**Census Tract Prevalence Estimate Methodology**

The census tract prevalence calculations were derived from the county and zip code level prevalence measures. The details for those measures are described in a separate document. The methodology for calculating the census tract prevalence estimates was used for all states across a variety of diseases. In order to calculate these estimates, the zip code level prevalence estimates, county level prevalence estimates, and census tract-county mapping file had to be created. The census tract-county mapping file contains the county with which each census tract lies within.

Once the county and zip code prevalence measures were calculated for each disease, the difference between each zip code prevalence and corresponding mean state prevalence was calculated. The absolute value of these differences were used to fit a beta distribution for each state. Next, the beta distribution output a list of random errors to be applied to each census tract in each state. For example, if a state had 100 census tracts, the code would generate 100 random error values to be applied to each census tract. Each random error was then added to the county prevalence estimate for which each census tract was in. For instance, if a county had five census tracts within it, all five census tracts would have their respective beta errors applied to the same county prevalence estimate. Since the random errors generated from the beta distribution were between 0 and 1, each value was randomly chosen to be positive or negative.