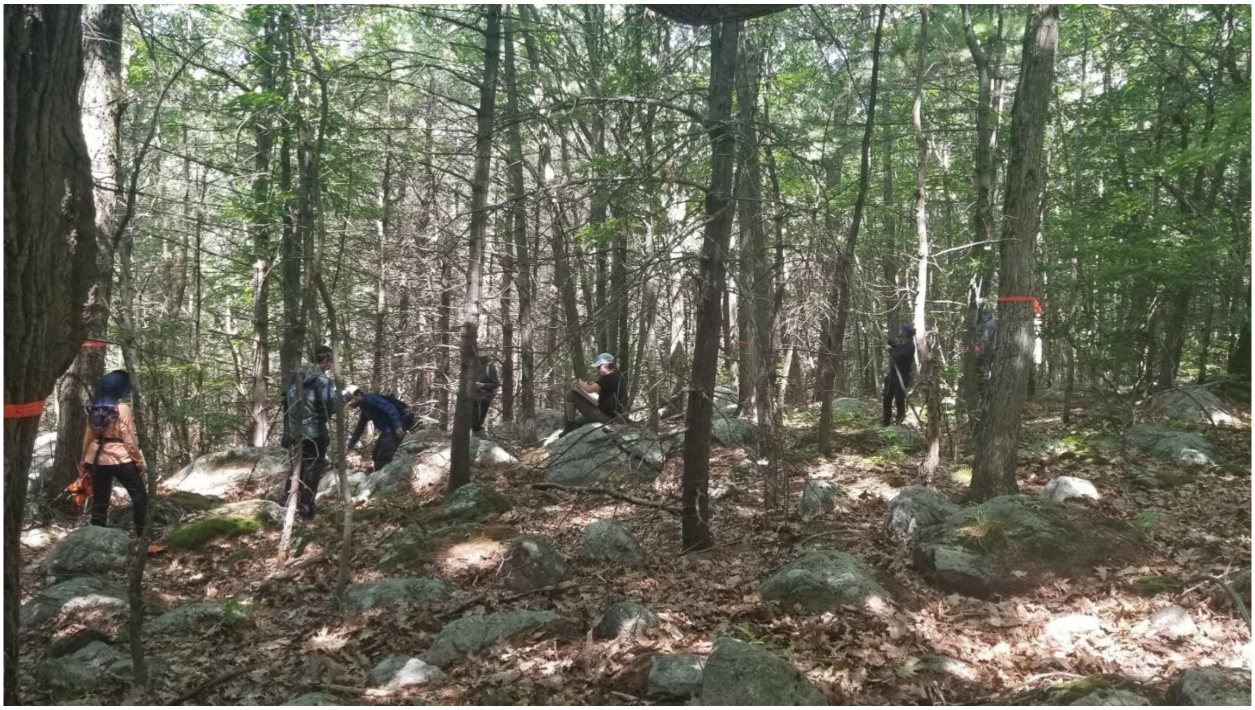
Forest Vegetation Characterization

SMAPVEX19 Cal/Val



PI: Laura Bourgeau-Chavez,

Co-Is: Michael Battaglia, Dorthea VanderBilt, Chris Cook, Mary Ellen Miller, Anthony Chavez, Nancy French

Michigan Tech Research Institute, Michigan Technological University

3600 Green Ct, Suite 100, Ann Arbor, MI 48105

POC: lchavez@mtu.edu

1 Overview

1.1 Background

This document describes the forest vegetation characterization for SMAPVEX19/22. Successful and accurate retrieval of soil moisture beneath a forest canopy using microwave data requires quantification of the aboveground biomass and structure. While soil moisture can vary considerably over the course of hours, days and weeks depending on weather and climate, changes to the structure and biomass of the vegetation is more gradual and predictable. As such, biomass measurements can be taken before or after passive or active microwave sensor data collection, while measurements regarding soil moisture and vegetation moisture must be sampled during data collection. The SMAPVEX19/22 vegetation sampling occurred in Spring and Summer 2022. Some variables were best sampled before leaves flushed in spring.

1.2 Study Domains

SMAPVEX19/22 occurred over two study domains in northeastern US. One of the sites is located (Fig. 1) in Massachusetts (MA) and the other one in Millbrook, upstate New York (MB). The outlines of the domains are based on the SMAP grid (EASE ver. 2); each encompass the retrieval domain of a 9-km pixel that is located in the center of the domain. Hence, the retrieval domains consist of 11 3-km EASE grid pixels in north-south and east-west directions. The actual sizes of the study domains are about 40 km by 30 km (because of the shape of the grid). The MA domain has a relatively uniform coverage of temperate forests while the MB domain has mixed distribution of temperate forests (70%) and fields (pasture and some cultivated crops). These domains were selected because they fit the desired land cover distribution and logistical feasibility.

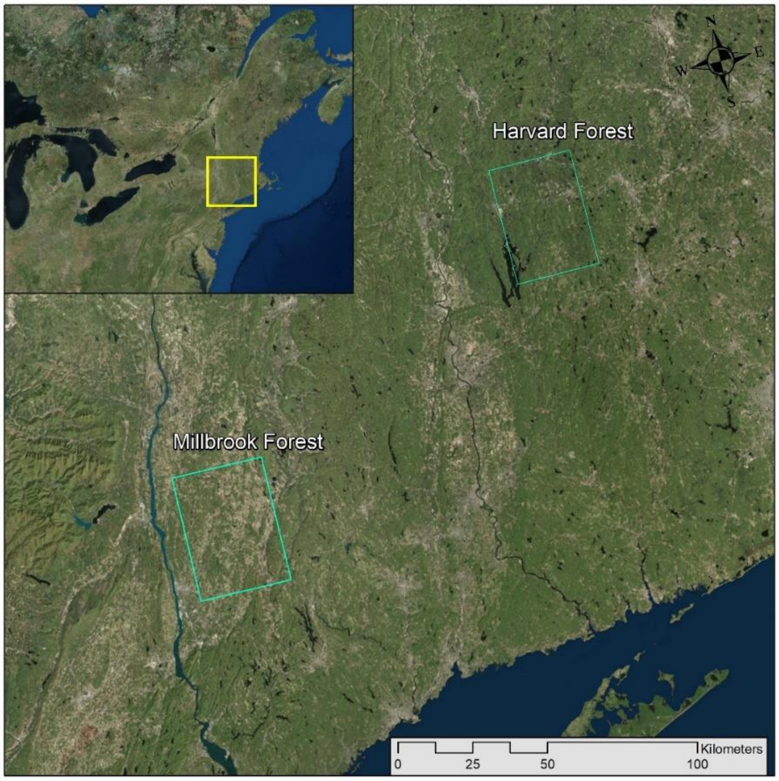


Figure 1. Map of the locations of the two experiment domains (green boxes): The Massachusetts (MA) domain in the northeast and the Millbrook (MB), New York domain in the southwest.

Proper characterization of the spatial and temporal radiometric variation due to landscape and ecosystem cover effects across the entire SMAP grid cell is required for soil moisture Cal/Val. To field measure the study domains, representative dominant forest cover types were chosen for sampling within each domain. The data from these representative types are then scaled up with a weighted averaging approach based on percent cover of these types across the grid cell (Fig. 2).

1.3 Massachusetts Domain – MA

Figure 2 shows the land cover distribution over the Massachusetts domain (MA).

The MA domain incorporates the Harvard Forest within its boundaries. The operations for the MA domain were staged out of Amherst. The Microwave Remote Sensing Laboratory of UMass, Amherst served as the logistical center with the storage for equipment and soil and vegetation drying ovens.

MA had 15 intensive sampling sites where vegetation was characterized. All 15 of MA intensive sites are forested. The SMAP grid cell for MA is only ~16% non-forest, with a dominance of beech-maple (~46%) followed by pine forest (~24%) and oak –hickory (12%). This grid cell also has ~13% wetlands (12% forested, 1% herbaceous) and only ~4% grassland/hay fields (based on the NLCD).

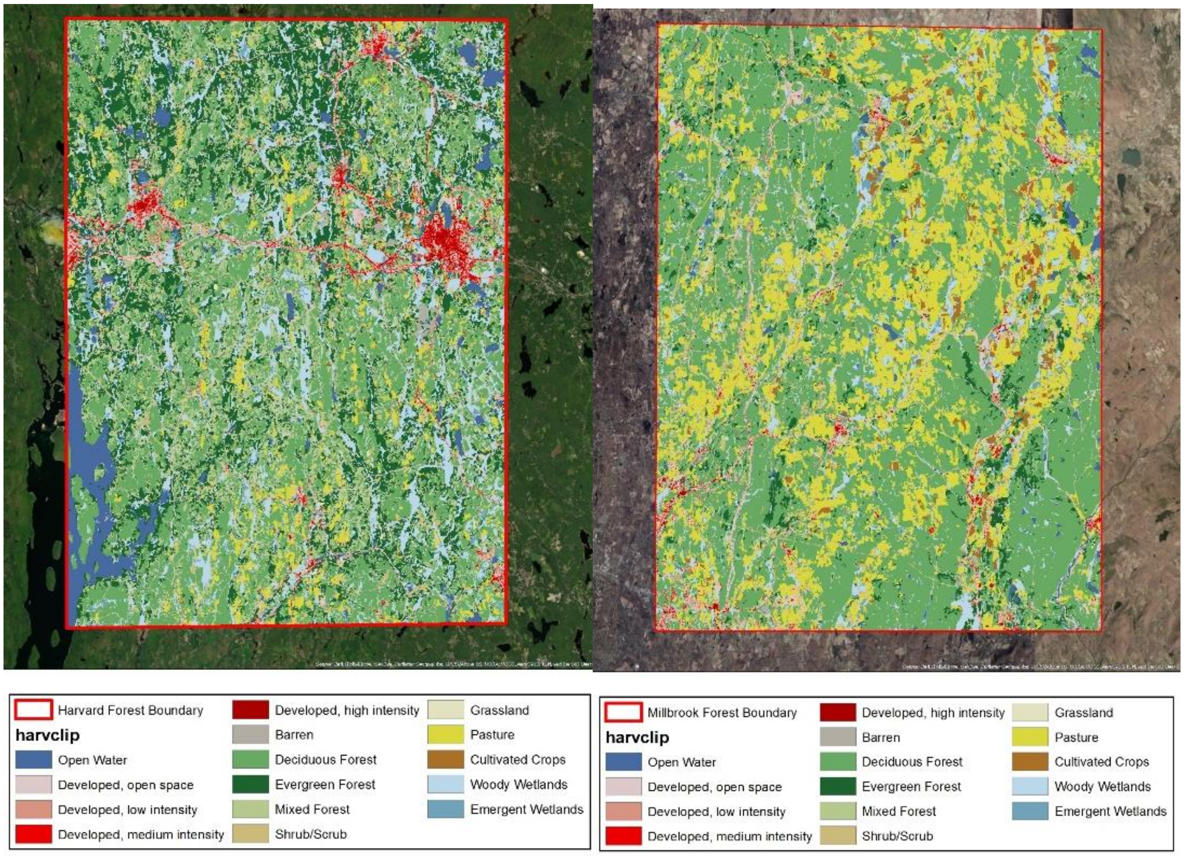


Figure 2. Land cover distribution over the Massachusetts (left) and Millbrook, NY (right) domains.

1.4 Millbrook Domain – MB

Figure 3 shows the land cover distribution over the Millbrook domain (MB).

The operations for the MB domain were staged out of Poughkeepsie, NY. The Cary Institute, located within the grid cell, served as the logistical center with the storage for equipment and soil and vegetation drying ovens.

There were 10 intensive sites at MB that were sampled for vegetation. Most of the forested sites in the SMAP grid cell are oak-hickory (~30%) or beech-maple (~30%), with a few conifer forests (~4%). 36% of the SMAP grid cell is non-forested, with 23% of the total grid cell area mapped as pasture/hay fields by NLCD (Fig. 2).

2 Measurements

The SMAPVEX19/22 measurements consisted of in situ instrumentation, manual sampling, aircraft instruments and ground-based radiometer measurements. The forest biometrics sampling scheme and protocol were designed to support the coincident soil moisture, satellite and aircraft measurements over the domain.

2.1 Sampling Strategy

Sites were set up in areas that are relatively homogenous in terms of vegetation, topography, and soil. These sites were 200 m x 200 m (4-ha) with 2 transects containing 4-20 x 20 m (nominal size) subplots each, for a total of 8 subplots. The length and width of the sites were flexible to accommodate for site conditions (such as rock walls or adjacent land covers), and the size of the plots were adjustable dependent on density of trees; we need to measure enough trees to properly quantify basal area and tree density. It was decided that a minimum of 10-20 trees were needed per plot. Sites were selected after analyzing aerial imagery for suitability, homogeneity, and accessibility followed by a site visit. Plots within sites were systematically located along the two transects in the GIS and each location was navigated to in the field via field GPS units. Data to calculate biomass, stand density, and other geometric measurements were collected one time. While leaf area index (LAI), canopy closure, ground cover, shrub cover, etc were collected once per season (spring and summer). Soil moisture and vegetation moisture were collected coincident with PALS/UAVSAR/SMAP and other sensor collections and are not described in this document.

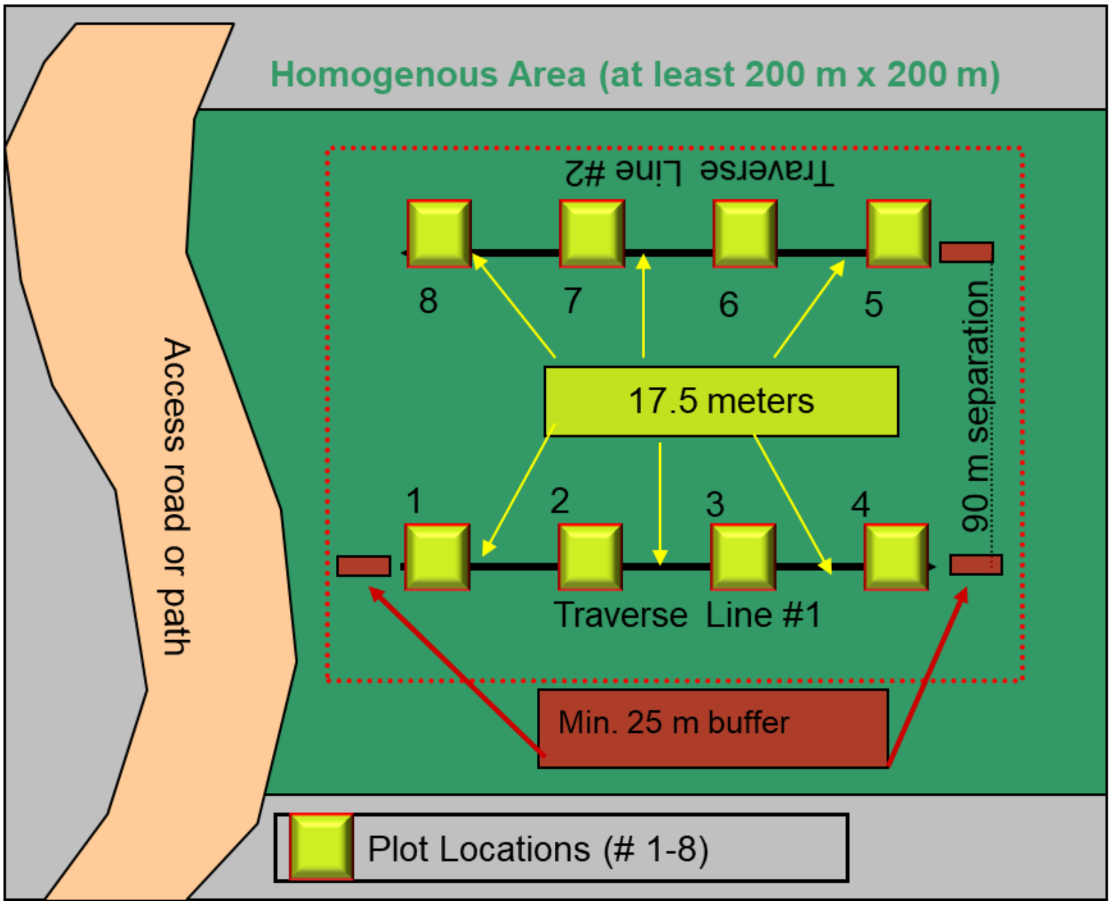
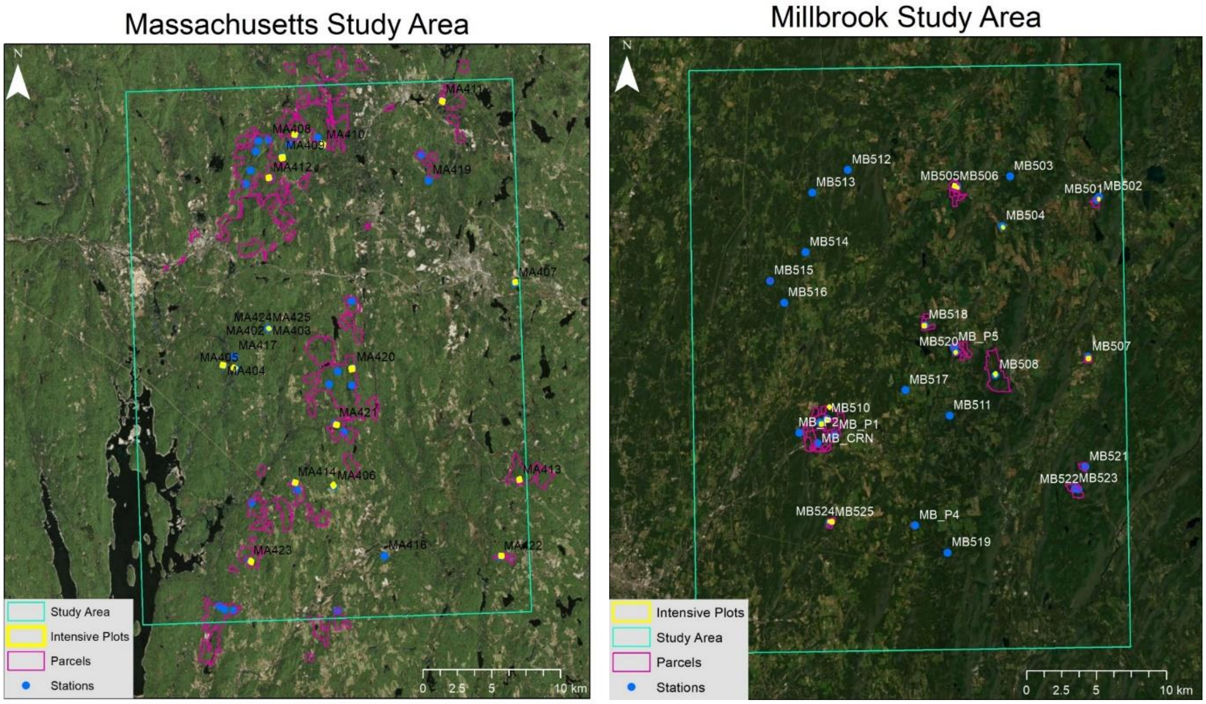


Figure 3. Nominal site and subplot layout for each 0.4 ha site at MB and MA during the SMAPVEX19/22 field campaign.


Massachusetts Study Area

Millbrook Study Area

Figure 4. Map of each study area with yellow points showing the intensive sites for sampling vegetation. Note that 16 were planned at MA, but 1 was unaccessible when the campaign began. 15 were planned at MB, 10 were accessible when the field campaign began and one became too difficult due to heavy poison ivy and prickly rose and was dropped (final number for vegetation sampling was 9 for MB and 15 for MA).

One Time Collections

Within each of the 200 m x 200 m plots the biophysical measurements (tree height, stem density, canopy height, branch angles, primary and secondary branch counts, distances and bearings between trees) were measured once. Every tree/shrub (including understory small trees) > 2 m in height (and >= 5 cm diameter) was measured for diameter at breast height (~1.37 m from ground, DBH) and common name or genus species recorded. If 2 or more trunks branched from the same tree base below breast height, DBH was measured for each trunk and noted on the field sheet. Dead trees were measured and marked as dead. Fallen trees were measured if a recent fall or partial fall (not downed woody decaying debris). Trees were noted as "standing" or "fallen". For areas with greater than 50 trees/plot, only ½ the plot was sampled (e.g. 10 x 20 m) and this was recorded on the field sheet. The heights of 5 representative trees and their lowest living branch height were also measured. For one overstory tree that was dominant in the plot, a count of number of primary branches and for one primary branch a count of secondary branches was sampled.

Allometric equations for DBH to biomass were used for the different tree/shrub species and biomass was calculated and summed over the area sampled for conversion into biomass per area unit. Stem density and basal area were calculated from the counts of all trees > 2 m in height. Shrub/understory small tree biomass was also measured when present.

Distances between pairs of trees were sampled for the NMM3D modeling, however, at the start of the field campaign, CUNY joined the field team in collecting backpack terrestrial LiDAR data. Thus, the sampling was adjusted to measuring, marking and recording data for a "LiDAR tree" at the plot corner (including GPS position), and then the 4-5 closest trees were sampled for bearing and distance. This adjustment was made to cal/val the backpack LiDAR, while also collecting field data for the modeling. Note that for some sites one additional tree was measured for height in each quadrant (10 x 10 m quadrant of the 20 x 20 m plot) the bearing and distance to those trees was what was sampled.

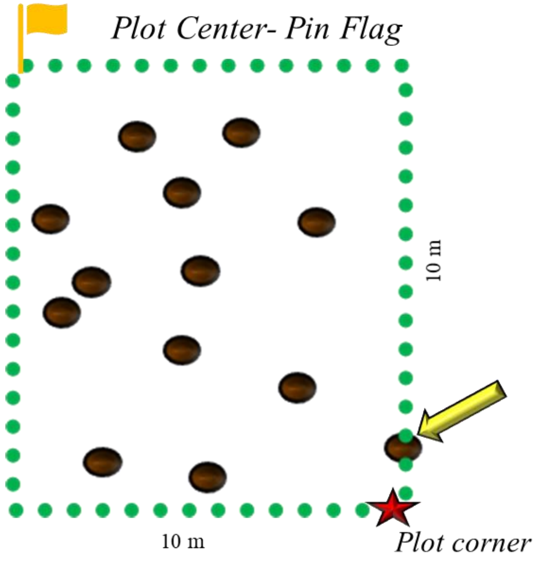


Figure 5. Bottom quadrantr of 20 x 20 m plot shown where the tree closest to the plot corner (navigated to in the field) was marked as the "LiDAR tree" with a GPS location and flagging for the Terrestrial LiDAR samplers. Then the distance from that tree to the closest 4-5 trees and bearing to the tree from the LiDAR tree was measured and recorded.

2.1.1 Spring Only Measurements

Photos of the tree canopy at the angle that SMAP is oriented (40°) in the four cardinal directions to see the branch angles, thus this was only done in leaf off conditions (spring 2022). This was done by mounting a camera on a tripod, leveling it, and then angling the camera at 40°. Note that CUNY led collection of backpack terrestrial Lidar data over the sites, which will provide further detail on the branch angles, lengths and tree distribution.

2.1.2 Collections Each Season

Six field photos were taken per plot center, including nadir, overhead (looking up), and the four cardinal directions. Percent ground cover was estimated from a qualitative assessment of plot area. Leaf area index was measured (using LiCor2200). Described in more detail below. A visual estimate of canopy closure and abundance of understory growth (shrubs/trees > 30 cm but < 2 m) was sampled each season.

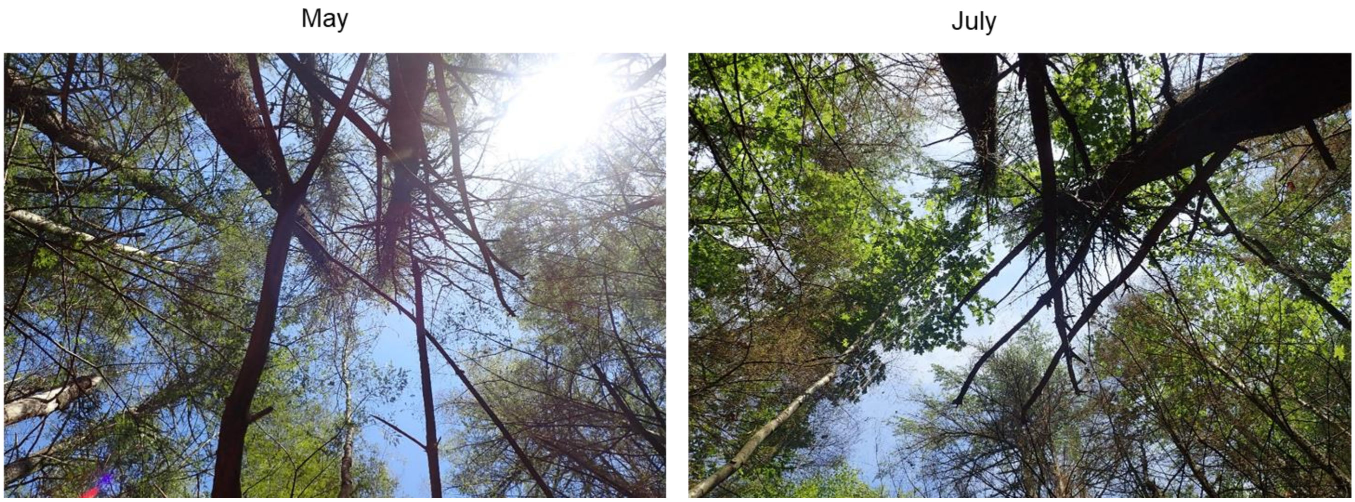


Figure 6. Canopy photos of Site MA411, plot 5 in May and July 2022. This site was affected by the spongy moth caterpillar and is not as dense in July as it otherwise would be.

2.2 LAI Sampling

Use the LiCor 2200 to sample leaf area index under canopy with reference to an open sky unit. Use LiCor2200 with diffuser cap with allows collection in full sun which is needed for the open sky unit. Set up open sky unit in field or place above canopy for reference collection. Set unit to collect automatically every few seconds, while traversing to forest area to sample (Figure 5). Once at the forest 4 ha site, sample along the predetermined transect lines. Collect at each end and center of each 20 x 20 m plot = 24 locations, Collect one sample between each plot = 6 locations, Collect 6 locations on route to traverse line 2 from plot 4, Collect 6 locations on route to traverse line 1 from plot 8 =Total 42 locations, Collect 3 samples at each location for a total of 126 LAI samples. These samples then are averaged for the site.

Figure 7. Design for set up of open sky (field without tree canopy) and forest sampling strategy for LAI using the LiCor2200.

3 Forest Biometrics Calculations and Results

Standard forest biometrics were calculated using the equations below.

Stem density = count of trees > 2 m tall/ unit area

Basal Area = $\boldsymbol{\frac{\left(\frac{1}{2}dbh\right)2}{unit\ area}\pi}$

Biomass Estimates

Equations from the literature were compiled to calculate total biomass per plot (e.g. 20 m x 20 m plot) and average biomass per unit area for the sites (0.4 ha). Species_data_dictionary.csv contains the summary of coefficients and reference article citations. For total biomass, equations were primarily from a compilation of Ter-Mikaelian and Korzukhin 1997 and used by Ahmed et al. 2013 in analysis of biomass allometry at Harvard forest.

Most of the equations were of the form

biomass = a * DBH^{b}

with biomass in kg and diameter in cm

Coefficients for "a" and "b" varied by species and source

Most allometric equations were for trees up to 40 or 55 cm DBH, but we did have trees as large as 96 cm DBH.

The species labeled as "small trees or shrubs" were understory species and were of low frequency or absent at most sites. These species were more difficult to find allometric equations and sometimes deviated from the formula above and also units varied. A complete data dictionary for the species equations by components of biomass is available in Species_data_dictionary.csv.

Python code was modified to estimate the biomass and other forest metrics including percent abundance for each species, biomass, mean DBH, mean overstory height, canopy depth, basal area, density, etc., by plot, by species, by site.

Python code was further modified to estimate biomass by component (foliage, stems, branches) as well as total biomass. However, equations for all components were not always available from the literature and additional sources were used (i.e. Jenkins 2004).

The python code for calculating biomass is available on GitHub (https://github.com/MTRI-AA/smapvex)

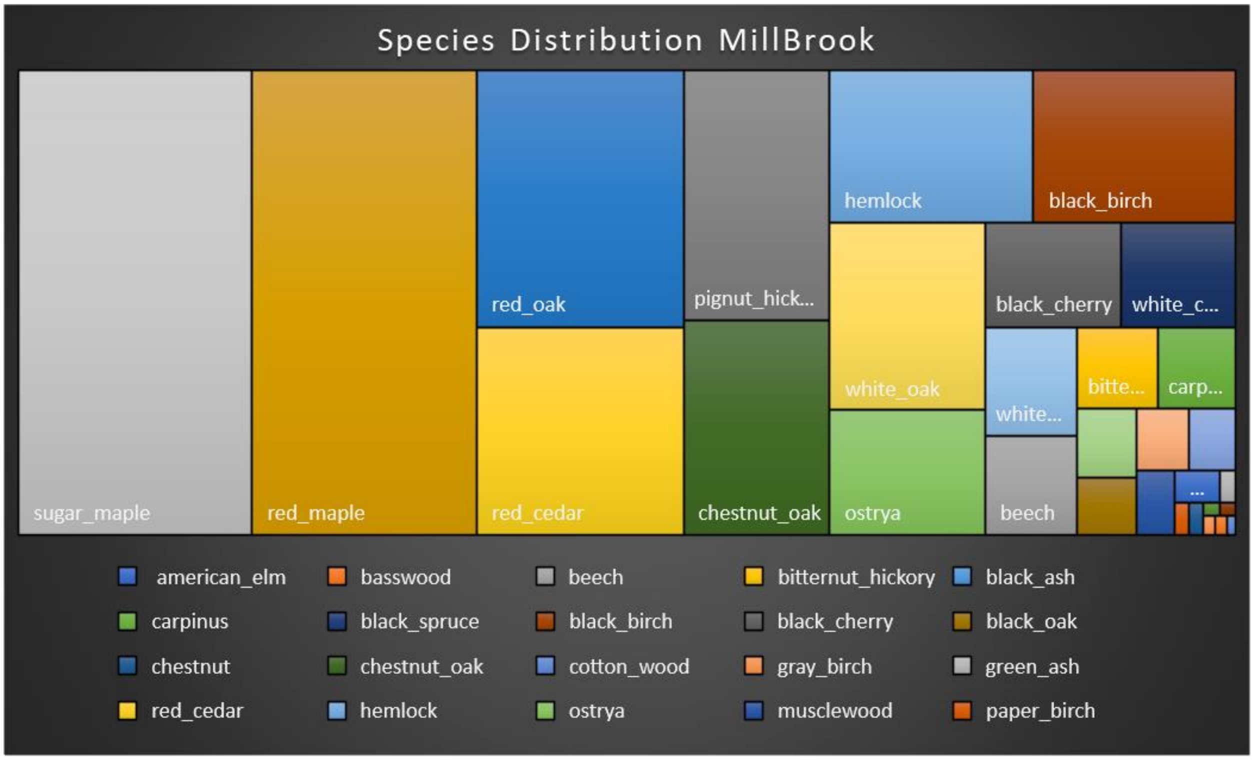
References:

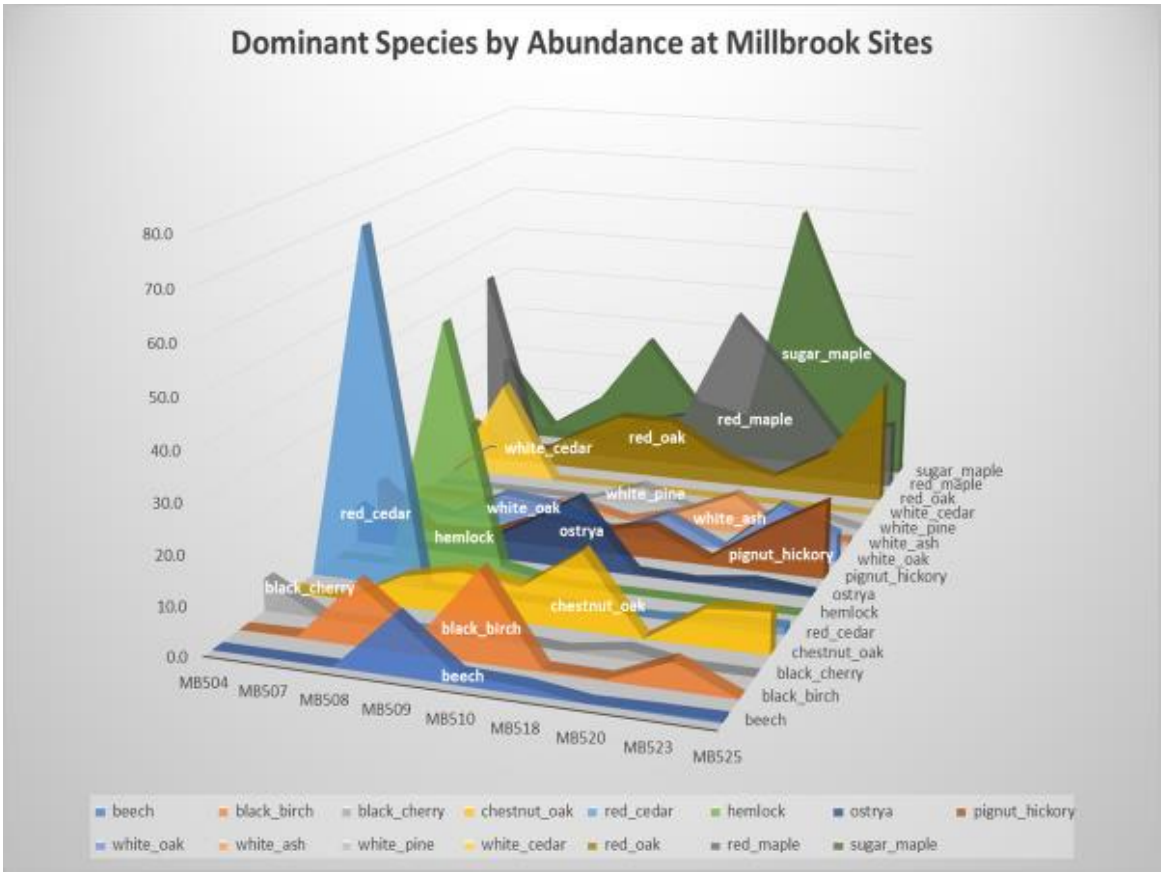
Ahmed, R., Siqueira, P., Hensley, S. and Bergen, K., 2013. Uncertainty of forest biomass estimates in north temperate forests due to allometry: implications for remote sensing. *Remote Sensing*, *5*(6), pp.3007-3036.

Jenkins, J.C., 2004. Comprehensive database of diameter-based biomass regressions for North American tree species (No. 319). United States Department of Agriculture, Forest Service, Northeastern Research Station.

Ter-Mikaelian, M.T. and Korzukhin, M.D., 1997. Biomass equations for sixty-five North American tree species. *Forest Ecology and Management*, *97*(1), pp.1-24.

3.1 Select MB Results:




Dominant Species by Abundance at Millbrook Sites
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
MB504
MB507
MB508
MB509
MB510
MB518
MB520
MB523
MB525
sugar_maple
red_maple
red_oak
white_cedar
white_pine
white_ash
white_oak
pignut_hickory
ostrya
hemlock
red_cedar
chestnut_oak
black_cherry
black_birch
beech
red_cedar
hemlock
white_oak
ostrya
white_pine
white_ash
pignut_hickory
black_cherry
chestnut_oak
black_birch
beech
white_cedar
red_oak
red_maple
sugar_maple
beech
black_birch
black_cherry
chestnut_oak
red_cedar
hemlock
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white_ash
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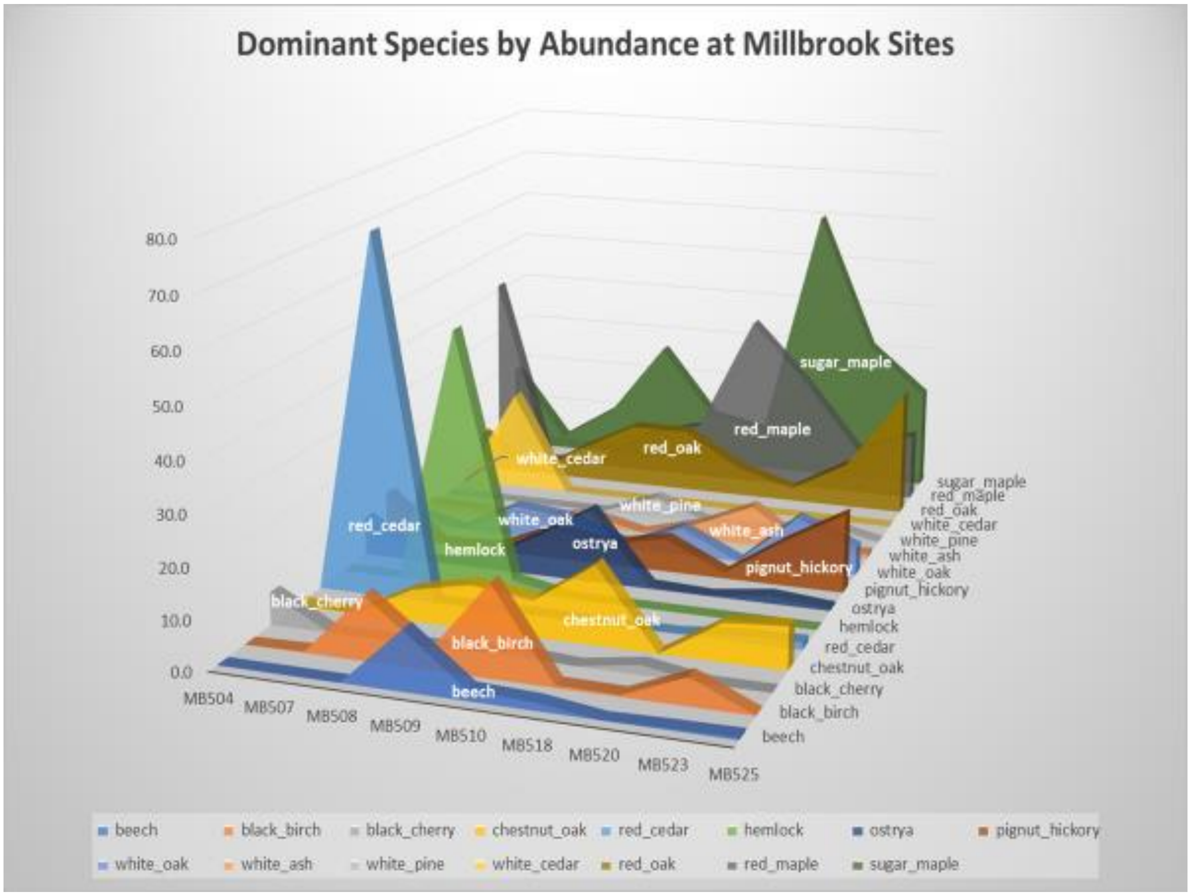
red_maple
sugar_maple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80.0
70.0
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MB504
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sugar_maple
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white_cedar
white_pine
white_ash
white_oak
pignut_hickory
ostrya
hemlock
red_cedar
chestnut_oak
black_cherry
black_birch
beech
beech
black_birch
black_cherry
chestnut_oak
red_cedar
hemlock
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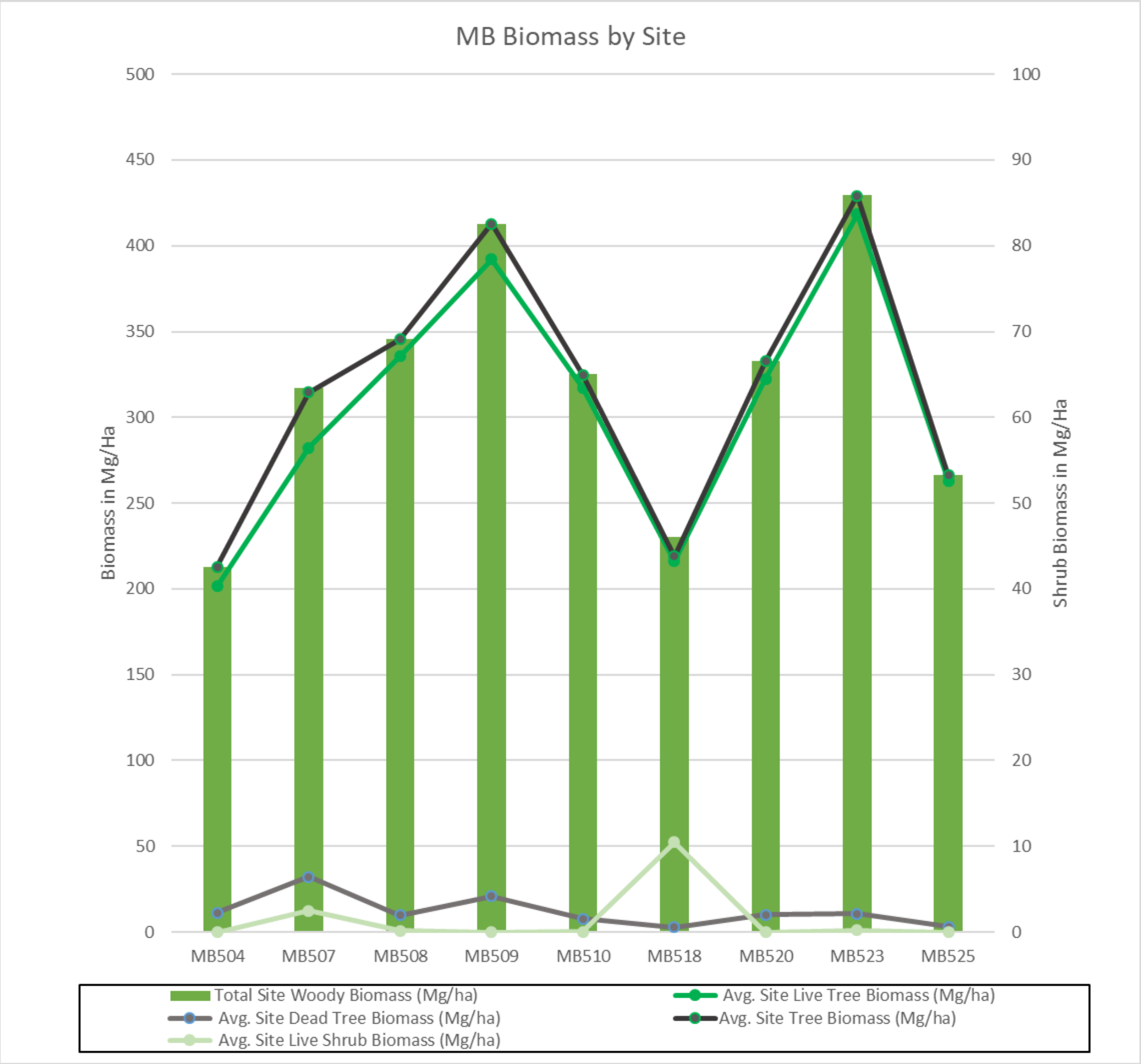
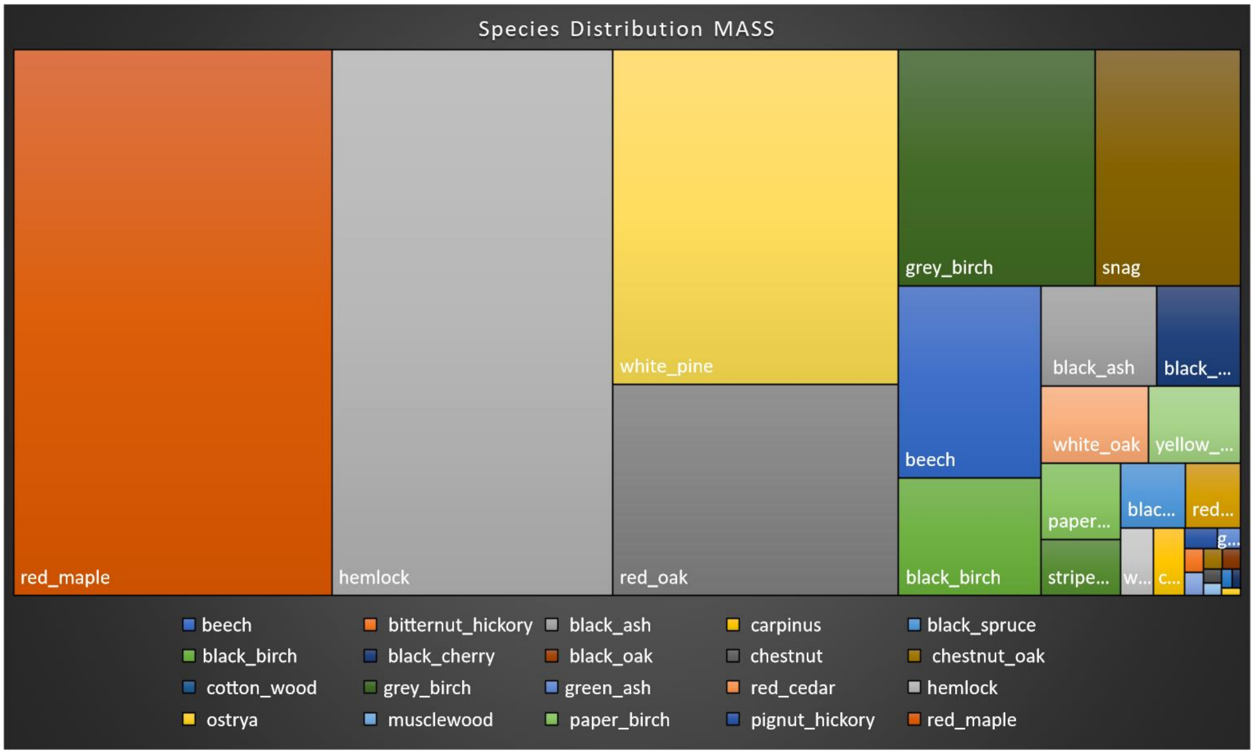
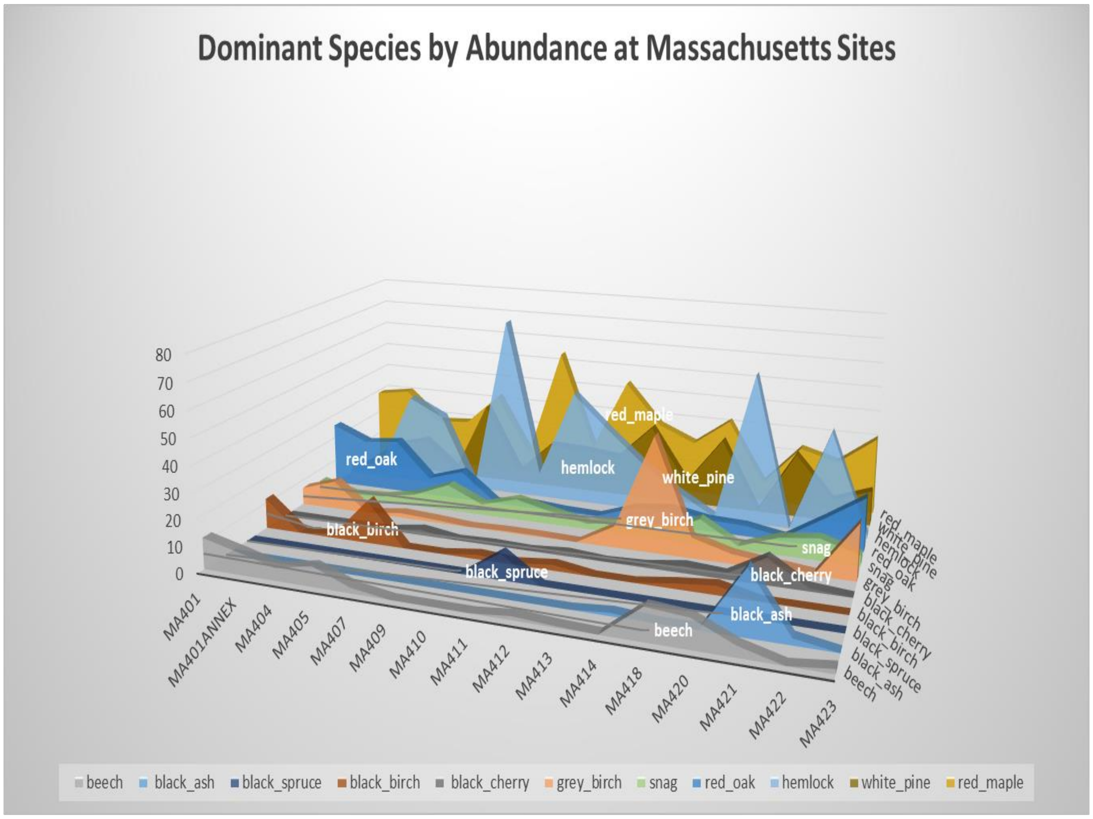
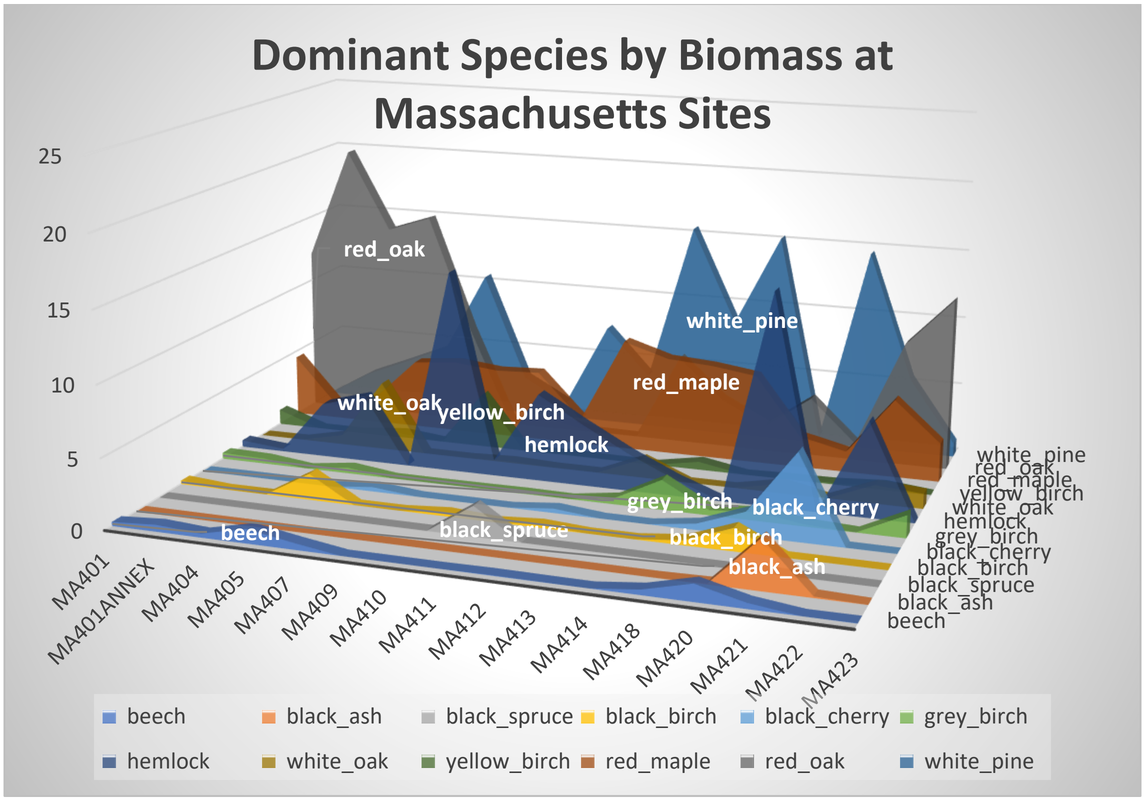
red_maple
sugar_maple

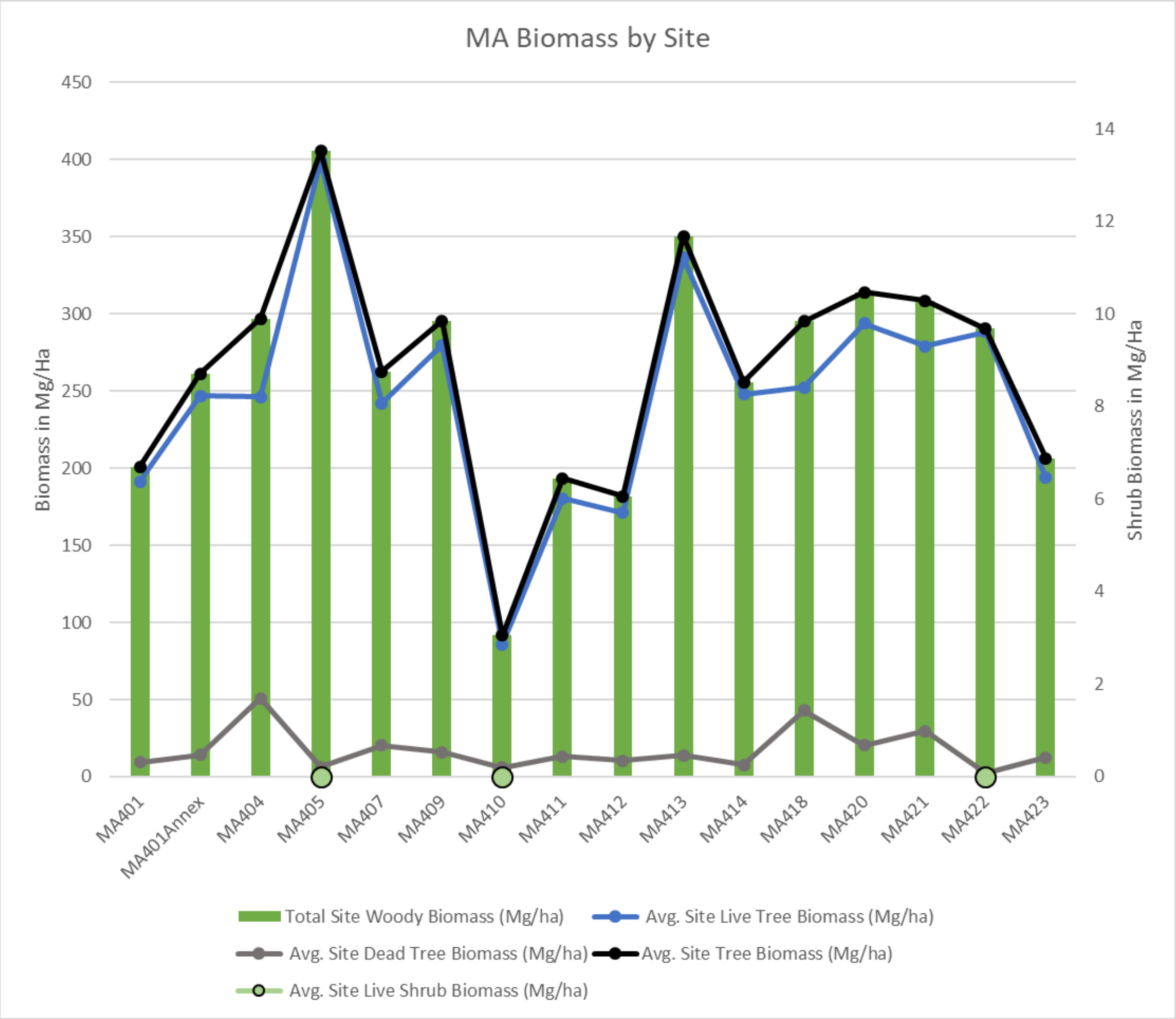

MB Biomass by Site
Biomass in Mg/Ha
500
450
400
350
300
250
200
150
100
50
0
Shrub Biomass in Mg/Ha
100
90
80
70
60
50
40
30
20
10
0
MB504
MB507
MB508
MB509
MB510
MB518
MB520
MB523
MB525
Total Site Woody Biomass (Mg/ha)
Avg. Site Live Tree Biomass (Mg/ha)
Avg. Site Dead Tree Biomass (Mg/ha)
Avg. Site Tree Biomass (Mg/ha)
Avg. Site Live Shrub Biomass (Mg/ha)

3.2 Select MA Results:






Dominant Species by Biomass at Massachusetts Sites
25
20
15
10
5
0
red_oak
white_pine
red_maple
white_oak
yellow_birch
hemlock
grey_birch
black_cherry
black_spruce
black_birch
black_ash
beech
MA401
MA401ANNEX
MA404
MA405
MA407
MA409
MA410
MA411
MA412
MA413
MA414
MA418
MA420
MA421
MA422
MA423
white_pine
red_oak
red_maple
yellow_birch
white_oak
hemlock
grey_birch
black_cherry
black_birch
black_spruce
black_ash
beech
beech
black_ash
black_spruce
black_birch
black_cherry
grey_birch
hemlock
white_oak
yellow_birch
red_maple
red_oak
white_pine


MA Biomass by Site
Biomass in Mg/Ha
Shrub Biomass in Mg/Ha
450
400
350
300
250
200
150
100
50
0
14
12
10
8
6
4
2
0
MA401
MA401Annex
MA404
MA405
MA407
MA409
MA410
MA411
MA412
MA413
MA414
MA418
MA420
MA421
MA422
MA423
Total Site Woody Biomass (Mg/ha)
Avg. Site Live Tree Biomass (Mg/ha)
Avg. Site Dead Tree Biomass (Mg/ha)
Avg. Site Tree Biomass (Mg/ha)
Avg. Site Live Shrub Biomass (Mg/ha)