

Niche hypervolume community vulnerability index

06/08/2020

Initial definitions

For calculating the NHCVI the following formula is applied to each species i :

$$NHCVI_i = 2N_{b,i} - N_{p,i} \quad (1)$$

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 **Euclidean distance** between the i -th species centroid and the community-wise general centroid.

In a nutshell, this index intends to give maximum vulnerability for species with smaller niche breadth and higher marginality in the community environmental suitable/niche space. The index attributes more weight to niche breadth since this variable was selected in a greater number of times in models explaining range shifts. Nonetheless, this can be changed by defining specific weights to each component of the index as: $NHCVI_i = w_1 N_{b,i} - w_2 N_{p,i}$ with, w_1 and w_2 respectively as the weights for niche breadth and position.

After calculating the $NHCVI_i$ for each species i in the community, values are normalized within the 0 - 1 range as follows:

$$NHCVI'_i = \frac{NHCVI_i - \min(NHCVI_{i=1,\dots,N})}{\max(NHCVI_{i=1,\dots,N}) - \min(NHCVI_{i=1,\dots,N})} \quad (2)$$

The $NHCVI_{i=1,\dots,N}$ represents a vector containing all species values in the community.

Because $NHCVI'_i$ attributes higher values to species less vulnerable, we calculate the reciprocal to make it more easily interpretable as:

$$NHCVI''_i = 1 - NHCVI'_i \quad (3)$$

After calculating [3] we obtain the final vulnerability score for each species in the community. It should be noted that a score of zero in index $NHCVI''_i$ does not mean a species is not vulnerable, this simply derives from the normalization of the score across species in the target community.

Next, to generate a spatial representation of the index we multiply this score by the habitat suitability of each species from the habitat suitability maps from biomod2. This way we attribute higher vulnerability to those locations where the species is more likely to have suitable environmental conditions. Calculations are performed at pixel-level for each species $i = 1, \dots, N$ in the community (with N equal to the total number of species) and implement the following simple formula:

$$NHCVIhs_i = H_{s,i} \times NHCVI''_i \quad (4)$$

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

By applying eqn. [4] we obtain a stack of vulnerability maps, one for each species with each pixel, p (in a particular x,y location) - mapped as: $p \rightarrow (x, y)$ - having a distribution of vulnerability values for the whole community. From this we can aggregate those values, noted as: $NHCVIhs_{i,x,y}$ and calculate certain quantities of interest, such as:

- the **average** / **median** for understanding centrality of vulnerability distribution;
- the **standard-deviation** / **median absolute-deviation** as a measure of dispersion of vulnerability rankings;
- the **Maximum**, as a representation of the greatest level of vulnerability found in a certain x,y location.

Results

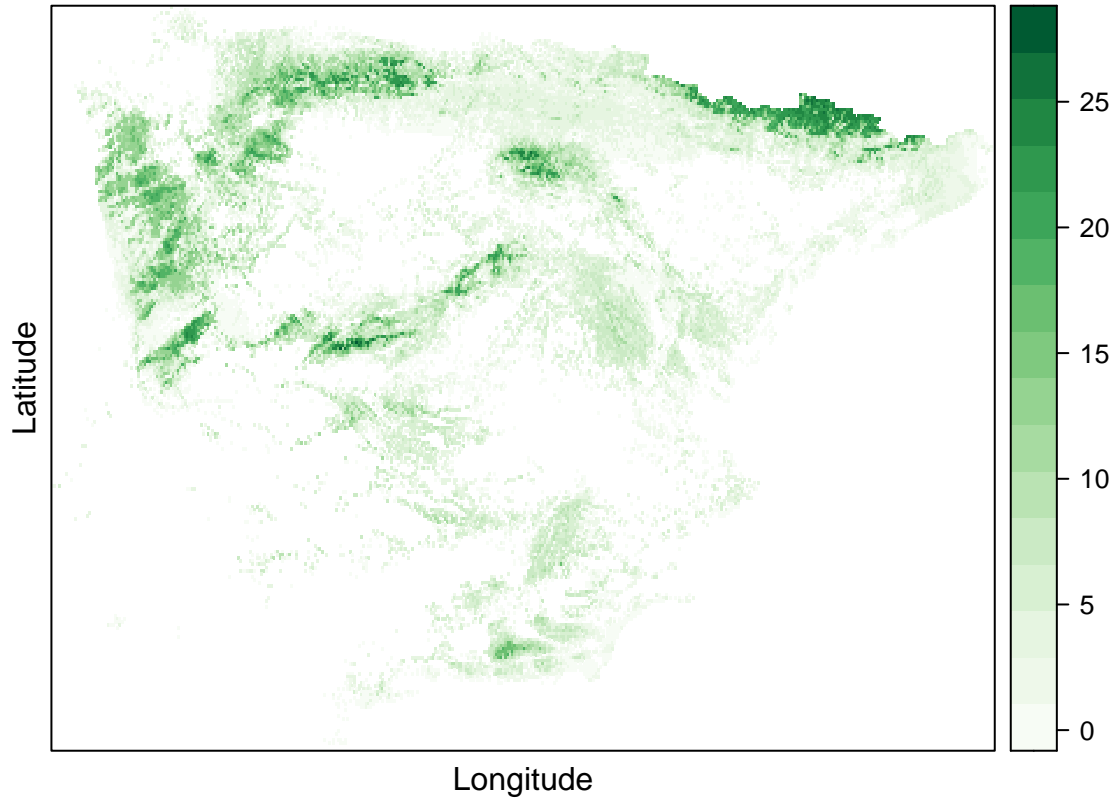
Species ranking in terms of vulnerability

The table is sorted by $NHCVI''$ (eqn. 3) 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

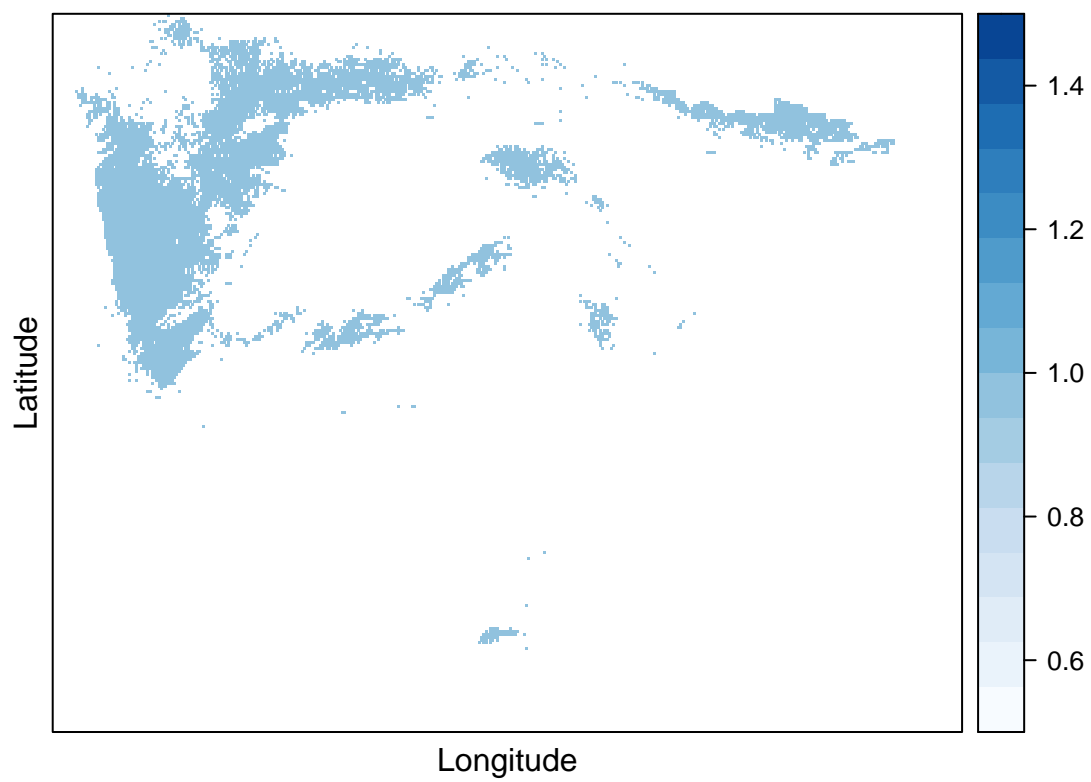
Darker green tones depict highest levels of species richness in the map (pixels with zero species have been converted to NODATA for better visualization):



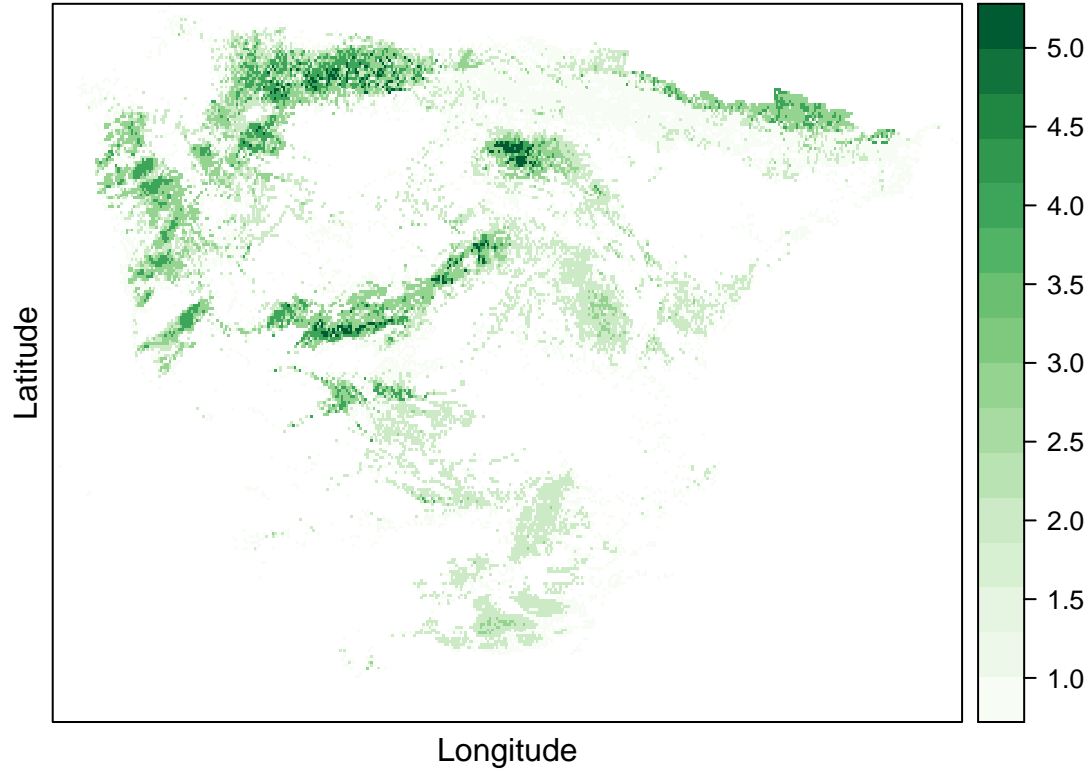
The following maps present species richness across four different levels of species vulnerability:

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

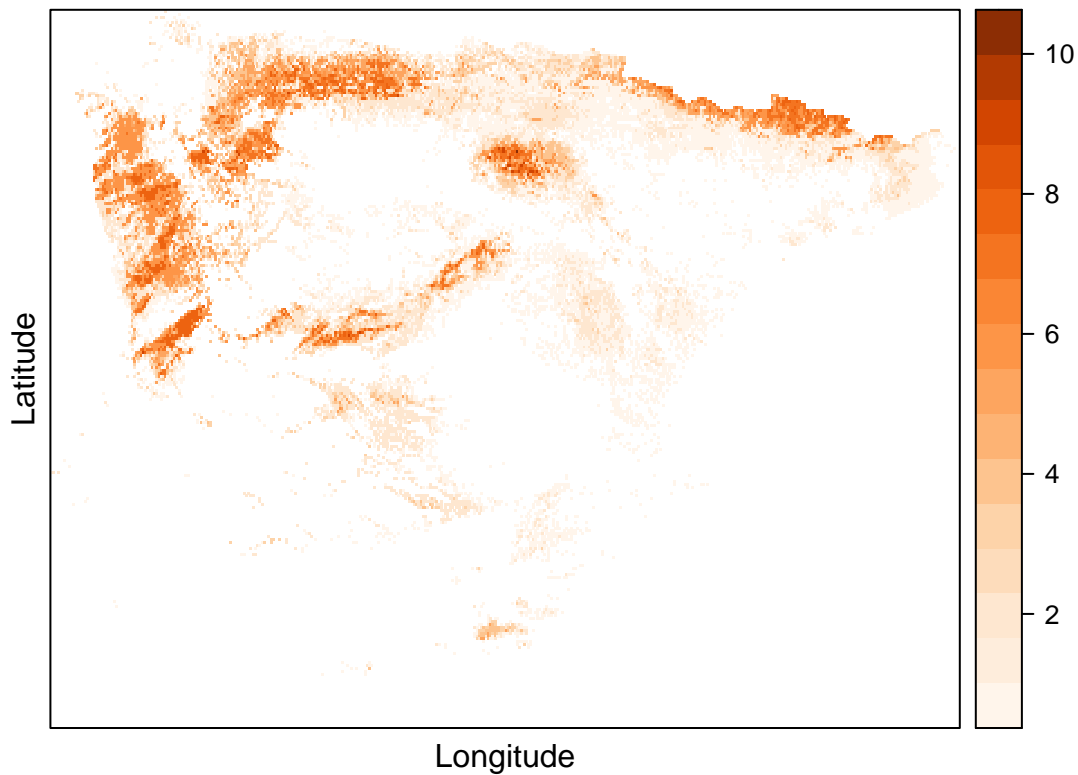
Very-low vulnerability



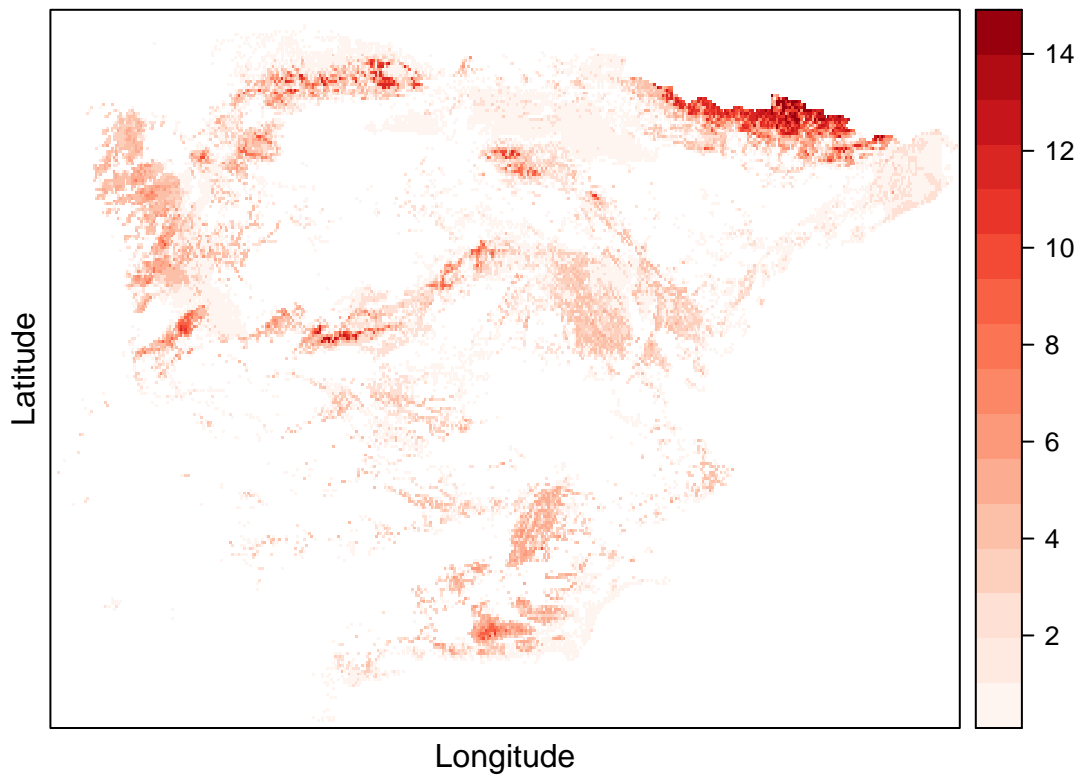
Low-Medium vulnerability



Medium-High vulnerability



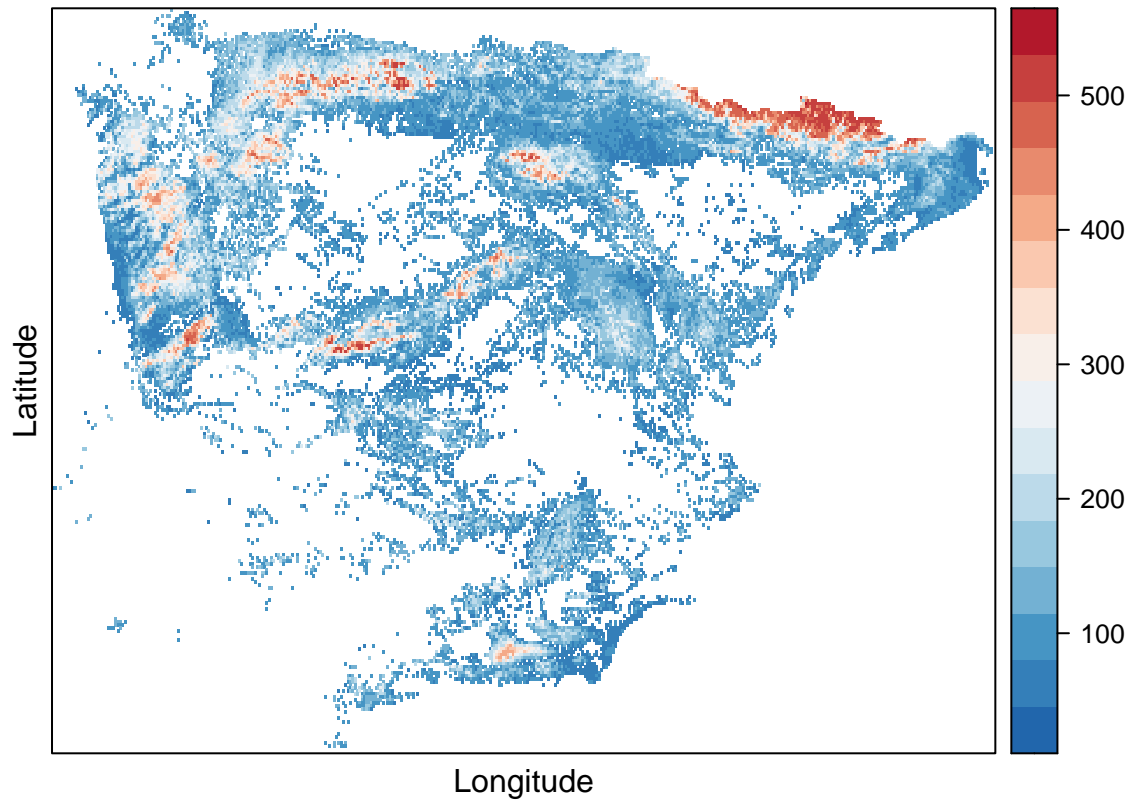
Very-high vulnerability



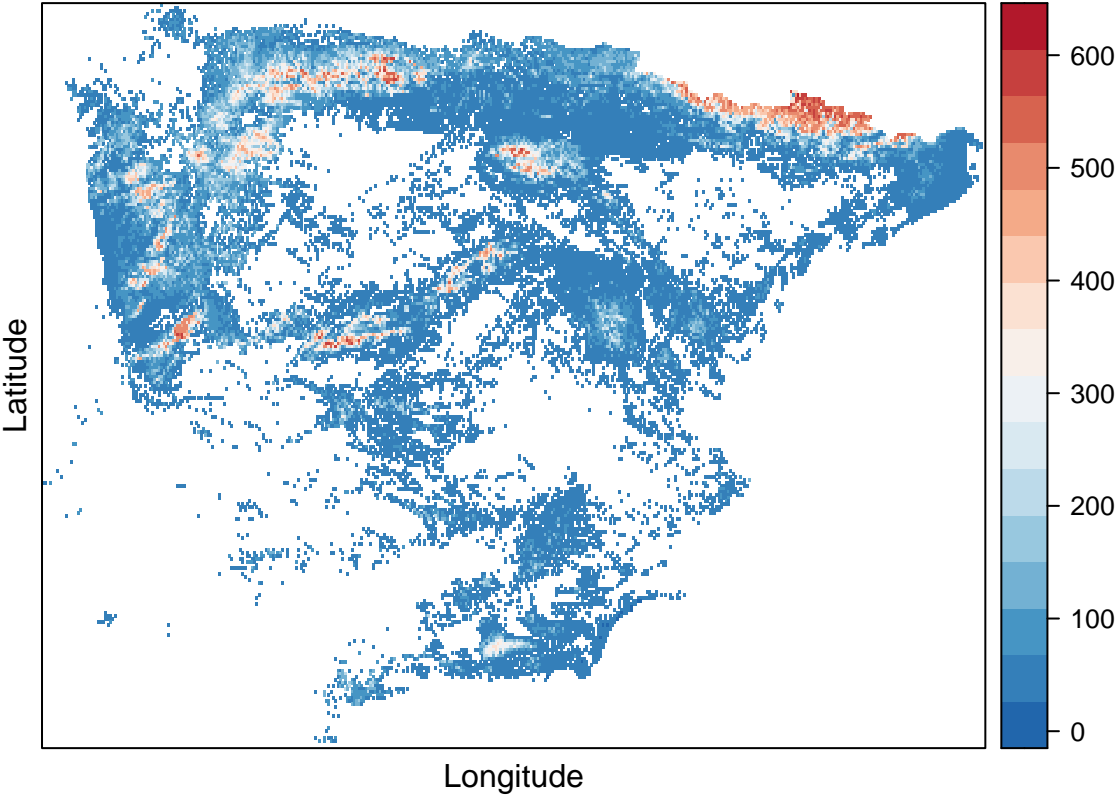
NHCVI_HS

The following map shows the application of different statistical aggregation measures to NHCVIhs with red tones showing less vulnerable areas in contrast to blue tones highlighting more vulnerable areas.

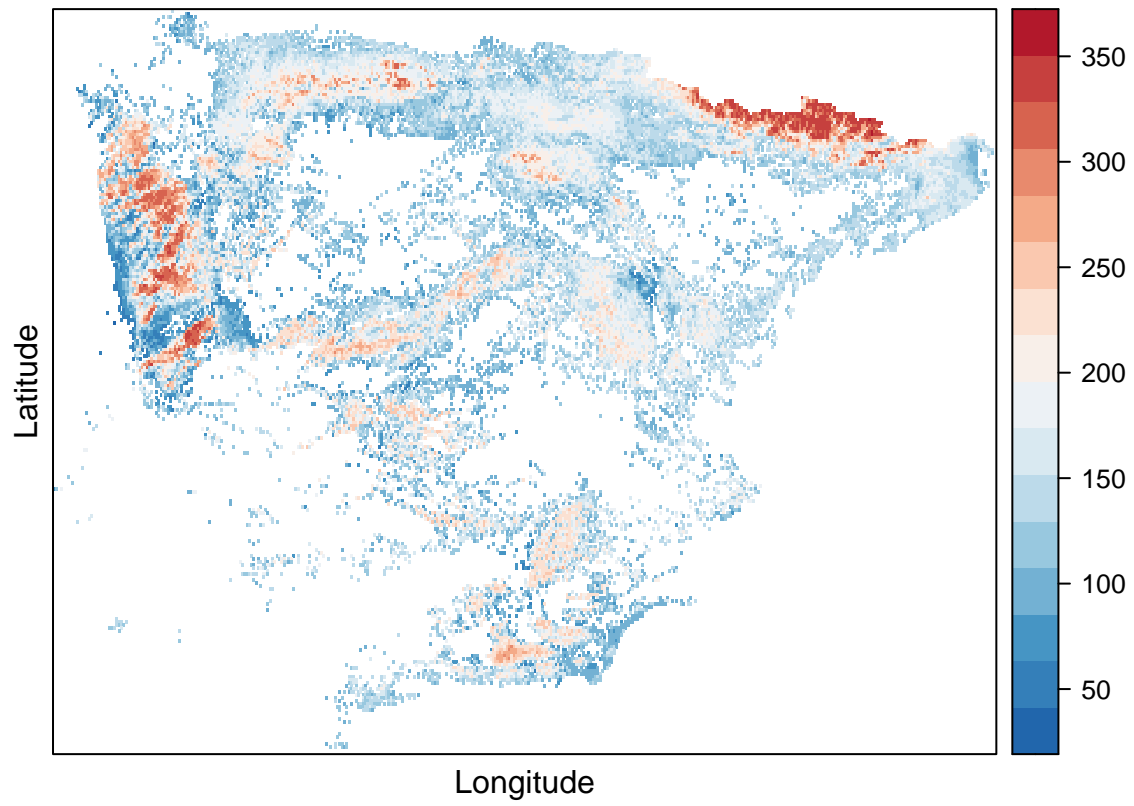
NHCVI_HS average NHCVI_HS average



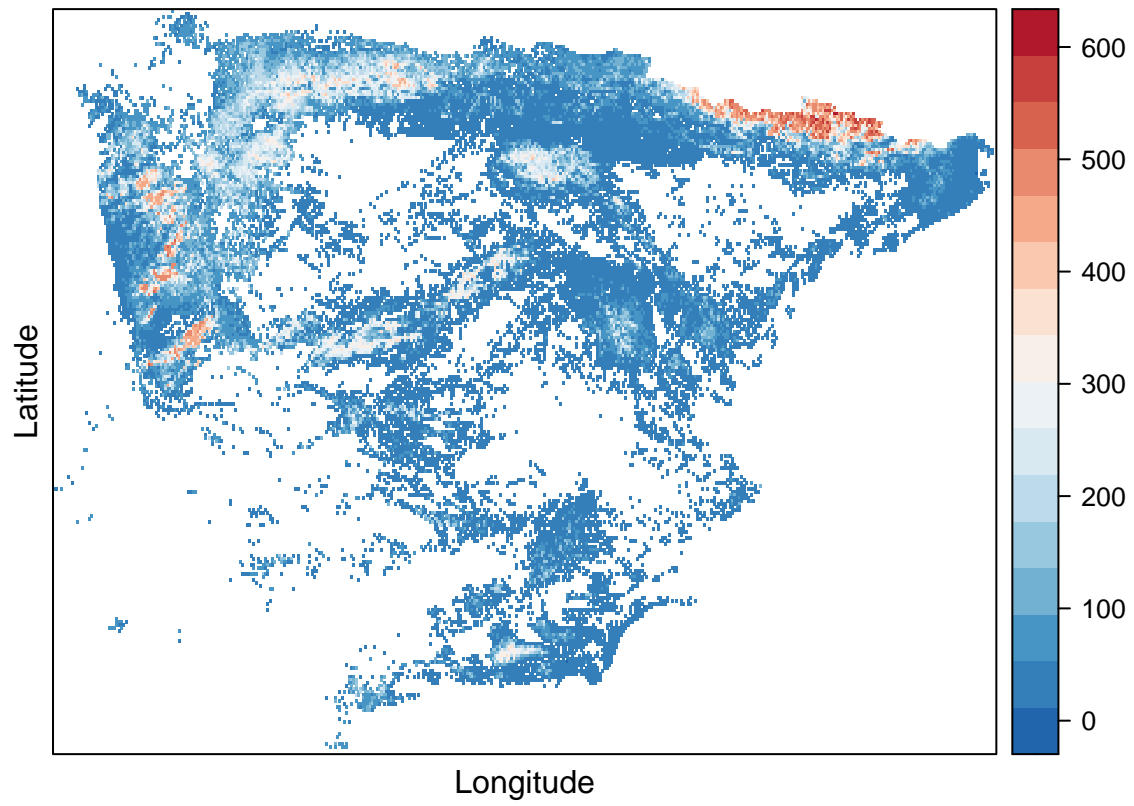
NHCVI_HS median NHCVI_HS median



NHCVI_HS standard-deviation NHCVI_HS standard-deviation



NHCVI_HS median absolute-deviation NHCVI_HS median absolute-deviation



NHCVI_HS maximum NHCVI_HS maximum

