

Evaluation of Human Population Density as a Predictor for Raptor Phylogenetic and Functional Diversity in Costa Rica

Sophie Barno, Shanta Hejmadi, Dr. Keith Barker
University of Minnesota Department of Ecology, Evolution, and Behavior

Background & Introduction

This project explores whether human population density is associated with diversity in diurnal raptors via the application of both phylogenetic and functional measures of diversity. Phylogenetic and trait dispersion are measures of diversity that refer to the ancestral and functional similarity within a population, respectively (Cadotte et al., 2013). I focus on the guild of diurnal raptors in the orders Cathartiformes, Accipitriformes and Falconiformes in the tropics of Central and South America. I will use and compare raptor presence-absence datasets from eBird (citizen observed ranges) and Birdlife International (polygon range map) to conduct this spatial analysis.

Question & Hypothesis

Can differences in human population density in Costa Rica be used to predict trait and/or phylogenetic diversity in communities of diurnal raptors?

I hypothesized that regions of high human population density are associated with clustered phylogenetic and trait dispersion. I expect these high population density areas to be associated with habitat destruction, which replaces the natural ecosystems that promote niche differentiation (De Palma et al., 2017; Laliberté et al., 2010). I reason that fewer available niches are associated with clustered trait dispersion, and since functional traits are typically phylogenetically conserved, I expect this trend to be the same in phylogenetic dispersion. Additionally, I expect clearer diversity trends to appear with the eBird analysis rather than Birdlife International because the eBird data will be weighted by abundance.

Methods

- I analyzed species presence and absence data in Costa Rica using eBird, a citizen science database and Birdlife International (*Birdlife International*, 2018; eBird Basic Dataset, 2021).
- Human population density data available from NASA (*NASA Earth Data*, 1995)
- QGIS used to crop and process raster and shapefile layers. (*QGIS Development Team*, 2009). *raster* package in R Studio used to process and stack raster layers (Hijmans, 2020)
- Trait data obtained through landmarking 3D beak scans for the raptors present in the spatial range of CR. Stratovan Checkpoint was employed for landmarking purposes (Stratovan Corporation, 2018)
- MTD calculated using Euclidean pairwise distances between 14 principal components accounting for ~95% of the total variance.
- MPD calculated from branch lengths of Jetz et al. (2012) phylogeny.
- Standardized effect size (ses) of MPD and MTD were calculated for each community in Costa Rica using R package *picante* (Kembel et al., 2010).
- Model 2 linear regression was performed for log transformed population density against *picante* trait dispersion and *picante* phylogenetic dispersion.

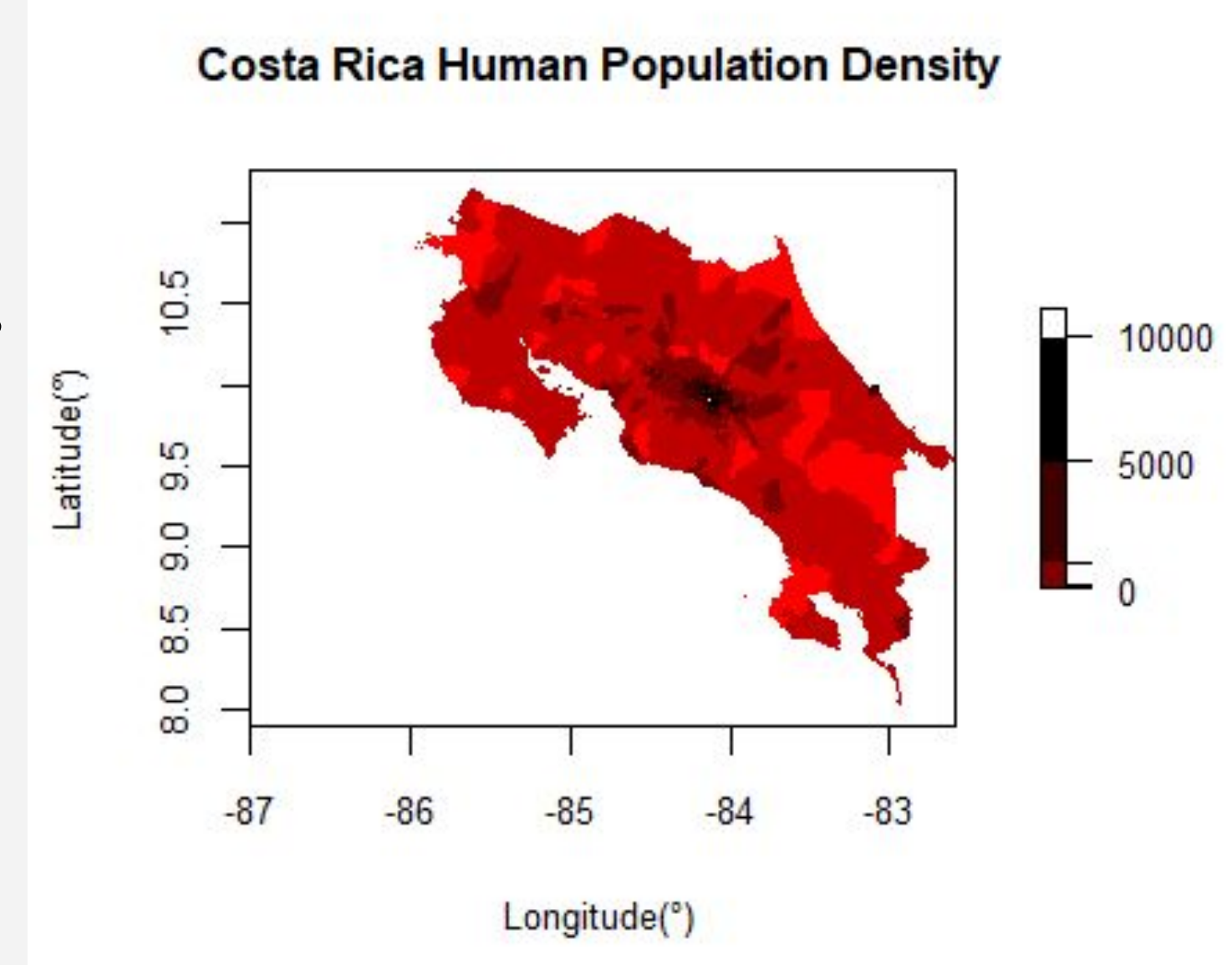


Figure 1: Raster layer of population density in Costa Rica in persons per square kilometer. Darker regions represent greater human population density.

Results

Linear Models

- Purple density plots show trait and phylogenetic distances in raptor communities located in regions with low and high population densities. (Fig. 2, 3).
- For both Birdlife and eBird data, model II linear regression of trait and phylogenetic dispersion vs log population density yielded extremely low coefficients of determination (R^2) (Fig. 2, 3). The small magnitude of the slopes and very low R^2 values indicate that, while there is a statistically significant effect ($p < 0.05$ for all regressions), its size is so small that it is not likely to be biologically meaningful.

Standard Effect Size Rasters

- Rasters of ses MTD and MPD values of communities in Costa Rica reveal areas of significant overdispersed and clustered trait and phylogenetic distances (Fig. 4). Birdlife MPD and MTD rasters display more concentrated areas of clustering and overdispersion, whereas the eBird rasters show more diffuse geographic patterns of MPD and MTD.

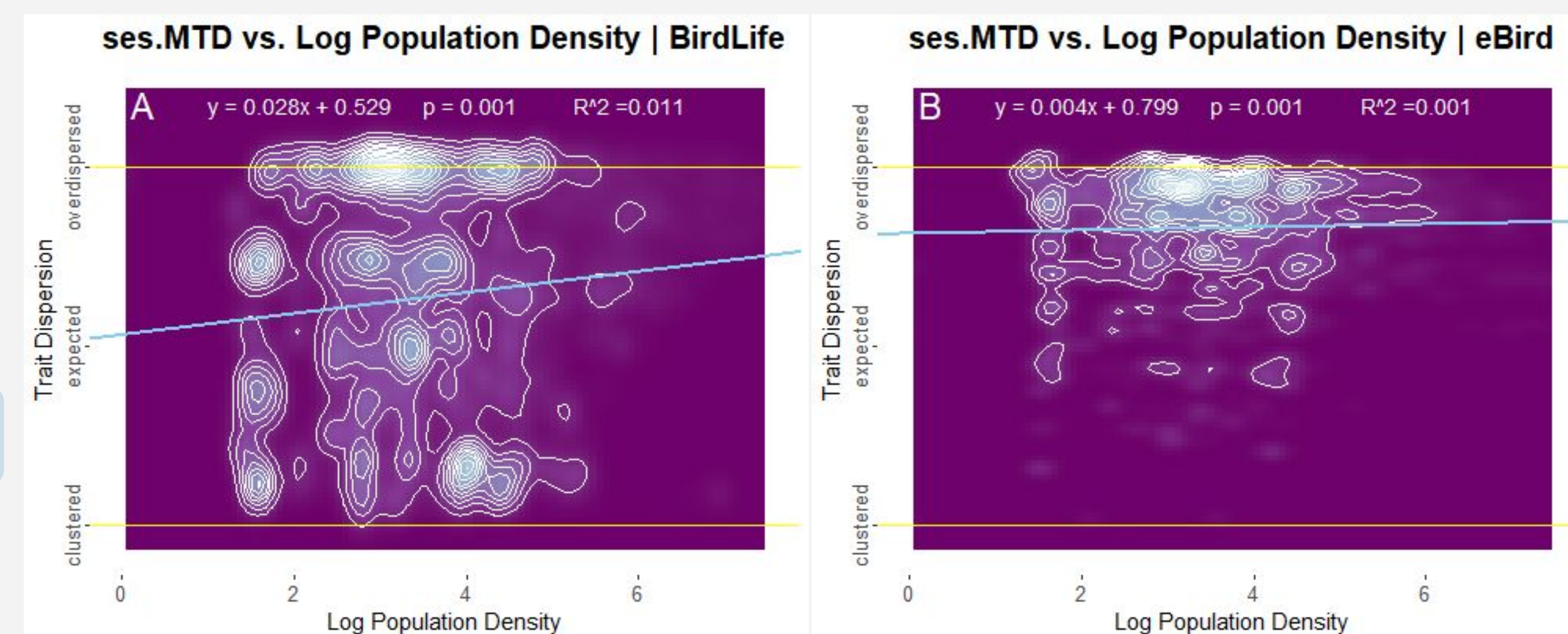


Figure 2: Mean trait dispersion vs log population density plot using Birdlife International (2a) and eBird (2b) distribution data. ses.MTD is regressed against log transformed population density in Costa Rica using linear model 2 regression. Lighter color indicates a higher density of communities, white lines are contour lines. Communities that fall outside yellow lines are considered significantly overdispersed ($p > .975$) or clustered ($p < .025$). Line of best fit (blue), p-value, and R square shown.

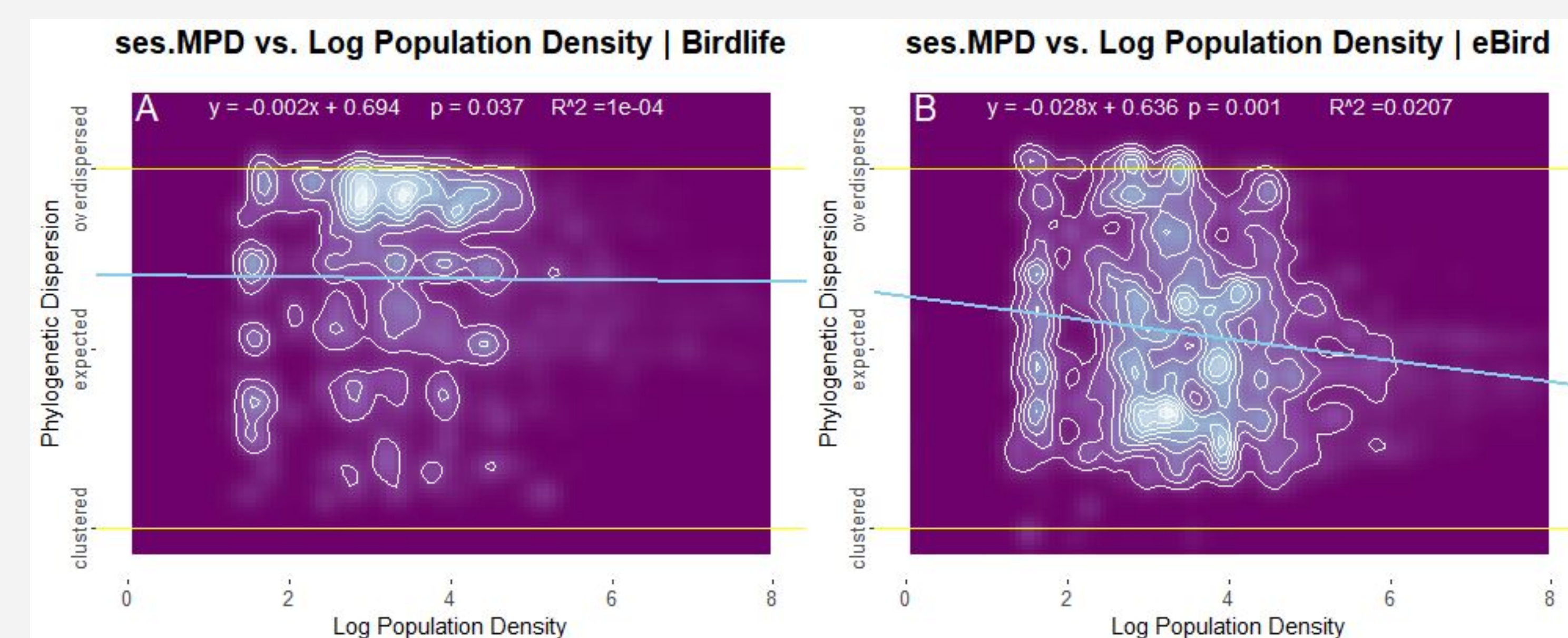


Figure 3: Mean phylogenetic dispersion vs log population density plot using Birdlife International (3a) and eBird (3b) distribution data. ses.MPD is regressed against log transformed population density in Costa Rica, using linear model 2 regression. Lighter color indicates a higher density of communities, white lines are contour lines. Communities bounded by yellow lines are not significantly different from the null model. Communities that fall outside yellow lines are considered significantly overdispersed ($p > .975$) or clustered ($p < .025$). Line of best fit (blue), p-value, and R squared values shown.

Results cntd.

Birdlife International vs eBird Data

- Both eBird and Birdlife communities have a wide range of trait clustering and overdispersion. However, eBird communities are more strongly weighted towards overdispersion (Fig. 2; Fig. 4a,b).
- Similarly, eBird and Birdlife communities have a wide range of phylogenetic and overdispersion, but the eBird communities are more strongly weighted towards phylogenetic clustering (Fig. 3; Fig. 4c,d).

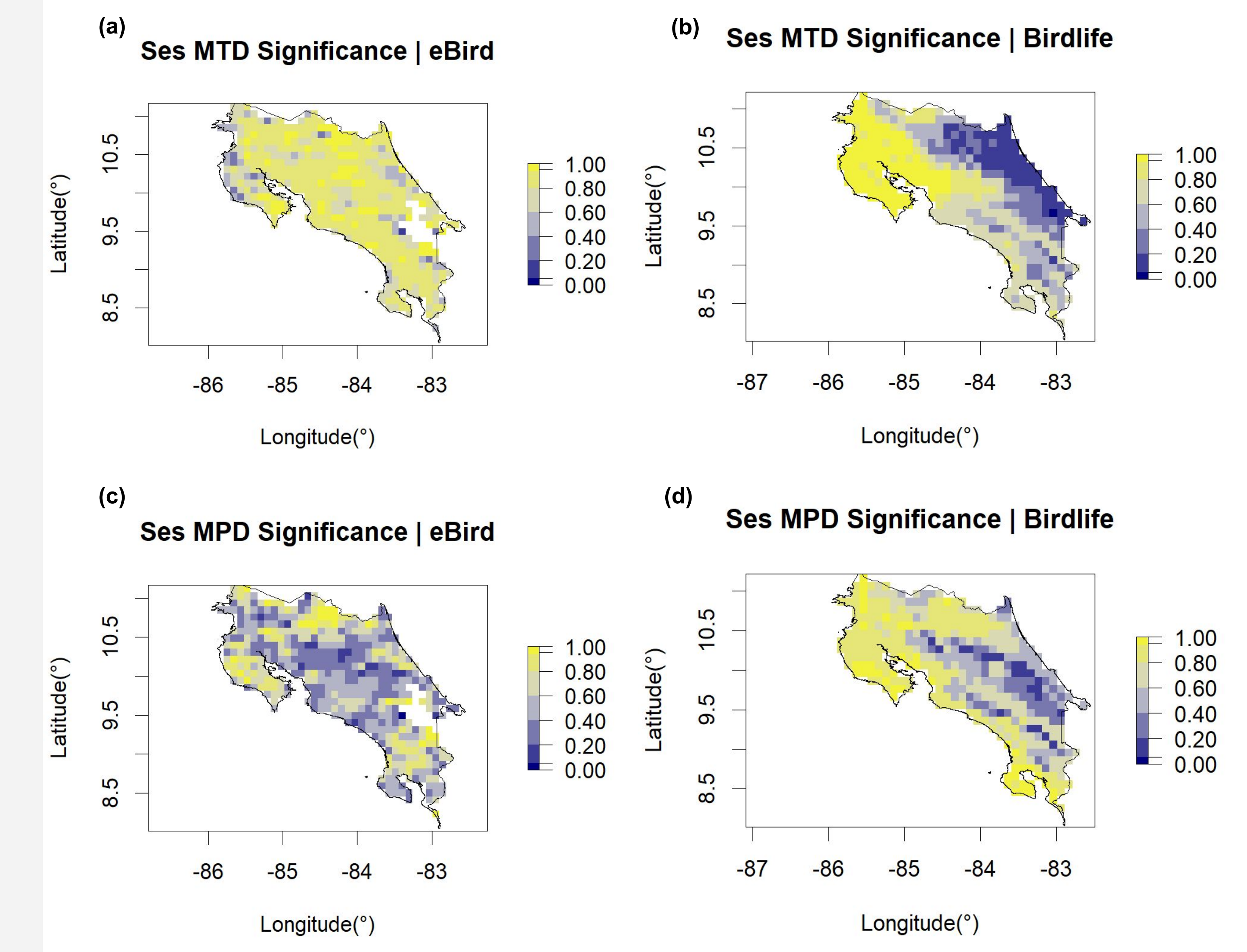


Figure 4: Trait and phylogenetic dispersion in Costa Rica based on raptor presence absence data from eBird (4a,c) and Birdlife International (4b,d). a and b display results for trait analysis using Euclidean pairwise distances between principal components. c and d display results for phylogenetic dispersion based on Jetz (2012) phylogeny. Colors represent p-values for the significance of MTD and MPD standard effect size (ses) 0.1x0.1 degree grid cell communities that range from 0 to 1. Darker cells represent more clustered dispersion and brighter yellow cells represent more overdispersion.

Discussion & Future Directions

- In Costa Rica, human population density cannot be used to predict MTD or MPD.
- There is a clear difference in patterns of MTD and MPD distribution between eBird and Birdlife International presence-absence data. This is due to the differences in theoretical species ranges (BirdLife) and observed ranges (eBird). Additionally, eBird distributions were weighted by abundance, and BirdLife distributions were not.
- Costa Rica may not be a good representation of anthropogenic population stress on biodiversity due to its relatively sparse population and abundance of ecotourism that has aided in preservation of the country's natural habitat (Hunt et al., 2015).
- Areas of high population density in this country may not represent areas of high habitat destruction (e.g. agricultural land is highly disturbed but has low population density). Future studies should expand their geographic scope to countries with greater geographic heterogeneity in human population density.

References

BirdLife International. (2018). Retrieved August 1, 2021, from <https://www.birdlife.org/>.
Cadotte, M., Albert, C. H., & Walker, S. C. (2013). The ecology of differences: assessing community assembly with trait and evolutionary distances. *Ecology Letters*, 16(10), 1234-1244. <https://doi.org/10.1111/ele.12161>.
De Palma, A., Kuhlmann, M., Bugter, R., Ferrer, S., Hoskins, A. J., Potts, S. G., Roberts, S. P. M., Schweiger, O., & Purvis, A. (2017). Dimensions of biodiversity loss: Spatial mismatch in land-use impacts on species, functional and phylogenetic diversity of European bees. *Diversity and Distributions*, 23(12), 1435-1446. <https://doi.org/10.1111/ddi.12638>.
Faber, J., & Fonseca, L. M. (2014). How sample size influences research outcomes. *Dental Press Journal of Orthodontics*, 19(4), 27. <https://doi.org/10.1590/2176-9451.19.4.027-029.EBO>.
Hijmans, Robert J. (2021). raster: Geographic Data Analysis and Modeling. R package version 3.4-13. <https://CRAN.R-project.org/package=raster>.
eBird Basic Dataset. Jan 2022. Version: EBD_reJan-2022. Cornell Lab of Ornithology, Ithaca, New York. Hunt, C. A., Durham, W. H., Driscoll, L., & Honey, M. (2015). Can ecotourism deliver real economic, social, and environmental benefits? A study of the Osa Peninsula, Costa Rica. *Journal of Sustainable Tourism*, 23(3), 339-357. <https://doi.org/10.1080/09669582.2014.965176>.
Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K., & Moores, A. O. (2012). The global diversity of birds in space and time. *Nature*, 491(7424), 444-448. <https://doi.org/10.1038/nature11631>.
Kembel, S., Cowan, P., Helmus, M., Cornell, W., Morlon, H., Ackerly, D., Blomberg, S., Webb, C. (2010). "Picante: R tools for integrating phylogenies and ecology." *Bioinformatics*, 26, 1463-1464. <https://doi.org/10.1093/bioinformatics/btq100>.
Laliberté, F., Wells, J. A., DeClerck, F., Metcalfe, D. J., Catterall, C. P., Queiroz, C., Aubin, I., Bonser, S. P., Ding, Y., Fraterrigo, J. M., McNamara, S., Morgan, J. W., Merlos, D. S., Vesik, P. A., & Mayfield, M. M. (2010). Land-use intensification reduces functional redundancy and response diversity in plant communities. *Ecology Letters*, 13(1), 76-86. <https://doi.org/10.1111/j.1461-0248.2009.01403.x>.
NASA Earth Data. (1995). Retrieved August 1, 2021, from <https://sedac.ciesin.columbia.edu/data/collection/gpw-v4/sets/browse>.
QGIS Development Team (2009). QGIS Geographic Information System. Open Source Geospatial Foundation Project. Retrieved June 1, 2021, from <http://qgis.osgeo.org/>.
Stratovan Corporation. Stratovan Checkpoint [Software]. Version 2018.08.07. Aug 07, 2018. URL: <https://www.stratovan.com/products/checkpoint>