CHAPTER 7.

Advancing Broad-scale Forest Health Evaluation and Monitoring with rFIA

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INTRODUCTION

The U.S. Department of Agriculture Forest Inventory and Analysis (FIA) program collects data describing the condition and change of forest ecosystems across all lands in the United States (Smith 2002, USDA Forest Service 2019b). The extraordinary size of the spatial domain and breadth of forest variables sampled by the FIA program make it a unique and powerful resource for determining the extent and severity of undesirable changes in forest health across large spatial domains in the United States. Due to a lack of flexible, user-friendly tools for estimation of forest variables (Tinkham and others 2018), the richness and utility of the FIA data are not always realized for forest health assessment. We developed rFIA (Stanke and others 2020, https://rfia.netlify.app/), an open-source R package (R Core Team 2020), to reduce these data accessibility hurdles and unlock the potential of FIA for broad-scale forest health evaluation and monitoring.

rFIA achieves two primary objectives: (1) improve the accessibility of FIA data for the estimation of status and change in forest ecosystems and (2) offer enhanced flexibility in estimation strategies and defining populations of interest. Using a simple yet powerful design, rFIA implements the design-based estimation procedures described in Bechtold and Patterson (2005) for more than 60 forest variables and allows users to return intermediate (i.e., plot, condition, and/or tree-level) estimates of all variables for use in modeling studies. With rFIA, users can easily summarize forest variables for populations defined by any combination of spatial units (i.e., spatial polygons), temporal domains (e.g., most recent measurements), and/or biophysical attributes (e.g., species, site classifications). Furthermore, rFIA implements five design-based estimators that enhance the value of FIA for temporal change detection and offer flexibility in a tradeoff between precision and temporal specificity.

Here we present three case studies chosen to demonstrate some aspects of rFIA's potential to advance forest health evaluation and monitoring in the United States. First, we highlight rFIA's spatiotemporal estimation capacity by estimating current down woody material (DWM) biomass within HUC6 watershed boundaries across the conterminous United States (CONUS) by combining the most recent FIA inventories available in each State. We next illustrate how rFIA enhances the value of FIA for temporal change detection by examining trends in lodgepole pine (*Pinus contorta*) mortality in Colorado using multiple design-based estimators. Finally, we use rFIA to estimate plot-level live tree density and develop a Bayesian hierarchical model to estimate changes in live tree abundance (i.e., net response of recruitment, growth, and mortality) within ecoregion subsections (Cleland and others 2007) across the CONUS (excluding Wyoming due to a lack of remeasurements), thereby demonstrating how rFIA can aid model-based analyses.

METHODS

Data

Since 1999, FIA has operated an extensive, nationally consistent forest inventory designed to monitor changes in forests across all lands in the United States (Smith 2002). The program measures forest variables on a network of permanent ground plots that are systematically distributed at a rate of approximately one plot/2428 ha (one plot per 6,000 acres) across the United States (Smith 2002). Ground plots are remeasured approximately every 5 to 7 years in the Eastern United States and 10 years in the Western United States, with remeasurements currently available in most States. Data collected on ground plots are stored in a large public database (i.e., the FIA Database) (USDA Forest Service 2019a). rFIA includes utility functions to retrieve, process, and visualize data stored in the FIA Database (Stanke and others 2020). Herein, we demonstrate potential applications of rFIA to forest health evaluation and monitoring, drawing solely from data collected by the FIA program. The code to reproduce these analyses (including sample sizes and results) are available at our official website (https://rfia.netlify.app/project/fhm2020/).

National-scale DWM Biomass Stocks

The FIA program measures variables related to DWM volume, biomass, and carbon on a subset of ground plots in most FIA regions (i.e., intensive or forest health plots). The *dwm* function in rFIA uses FIA data to produce plot-level or population estimates of DWM variables by ecosystem components, including: coarse woody debris (i.e., 1,000-hour fuels), fine woody debris (i.e., 1-, 10-, and 100-hour fuels), slash piles, litter, and duff. We used the *getFIA* function in rFIA to download an appropriate subset of the FIA Database from the FIA DataMart and selected the most recent subset of inventories within each State using the *clipFIA* function. We then used the most recent subset of the FIA Database to estimate the current biomass density of 100-hour fuels (1.00–2.99-inch diameter) on forest land (including public and private lands) within HUC6 watershed boundaries across the CONUS. All estimates were produced using the temporally indifferent (TI) estimator (i.e., the same methods implemented by FIA’s flagship online estimation tool, EVALIDator [Miles 2019]).

Trends in Colorado Lodgepole Pine Mortality

The FIA program uses an annual panel system to estimate current inventories and change, where inventory cycles consist of multiple panels, and individual panels comprise mutually exclusive subsets of ground plots measured in the same year within a region. Precision of point and change estimates can often be improved by combining annual panels within an inventory cycle (i.e., by augmenting current data with data collected previously). While FIA does not prescribe a core procedure for combining panels (Bechtold and Patterson 2005), the TI estimator, which effectively pools data from annual panels into a single periodic inventory, is likely the most widely known and used.

rFIA implements the TI estimator by default for consistency with EVALIDator (Miles 2019). Alternatively, users may choose to return estimates from individual annual panels (ANNUAL estimator) or use one of three moving-average-based estimators, including the simple moving average (SMA), linear moving average (LMA), and exponential moving average (EMA). The SMA estimator applies equal weight to all annual panels within an inventory cycle; hence, its estimates tend to align closely with those of the TI estimator. In contrast, the LMA and EMA estimators apply weights that decay linearly or exponentially as a function of time since measurement, respectively. The EMA estimator requires specification of a decay parameter, λ (ranging between 0 and 1, default 0.5), that controls the rate at which panel weights decline with time (higher values of λ indicate more even distribution of weights across panels).

The FIA program calculates growth, mortality, and removals between repeated measurements of inventory plots. To provide early estimates of mortality (i.e., prior to availability of remeasurements on annual inventory plots), FIA draws on inventory data collected prior to the implementation of the annual design (i.e., periodic inventory plots; where many annual plots were established on top of previous periodic plots). The *growMort* function in rFIA seamlessly integrates both procedures (periodic-annual and annual-annual) to provide unbiased estimates of tree mortality processes over time.

We used the *growMort* function to estimate trends in the mortality rate (trees per acre per year) of lodgepole pine in Colorado over the period 2002–2018. We estimate mortality rates and associated uncertainty using each design-based estimator currently offered in rFIA (i.e., TI, SMA, LMA, EMA, and ANNUAL estimators) and visually compare trends across estimators. To highlight the flexibility and utility of the EMA estimator for use in temporal change detection, we estimate mortality rates and associated uncertainty with multiple values of λ (i.e., effectively varying the temporal kernel from which mortality rates are estimated) and visually compare short-range and long-range trends.

National-scale Shifts in Live Tree Abundance

Traditionally, FIA has relied on sample plot data and design-based estimators to produce point and change estimates of forest variables (Tinkham and others 2018). These estimators are familiar and generally unbiased (McRoberts 2010), though low sample sizes often limit their ability to yield sufficiently precise estimates for small populations (e.g., small spatial domains, rare species/events). Model-based estimators offer a versatile alternative to design-based estimation, relying on predictions from models and ancillary variables to produce estimates of forest variables and often yielding more precise estimates for small populations. To aid model-based analyses using FIA data, rFIA allows users to return estimates of all forest variables within subpopulation response units (e.g., plot, subplot, condition, tree-level). These estimates can then be used (along with ancillary variables) to develop models of ecological patterns and processes, estimate population parameters, and predict to unobserved domains (e.g., forecast future change).

Here, we use the *tpa* function in rFIA to estimate plot-level number of live trees per acre (TPA) and live tree basal area per acre (BAA) for all plot visits under the annual inventory design across the CONUS. Using estimates from plots visited more than once (i.e., remeasured annual plots), we construct a Bayesian hierarchical model to estimate the average rate of change in live TPA and BAA at individual plots, within ecoregion subsections (Cleland and others 2007), and across the CONUS over the period 1999–2019:

$$y_{i,j,k} \sim normal(\beta_{j,k} t_{i,j,k} + \alpha_{j,k}, \varsigma^2_{j,k}) \qquad (1)$$

$$\alpha_{j,k} \sim normal(\alpha_k, \sigma^2_{\alpha,k}) \qquad (2)$$

$$\beta_{j,k} \sim normal(\beta_k, \sigma^2_{\beta,k}) \qquad (3)$$

$$\alpha_k \sim normal(\alpha, \sigma^2_{\alpha}) \qquad (4)$$

$$\beta_k \sim normal(\beta, \sigma^2_{\beta}) \qquad (5)$$

where

y = the log of live TPA or BAA at visit i, on plot j, in ecoregion subsection k

t = year of visit

α = a random intercept describing y at $t = 0$

β = a random slope describing the average annual rate of change in y

$\varsigma^2_{j,k}$ = the residual variance of the linear model relating log TPA/BAA to time at the plot level [equation (1)]

We allow $\alpha_{j,k}$ and $\beta_{j,k}$ to vary across plots, with their values drawn from subsection-level distributions [equations (2–3)] characterized by a corresponding mean (α_k and β_k) and variance ($\sigma^2_{\alpha,k}$, $\sigma^2_{\beta,k}$) for each coefficient. Parameters of subsection-level distributions are in turn drawn from a CONUS-level distribution defined by means (α and β) and variances (σ^2_{α}, σ^2_{β}) of each coefficient. As our response (live TPA or live BAA) is log scaled, we can transform estimates of β_k and β to annual rates:

$$r_k = 100(e^{\beta_k} - 1) \qquad (6)$$

$$r = 100(e^{\beta} - 1) \qquad (7)$$

where

r = percentage of annual change in live TPA or BAA (Crawley 1993)

The hierarchical form of our model allows us to draw inference regarding temporal trends in live tree abundance across multiple ecological scales (i.e., stand, landscape, and subcontinental). For brevity, we highlight results at the landscape and subcontinental scale here. Specifically, we estimate the percentage of annual change in live TPA and live BAA of tree populations [equations (6 and 7)] within ecoregion subsections and across the CONUS. We estimate the probability of direction, or probability that the estimated rate for each population excludes 0, to highlight the "significance" of the estimated trends.

RESULTS AND DISCUSSION

National-scale DWM Biomass Stocks

We mapped estimates and associated uncertainty of current 100-hour fuel biomass density (tons per acre) by HUC6 units across the CONUS to demonstrate the spatiotemporal estimation capacity of rFIA (fig. 7.1). In the Eastern United States, 100-hour fuel density generally appears to be higher in regions dominated by oak-hickory forest types relative to regions dominated by southern pines, northern hardwoods, and spruce/fir forest. In the Western United States, 100-hour fuel density appears to be elevated in regions dominated by Douglas-fir forest types (e.g., Pacific Northwest) relative to other regions. Uncertainty (measured as sampling error percentage, or coefficient of variation percentage) tended to be highest in the Plains and desert Southwest, presumably due to low sample sizes. Estimates presented herein are similar to those from previous efforts to characterize DWM biomass in U.S. forests (Chojnacky and others 2004, Woodall and others 2013).

Down woody material is an important component of forest ecosystems across the United States. Specifically, DWM biomass may help describe fuel loading, wildlife habitat, structural diversity, and biogeochemical processes in forests (Woodall and Monleon 2008). The national-scale DWM inventory provided by FIA is unprecedented in scope and spatial extent, and of extraordinary value in many forest health monitoring efforts. We anticipate the *dwm* function in rFIA will be of particular interest to wildlife biologists, ecologists, mycologists, foresters, and fuels specialists seeking to estimate the status, change, and future states of DWM stocks. For brevity, we only present results of 100-hour fuel density (biomass per acre). However, it is important to note that our analysis (i.e., a single call to *dwm*) simultaneously produced estimates of DWM biomass, carbon, and volume (totals and density) for the following ecosystem components/fuel classes: litter, duff, 1-hour (0.00–0.24-inch diameter), 10-hour (0.25–0.99-inch diameter), 100-hour (1.00–2.99-inch diameter), and 1,000-hour fuels (≥3 inch diameter).

While the analysis presented here is relatively simple, it represents a substantial advance in spatial estimation capacity relative to other FIA estimation tools (USDA Forest Service 2019a). That is, we used unique areal units (i.e., HUC6 watershed boundaries) to define populations of interest, rather than relying on fields recorded in

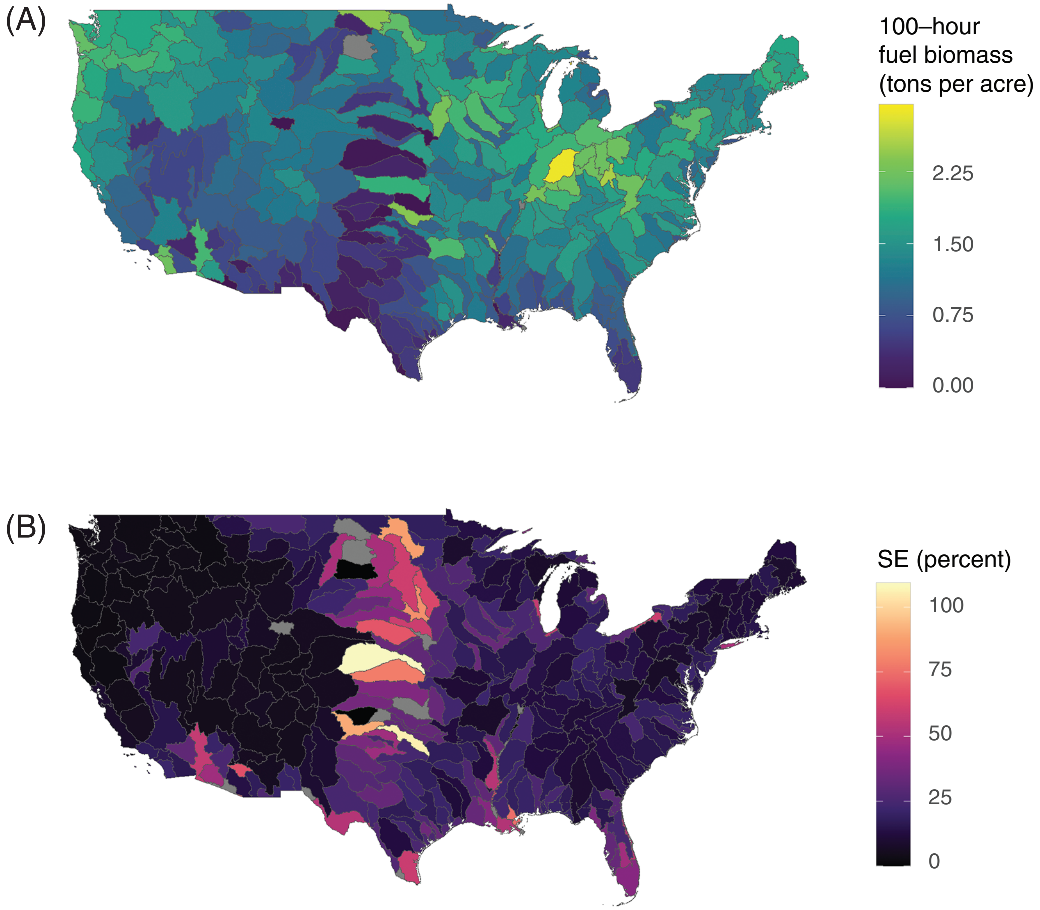

Figure 7.1—(A) Estimated current 100-hour fuel biomass (tons per acre) and (B) associated uncertainty (percent sampling error [SE]) within HUC6 watershed boundaries across the conterminous United States. All estimates produced using the dwm *function in the rFIA package, using the temporally indifferent estimator.*

the FIA Database. With rFIA, users can specify any spatial polygon object to use as a grouping variable (i.e., region contained within each areal unit is treated as a unique population). For example, spatial polygons describing historic fire regimes could be used to group estimates of current DWM fuel stocks (or other variables of interest, e.g., size-class distributions, mortality, invasive species abundance). While we use the *dwm* function to highlight rFIA's spatial estimation capacity, all rFIA estimator functions have been designed with the same functionality.

Trends in Colorado Lodgepole Pine Mortality

We used multiple design-based estimators to examine temporal trends in Colorado lodgepole pine mortality (TPA per year) and highlight how rFIA enhances the value of FIA for temporal change detection. A general pattern of increasing mortality through time was evident across all estimators, likely linked to recent outbreaks of mountain pine beetle (*Dendroctonus ponderosae*) in the region (Page and Jenkins 2007). Specifically, we observe an approximately fourfold increase in lodgepole pine mortality across all estimators in 2015 relative to 2005 levels. Point-estimates of mortality (estimated mortality in any given year) and associated uncertainty (i.e., sampling error percentage) varied considerably among estimators, with the ANNUAL estimator exhibiting the highest degree of interannual variability and uncertainty and the SMA and TI estimators exhibiting the smoothest temporal trends and lowest uncertainty (fig. 7.2). In general, a decrease in uncertainty was evident across estimators over

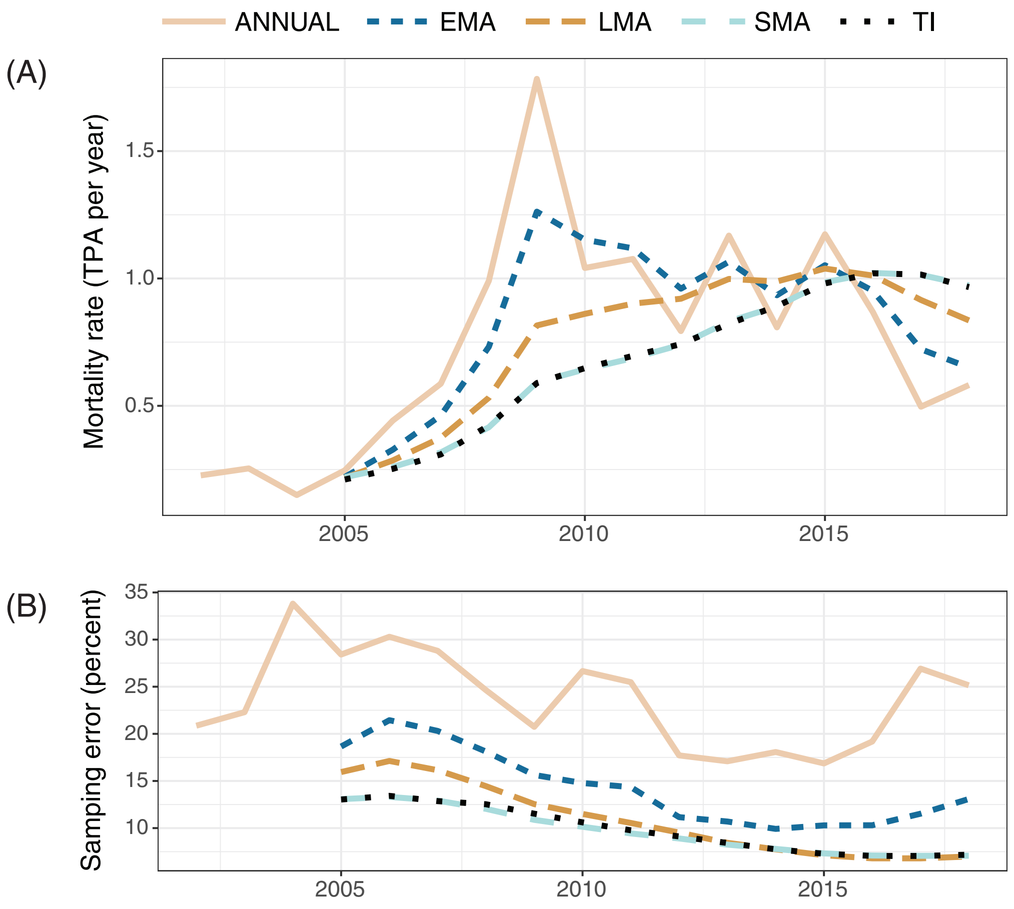

*Figure 7.2—(A) Estimated trends in lodgepole pine (*Pinus contorta*) mortality rates (trees per acre [TPA] per year) and (B) associated uncertainty (percent sampling error) in the State of Colorado over the period 2002–2018. Estimates were produced using five design-based estimators: annual (ANNUAL), exponential moving average (EMA), linear moving average (LMA), simple moving average (SMA), and temporally indifferent (TI). All estimates were produced using the* growMort *function in the rFIA package.*

time, likely due to increasing sample size (i.e., availability of plot remeasurements). While the estimators presented herein vary considerably in their temporal specificity, it is important to note that plot remeasurements occur on 10-year intervals in the Western United States. Hence, all estimates of mortality should be interpreted as an average over a decade (ANNUAL) or more (SMA, LMA, EMA, TI).

Point-estimates of mortality and associated uncertainty varied with the value of λ (i.e., decay parameter controlling distribution of weights across an inventory cycle) specified in the EMA estimator, illustrating the estimator's pronounced flexibility and an inherent tradeoff between precision and temporal specificity (fig. 7.3). As λ approaches 0, higher weight is given to more recent panels in the inventory cycle, and the behavior of the EMA approaches that of the ANNUAL estimator (high temporal specificity; increased uncertainty). In contrast, as λ approaches 1, panel weights are distributed more evenly across inventory cycle, and the behavior of the EMA approaches that of the SMA (low temporal specificity; decreased uncertainty). Sample variance is generally minimized when panel weights are evenly distributed across the inventory cycle, though improved precision comes at the cost of introducing temporal lag-bias (Bechtold and Patterson 2005). Hence, equal weighting schemes (e.g., SMA, TI, or EMA with a high λ) could be undesirable in settings where the variable of interest is suspected to change rapidly over time (as seen here).

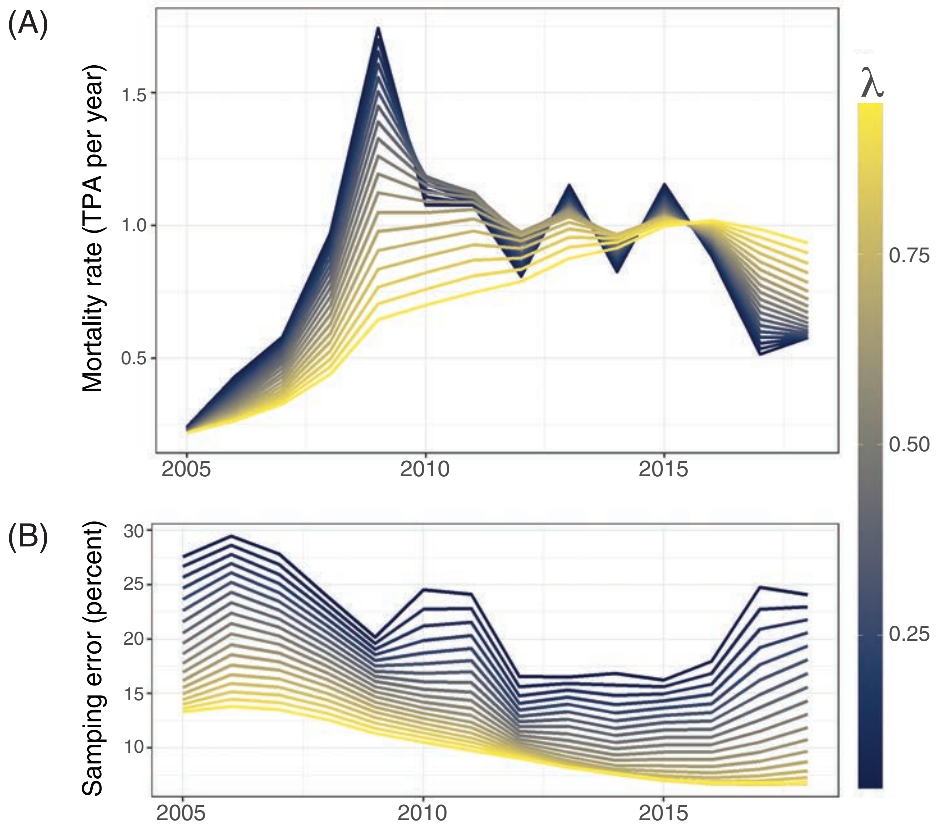

*Figure 7.3—(A) Variation in short-range and long-range temporal trends of lodgepole pine (*Pinus contorta*) mortality rates (trees per acre [TPA] per year) and (B) associated uncertainty (percent sampling error) in the State of Colorado over the period 2002–2018. Estimates produced by varying the value of λ specified in the exponential moving average (EMA) estimator, where high values of λ characterize long-range temporal trends and low values characterize short-range temporal trends. All estimates produced using the* growMort *function in the rFIA package.*

In practice, the choice of estimator should be guided by user objectives. That is, no single estimator presented herein is “best” for all estimation objectives or across a wide variety of spatial, temporal, and population conditions. As a general guide, estimators that distribute weights approximately evenly across panels (i.e., SMA, TI, or EMA with a high λ) should be employed when users seek to minimize uncertainty around estimates and no considerable change is suspected in the underlying population. In contrast, if users are primarily interested in characterizing temporal change in the population of interest, estimators that give higher weight to more recent observations (i.e., ANNUAL, LMA, EMA with low λ) are likely to be more suitable.

In rFIA, users can easily produce “moving-average ribbons” as seen in fig. 7.3 where estimates are produced for multiple, sequential values of λ using the EMA estimator (i.e., effectively characterizing change across multiple temporal scales). Such plots are particularly useful for detecting periods of rapid change in a population. That is, rapid change is likely when large gaps appear between point-estimates produced with different values of λ, with increases in the state variable indicated when short-range (i.e., low λ) estimates exceed long-range estimates (i.e., high λ) (fig. 7.3, 2008–2012) and decreases indicated when long-range estimates exceed short-range estimates (fig. 7.3, 2017–2018).

National-scale Shifts in Live Tree Abundance

To demonstrate how rFIA can aid model-based analyses using FIA data, we use rFIA to estimate plot-level live tree TPA and BAA and develop a Bayesian hierarchical model to estimate temporal changes in each variable across multiple ecological scales. Across the entire CONUS (i.e., subcontinental scale, excluding Wyoming due to a lack of remeasurements), we found a decline in live TPA at a rate of 0.41 percent per year (probability of direction = 99.9 percent, i.e., very high confidence rate is different from 0). In contrast, we found live BAA to be expanding at a rate of 0.99 percent per year across the CONUS (probability of direction = 99.9 percent). Considerable variability was evident across ecoregion subsections (i.e., landscape scale; fig. 7.4); however, broad-scale patterns of decline in live TPA and expansion in live BAA emerge across much of the CONUS. Notable exceptions appear in northern Minnesota, where both variables are expanding, and in the southern Rocky Mountains, where both variables frequently indicate decline or zero net change in live tree abundance.

Shifts in live tree abundance emerge from the net demographic response of tree populations to endogenous (e.g., competition) and exogenous drivers (e.g., climate, disturbance). Hence, the patterns we observe in figure 7.4 represent the net result of spatially varying tree mortality, recruitment, and growth (BAA only) processes in U.S. forests over the period 1999–2019. General patterns of decline in live TPA and

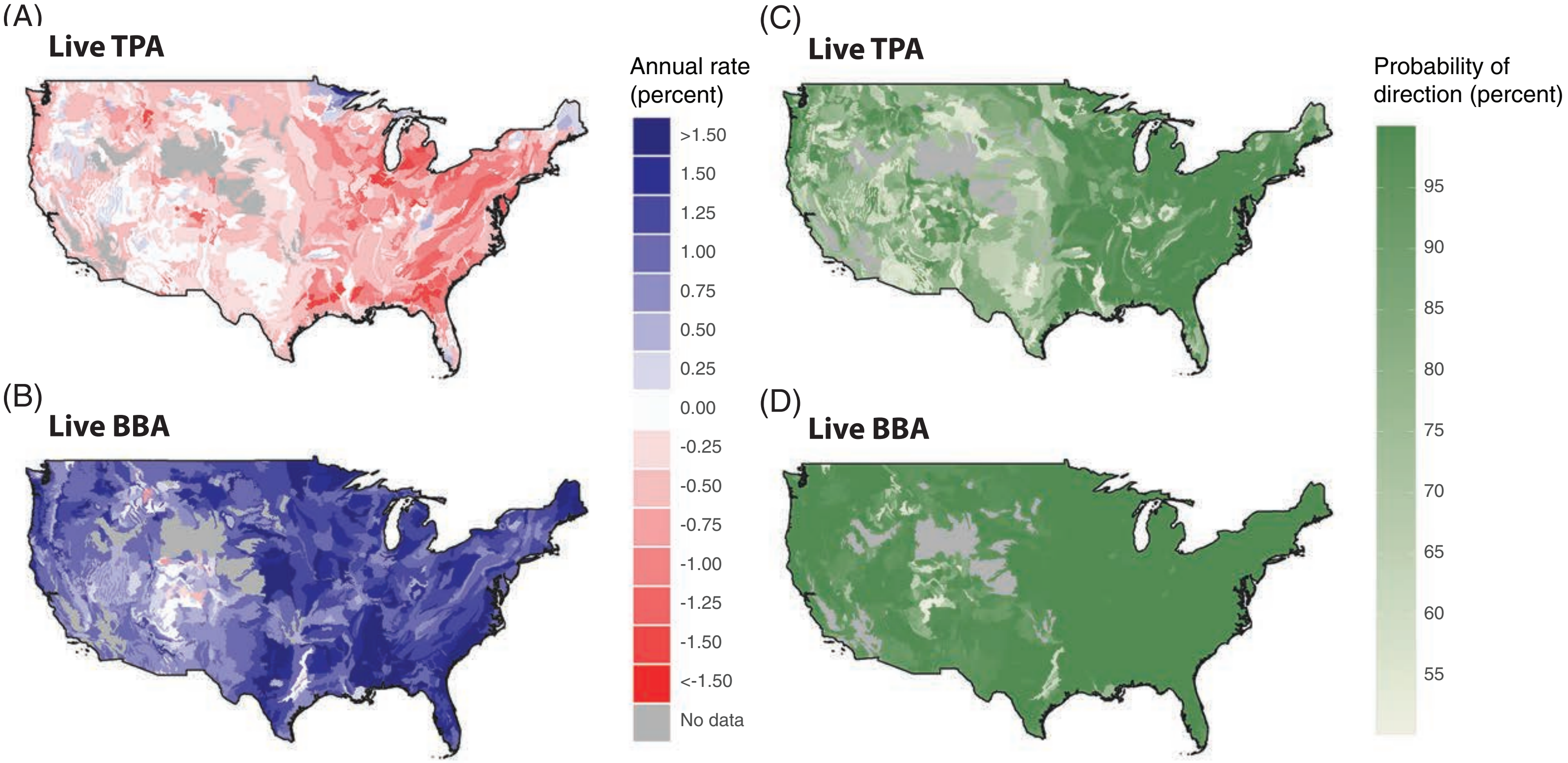

Figure 7.4—Estimated annual rate of change (percent per year) in (A) live number of trees per acre (TPA) and (B) live basal area per acre (BAA), and (C, D) associated indices of significance (probability of direction) within ecoregion subsections (Cleland and others 2007) across the conterminous United States from 1999–2019. All estimates produced using a Bayesian hierarchical model fit to plot-level indices of live TPA and BAA on remeasured Forest Inventory and Analysis (FIA) plots. Plot-level indices of live tree abundance produced using the tpa *function in the rFIA package.*

expansion in live BAA likely emerge in part from transient dynamics associated with stand structural development and succession (Franklin and others 2002) (synchronous maturation of secondary forest across broad spatial domains); hence, it is difficult to determine if/when shifts result primarily from exogenous stressors. Previous efforts have restricted their population of interest to old forest to account for such dynamics (Van Mantgem and others 2009); however, these analyses are unlikely to properly characterize demographic responses at the landscape level, where tree populations are dispersed amongst a mosaic of stand structural classes and successional stages.

rFIA's capacity to return estimates of forest variables within subpopulation response units (e.g., plot-level estimates, as used here) is unique relative to other public FIA estimation tools (i.e., others are designed primarily for design-based population estimation). This capacity eliminates the need for users to navigate the complex structure and data coding of the FIA Database to retrieve data for use in modeling or other applications (e.g., plot-level mapping). We anticipate this capacity will be particularly valuable in applications related to forest health evaluation and monitoring by allowing users to: (1) draw on auxiliary variables to augment sparse FIA data (e.g., Phase 2+ and Phase 3 plot networks) and improve estimation of forest health variables; and (2) draw on multiple remeasurements of FIA plots (when available) to improve estimation of demographic indices and change attributes (as shown here).

Future Extensions of rFIA

In short, we designed rFIA to reduce the hurdles of accessing and manipulating FIA data. Specifically, we aim to improve the accessibility of FIA data for the estimation of status and change in forest ecosystems, and to offer enhanced flexibility in estimation strategies and defining populations of interest. At present, rFIA is capable of estimating more forest variables (>60) from FIA data than any other publicly available tool. This suite of forest variables includes multiple important forest health indicators, including: tree mortality, tree growth, DWM, and tree diversity (i.e., species diversity, structural diversity). Current development aims to broaden the scope of rFIA to provide advanced estimation capacity for indicators of ozone damage, tree crown condition, soil quality, lichen diversity, and understory plant diversity.

Furthermore, we intend to expand the capacity of rFIA to include a suite of spatially enabled model-assisted estimators aimed at improving estimation within small domains (e.g., spatial/temporal extents, rare events). Model-assisted estimators will allow users to easily incorporate auxiliary data in the estimation of forest variables, offering substantial improvements in spatial prediction and change detection for sparsely sampled forest health variables.

Interested users can track updates to rFIA at our official website (https://rfia.netlify.app/). We encourage users to report any issues and/or desired extensions on our active issues page (https://github.com/hunter-stanke/rFIA/issues).

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