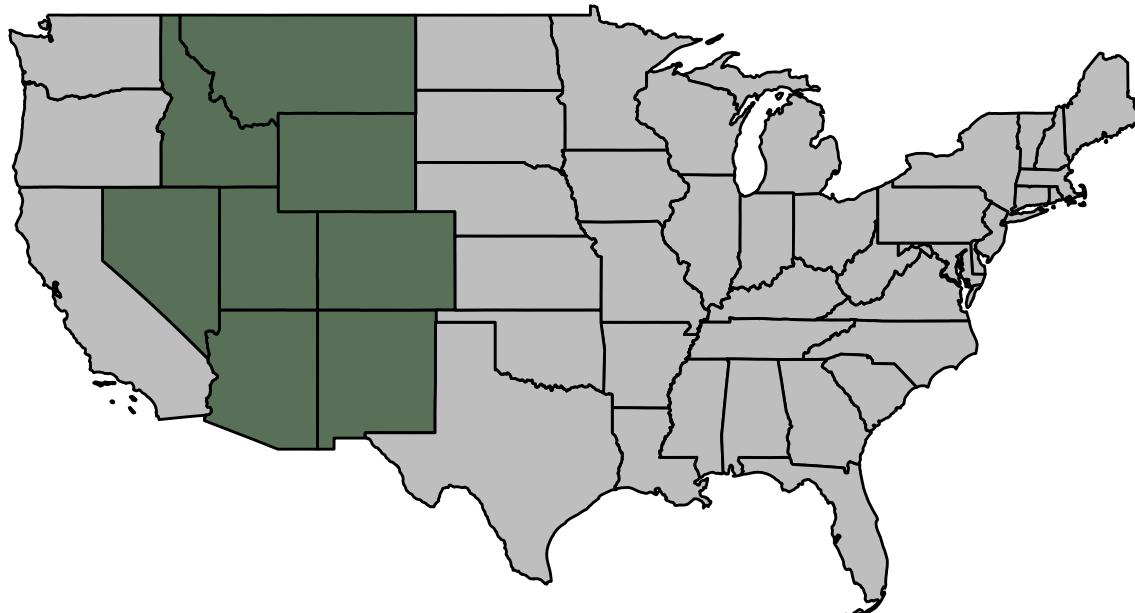


Data

The data used in this thesis was collected by the Forest Inventory and Analysis Program (FIA) in the span of 10 years from 2007 to 2017. While this data was collected over this 10 year period, the analyses done throughout this thesis are under the assumption that this is a “snapshot” of the Interior West at some moment in time. Thus we do not consider any temporal features of this dataset. The data we have is plot-level data for the Interior West region of the United States, where the data for each plot is collected by FIA and its crew members. The units measured by the FIA and their ground crews are approximately 30 m by 30 m hexagonal units. Since the Interior West covers over 140 million acres of forestland, it is extremely impractical for FIA to measure every unit (Source: <https://www.fs.fed.us/rm/ogden/lib/interiorwest2.pdf>). Instead, they sample from the population of 30 m by 30 m hexagonal units by using a geographically-based systematic sampling design (Source: McConville et al, 2020). The FIA chooses these samples by first overlaying a hexagonal grid over the United States where each hexagon contains 6000 acres of land. Then, they fill these hexagons with much smaller hexagons and randomly sample from the population of small hexagons. Then, ground crews go to these sampled small hexagons and collect variables such as basal area, trees per acre, etc. This plot level data is what we are working with throughout the duration of the thesis. In particular, the dataset contains 86085 plots.

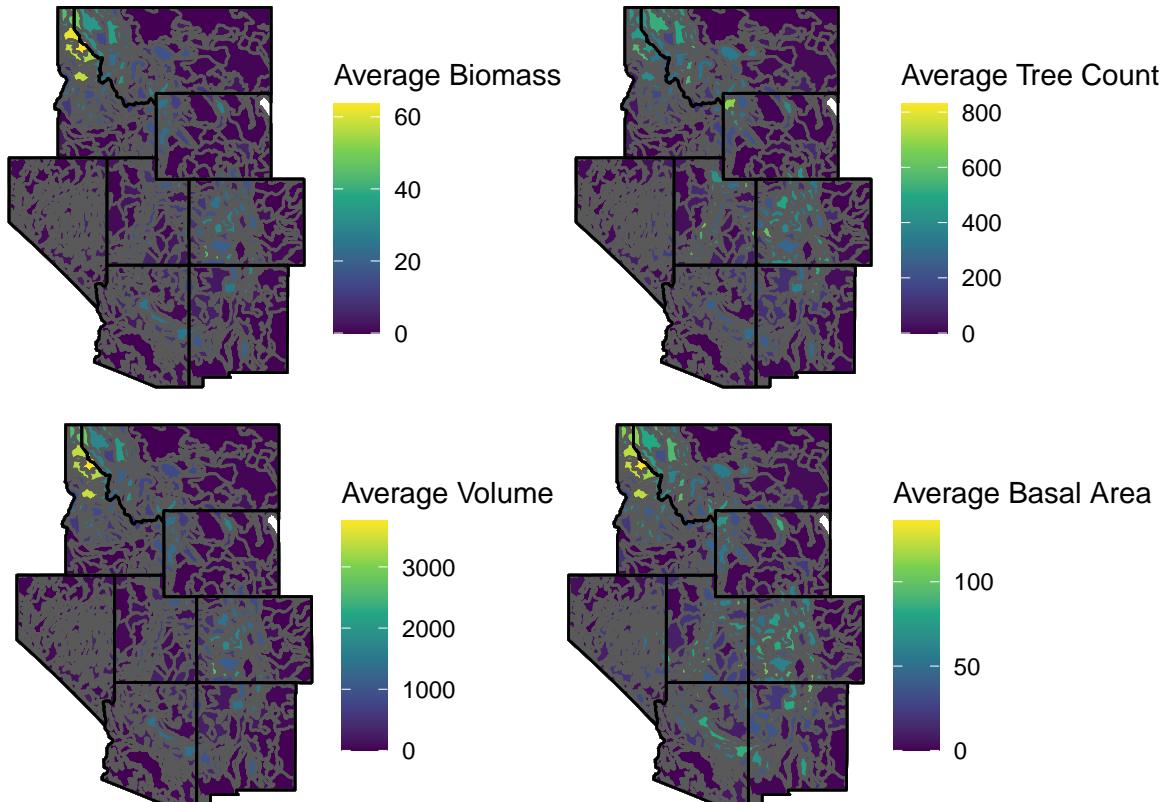
Again, the data we have is from the Interior West, and the FIA defines the Interior West as Arizona, Colorado, Idaho, Montana, Nevada, New Mexico, Utah, and Wyoming. For reference we have provided the Interior West colored green on a map of the continental United States:



While the data covers the Interior West as a whole, we have very granular information, as each row represents a plot sampled by FIA. The data also includes variables that subset the Interior West into provinces which contain ecosections, and these ecosections contain ecosubsections. In our data, on average, each ecosection contains approximately 7.06 ecosubsections, and each province contains an average of 4.86 ecosections. So,

an average province then contains just over 34 ecosubsections. The data we have covers a total of 14 provinces, 68 ecosections, and 480 ecosubsections. The hierarchical struture of the data and nestedness of the ecosubsections within ecosections within provinces lends itself to be able to create hierarchical models which borrow strength from surrounding areas.

While this data contains a multitude of variables, the analyses done in this thesis focus on four key response variables and two explanatory variables. The response variables used are basal area (square-foot), trees per acre, above-ground biomass (lbs), and net volume (ft^3). These variables are coded as `BALIVE_TPA`, `CNTLIVE_TPA`, `BIO LIVE_TPA`, and `VOLNLIVE_TPA`, respectively. We can look at the average of these variables across the Interior West region by ecosubsection in the plots below.



While we have four variables which we will model as response variables throughout the analyses, we also have two predictor variables which will be of much use to us. In particular, forest probability and forest biomass (coded as `forprob` and `forbio`). These variables which we will treat as predictors are remotely sensed data, meaning that they were not collected by FIA crew members and are truly estimated quantities. However, we will be using these variables to attempt to predict our response variables in order to understand how good of estimates we can make based off of remote data that does not require as much effort to collect. While it may seem unnatural to attempt to predict forest biomass with forest biomass, the differences in the data collection process between the ground level data and remotely sensed data are quite different.

Summary of the data:

```
## # A tibble: 6 x 6
##   variable      mean   median     min     max na_count
##   <chr>        <dbl>    <dbl>    <dbl>    <dbl>    <int>
## 1 forbio       6.66      0        0     118        0
```

```
## 2 forprob      0.272 0.0685      0      1      1
## 3 BIOLIVE_TPA   6.23   0          0    244.      0
## 4 BALIVE_TPA    22.7   0          0    469.      0
## 5 CNTLIVE_TPA   98.6   0          0   6678.      0
## 6 VOLNLIVE_TPA  342.    0          0  16436.      0
```