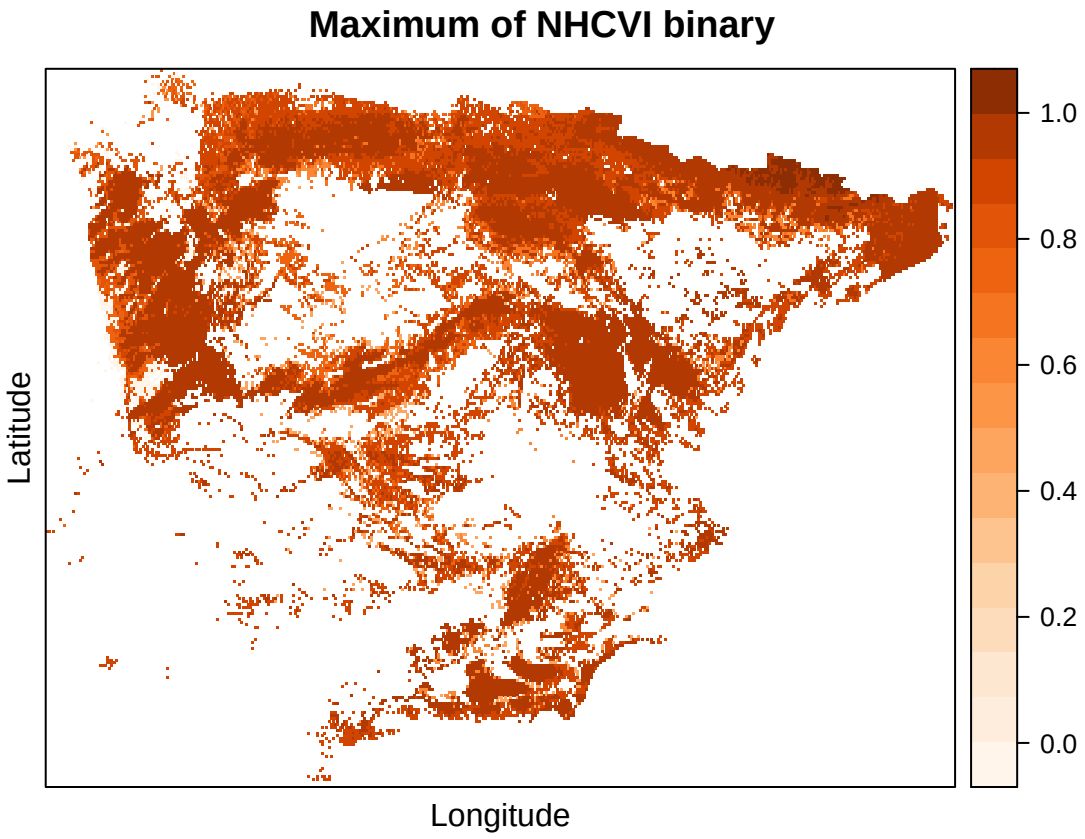


NHCVI_bin (binary version, normalized by species richness)

The following map shows the application of (4) with red tones showing less vulnerable areas in contrast to blue tones highlighting more vulnerable areas.

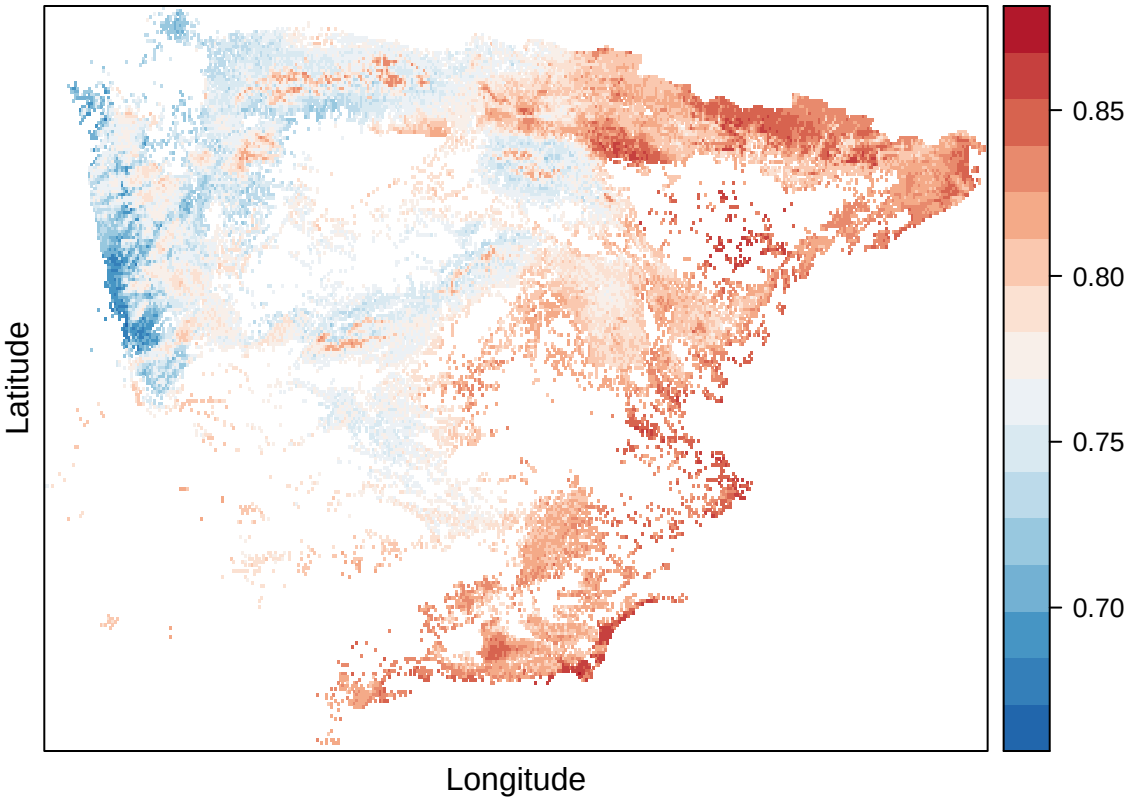

Latitude
Longitude
1.0
0.8
0.6
0.4
0.2
0.0

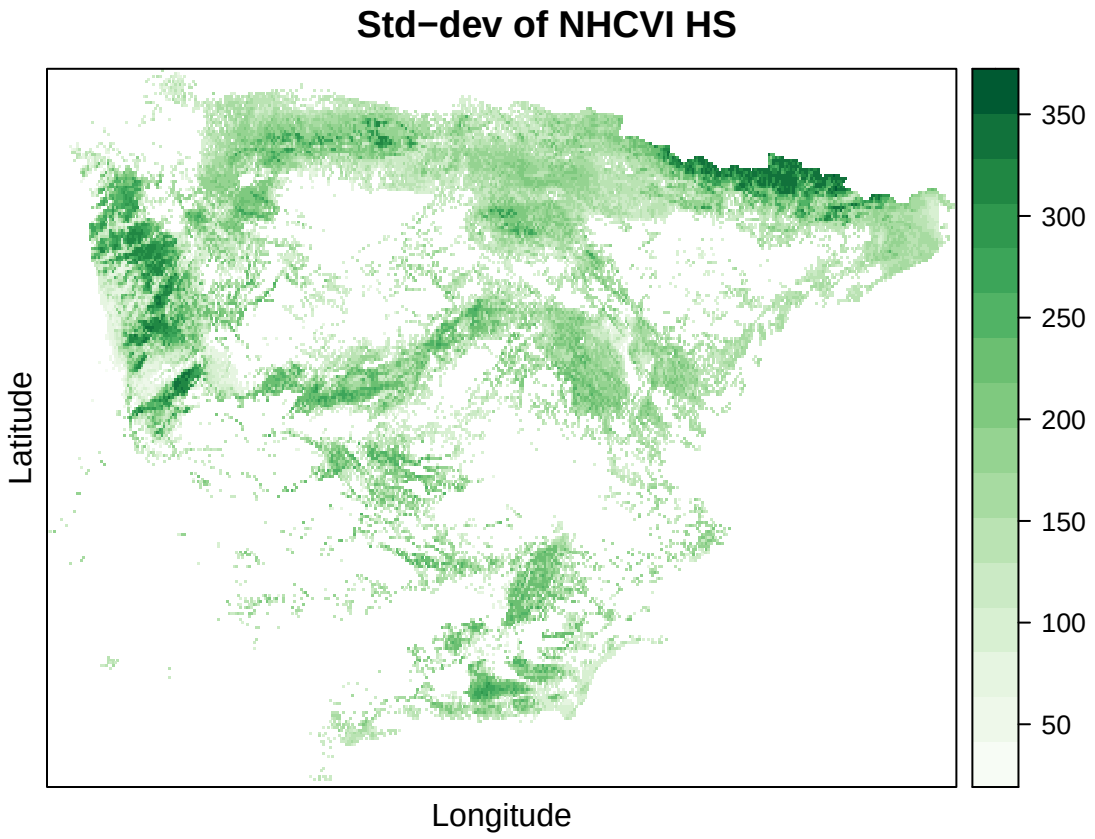

Std−dev of NHCVI binary
Latitude
Longitude
0.4
0.3
0.2
0.1
0.0

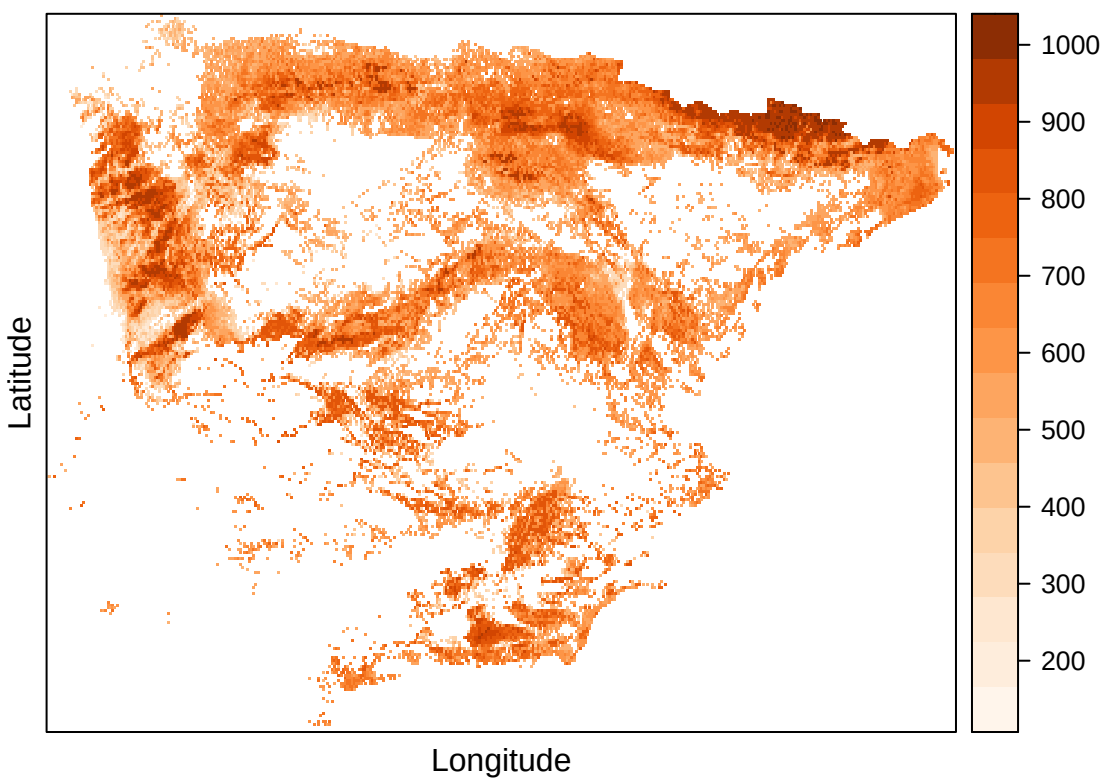


NHCVI_HS (Hab. suit., normalized by habitat suitability sum across all species)

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


Latitude
Longitude
0.85
0.80
0.75
0.70


Std−dev of NHCVI HS
Latitude
Longitude
350
300
250
200
150
100
50


Maximum of NHCVI Hab suitb.
Latitude
Longitude
1000
900
800
700
600
500
400
300
200