Packaged alongside the BIGMAP layers is an additional layer of validation data, modeling a comparative accuracy assessment at three different scales. These layers are possible through the FIA sampling design, of hexagonal grids which account for 6,000 acres (24.29 km2) of forested lands. To be included in the validation assessment hexagons and hex aggregations need to have enough plots to ensure that the summed scaling factor accounts for at least 10% of the assessment area. To be included in the validation set, there needs to be three plots with a specific observation recorded bringing the expansion factor above 64.8 km2 example: If one Dogwood tree is found on a 2 plots in a 3 hexagon range, then you would need to scale this to account for 10% of the total inventory. Along the coast and the borders many of the hex aggregations did not contain the full number of hexagons to ensure the assessment area were of similar size scaling methods were used to ensure consistency (or accuracy). For level 2 aggregations, there needs to be a minimum of 6 hexagons present with observations on them and level 3 needs a minimum of 37 hexagons with observations.

For each level and species, two graphs are created: reduced major axis (RMA) regression and a species level line graph. These graphs aid in analyzing the error and biases associated with modeling FIA data. Along with the graphs, different variables are calculated to aid in the standardization and analysis between the different species and levels. The variables calculated are: Agreement Coefficient (AC), Systematic Agreement Coefficient (ACsys), Unsystematic Agreement Coefficient (ACunsys), RMA Relationship (y=mx+b), and R2 values.

A reduced major axis regression is a method meant to handle errors in both the x and y variables and find biases in the estimates. The Agreement coefficient is a measure of interrater reliability for qualitative items and aids in the calculation of Systematic and Unsystematic coefficients. The Systematic agreement coefficient, ACsys calculates the difference between the 1:1 line and the geometric mean functional relationship (GMFR) regression, which describes the bias present. The Unsystematic agreement Coefficient calculates the scatter around the GMFR line. A high scatter of points suggests a difficult set of predictor variables to model.

Species level line graph depicts the local variability of the pixels and their differences between mapped estimates and increasing plot-based means. [Description of how to interpret the points on a species level line graph]