

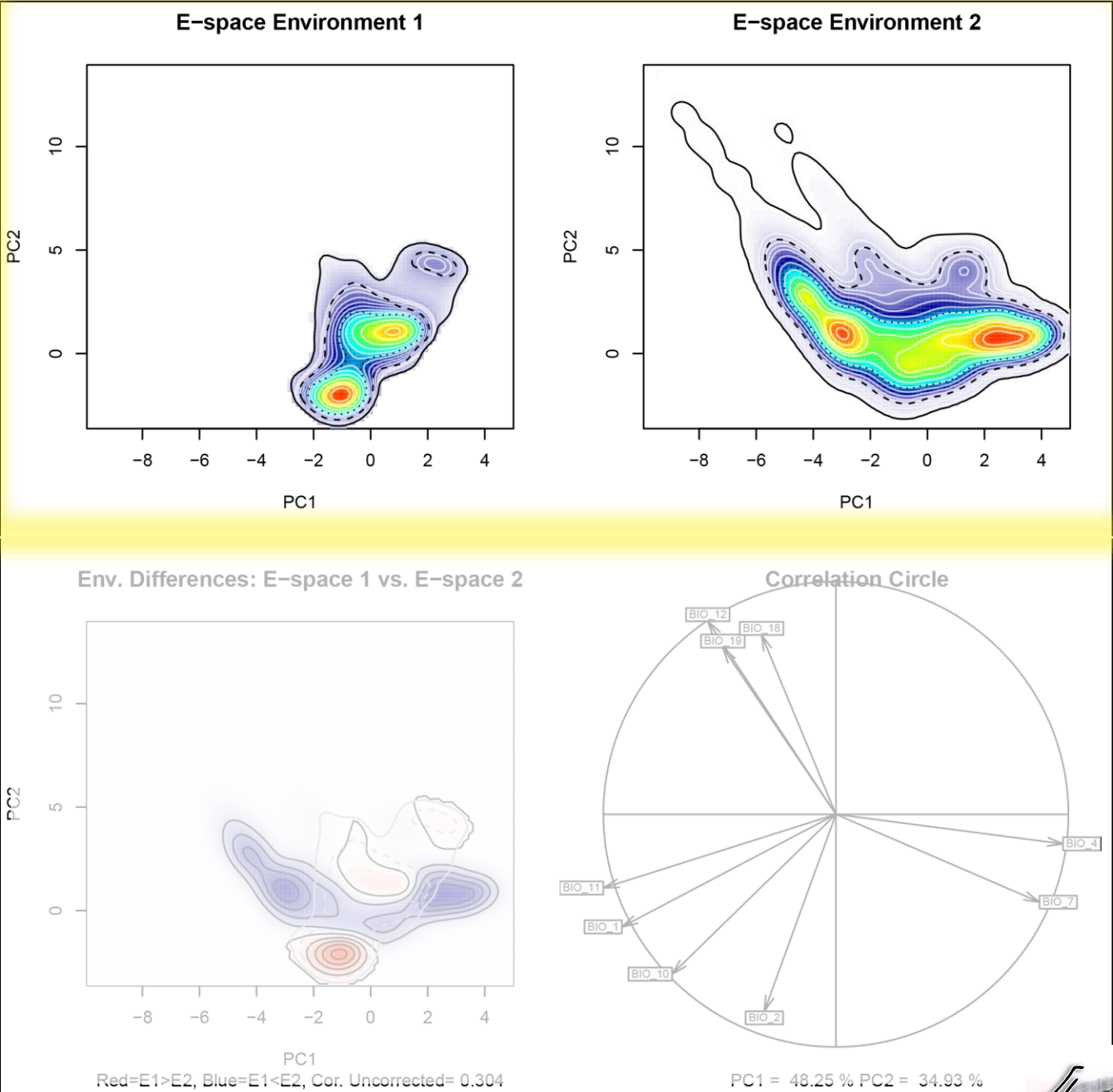
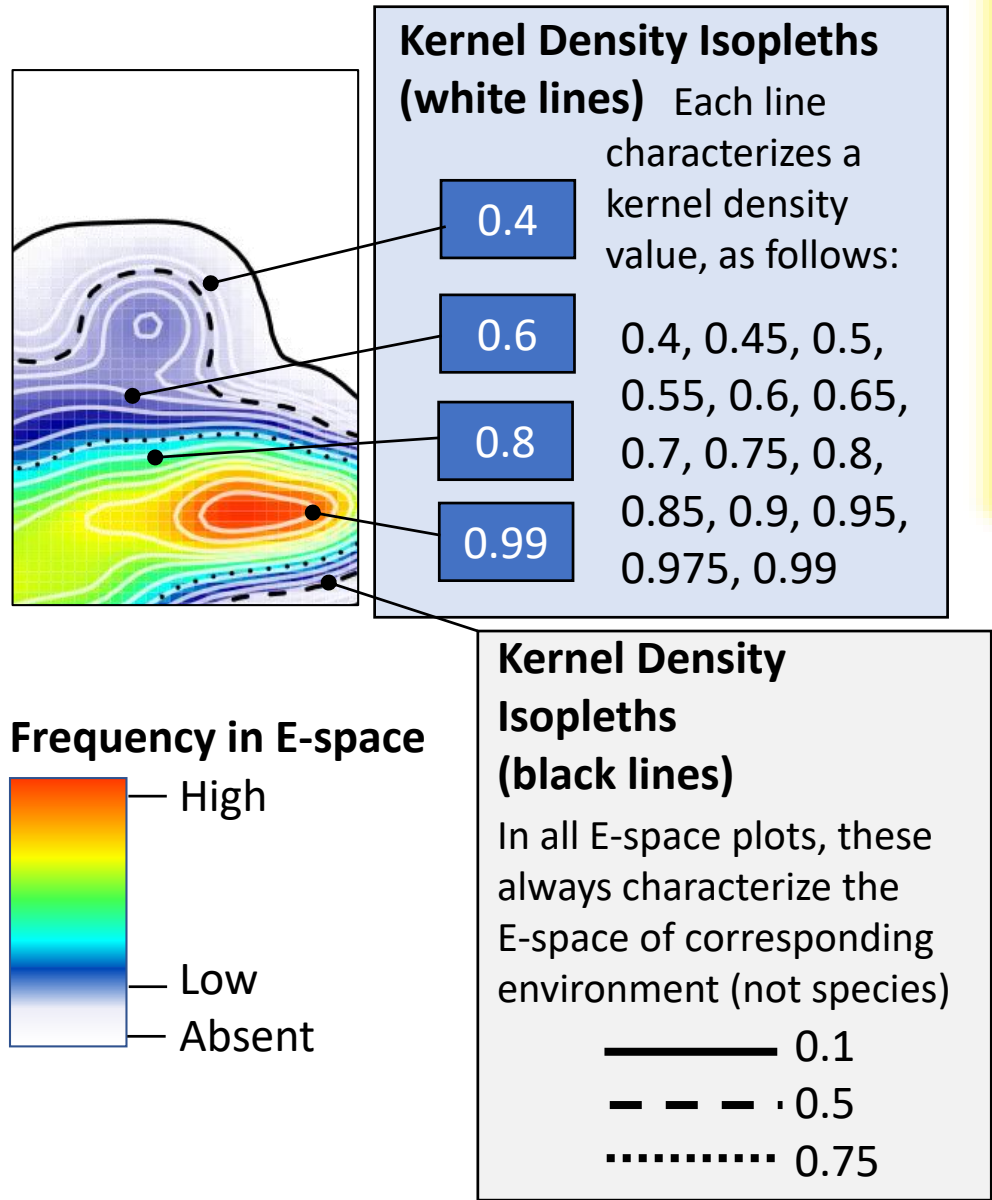
Explanation of figures output from *humboldt::humboldt.doitall*

<https://github.com/jasonleebrown/humboldt.git>

<http://www.jasonleebrown.org>

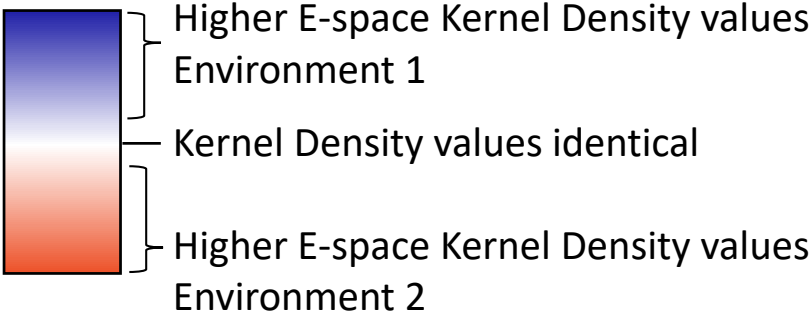


Plots of E-space of Environment 1 & 2



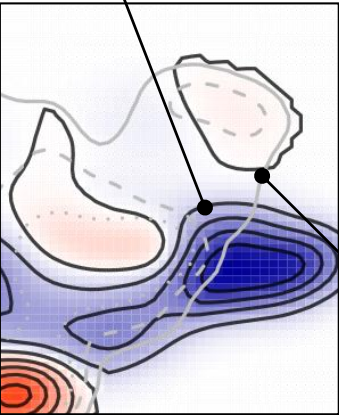
Environment Differences in E-space

Comparison of Environment E-space Frequencies



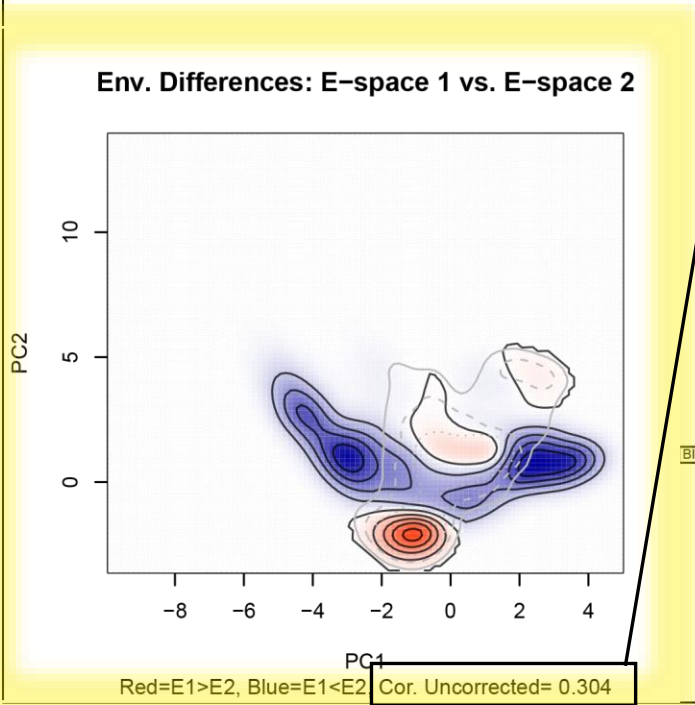
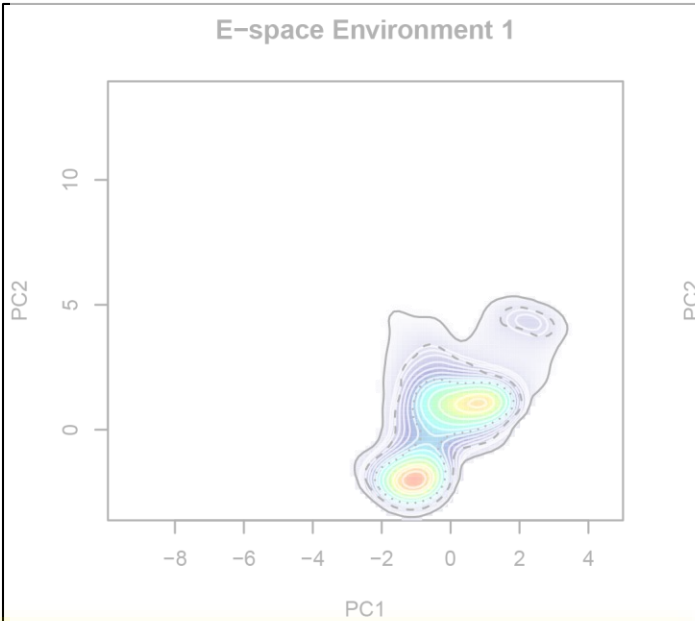
Difference Isopleths (black lines)

In all E-space Difference plots, the black lines characterize isopleths of corresponding to the differences between two E-spaces. The values vary among situations and represent equal intervals between max and min values.



Kernel Density Isopleths (grey lines)

In all E-space Difference plots, the grey lines characterize the E-space of corresponding to environment 1



E-space correction of environmental abundance test

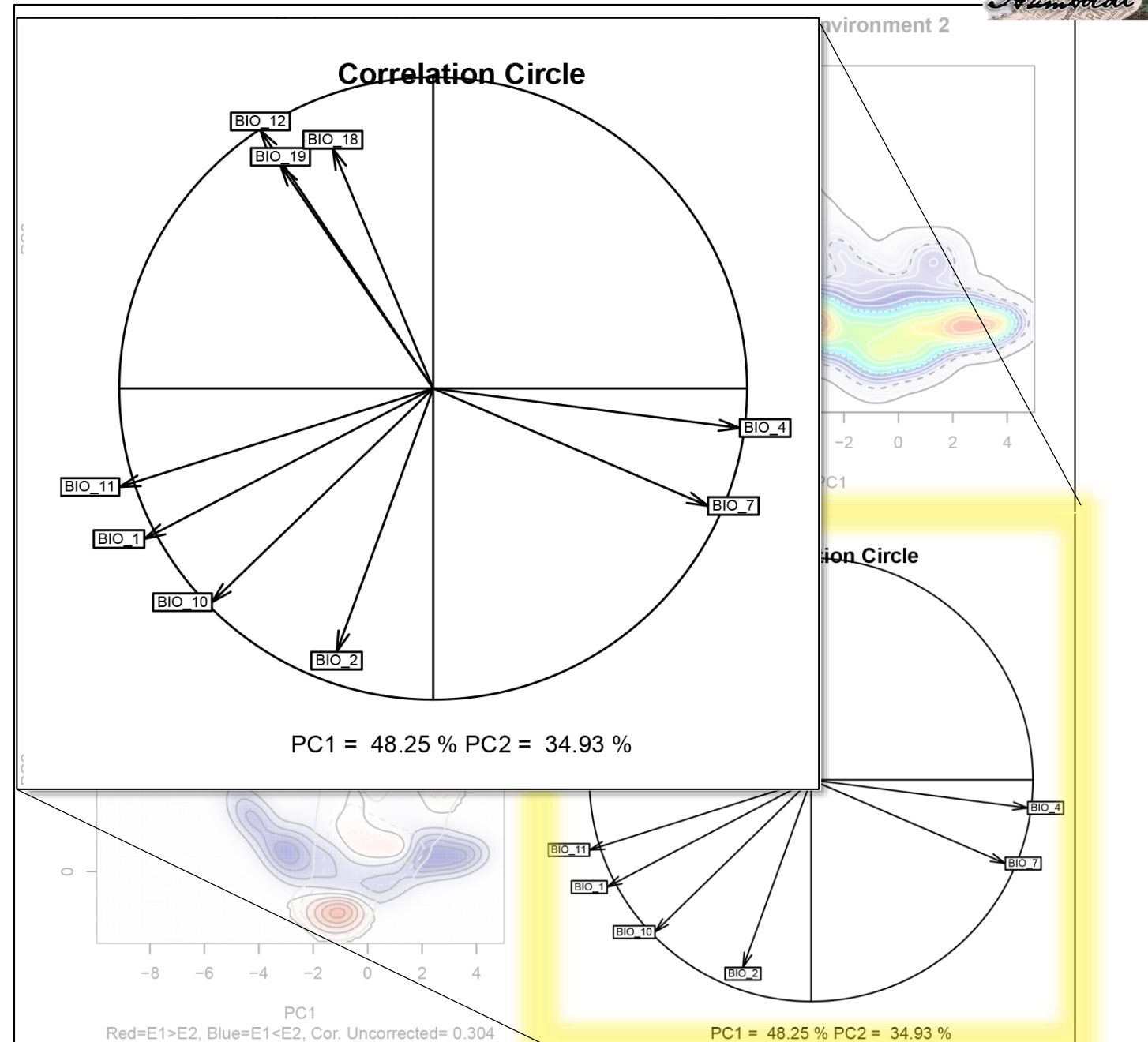
Determines if users should correct occurrence densities of each species by the prevalence of the environments in their range for Equivalency, Background, and overlap analyses (correct.env=T). Often datasets have high overlap among the differences between input environments and the differences between species distributions in environmental space. If ignored, equivalency tests are prone to type I errors and you may observed statistical differences that are entirely due to differences in the availability of environments vs. actual differences in occupied environmental space. When highly correlated, it is strongly encouraged to use 'correct.env=T' to correct E-space observations by abundance of environments.

The value depicted is the uncorrected value.

E-space correlation circle of original data

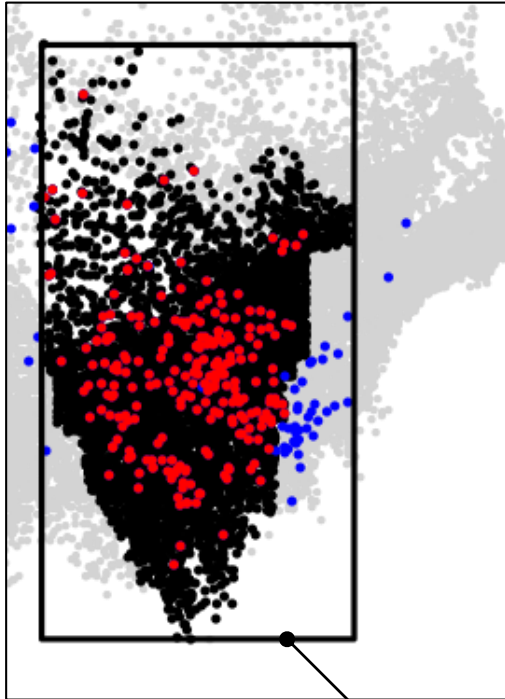
Our PCA reveals that 83.18% (or separately, PC1= 48.25% and PC2= 34.93%) of the variance in my environmental data input can be represented in a 2-dimensional E-space. The dimension with the most explained variance is called PC1 and plotted on the horizontal axes, the second-most explanatory dimension is called PC2 and placed on the vertical axis. Inside this 2-dimensional circle the original 10 variables are projected onto this 2-dimensional E-space. If 2 arrows are pointing in the same direction (i.e. Bio_19 and Bio_12) then they are highly correlated. If they are orthogonal (at a 90 degree angle, i.e. Bio_2 and Bio_4) they are unrelated and if they are pointing in opposite directions they are negatively correlated (i.e. Bio_11 and Bio_4). Some are best represented by only 1 PC axis (i.e. Bio_4) and others are represented by both PCs (i.e. Bio_10).

The length of the an arrow represents how well the parameter explains the distribution of the data. A parameter with an arrow that is clearly longer than others has a better correlation (i.e. Bio_12 vs Bio_19). Here, most arrows have a similar length, so the parameters contribute equally.



File name: *_ENV2.pdf

Plots of G-space vs. E-space of Environment 1 & 2

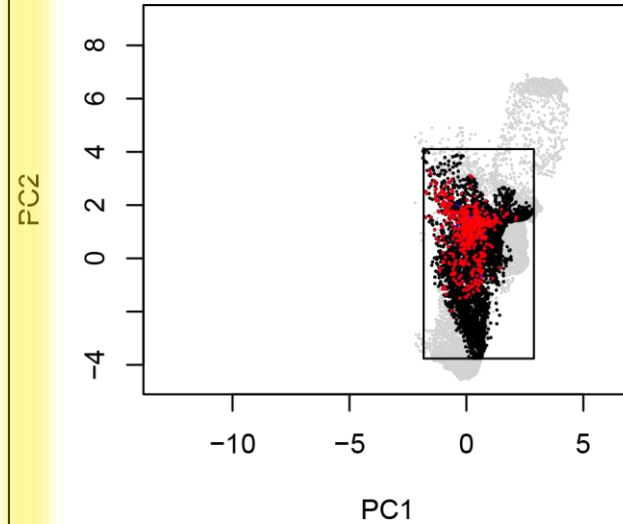


- Occurrence localities **retained** after E-space is reduced to analogous environments
- Occurrence localities **removed** after E-space is reduced to analogous environments
- E-space **retained** after E-space is reduced to analogous environments
- E-space **removed** after E-space is reduced to analogous environments**

Black box depicts shared E-space (based only on maximum and minimum values of each PCs). If non.analogous.environments= "YES", all values within this box will be retained** If non.analogous.environments= "NO", only areas shared between both environments are retained within this box.

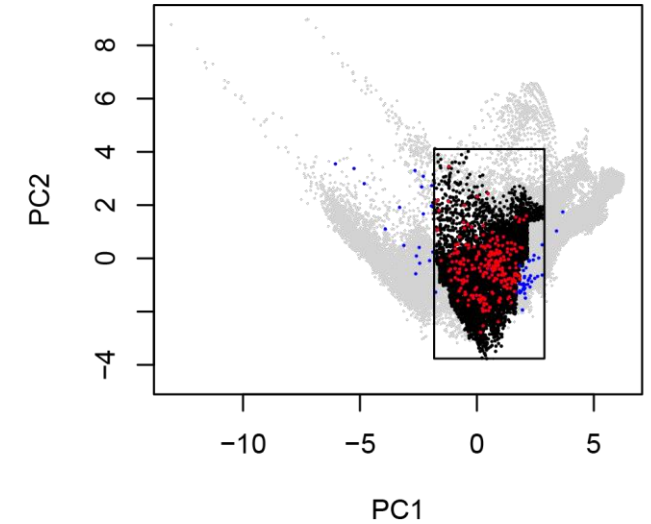
***points can also be removed via the 'env.trim' parameter, which trims input environments in geographic space to a buffered minimum convex polygon of the focal species occurrence localities. This reduces the input environmental space to accessible habitats to the focal species.*

E-space Environment 1



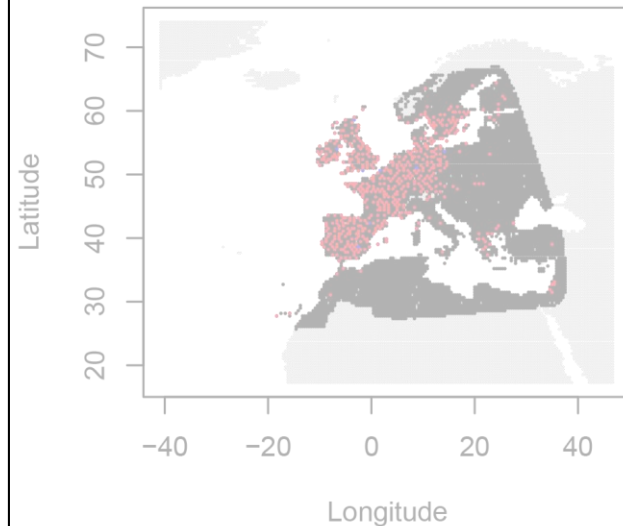
Removed: 8185 sites of 14095 (58.1 %); 8 locs of 554 (1.4 %)

E-space Environment 2



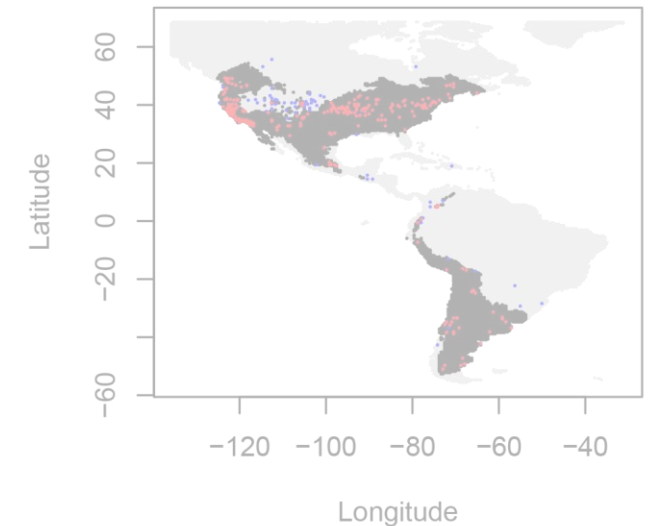
Removed: 17231 sites of 23758 (72.5 %); 60 locs of 299 (20.1 %)

G-space Environment 1



Removed: 8185 sites of 14095 (58.1 %); 8 locs of 554 (1.4 %)

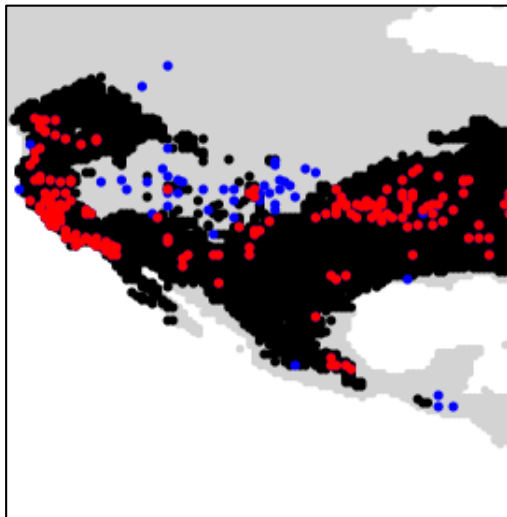
G-space Environment 2



Removed: 17231 sites of 23758 (72.5 %); 60 locs of 299 (20.1 %)

File name: *_ENV2.pdf

Plots of G-space vs. E-space of Environment 1 & 2

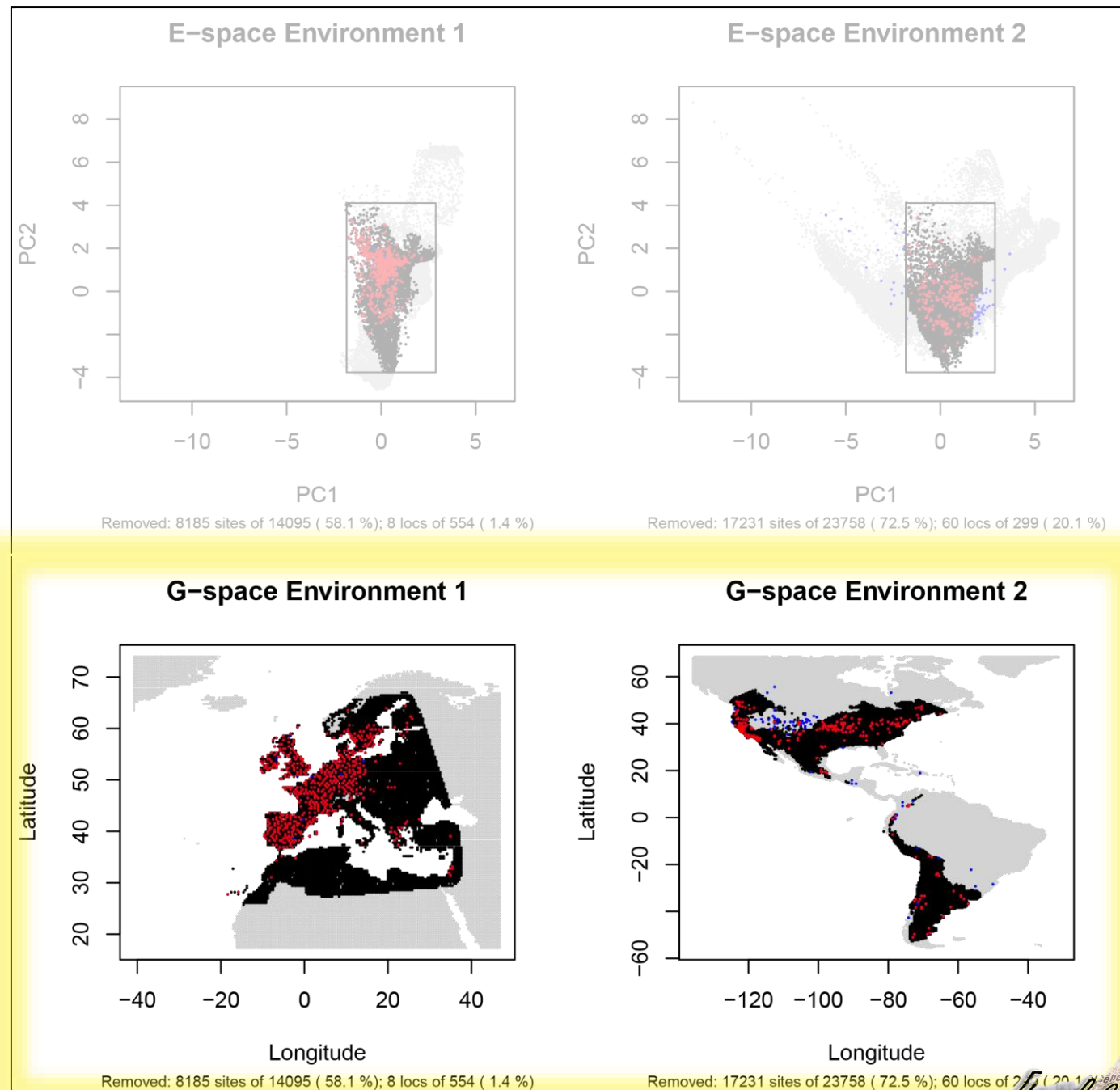


Removed: 17231 sites of 23758 (72.5 %); 60 locs of 299 (20.1 %)

Locations removed. Values are: 'Number of removed' sites of 'total number of sites' (percentage removed)

-First set of values is for landscape, second is for species

***points can also be removed via the 'env.trim' parameter, which trims input environments in geographic space to a buffered minimum convex polygon of the focal species occurrence localities. This reduces the input environmental space to accessible habitats to the focal species.*



File name: *_ENV3.pdf

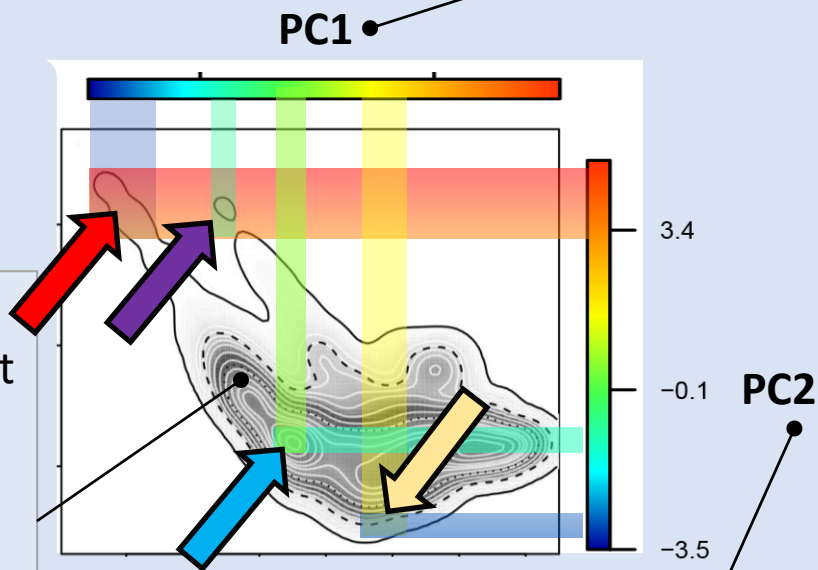
Plots of E-space in G-space of Environment 1 & 2

E-space plot of Environment 2 from *_ENV.pdf

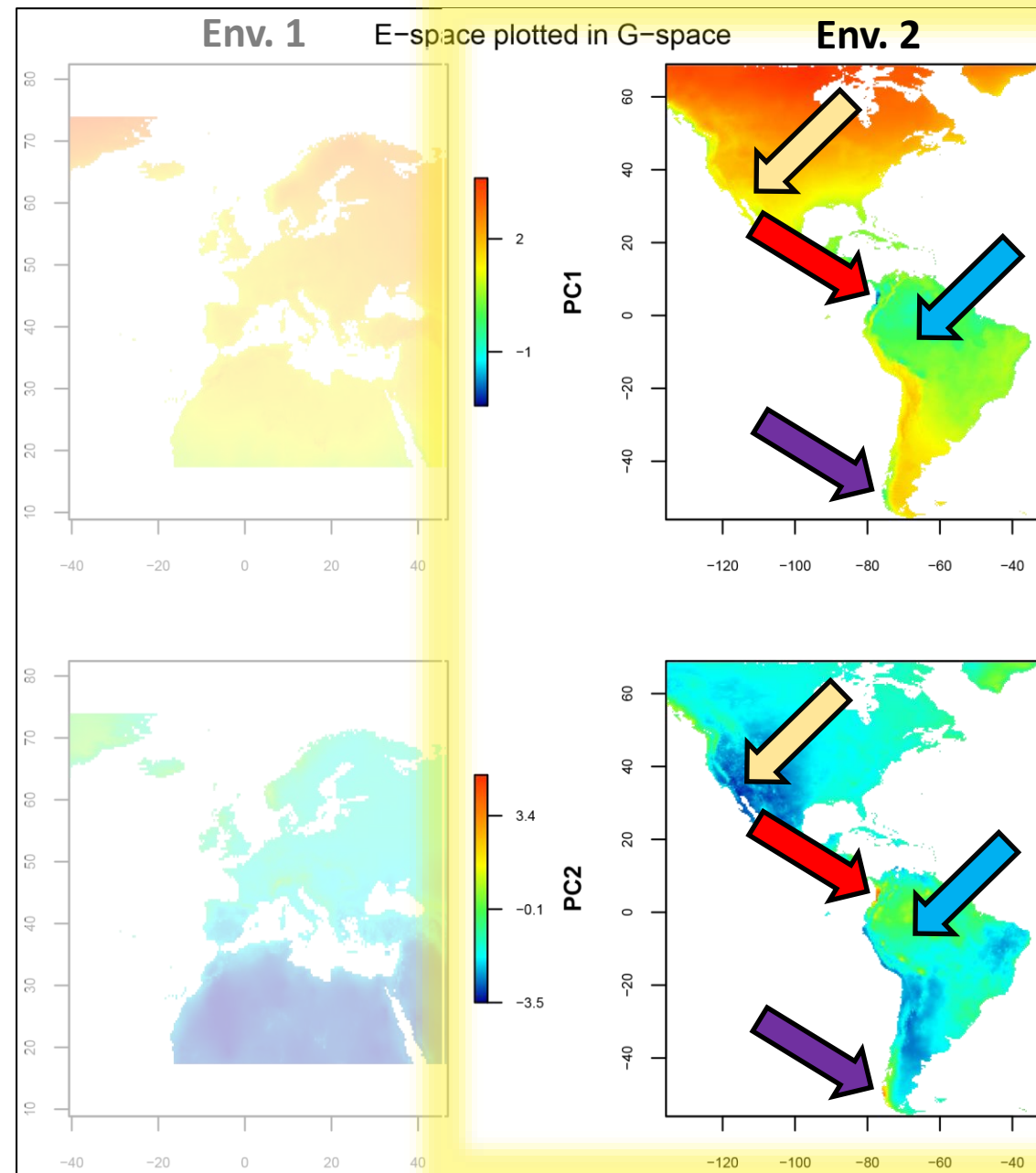
Top right plot. How PC1 of E-space is characterized in geographic space

Arrows depict corresponding E-space & G-space

Note: Color of kernel density plot does **NOT** correspond with E-space's plot color in geography. Look at PC values between plots



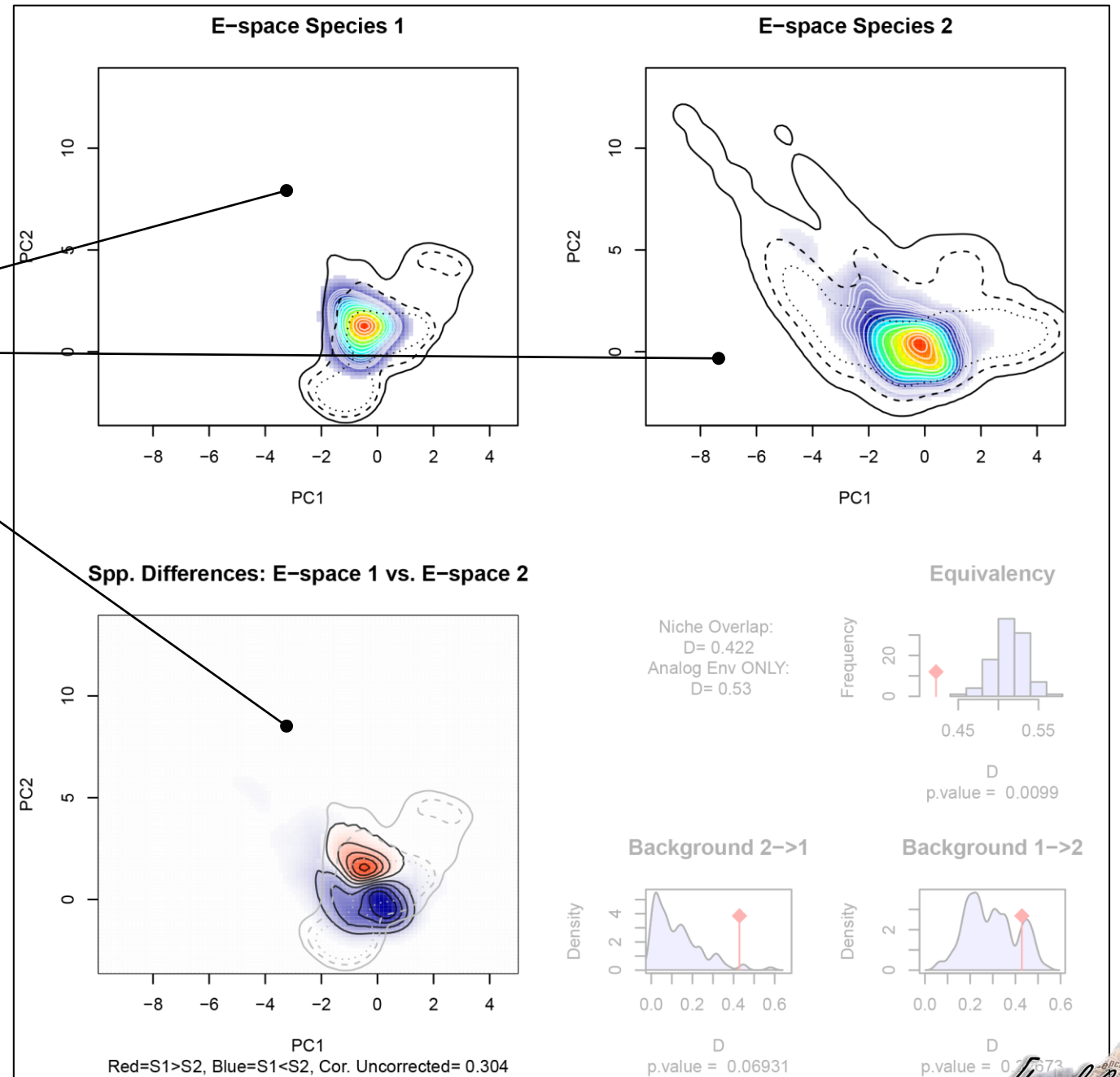
Bottom right plot. How PC2 of E-space (PC2) is characterized in G-space



File name: *_SP.pdf

Plots of Species E-space and Results

See Explanation of *_ENV.PDF



File name: *_SP.pdf

Plots of Species E-space and Results

Niche Similarity

Schoener's D Niche Similarity value. A numeric value from 0-1 reflecting the niche similarity among two niches.

A value of 1 equals identical niches and a value 0 is completely different niches.

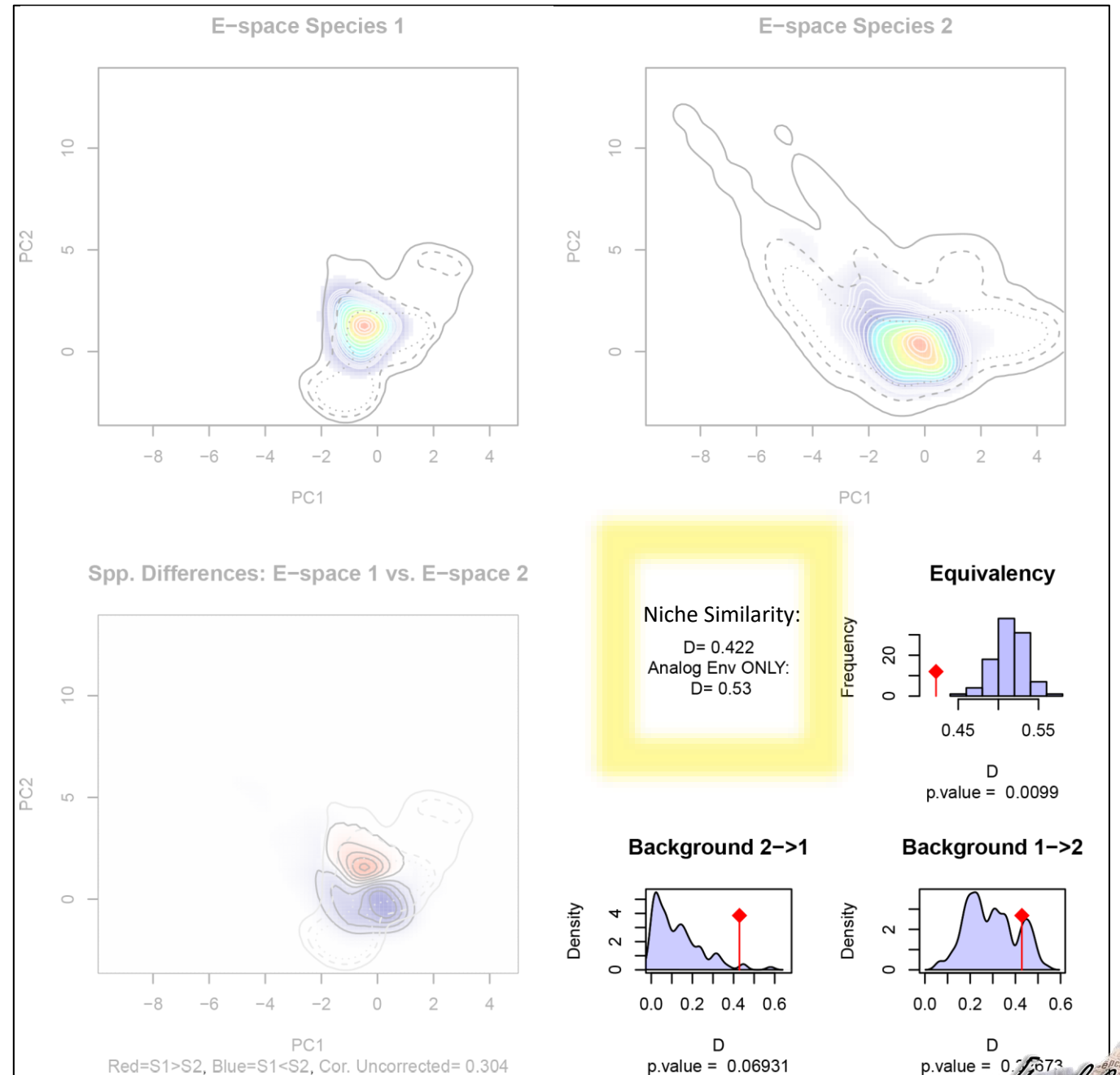
The second value measures niche similarity only in analogous environmental space. See description of 'nae=' parameter for more info.

Niche Similarity:

D= 0.422

Analog Env ONLY:

D= 0.53

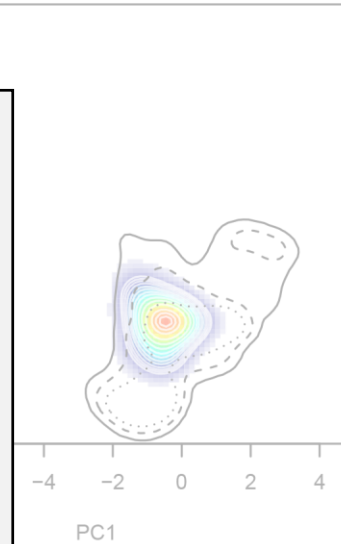


Plots of Species E-space and Results

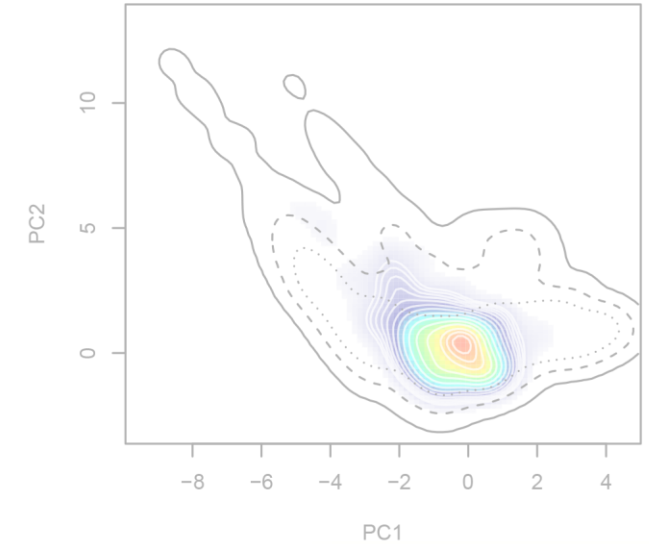
Niche Equivalency Test

A one-tailed statistical test of the null hypothesis that niches are equal. The test compares the observed niche similarity between two species (depicted by red diamond) and the overlap of niches built from the repeated resampled of occurrences of species 1 and 2 (depicted by blue histogram). During each resampling iteration, occurrences of species 1 and 2 are pooled and then randomly assigned to one of two groups. The number of occurrences in the two groups match the number of observations for species 1 or species 2, and each iteration, niche similarity is measured between the two reshuffled groups. A null distribution is created from all iterations of niche similarity values from the reshuffled occurrences. The observed niche similarity between species 1 and 2 is then assessed against the null distribution. A significant value states that the two species datasets are not statistically equivalent and rejects the null hypothesis that species' niches are equivalent.

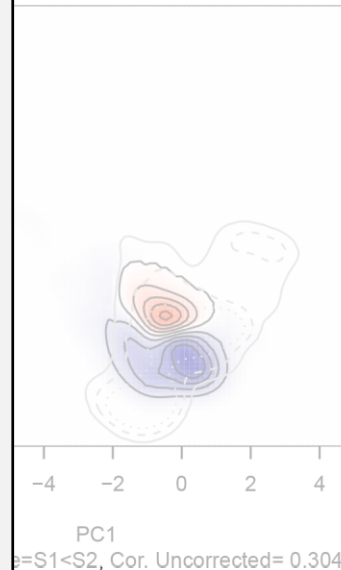
E-space Species 1



E-space Species 2

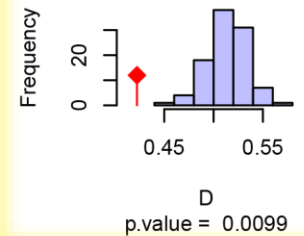


Species: E-space 1 vs. E-space 2

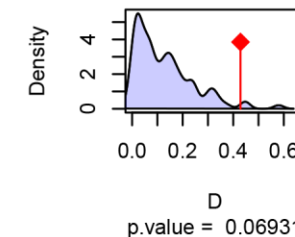


Equivalency

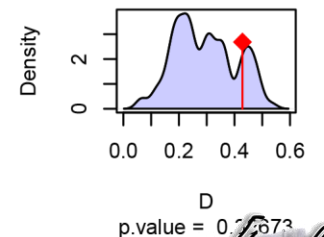
Niche Overlap:
D= 0.422
Analog Env ONLY:
D= 0.53



Background 2->1



Background 1->2



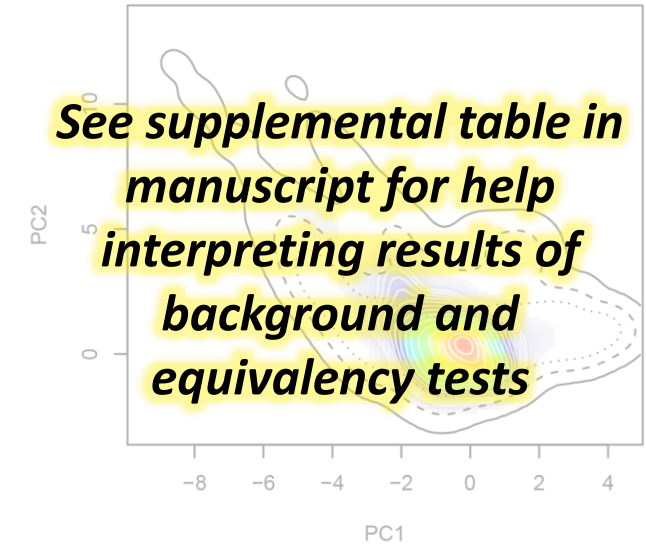
Plots of Species E-space and Results

Background Test

To assess the power to detect differences among the two species' distributions, Humboldt performs a Background Test based on the niche similarity two species' niches in E-space. The function compares the observed niche similarity between species 1 and 2 (red diamond) to overlap between species 1 and the random shifting of the spatial distribution of species 2 in geographic space, and then measuring how that shift in geography changes occupied environmental space (see manuscript for a detailed figure). The repeated random spatial shifting of localities creates and measuring similarity between this distribution and species 1 creates a null distribution of available E-space in the habitat of species 2 (blue density curve). The Background test asks if the two distributed populations/species are more different than would be expected given the underlying environmental differences between the habitats in which they occur. If the observed values of the niche similarity obtained from the two original populations are significantly higher or lower than expected from randomly shifted null distribution, then the null hypothesis that similarity between species is solely due to limits in habitat availability is rejected. The Background test measures the ability of the Equivalency test to detect differences based on the available e-space. If both the Equivalency test and Background test are non-significant, this means the two species occupied environmental spaces are not significantly different and resulting niche 'equivalence' is likely a result of the limited environmental space present in the habitats (See table 1 for a breakdown of interpreting results). Basically, in these situations, there is limited power for the Equivalency test to actually detect significant differences.

E-space Species 1

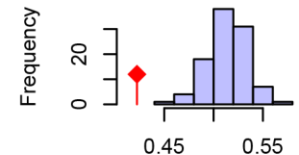
E-space Species 2



ce 2

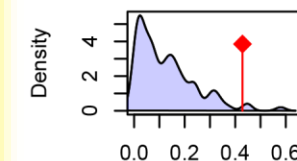
Equivalency

Niche Overlap:
D= 0.422
Analog Env ONLY:
D= 0.53



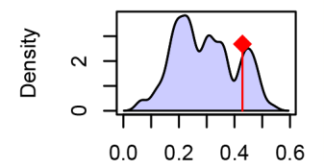
p.value = 0.0099

Background 2->1



p.value = 0.06931

Background 1->2



p.value = 0.32673

File name: *_SP-OVERLAP.pdf

Optional Plot: p.overlap=T

Plots of both species in E-space

Histogram Density Plots

For each PC, the density of each species E-space is displayed

Filled Kernel Density Isopleths

(red= sp1 and blue= sp2*)

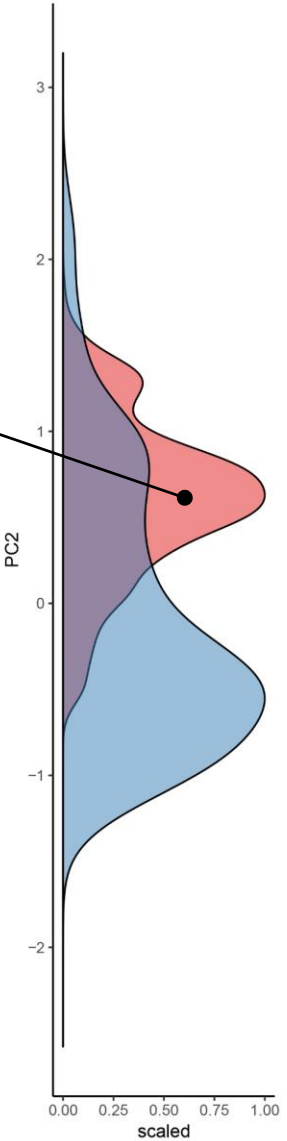
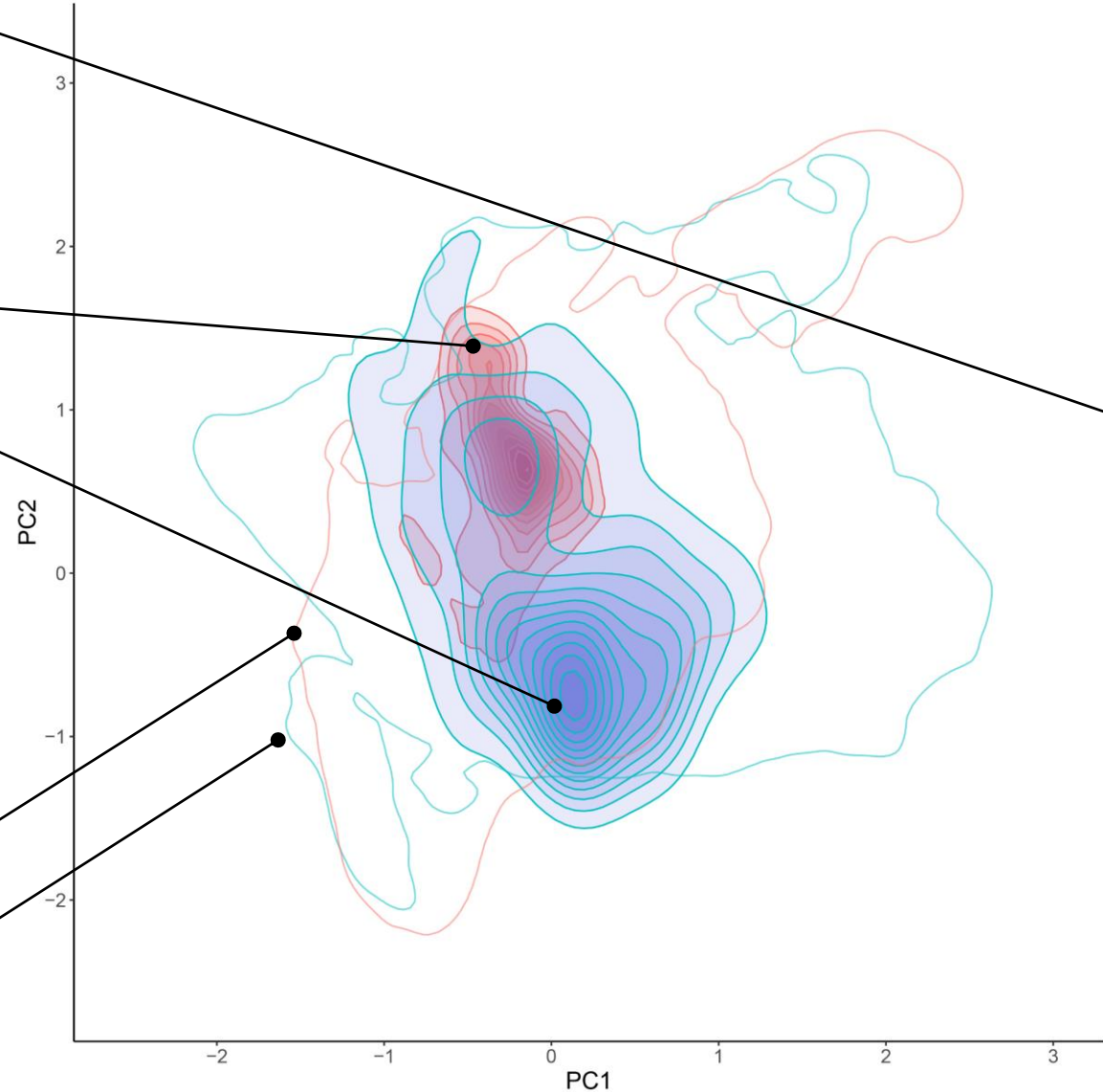
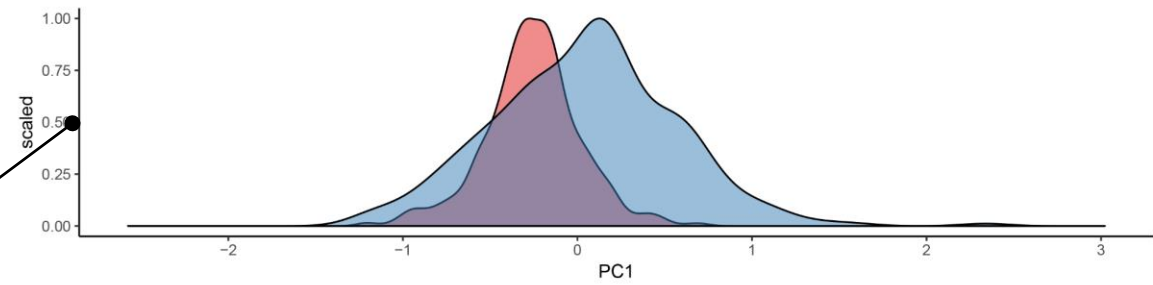
Lines representing the kernel density isopleths from 1-100% kernel densities. The number of bins is set at default and adjusts so that the number contour bins best display the data. Here 11 were selected, thus, as follows are the plotted kernel isopleths: 0.01,0.1,0.2,0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 ,1

Empty Kernel Density Isopleths

(red= env1 and blue= env2*)

Lines representing the 1% kernel density isopleths of the environments (not species) depicting outside boundaries of E-space. Sometimes species values erroneously exceed these due to the smooth parameter of kernel densities estimates.

***if swap=T, colors will be switched in plots**



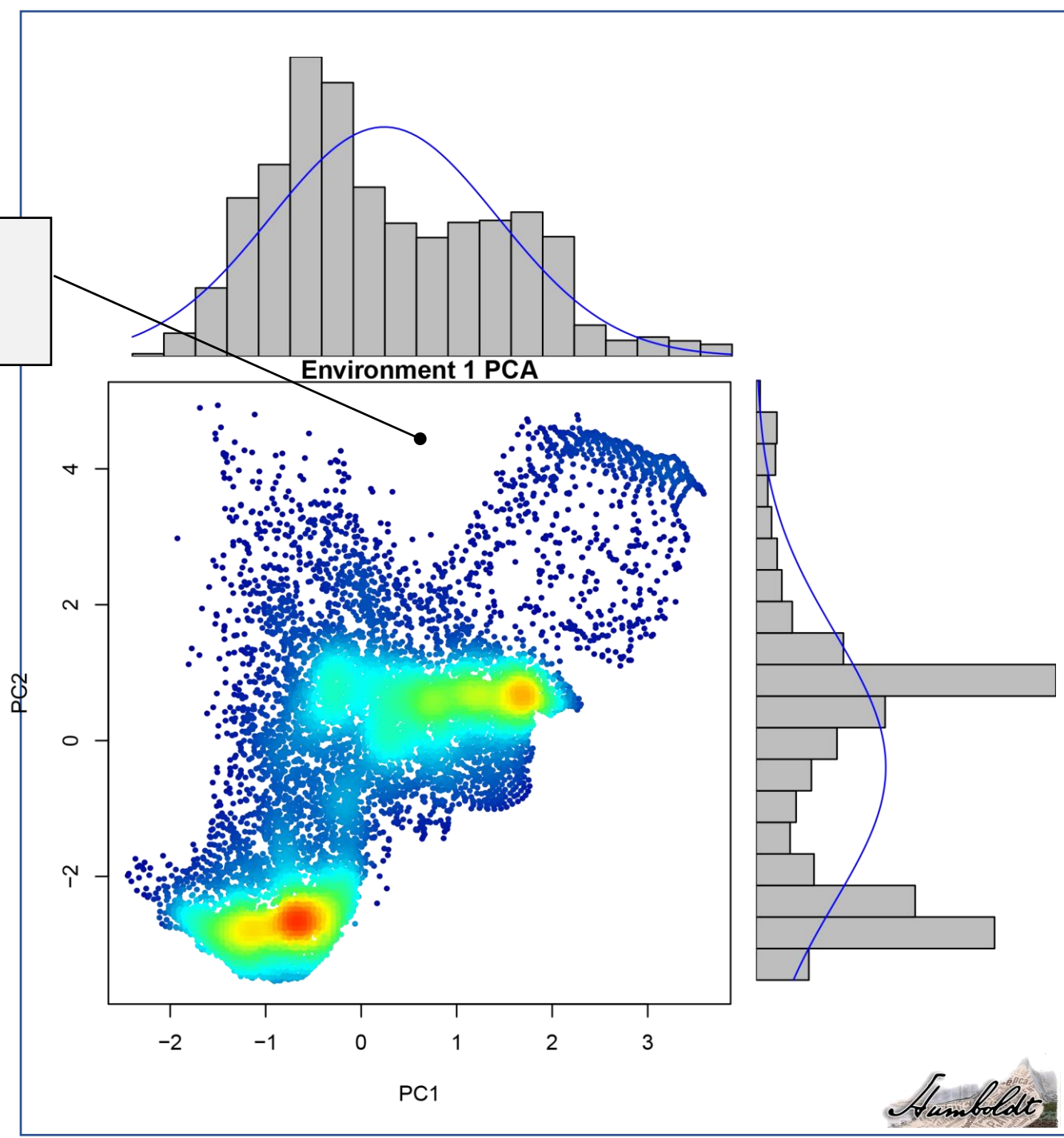
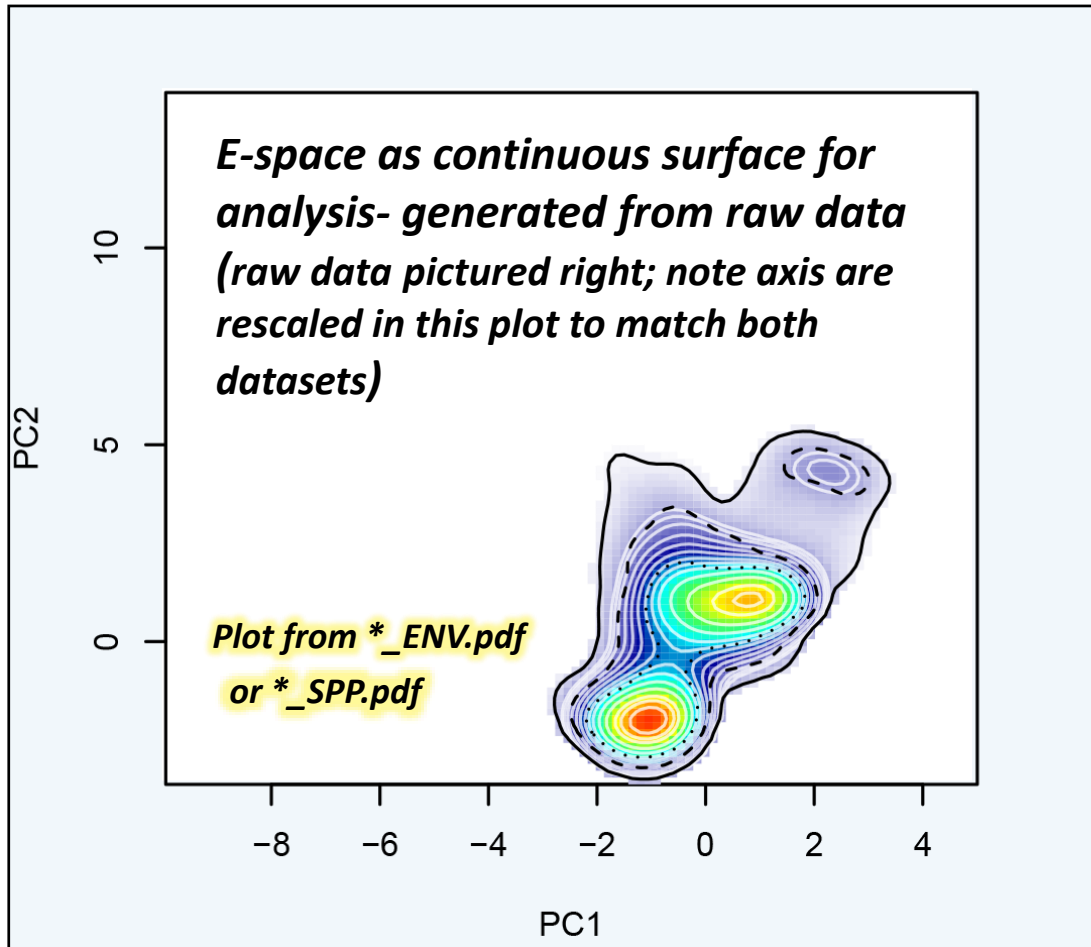
File name: *_SCATTER.pdf

Optional Plot: p.scatter=T

Raw Plots of both species and environment E-space

Density Plots of Raw E-space Data

A plot of raw data of species' and environment E-space. Cooler colors represent lower and warmer higher densities of E-space.



File name: *_BOXPLOT.pdf

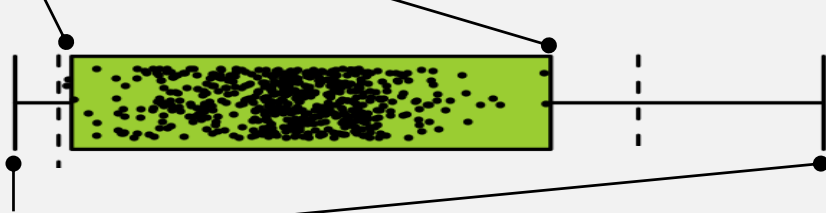
Optional Plot: p.boxplot=T

Plots of both species E-space in single dimensions

E-space Box Plots

For each PC, the one dimensional E-space is Displayed.

Lower and Upper Box: Minimum and Maximum PC values for species' E-space



Lower and Upper Whiskers: Minimum and Maximum PC values for each environment' E-space

Dotted lines: Maximum and Minimum value of shared (analogous) E-space of both environments

Dots: PC values for each occurrence record

E-space truncation in 1 dimension can affect other

Sometimes the reduction of E-space in PC1, results in truncation of E-space in PC2. In absence of trimming E-space of PC1, the upper shared limit of E-space for PC2 should be ~7 (red arrow). Those values were lost in trimming PC1 and within the remaining analogous E-space, ~4 (yellow arrow) becomes the shared upper limit for PC2.

