Ecological Factors Associated with Self-Reported Mental Health Status

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# Abstract

***Background:*** Ecological factors are known predictors of many health outcomes. However, there are many complex ecological factors that have not yet been thoroughly identified and spatial analysis used for non-infectious public health outcomes, particularly for mental health, is limited. ***Aims:*** We aimed to utilize machine learning and spatial statistics to identify significant search among many possible zip code or county predictors (N > 2000). We also aimed to identify informative associations between ecological variables and mental health outcomes available from public data sources (CDC Places). This study seeks to identify local socioeconomic factors and area health resources associated with poor self-reported mental health status. ***Methods:*** This study combines feature selection, spatial regression, to identify a small set of important variables representing possible effects. Hierarchical linear models and artificial neural networks to identify the effects and their predictive ability. ***Results:*** The approach identified a final model consisting of (N = 5) zip code variables related to families, education, or employment. Designation as manufacturing dependent accounted for a significant variation in poor mental health (71% based on ICC). Based on the presence of statistically significant, meaningful, and informative results developed without direct researcher engagement with the content, this process of “algorithmic triangulation” was relatively effective. ***Conclusions:*** Types of employment and educational opportunities may be related to population level mental health, but more research is needed. This methodology can be applied to many other outcomes for the purpose of generating hypotheses that can be further investigated with relevant domain area knowledge.

Ecological Factors Associated with Self-Reported Mental Health Status

# Introduction

Ecological factors are known predictors of many health outcomes (1–7). Neighborhood level deprivation is a useful measure in assessing risk for negative health outcomes and creating targeted interventions within population health management (8–13). However, there are many complex ecological factors that have not yet been thoroughly identified. With the advent of ‘big data,’ there is increased availability of ecological data that can measure these effects as well as machine learning algorithms that can analyze large datasets.

Alongside geographic information systems that can model complex associations, new computational approaches have great potential to improve public health research and population health management efforts (14–17). However spatial analysis used for non-infectious public health outcomes is limited (18) and the use of machine learning often provides little benefit over traditional approaches (19,20). Machine learning needs methodological improvement (21–24) to better assist population health management efforts (25–27). There is a need for expanded scope in spatial analysis to better inform translational science in public health (28–30).

***Purpose of this Study***

The purpose of this study is to utilize machine learning and spatial statistics to identify significant associations between ecological variables and health outcomes available from public data sources. This study seeks to identify local socioeconomic factors associated with a higher prevalence and health resources that are associated with a lower prevalence of poor self-reported mental health status. Once identified, hierarchical linear models can be developed to display these relationships and artificial neural networks can be used to predict future outcomes. By searching among large numbers of candidate predictors, informative relationships that may not be already considered in previous research can be used to develop targeted future population health management efforts.

**Methods**

Due to the inability for traditional statistical approaches to search among candidate predictors in multi-dimensional data, this study has developed a novel approach that combines several previously established methods for feature selection, spatial regression, hierarchical linear modeling, and artificial neural networks. Together these methods provide a process for hypothesis generating observational research able to identify candidate predictors, adjust for spatial relationships, model multi-level interactions, predict future outcomes. This process consists of four steps: feature selection, spatial regression, hierarchical linear modeling, and artificial neural networks.

***Feature Selection***

Feature selection (FS) is a quantitative approach designed to identify predictors that are most important for a given outcome of interest among a large number of candidates. FS techniques fall are often described as *wrapper*, *filter,* and *embedded* methods(31–33)*.* Wrappers select subsets of features for classification to compare results and include approaches such as Recursive Feature Elimination with Support Vector Machines (SVM-RFE) (32). Filters use metrics to rank features individually and include Linear Discriminant Analysis (LDA) (34,35) and certain applications of Principal Component Analysis (PCA) (36). Embedded methods combine qualities of both by including ranking into the classification process and include Random Forests (RF) (37). This study utilizes an approach that combines embedded (RF), filter (PCA), and wrapper methods (SVM-RFE) together to identify the smallest set of predictors that have both high variation and high importance in the context of all other candidates.

RF create an ensemble of decision trees with bootstrapped sampling of predictors fit to a given outcome (38,39) providing an aggregate measure of importance for each candidate predictor that is useful for variable selection (40–44). RF rely on less assumptions that traditional variable selection methods (40,42) and can integrate multiple statistical approaches (45,46) allowing RF to remain highly accurate with high collinearity (43), significant noise (42,47), or complex interactions (48–50). RF are easily adaptable for various applications (51,52), are relatively resource efficient (38), and available in many open-source libraries (52). RF have bene used widely in bioinformatics (53) for disease risk prediction (54–57) and genome wide association studies (GWAS) (41,43,47,50,58), but recently have begun to be used for spatial analysis in public health research (59,60). RF were then used to identify predictors with above average importance measured by Gini impurity. This allowed for variables to be independently evaluated for predictive ability that adjusts for collinearity and confounding.

Principal Component Analysis (PCA) constructs orthogonal linear combinations of features that account for a given amount of variation within a dataset (61,62) and is commonly used in bioinformatics for dimensionality reduction through variable aggregation (63–65) or component loading (66–68). PCA is applicable to high dimensional data (69), does not require distribution assumptions (70), and can be conducted with widely available computational resources using open-source software (71). For variables at the zip code level, PCA was used to identify predictors with above average eigenvectors for all components with an eigenvalue above 1.0. This allowed for predictors with higher variation to be identified from among possible candidates.

SVM-RFE is a simple approach to feature selection that identifies a reduced set of predictors that provide the highest prediction accuracy through iterative cross validation (72–75). SVM-RFE can be deployed in similar settings to stepwise regression but avoids the many established drawbacks by utilizing Support Vector Machines which requires minimal assumptions related to the distribution of the data to be met (76). In this study, predictors that had both above average variation (from the PCA model) and importance (from the RF model) were selected for RFE-SVM with cross validation. This process calculates AIC values for all possible combinations of selected predictors and identified the best possible selection with the lowest number of candidate predictors.

***Spatial Regression***

Since health outcomes and ecological predictors may exhibit geographic similarity, regression methods that display these differences are used to identify areas where multi-level effects may be present. These models use features identified from the feature selection process at some geographic layers and will inform feature selection at other geographic layers.

Multi-scale geographic weighted regression (GWR) is spatial regression (SR) for identifying spatial variations in an independent-variable’s estimated effect on the outcome of interest. Rather than globally identifying parameter estimates, GWR modifies parameters for each individual area based on the relationship to other spatially adjacent areas. This provides for areas to be identified where a given independent variable has a greater or lesser effect on the same outcome, indicating that higher level effects may be present.

The list of zip code variables from the FS process is used for GWR and areas where zip code level predictors had higher predictive ability are identified. These areas represent locations where infrastructural differences have a possible interaction with socio-economic factors leading to an increased effect on the outcome. To identify these interactions, each county is coded with a multi-level categorical variable indicating which zip code variable had the highest GWR coefficient. Due to the ability for SVM to handle a low number of observations with high variable counts, SVM is used to identify county level predictors from the county predictors with the highest coefficients for each zip code variable. These county-zip code predictor pairs are kept as possible multi-layer interactions. Using local Empirical Bayes smoothing and local Moran’s test for spatial autocorrelation (LISA) quadrants, ‘hot and cold spot’ regions are created that represent significant autocorrelation in the outcome. These regions are overlayed to county boundaries and provided with nominal labels. SVM are used to identify independent county level predictors.

***Hierarchical Linear Modeling***

After significant features are identified and spatial relationships are quantified, a hierarchical linear model (HLM) model is used to identify parameter estimates for ecological predictors that can illustrate the relationship between variables with statistical tests.

***Artificial Neural Networks***

In order to compare the selected predictors used in the HLM model to all candidate predictors, a multi-layered perceptron (MLP) with an artificial neural network (ANN) architecture is used to predict a zip code being in the 75th percentile for the outcome. An MLP using all possible candidate predictors, a random selection of candidate predictors, and an MLP for the selected multi-level predictors that are included in the HLM are both trained and tested on a 50-50 random split on the original data (with standard scaling and missing data imputation). A Receiver Operator Curve (ROC) and the corresponding C-statistics are used to compare the accuracy of each variable set.

During the FS, SR, and ANN processes, all candidate predictors with less than 75% non-missing data are removed and the remaining missing values are imputed with median values. During the HLM process, a significantly smaller set of predictors are used and observations with missing values are removed due to low infrequency.

Each of the machine learning, spatial regression, and traditional statistical models used open-source libraries available in the Python Programming Language (Python) version 3.6 and R Project for Statistical Computing (R) version 3.0. The ANNs utilized the Keras API for TensorFlow v2.4.1. Datasets and code scripts are available as under open-source license from GitHub for the purpose of dissemination and replication.

## Data Collection

US Census American Community Survey (ACS) five-year percent estimates by zip code are collected from the 2020 data release to represent socio-economic ecological predictors. The Health Services Resource Administration (HRSA) Area Health Resource File (AHRF) 2020 data release is collected and five-year averages are calculated by county to represent infrastructural ecological predictors. The CDC and RWJF PLACES 2020 data release (formerly 500 Cities project) provided zip code level prevalence estimates of many common diseases, health conditions, and preventive care services. Zip codes were joined to county using crosswalk files from the Department of Housing and Urban development so that each zip code could be contained within a specific county based on where a majority of the population is located. Together these datasets provide a comprehensive list of approximately 2500 possible candidate predictors at zip code and county levels for all 50 states and include individual demographics, housing types, economic status, education levels, employment types, health workforce availability, insurance markets, and inpatient facilities, and hospital quality metrics.

For each of the datasets, the 2020 release was created based on data collected during 2014-2019. This time period was selected due to its timing immediately after the most significant period of ACA implementation and preceding the SARS-Cov20 pandemic. When compared to other time periods, this 5-year window represents a relatively stable healthcare environment that can be useful in determining the direction for future reforms.

# Results

Self-reported mental health status from (N = 969) zip codes in Florida were collected from the CDC PLACES dataset (Figure 1) and descriptive statistics were calculated for crude rate per 1000 residents (quartiles = 0, 128, 149, 146, 167). At the zip code level (N = 366) socioeconomic variables were collected from the ACS and (N = 28) were collected from the CDC. At the county level (N = 1802) variables were collected from the AHRF.

A generalized GWR model was created using the natural log of the crude rate (Adj. R-squared = 0.9577, F-statistic = 10970, p-value < 0.001, AIC -3985) with composite index of both social variables from the ACS (Estimate = 0.005, p < 0.001) and health variables from the CDC (Estimate: 0.021, p < 0.001). The weighted coefficients for local health (Figure 2) were calculated, normalized, and averaged among zip codes by each (N = 67) county (quartiles = 18.38, 18.90, 19.45, 20.12, 22.87). Gini coefficients for each county (Figure 2) were calculated (quartiles = 0.00, 0.03, 0.05, 0.07, 0.09).

Using PCA, RF, and RFE-SVM a set of (N = 21) predictors were selected based on predicting the crude rate (Figure 3). Using SVM, (N = 10) county level predictors were selected based on predicting the different county level rates (Figure 3). The selected zip code predictors were used to create a simple ordinary least squares (OLS) model for crude rates (Figure 4). OLS assumptions were checked by Utt’s rainbow test (p < 0.001, indicating non-linearity), the Jarque-Bera test (p < 0.001, indicating non-normal errors), the Anderson-Darling test (p < 0.001, indicating non-normal errors), the Durbin-Watson test (p = 0.761, indicating no generic autocorrelation), the Moran’s I test (p < 0.001, indicating spatial autocorrelation), the Breusch-Pagan test (p < 0.001, indicating homoskedasticity), the Goldfield-Quandt test (p = 0.995, indicating no heteroskedasticity). A Q-Q plot and residuals plot (Figure 5) were further used to confirm non-normality and homoscedasticity within the sample. A correlation matrix (Figure 6) was used to identify colinear variables with a Spearman’s rank r above 0.5 (N = 7).

These results show that the homoscedasticity, and independent sampling assumptions were met, but non-normality, non-linearity, spatial autocorrelation, and collinearity was present. Multiple generalized linear models (GLM) were created using different approaches to addressing these concerns and compared. A GLM was created for the standardized rate (SMR) with an identity link and normal distribution (AIC = 1304.5), the crude rate with log-link and normal distribution (AIC = 1152.8), the binary outcome (SMR > 1) with a logit link and binomial distribution (AIC = 547.3), the crude rate with a log-link and Poisson distribution (AIC = 10219.0), the crude rate with a log-link and a negative binomial distribution (AIC = 9401.4). The most simple and accurate approach for addressing non-normality was a GLM with a natural log transformation of the crude rate. This model was implemented along within a hierarchical linear model to further account for spatial autocorrelation.

A HLM was created for the natural log crude rate assuming random-effects with fixed coefficients and varying intercepts for each selected county variable. Zip code predictors for the HLM models were excluded if they were collinear (r > 0.5) and less “important” based on scores from the RF model. (N = 1) county variables were significant (alpha = 0.001) based on a One-Way ANOVA test when models with or without the randomized terms were included and (N = 5) zip code variables had significant parameter estimates in each HLM model.

A final model using these selected predictors (Figure 7) was created (AIC = 1283.3, log-likelihood = -633.65) and the adjusted intraclass correlation coefficient was calculated (ICC = 0.714). A MLP with 50-50 random split was trained and used to calculate the C-statistic for all predictors (AUC = 0.91, epochs = 100, loss < 0.01) and the selected predictors (AUC = 0.87, epochs = 100, loss = 0.09).

Immediately upon download (using public APIs) all predictors were given generic labels and blinded to the software user until the above results were collected. Once the final HLM and MLPs were created, the feature labels were used to identify each of the selected zip code level predictor with relevant definitions. This allowed for the final selection to be chosen without bias from the researcher and rely entirely on quantitative assessment. The list of selected zip code predictors (Table 1) with significant parameter estimates in the final model included: average household size (B = -0.075, 95CI = -0.060 to -0.090, p < 0.001), population 25 years and over with a bachelor's degree or higher (B = -0.159, 95CI = -0.141 to -0.176, p < 0.001), total population female (B = 0.249, 95CI = 0.235 to 0.264, p < 0.001), percent of civilian employed population as government workers (B = 0.093, 95CI = 0.078 to 0.108, p < 0.001). The final list of selected county predictors (Table 1) with significant ANOVA tests comparing the presence of a random effect in the model included: manufacturing dependent designation (p < 0.001).

**Discussion**

The purpose of this study was to explore social determinants of health resources associated with self-reported poor mental health status in Florida. A novel approach was utilized which included methodology incorporating machine learning and spatial statistics to search among many possible predictors of hospital discharges. This methodology sought to identify informative associations regarding mental health outcomes that may not be considered in previous research excluding spatial data. Additionally, there were a variety of quantitative methods applied to minimize intrinsic biases among various modeling techniques with a process commonly deployed in qualitative research.

Overall, findings from this study discovered many variables that reflect previous findings, but also variables that provide greater nuance on social factors associated with mental health status. Evidence from this study can be used for hypothesis testing and intervention design for population health management. Based on the presence of statistically significant, meaningful, and informative results developed without direct researcher engagement with the content, this process of “algorithmic triangulation” was relatively effective. Due to the automation involved in the process, this methodology can be applied to many other outcomes for the purpose of generating hypotheses that can be further investigated with relevant domain area knowledge.

The most significant finding in the study was the level of variation in poor mental health (71% based on ICC) attributed to being labeled as manufacturing dependent. Although this is not applicable to all studies, it can provide relevant information when assessing for accessibility and availability of resources in areas of target populations. These findings may also raise important questions regarding finances and economics within residence of these target populations. Types of employment and educational opportunities may be related to population level mental health, but more research is needed to identify these possible effects. Despite more research being needed to draw these direct conclusions and direct causations, studies such as these are useful in obtaining spatial information that may not be known form assessing the literature alone or from talking to community members alone.

***Limitations***

There are several important limitations to acknowledge, particularly in relation to the exploratory nature of this study. Since this study did not seek to test a hypothesis, involve longitudinal data, or utilize any experimental (or quasi-experimental) designs the results should be interpreted carefully. However, it is important to note the value in hypothesis generating studies for mental health, especially in connection to ecological data. Although this study was broad in nature, it is a first step in further understanding how spatial data can benefit psychiatric epidemiologic research.

The final model is a reflection of what possible effects may be present when these other research processes take place. These results are designed to inform future studies and not to replace or contradict them. Domain knowledge and researcher input is necessary for these results to help translational research. The goal of this study was to simply identify through advanced computational techniques what effects may be present, but not yet fully investigated for mental health outcomes. This hopefully can provide a starting point for future innovative research.

Due to the level of precision in the selected variables, there is a temptation to explain each one as a proxy for broader effects (age, neighborhood deprivation, poverty etc). However, the datasets included robust measures for all general variables and the algorithms were designed to account for each variable in context through multiple and repeated ways. If variables are not fully represented in the final selection, there is strong evidence that they may not be representative of the true possible effect. These would need to be further verified by future study, but dismissal due to other factors considered by the algorithms would not be accurate.

Due to the fact that many different methods were used in the process of “algorithmic triangulation”, there is a possibility that a different combination may yield more informative results. Each algorithm or model was chosen due to their previously validated uses and mathematical relevance to the research question, however this exact combination has not been yet utilized.

Florida was chosen as a focus area for two reasons: 1) It is the home state of the research institution and 2) The computational resources required to conduct analysis among multiple states far exceed the capability of everyday devices (The analysis was conducted on an Intel i7 CPU with 16GB DDRAM running Ubuntu 20.04. Some algorithms took over a week to run when using data from all 50 states). GPUs have shown great potential in advancing processing speed for many algorithms that benefit from the parallel structure used for graphics (RF, ANN, GWR) and NVIDIA’s RAPIDS architecture provides a Python library capable of utilizing the same algorithms on their GPUs. If the code scripts could be adapted to GPU use, access to resources that are commercially available as ‘gaming’ devices (or furthermore advanced research computers) would provide a significant boost in speed allowing for a much wider analysis.

**Conclusion**

When considering potential social determinants of health and associated resources in Florida, there is significant evidence that types of employment and educational opportunities may be related to population level mental health, but more research is needed to identify these possible effects. Future research should use these results to more specifically identify why there is such variation in self-reported mental health. Understanding the context behind this quantitative data will better inform hospitals, neighborhoods, and public health professionals on how to collaborate in creating enhanced targeted interventions to overall improve population health and other potential impeding financial constraints.

**Tables and Figures**

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| --- | --- | --- |
| *Table I.* Final list of selected zip code and county predictors used in mixed-effects model using natural log of crude prevalence as outcome. | | |
| **Feature** | **Layer** | **Description** |
| D2\_T1\_17 | Zip Code | Average Household Size |
| D2\_T1\_46 | Zip Code | Population 25 Years And Over Bachelor's Degree Or Higher |
| D2\_T2\_39 | Zip Code | Civilian Employed Population Government Workers |
| D2\_T2\_90 | Zip Code | Percentage of Families with Income Below The Poverty Level |
| D2\_T4\_5 | Zip Code | Total Population Female |
| D3\_1029 | County | Manufacturing-Dependent Designation |

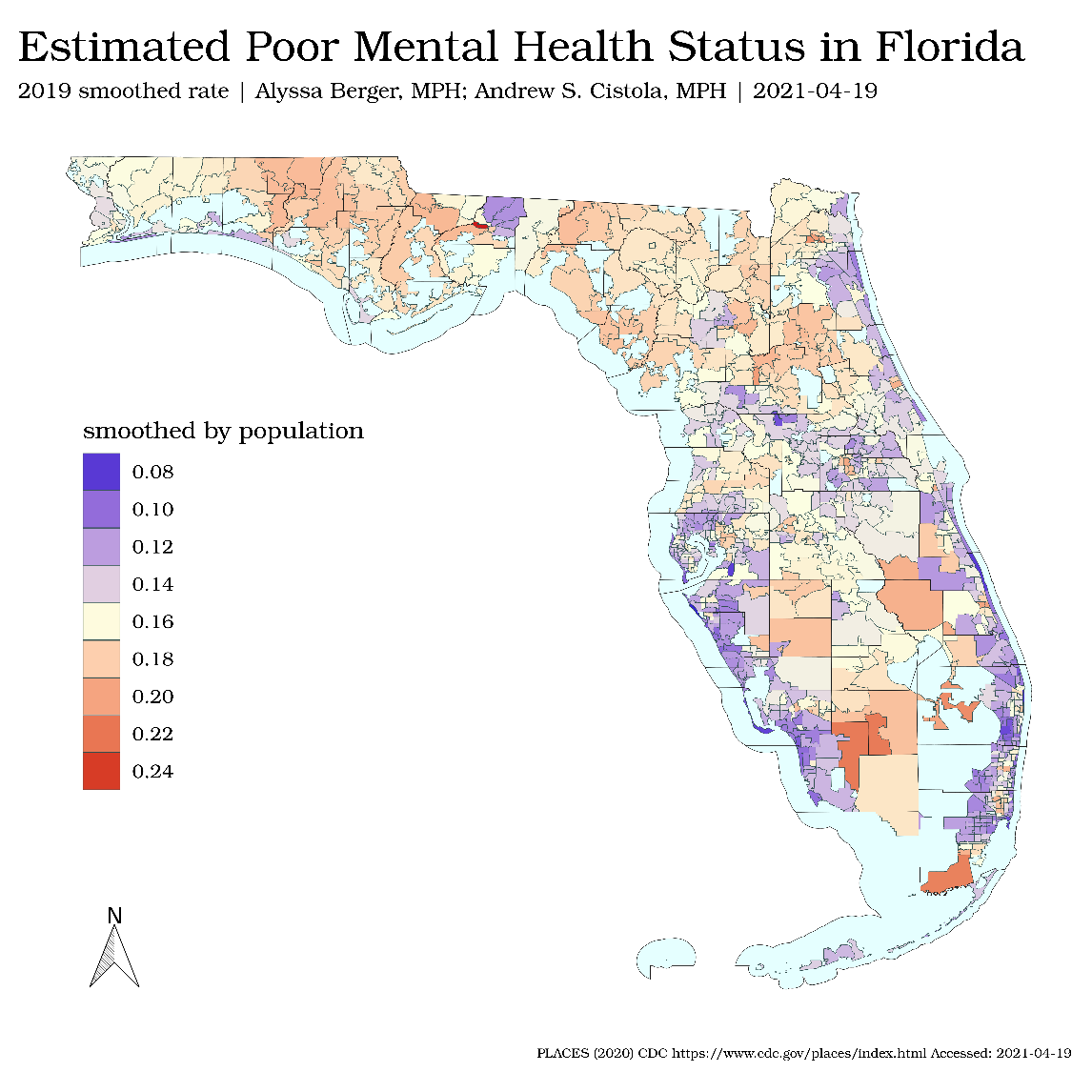
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Figure 1. Estimated zip code prevalence of self-reported poor mental health using local empirical bayes smoothing.

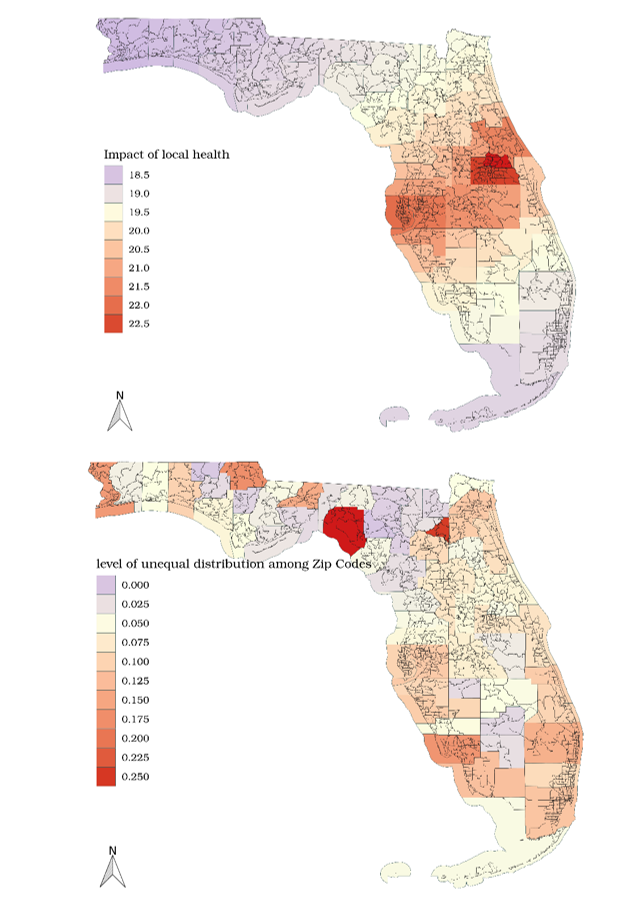


Figure 2. (above) coefficient variation of aggregated local health status in a geographically weighted regression model (below) Gini index measuring level of unequal distribution of higher rates among zip codes within counties.

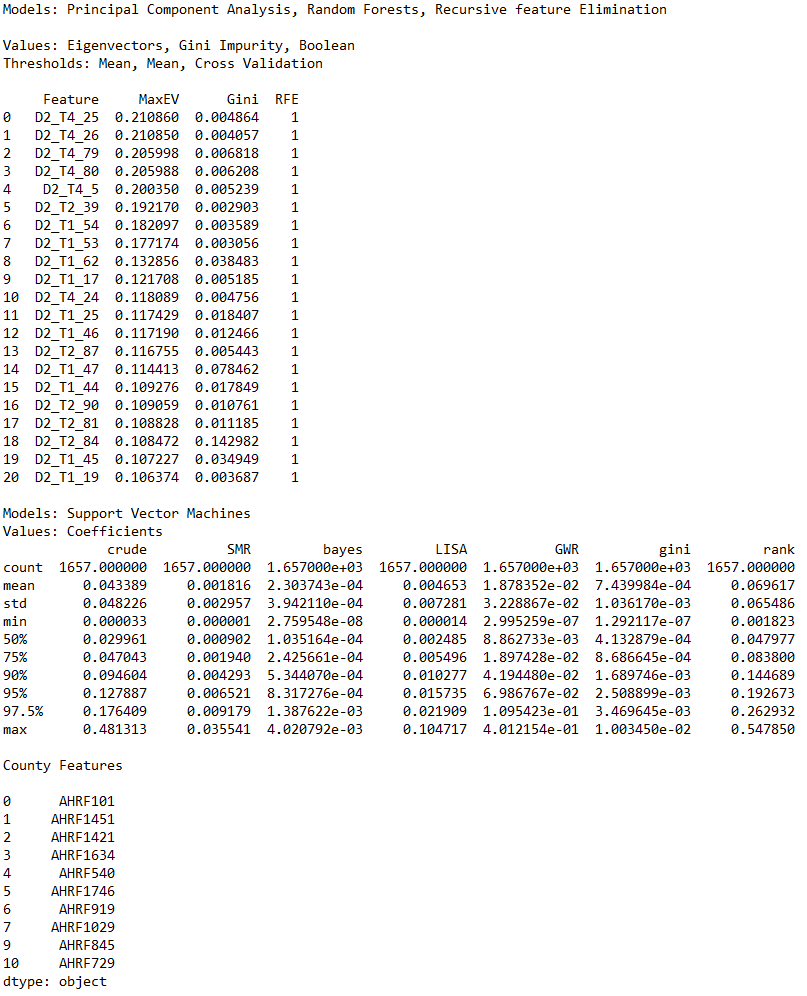
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Figure 3. Raw output from Python ‘scikit-learn’ library showing results from algorithms used in feature selection for zip codes (above) and counties (below). These features were selected for use in the ANN and HLM models.

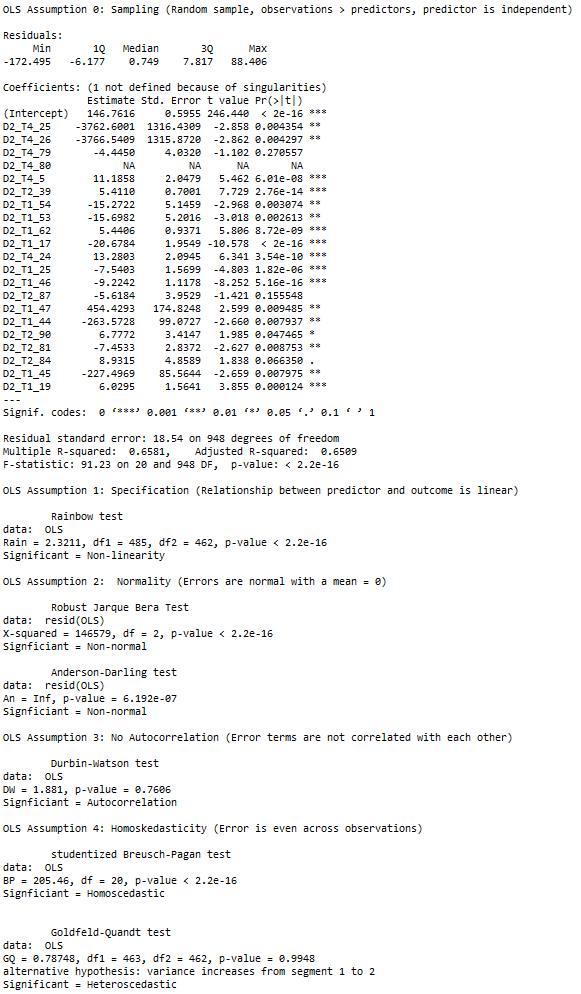
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Figure 4. Raw model summary from R ‘stats’ library for initial OLS model using selected zip code predictors as well as test results checking OLS assumptions.

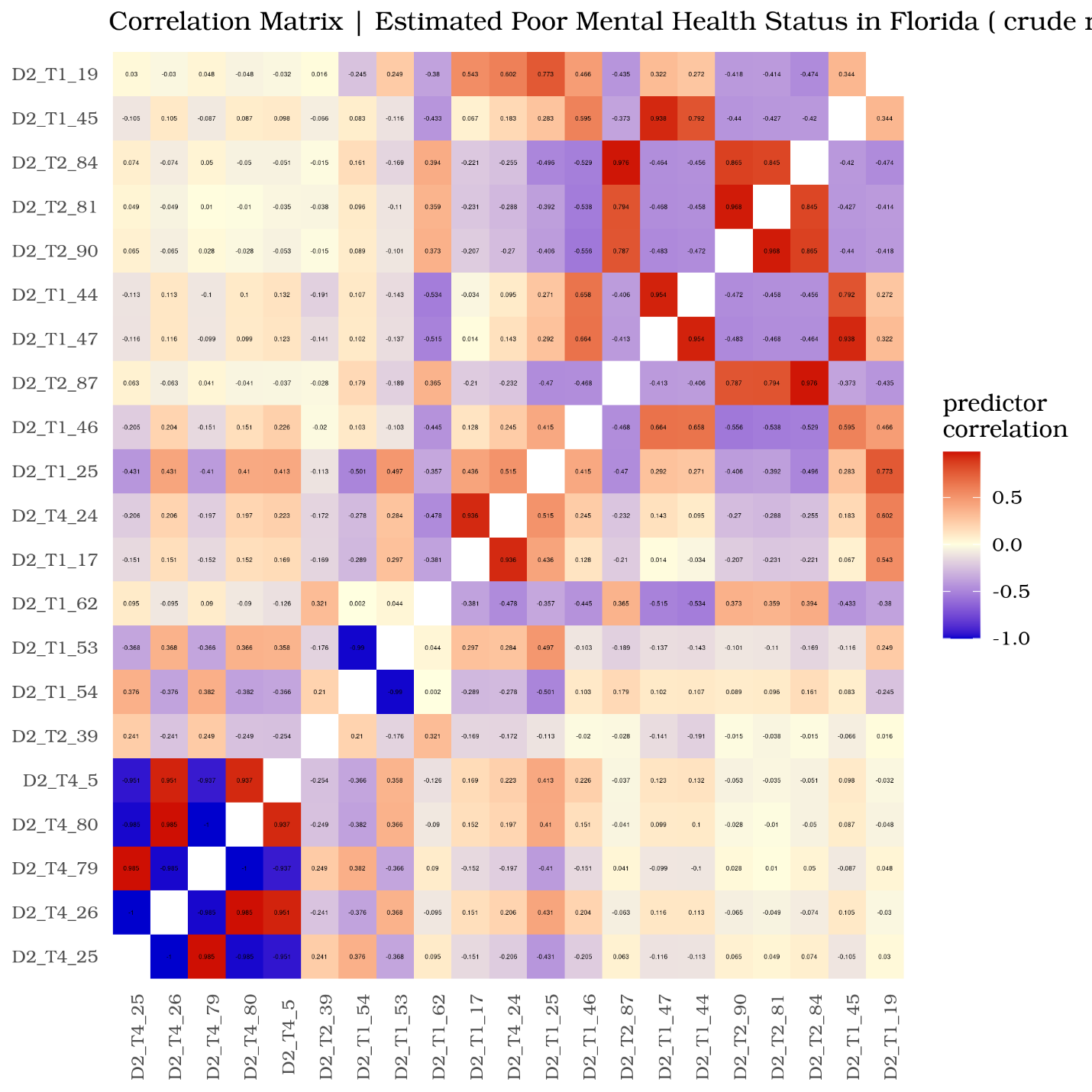
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Figure 5. Correlation matrix of zip code level predictors

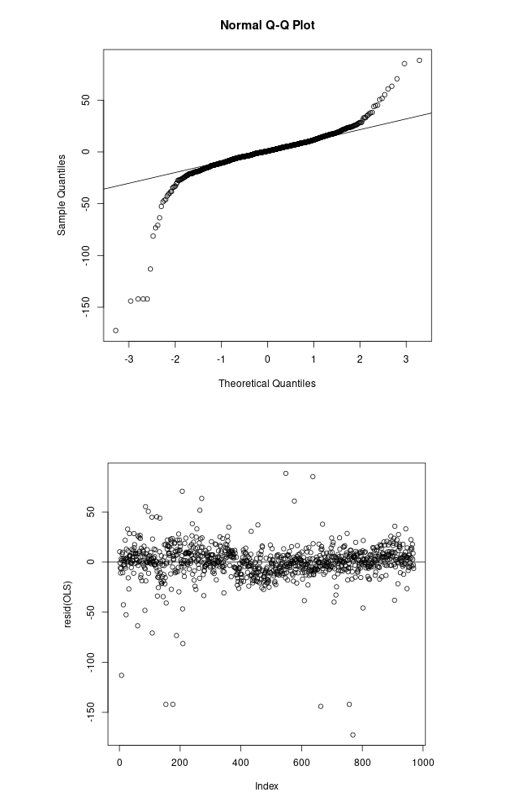
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Figure 6. Q-Q (above) and residuals plot (above) from original OLS model.

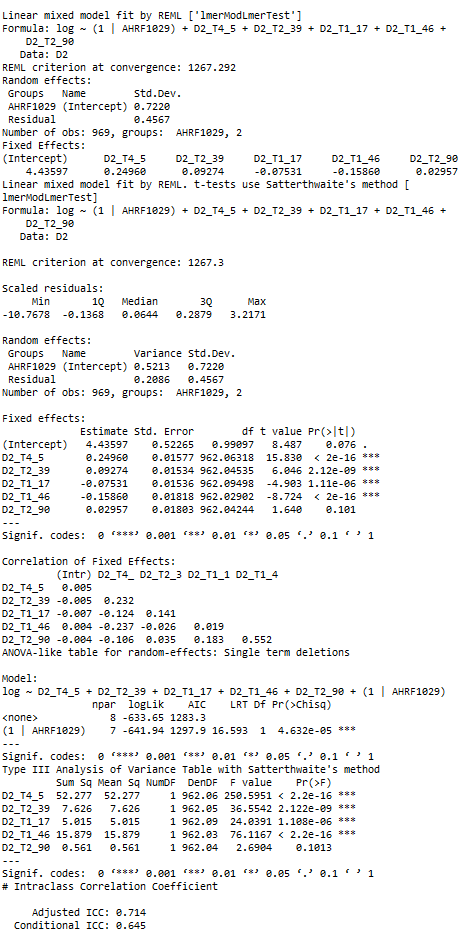
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Figure 7. Raw model summary from R ‘lme4’ library for final mixed-effects model and intraclass correlation coefficient result.

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