Ecological Factors Associated with Self-Reported Mental Health Status

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# 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 for expanded scope in spatial analysis to better inform translational science in public health (28–30).

***Background***

* % of adults report their mental health status and % report that they have struggled from symptoms of a mental health condition(s)
* Among these adults, various sociodemographic factors such as age, marital status, socioeconomic status, household size, education, pet size, domestic violence, and social support are all known factors that influence various mental health conditions
* These sociodemographic factors have been well researched in connection to adults’ mental health conditions yet spatially, little is known on where each of these factors are in relation to all mental health conditions
* Despite limited information on ecological factors associated with mental health, the information that has been studied has been proven to be effective in enhancing education, mental health consultations, and targeted interventions
* This study aims to serve as a top-down approach to assess the impact ecological factors can have on self-reported mental health outcomes utilizing recent Places data
* In evaluating this impact, we hope this study can move towards more hypothesis generating research that considers the importance of ecological factors as it relates to mental health

***Literature Review***

***Theoretical Framework***

***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 a number of 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.

**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 |

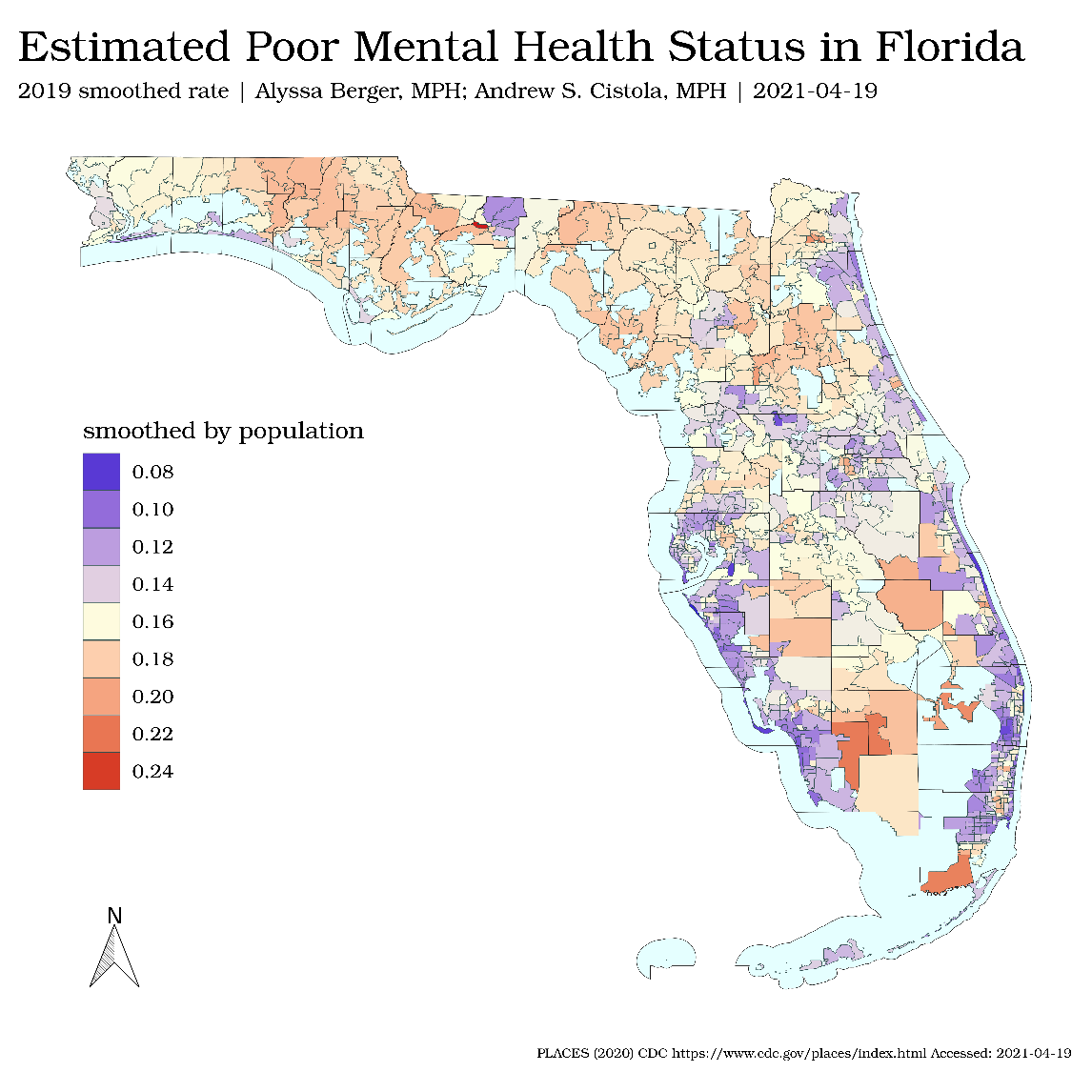
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Figure 1. Estimated zip code prevalence of self-reported poor mental health using local empirical bayes smoothing.

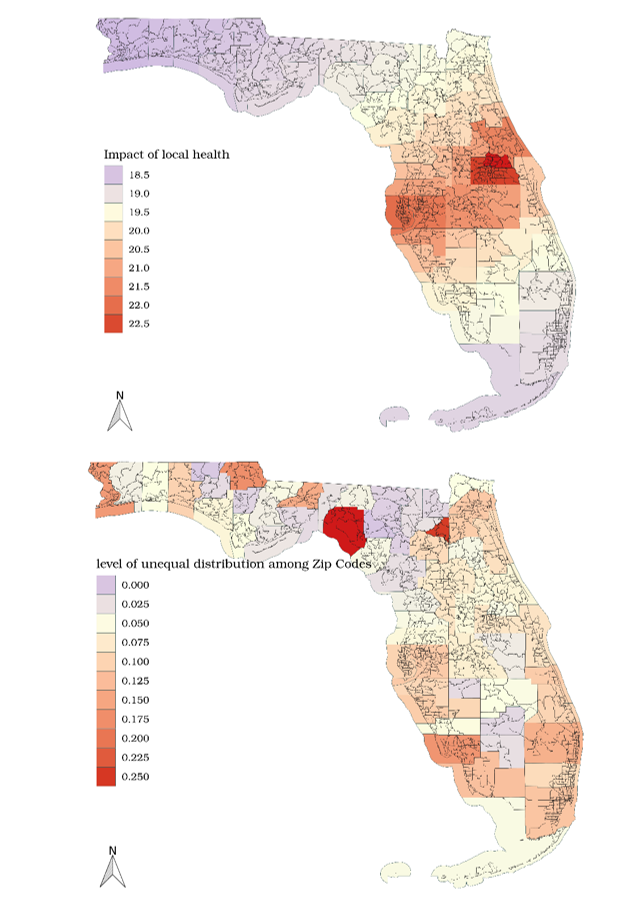


Figure 2. (above) coefficient variation of aggregated local health status in a geographically weighted regression model (below) Gini index measuring level of unequal distribution of higher rates among zip codes within counties.

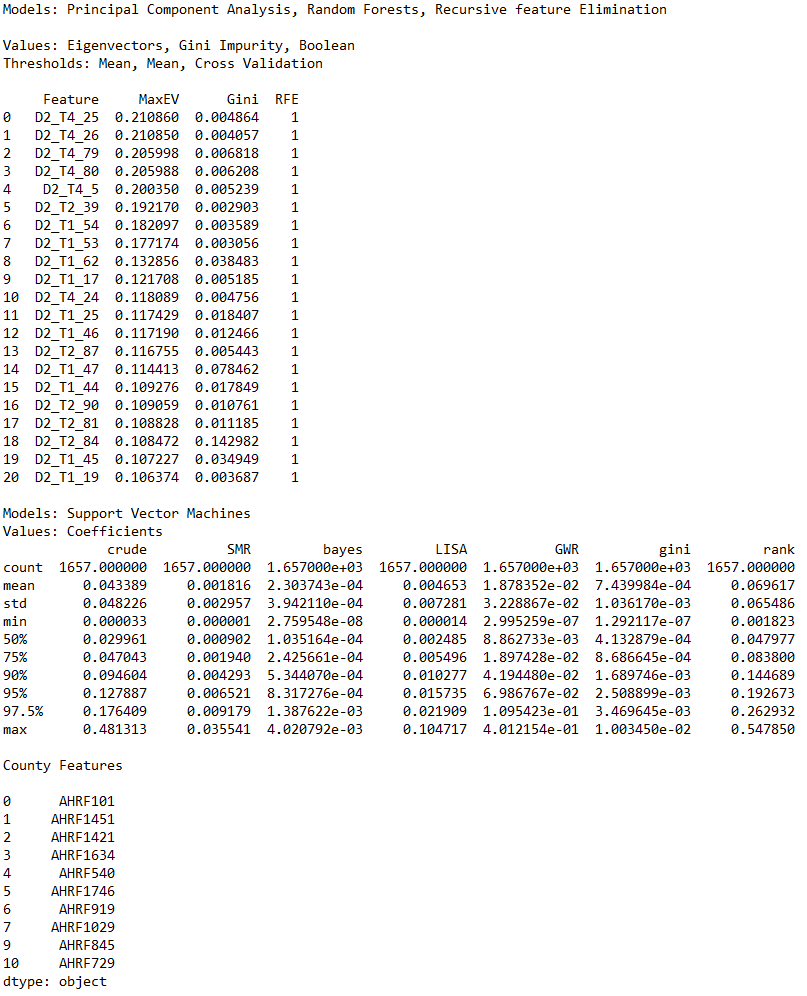
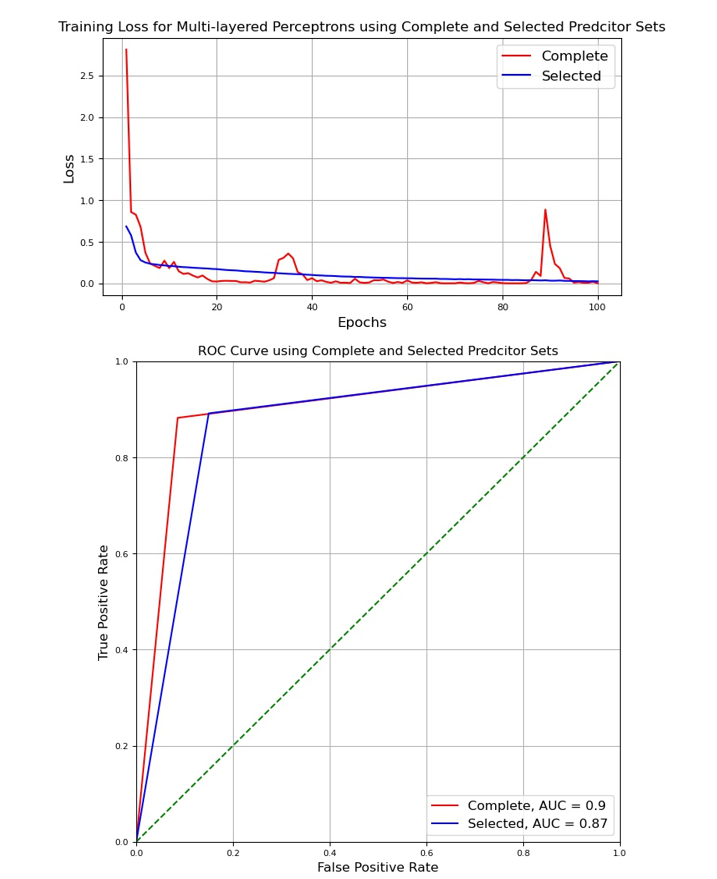
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Figure 3. Raw output from Python ‘scikit-learn’ library showing results from algorithms used in feature selection for zip codes (above) and counties (below). These features were selected for use in the ANN and HLM models.

Figure 4. (above) Training loss for each multi-layered perceptron used to compare complete and selected predictor sets (below) ROC with AUC tests comparing complete predictor set (N > 2000) and selected county/zip code predictors (N = 25).

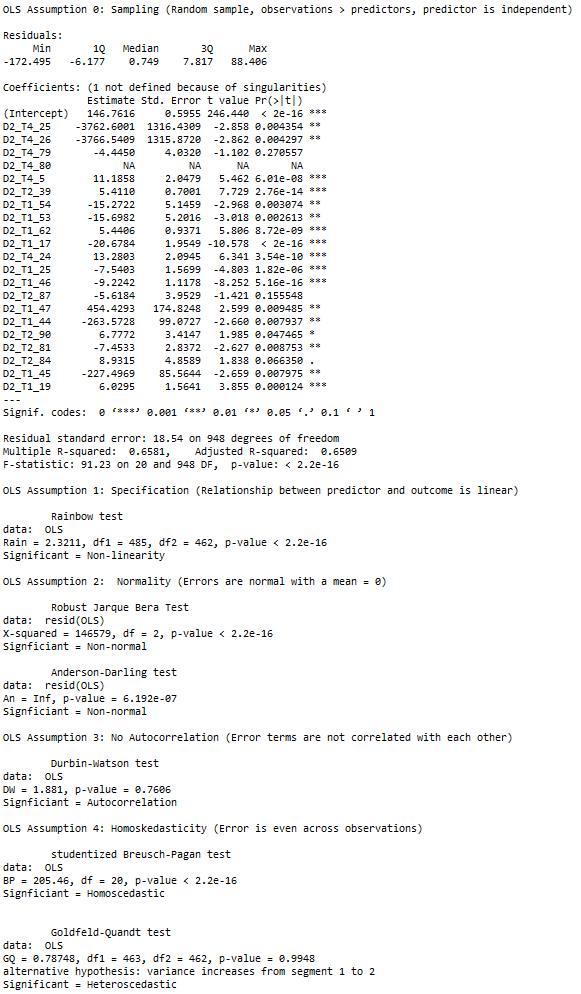
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Figure 5. Raw model summary from R ‘stats’ library for initial OLS model using selected zip code predictors as well as test results checking OLS assumptions.

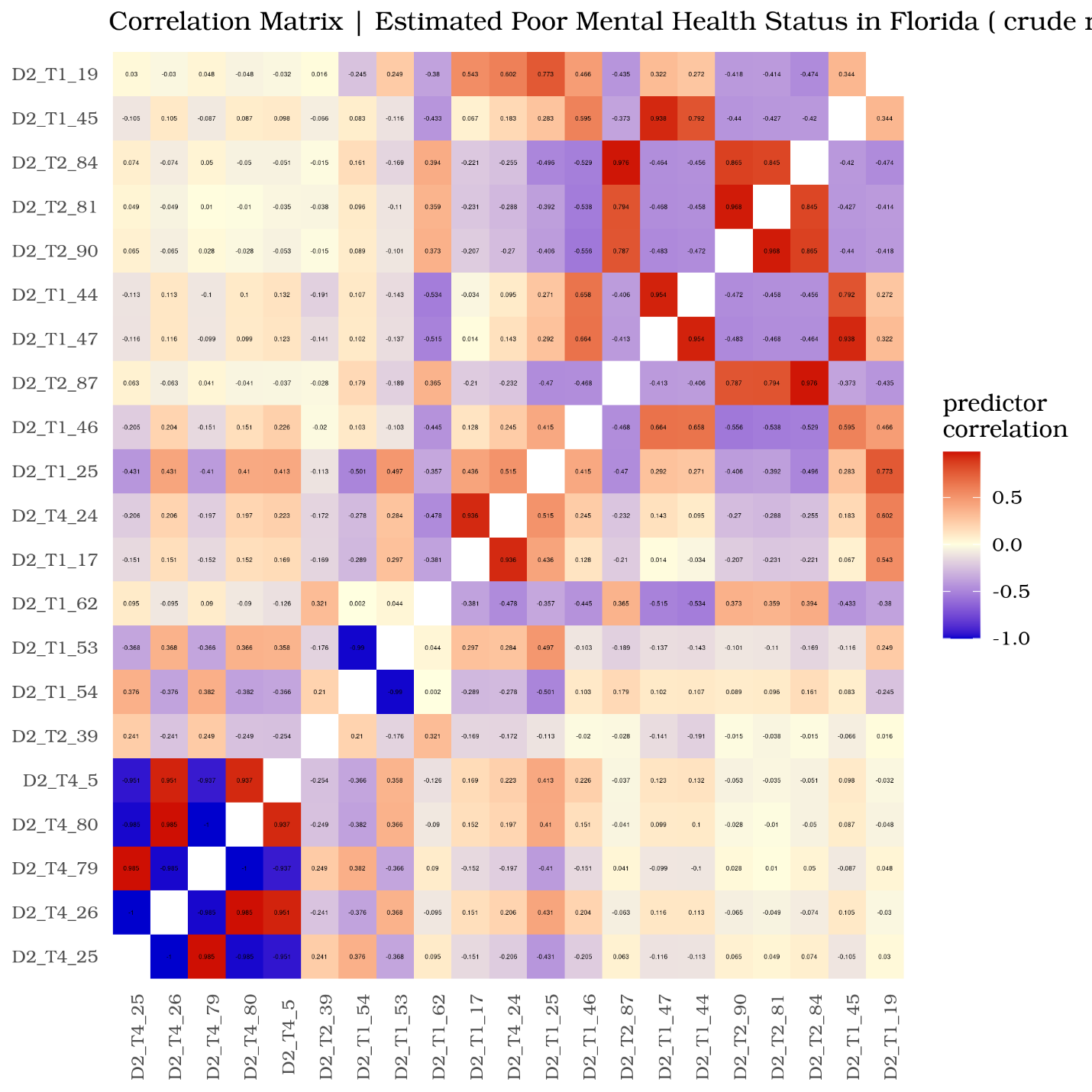
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Figure 6. Correlation matrix of zip code level predictors

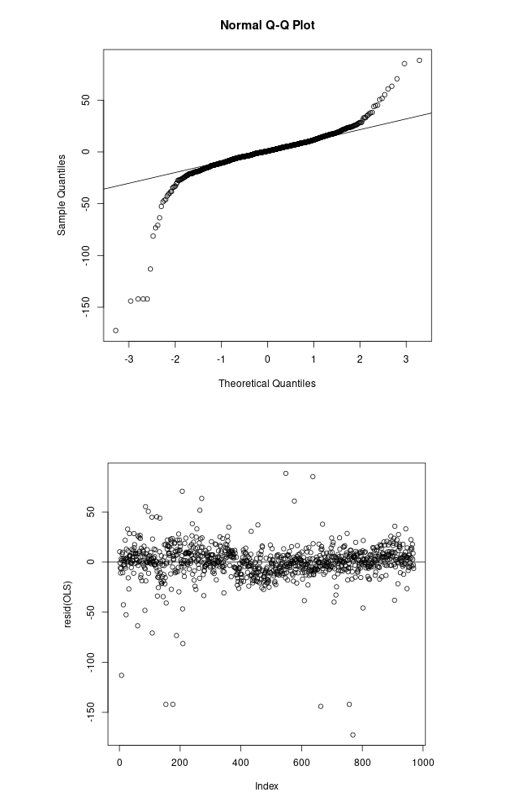
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Figure 7. Q-Q (above) and residuals plot (above) from original OLS model.

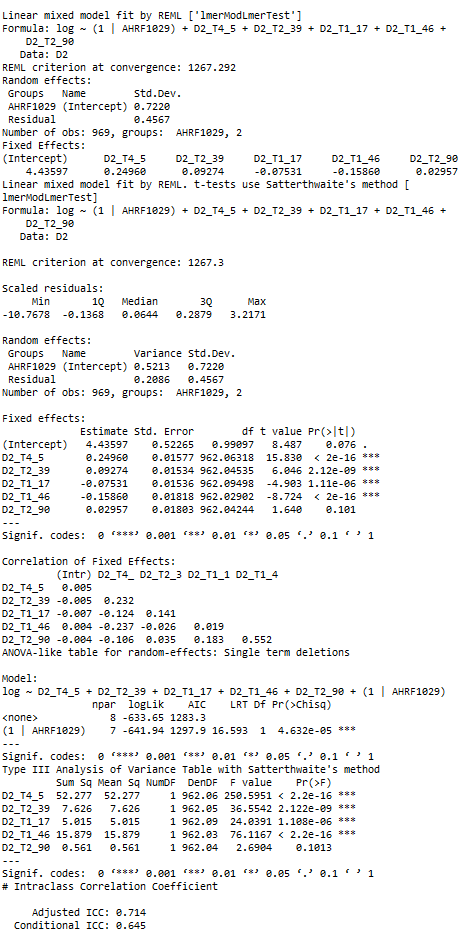
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Figure 8. Raw model summary from R ‘lme4’ library for final mixed-effects model and intraclass correlation coefficient result.

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