SOP 7: Herbaceous Plant and Seedling/Sapling Measurements

Version 1.34 (August 2020)

Time estimate: 120 minutes

Overview

This SOP documents data collection for overall plant species diversity and tree seedling/sapling counts in nested subplots within the 20 m x 20 m plot. Quantitative data are collected in eight sets of nested subplots, the 10 x 10 m module, and the entire 20 m x 20 m plot following a modified Carolina Vegetation Survey approach (Lee et al. 2008). While the tree data will help us understand long term patterns, the herbaceous data will potentially alert us to short term patterns and changes in the vegetation. As stressors affect the vegetation, seedling and herbaceous species composition and structure will respond more quickly than will large trees, coarse woody debris, or other measures we are actively monitoring. The data will help to discern trends including invasive exotic plant species numbers and seedling regeneration rates for key canopy tree species.

Most of the monitoring SOPs can be completed with basic plant identification skills. However, this SOP requires at least one team member to have demonstrated expertise and experience with the full diversity of vascular plant species in the park and to be able to quickly identify each plant species as data are collected. This protocol will be applied in late spring – late summer (late April to late September). Efforts will be made to revisit plots within two weeks of the time they were initially sampled (i.e., plots initially sampled in mid-June in 2011 were revisited in mid-June in 2016). To avoid over-trampling of the vegetation in the subplots, all crew members must be aware of the corner nested subplot locations and, to the extent practical, avoid walking in these areas.

Definitions

Cover is defined as the percentage of the ground that is covered by the vertical projection of the above ground material (leaves, branches, etc.) for a particular species (Lee et al. 2008). For this protocol, we record canopy cover. In canopy cover, unlike foliar cover, the tiny gaps between leaves and limbs are considered filled when estimating.

Height of a seedling or sapling is the distance from the soil surface to the top of the terminal bud (the large bud at the top of the stem). Do not include leaves or needles in this measurement. Seedling/sapling height is determined from stems as they are naturally growing. Height is measured vertically from the ground to the tip of the terminal bud, not along the axis of the stem. Stems should **not** be straightened for measurement.

Seedlings are live juvenile **trees** with at least two true leaves that are less than 1.37 meters (4.5 feet) tall. A seedling is counted only if it is rooted in the nested subplot. Seedlings <5 cm (2

inches) in height are not counted in the tally. Tree seedlings that originate at a common root collar but branch under the leaf litter are independent seedlings. If a tree seedling forks or branches above ground, measure the height of the tallest terminal bud and count the seedling as one. Do not count stump sprouts from a live tree as seedlings. Tally stump sprouts from standing dead trees, counting each sprout as a separate seedling. Refer to the Master Plant List to determine which species are considered trees.

Saplings are live juvenile **trees** that are more than 1.37 m (4.5 feet) in height but <10.0 cm DBH. If a sapling forks or branches above 0.5 m, measure the height of the tallest terminal bud and count the sapling as one; if a sapling forks or branches below 0.5 m, measure each fork or branch as a separate sapling. Saplings are alive if there are any living parts (i.e., leaves, buds, cambium) at or above 1.37 m (breast height). Saplings that have been temporarily defoliated are considered alive. A sapling is counted only if it is rooted in the nested subplot. Refer to the Master Plant List to determine which species are considered trees.

Vines are not tallied as a seedling or sapling. Presence of vine species is recorded in the nested subplots (depths 3 and 2), and 10 m x 10 m modules (depth 1) along with other plant species.

Step by Step Instructions

Each of the 10 m x 10 m modules (1-4) contains four numbered corners with teams sampling two of the corners within each of the modules for a total of eight corners sampled (Figure 7.1). Corners sampled are 1-2, 1-4, 2-2, 2-3, 3-2, 3-4, 4-2, and 4-3 (Figure 7.1), where the first number refers to the module # and the second refers to the specific corner within that module. In other words: corners two and four are sampled in module one; corners two and three in module two; corners two and four in module three; and corners two and three in module four. It is important for the field crew to keep themselves oriented, so that the correct corners are completed and documented. When in doubt, check with other crew members and/or the plot diagram included in the field datasheets.

Following the Carolina Vegetation Survey protocols (Lee et al. 2008), nested subplots in eight corners are sampled in a particular pattern. This is so that each corner sampled is not adjacent to another sampled corner and there is a permanent post anchoring each nested subplot. The corners are indicated at the top of the columns on the datasheet, as pairs, module number and corner number (e.g., 1-2, 1-4, etc.). Once at the nested corner location, take two meter sticks and use them along with the previously laid out tapes to form a square 1.0 m^2 nested subplot, which corresponds to depth three for that corner (Figure 7.2). If for some reason you cannot sample a corner, mark through the corner and module numbers at the top of the column on each page of the field datasheet for SOP 7 and replace with 0-0. Also, make a note of why the corner was not sampled in the Plot Layout Notes (e.g., very active yellowjacket nest in corner, concerned for crew safety).

In recent operational reviews concern has been expressed from multiple sources about the use of minimally trained and/or experienced field crew members as data recorders for the botanist. This role requires a great deal of experience and/or oversight from the botanist and whenever possible should be performed by someone with substantial and demonstrated experience. This may mean that if the individual responsible for completing tree work is the only experienced data recorder on the plot than they will need to alternate between recording for the botanist and collecting tree

data. One way to partition this workload that has worked well with two-person teams is to have the tree data collector record for the botanist when completing the two intensive corners within the module. When the two corners are complete the tree data recorder can hand the clipboard back to the botanist and switch to tree work, while the botanist collects the residual data for the module (i.e., level 1). This approach of putting the clipboard in the hands of the botanist in each module also allows an opportunity for the botanist to review the module data before moving on to the next module (i.e., it potentially benefits data quality). This increase in training and experience level requirements for data recorders also means that some thought needs to be given to engaging and utilizing the skills of "temporary" or minimally experienced field crew members. This shouldn't be forgotten! It is important to engage park staff and others in this process and utilize their help. Some potential tasks have been identified within this and other SOPs.

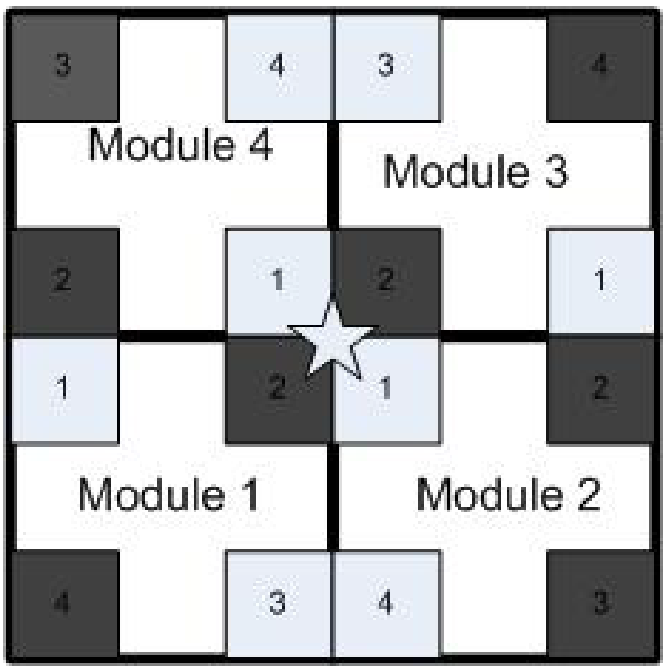

Figure 7.1. 20 x 20 meter plot diagram delineating location of eight sampled subplots (shaded dark).

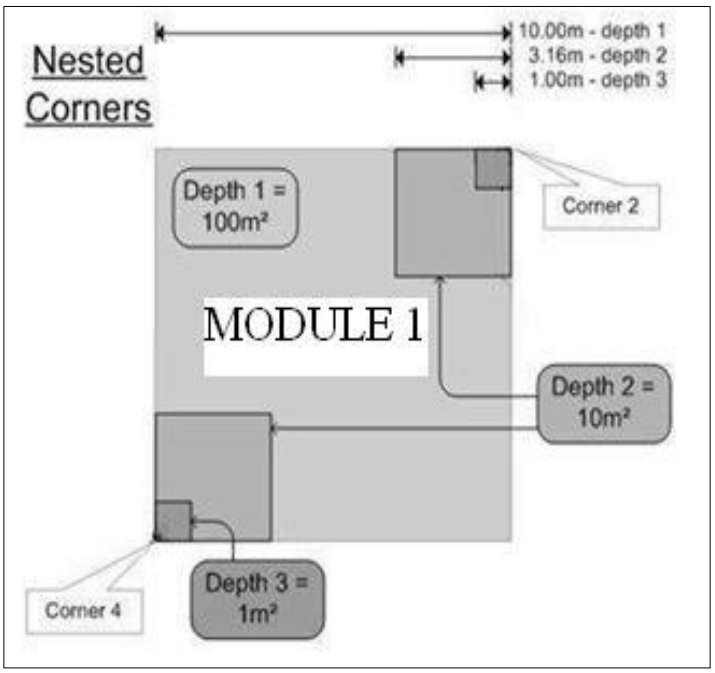

Figure 7.2. Diagram showing placement of sampled corners in module 1 (Lee et al. 2008).

1.0 x 1.0 m (Depth 3)

Once the 1.0 m^2 corner nested subplot is laid out, species presence data are collected. First, identify and record all plant species in the 1.0 m x 1.0 m nested subplot for module 1 (refer again to Figure 7.2). Skip over any plants that are very small (less than 5 cm) and cannot be attributed to a species. In the box for the nested subplot on the datasheet, mark a "3" to indicate that the species is present in module one, corner/subplot two at the 1.0 m x 1.0 m level. For plot revisits, the datasheets for the plot will be filled with a preprinted species list from the last survey, with species codes listed in alphabetical order and extra blank rows to add species not encountered during the last survey. Refer to SOP 14 for detailed information on species nomenclature. Certain species have duplicative seven letter codes, so eight letter codes are provided for these species on the species list. They include species such as *Acer saccharum* and *Acer saccharinum,*

Carya ovata and *Carya ovalis, Polygonum hydropiper* and *Polygonum hydropiperoides,* and *Polygonum virginianum and Polypodium virginianum*. Record your confidence in the identification value under the field of **ID conf** (Table 7.1).

If there is any doubt about species identification, an ID confidence of **P**robable or **U**ncertain is recorded instead of **C**ertain (Table 7.1). If needed, utilize the **Note#** column to reference a more detailed note about the species ID at the end of the species list. If a plant cannot be identified to species quickly and confidently, then identify the species to either family or genus and assign it with a descriptive name for later reference (for instance, "*Carex* slender rhizome" or "*Symphyotrichum* large purple flower" and utilize the **Note#** column to reference a more detailed note about the species ID at the end of the species list. If the species cannot be determined in the field, collect a sample with foliage, buds, cones, or flowers, and/or a photograph to make a positive identification later. Put a check in the **Collected** column on the data sheet to indicate that a specimen was collected. For more information on species collecting and identification, refer to the "Notes on Collecting" section at the end of this SOP.

Table 7.1. Species confidence level codes.

Certain	The person(s) making the taxon interpretation has a high confidence in the accuracy of the field or herbarium identification.	C
Probable	The person(s) making the taxon interpretation has a moderately high confidence in the accuracy of the field or herbarium identification, but uncertainly is typically recorded as "cf" or "?" (e.g., taxon is most likely the species named; occasionally another taxa may be listed as a possibility – it can be named in a comments field)	P
Uncertain	The person(s) making the taxon interpretation has only moderate confidence in the accuracy of the field or herbarium identification, as shown by "??" or other comments about uncertainty. (For example, taxon may be one of two or more species and although one name is chosen, it could as easily be another.)	U

Once you have collected species data at the 1.0 m x 1.0 m level (depth 3), then move on to the tree seedling tallies at the 1.0 m x 1.0 m level. Blank datasheets will be provided for seedlings and saplings for both plot establishment and plot revisit surveys. Identify tree species and tally (by species) all individual seedlings in the 1.0 m x 1.0 m nested subplot that are 5-15, 15-30, 30-50, or 50-137 cm tall. Skip over any plants that are very small (less than 5 cm) and cannot be attributed to a species. Use the dots and square method described at the top of the seedling and sapling datasheet to most easily document numbers of seedlings and saplings (Figure 7.3).

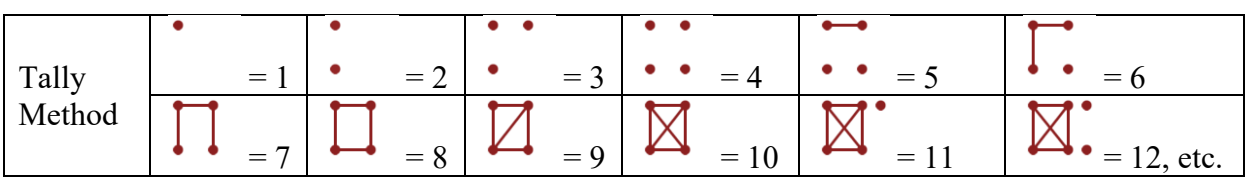

Figure 7.3. Tally method for recording (counting) seedling and saplings occuring within sampled corners.

3.16 x 3.16 m Corner (Depth 2)

At this point, you have completed the 1.0 m x 1.0 m nested subplot but still must complete the 3.16 m x 3.16 m (10 m^2) nested subplot in the same corner. The 3.16 m x 3.16 m (depth 2) nested subplot includes the 1.0 m x 1.0 m (depth 3) nested subplot that was already examined, so you simply need to expand the size to 3.16 m on each side (there are various ways to lay this out, such as to place meter sticks and pin flags at the module corners). This protocol relies on repeated measures (i.e., consistency). Thus, it is important to invest some effort in getting an accurate 10 m^2 subplot and doing it in such a way that the next team, whether that be a QA/QC team or another monitoring effort in five years, lays their subplot out in such a way as to be sampling the same 10 m^2 area.

<u>If</u> the tape measures delineating the module boundary are anchored in the corner conduit, then two of the sides of the 10 m^2 subplot are already established. Remember the "permanent marker" for the subplot is the conduit, not where your field crew happened to anchor the chaining pin when laying out the plot. So beginning at the conduit measure 3.16 meters up each tape from the conduit. A flag can be placed at each of these points along with a meter stick extending into the module along the two currently unmarked sides of the 10 m^2 subplot. Once the meter sticks are adjusted to right angles from the tapes a crew member can visually extend these lines to where they would meet at the opposite corner from conduit. A flag should be placed at this point, which should be 4.47 m at a 45° angle from the conduit.

A secondary and arguably more accurate approach to laying out the 10 m^2 subplot is with the use of pre-measured, light-duty chains or 30 m tape measure. These are marked in 3.16 m increments. An individual can hook one end of chain over the conduit, stretch along tape measure 3.16 m, then turn into the module (at a right angle from the tape), and stopping at the approximate location of the opposite corner of the subplot from the conduit. A second chain or tape measure can be run along the second boundary tape and meet the first chain at the opposite corner of the subplot from the conduit. As a final step the subplot diagonal is measured from the conduit. The opposite corner from the conduit should be established 4.47 m from the conduit.

If there are questions about whether large size class saplings should be included within the subplot, the previous sampling event's datasheets can be consulted. The chain approach delineates the full subplot boundary without relying on the meter sticks used by the botanist. As such, this is an excellent task for extra or minimally trained field crew members to perform and is a big help to the botanist.

Once laid out, identify, and **record only new species that were not already documented at depth three in this corner**. Instead of writing a "3" in the box for the corner to indicate presence, write a "2" to indicate the new "depth" (modified from Lee et al. 2008). Skip over any plants that are very small (less than 5 cm) and cannot be attributed to a species. Collect tree sapling data for the 3.16 m x 3.16 m subplot (including the 1.0 m x 1.0 m subplot) and tally numbers of each tree sapling (0-1.0 cm DBH, 1.0-2.5 cm DBH, 2.5-5 cm DBH, and 5-10 cm DBH). Do this in a similar manner to how tree seedling data were collected. **<u>Do not</u>** collect any data on **<u>seedlings</u>** (woody plants below 1.37 m tall) for the 3.16 m x 3.16 m nested subplot, as these are only recorded at level 3 in each corner. If after sampling a subplot at both depth 3 and 2 you do not encounter any seedlings or saplings at all, write a 0 (zero) on the datasheet for that module and corner in the seedling and sapling data section so it is documented that the field team

did survey that corner for seedlings and saplings and that the corner was not unintentionally missed. It is also imperative that the field team takes the time to tally all seedlings and saplings at the appropriate depth in each subplot because these are important data used for regeneration analysis. A quick check of tree species written on the species list for that subplot will let you know if there might be any seedlings or saplings missed in the seedling and sapling tallies.

Take up all nested subplot markers and repeat the previous steps in the second nested subplot for the module. Remember to start over with recording of species in the new corner. In other words, if a species occurs in both sampled corners within the module then it should be recorded in both corners. If you are recording data and are unsure about how to code a species presence on the datasheet, do not hesitate to stop and ask questions of other field team members. It is extremely important to get it right as there are no second chances to record the data.

10 x 10 m (Depth 1)

Move on to the whole 10 m x 10 m module, which is referred to as depth "1" (where 3.16 m x 3.16 m was depth "2" and 1 m x 1 m was depth "3"). Now identify and write down any new species that were not already documented in either corner of the module. Skip over any plants that are very small (less than 5 cm) and cannot be attributed to a species. This time, instead of writing a "2" in the box for the corner to indicate presence at that depth, write a "1" to indicate depth of 1 (modified from Lee et al. 2008). This is also a good time to look up at the trees in the module and consult with the team member surveying trees to make sure that you are in agreement on species ID and have accounted for species that may not be present as seedlings or saplings. While there is no strict time limit established on searching for residual species at level 1, the goal is to be thorough but at the same time recognize that invariably some species will be missed. As a general guideline, the botanist should keep track of the amount of time spent since they added a species to the module. If it has been two or more minutes of active searching without a new species being found, then this is probably a good indicator that it is time to move on to the next module.

Sample Remaining Modules

Move on to the next 10 m x 10 m module and repeat the steps above until you have completed all four modules of data collection.

Assign Cover Classes

After all four modules have been sampled, a cover value (see definitions) will be assigned for each plant species recorded in the plot. One way of estimating cover is to ignore all but one species and estimate the percent of the ground that would be shaded if the sun were directly overhead. When assigning cover **do not** assign separate cover classes for the canopy, subcanopy, shrub and herbaceous strata. Also, **do not** attempt to assign a separate cover value for each module. When finished you should have a single cover value for each species for the entirety of the 20 x 20 m plot. The cover classes are assigned rapidly (completed in 10 minutes or less) so teams should not spend extensive time equivocating between two cover classes for a particular species.

Data are recorded in cover classes which represent ranges of percent cover assigned to 10 categories (Table 7.2) (Lee et al. 2008). When assigning cover classes, the botanist should consult with the team member that surveyed the trees (SOP6) in order to make sure that all tree

species are accounted for correctly in the cover values. Also, do not forget about assigning cover values for species that overhang the plot but are not rooted in the plot. For those species a presence value of 0 is added to the module where it is overhanging.

Table 2. Canopy Cover Categories, Range and Notes on Cut-offs between Categories.

Category	Range and Cut-off Descriptors
1	<0.1%
	0.1% = 0.4 m^2 or ~ 0.6 x 0.6 m
2	0.1 - 1%
	1% = 4 m^2 or 2 x 2 m
3	1 - 2%
	2% = 8 m^2 or 2 x 4 m
4	2 - 5%
	5% = 20 m^2 or 4 x 5 m
5	5 - 10%
	10% = 40 m^2 or 5 x 8 m
6	10 - 25%
	25% = 100 m^2 or 1 module
7	25 - 50%
	50% = 200 m^2 or 2 modules
8	50 - 75%
	75% = 300 m^2 or 3 modules
9	75 - 95%
	95% = 380 m^2 or nearly covered
10	95% - 100%

Remember if reasonably continuous in outline, the canopy of a plant is considered continuous. However, if there are significant gaps within an individual canopy, it is not considered continuous. Cover ignores the vertical distribution of leaves and includes all leaves from those near ground level to those in the canopy (Lee et al. 2008)

Notes on Plot Revisits

For plot revisits, there are several notes to keep in mind when taking herb data:

1. When identifying additional plant species at depth 1, do not add additional search time to residual level searching for species found during the previous sampling event but not in the current sampling event at depths 2 or 3. In other words, don't go back just to locate species found in previous sampling events. Consistency in effort and independence between sampling events are important.

2. If the previous sample excluded a corner for a temporary reason (such as the presence of a yellowjacket nest) that is not applicable during the revisit, sample the corner during the revisit.

3. During plot revisits, there will be an established species list for the plot from the previous sampling event. This list will be in alphabetical order on the datasheet. If you notice obvious species ID errors or incorrect species code usage, cross out the original code on the datasheet and write in the correct code. If helpful, utilize the Note# column to explain why the previous ID was incorrect. It can also helpful to identify a previously identified genus to species if possible. Refer to "Changing/Amending Previous Sampling Event's Data" section below for more information.

4. For those species on the pre-populated species list that were detected during previous sampling events but not the current one, it is good practice to draw a horizontal line through the entire row of the datasheet to indicate that this species was not observed for the current sampling event. It is expected that some species found during previous surveys will not be seen during current surveys and that new species will be seen during the current survey. Add new species to the bottom of the species list.

Changing/Amending the Previous Sampling Event's Data

While changes to previous sampling event data should be rare, there are circumstances where such changes are valid. For instance, an obvious misidentification occurred or a data entry error was discovered in the field. Some examples include:

- Based on the presence of fertile material that was not present in the plot during the previous survey, the botanist changes an identification from *Lonicera standishii*-**P**robable to *Lonicera maackii*-**C**onfident.

- The botanist realizes he/she made an obvious mistake on the previous plot visit, such as using an incorrect code-an example is writing CHAMMAC instead of CHIMMAC.

One piece of evidence that may sway the decision on whether to make a taxonomic change is to consult the presence and cover values recorded during the previous sampling event. For instance, if a species was found in one and only one corner during both sampling events, or if a species was widely dispersed throughout the plot with a relatively high cover value during both sampling events, this would add greater evidence that both botanists were looking at the same taxon. Note the botanist should avoid consulting presence and cover values from the previous sampling event until after data collection for the current event is concluded, if possible. If the botanist concludes that a species name should be changed, he/she should indicate this by marking through the species code on the field form in pencil and writing the new "corrected" species code next to it. However, before such a change the botanist must consider the following questions:

- How do you know the proposed species change is not just a second species that was either missed or not present during the previous sampling event?

- If the previous field crew were present, would they quickly and easily agree that a data error occurred and should be corrected?

- Does the change improve the quality of the data, both in terms of accuracy and consistency?

In determining whether to make a species change, the botanist must also keep in mind that there are some taxonomic concepts where accurate identification from vegetative material alone is difficult at best and that there is going to be some disagreement even among trained, experienced botanists. A couple of examples where there appears to be some ambiguity in species calls include *Acer barbatum* vs. *Acer saccharum* and just about anything in the genus *Carex*. These are examples of "errors" that not every botanist may quickly agree upon. Also, because there is some ambiguity with these taxonomic concepts, the data are likely to be lumped for most if not all analyses. So, a proposed change may not necessarily improve the quality of the data. What we're trying to avoid are situations where taxonomic concepts are constantly changing and in the grand scheme these changes would have little impact on the overall quality of the data and subsequent analyses. Instead of making the change, another possible solution for consideration is to lower the **ID conf** from **C**ertain to **P**robable or **U**ncertain and adding a note that the "YYYY botanist believes species X may be species Y." The updated **ID conf** and note would then be on the field form for the next sampling event. The future botanist would thus be alerted to the fact that there was some uncertainty regarding that particular taxonomic concept.

Notes on Collecting

It is very important that all data collectors for this SOP attempt to thoroughly catalog the species within each of the nested subplots and the plot as a whole. By doing this, we hope to minimize the error associated with differences in data collectors' abilities to find the same specimens and maximize the power to detect change over time. A secondary goal of monitoring efforts should be to enhance plant species lists for each park, so any unusual plant that is suspected of being new to the park should be collected. All relevant specimens or photographs that are collected will be sent to Curatorial Specialist Brenda Wells, Cumberland Piedmont Network, P.O. Box 8 Mammoth Cave, KY 42259. Following are notes on specimen collection and subsequent identification:

- For any Early Detection species observed in the plot, make sure that the Incidental Observation form is completely filled out and a specimen and/or photo has been collected to accompany the form. Early detection plant species found on the plot will not be targeted for removal because a management action that specifically targets a plot will compromise the integrity of the plot. Instead, it is better to try to locate additional populations of the species outside of the plot so that those populations can be targeted, or if the species is very widespread, the plot will be part of a larger management action that doesn't specifically target the plot.

- Do not collect any plants represented by 3 or fewer individuals (i.e., locally sparse) in the general vicinity of the plot. If a plant is considered locally sparse and there are individuals outside of the plot, consider taking your collection from outside of the plot.

- Do not remove entire plants (including roots) from within the plot. If the plant occupies greater than 2 % cover and is sufficiently robust, a portion of the plant may be removed from within the plot such that the overall cover of the plant within the plot is not significantly affected.

- If it is not possible to collect a specimen, take a photograph instead. First take a photo of the plot sheet so that we can easily identify which plot the specimen photo is from. Then place a

ruler or an object of known size like a pencil or pen in the photograph for scale, and allow the camera to automatically select the appropriate aperture for the given light conditions. Use the Macro setting or Super Macro setting to take detailed close-up photographs of smaller plants.

If a specimen from what you believe is the same species has already been collected in a previous plot, then mark which plot it was from in the **Collected** column and rely on that previous specimen for specimen identification.

- For a specimen that isn't identifiable to species (particularly vegetative *Carex* sp. and *Dichanthelium* sp. specimens), it is ok to collect, but mark it clearly as not identifiable and continue to look for a viable specimen in other plots in the park that you can link this specimen to. Do not spend a lot of time on species identification, particularly if spikes or other distinguishing characters are absent. The recommended approach is to use **P** or **U** for **ID confidence** or write the genera, with notes on characters used to distinguish it from other species in the plot, and move on. Spending less time on these genera will increase efficiency both on the plot and during data validation, and reduce turnover between plot samples.

- Keep only quality specimens for vouchers. Voucher specimens must have clearly distinguishable features, such as flowers or fruit. Do not voucher specimens that were given an **ID confidence** of **P** or **U**.

- If you collect a specimen and check the **Collected** column, but later realize that you cannot use the specimen and discard it, please ensure that you cross out the checkmark in the **Collected** column so that other workers do not mistakenly think that a specimen has been lost.

Equipment List

DBH Tape (in cm)
2 Meter sticks
2 Measuring chains
Camera
Hand lens
Tree identification references
Vascular plant identification references
Field protocol manual
Plant press, plant press dividers/blotters, and old newspapers for pressing
Zip seal plastic bags
Compass
Datasheets for each type of data collected

References

Kelley, T.M. 1994. Effect of white-tailed deer on the understory vegetation of an oak-hickory forest and growth of trees in a white pine plantation. M.S. Thesis, Illinois State University. Normal, IL.

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Swift, E. 1948. Deer select most nutritious forages. Journal of Wildlife Management. 12, 109-110.

Taverna, Kristin, Robert K. Peet and Laura Phillips. 2005. Long-term change in ground-layer vegetation of deciduous forests of the North Carolina Piedmont, U.S.A. Journal of Ecology 93: 202-213.

Wentworth, T. R., R. K. Peet, M. T. Lee, and S. D. Roberts. 2008. Woody Plant Inventories, CVS-EEP Protocol. Version 4.2. Carolina Vegetation Survey. http://cvs.bio.unc.edu/protocol/woody-stems-protocol-summary-v4.2.pdf

Revision History

Version numbers are incremented by decimals where minor grammatical changes or textual clarifications are incremented by hundredths (e.g., 1.01, 1.02, 1.03, …, etc.) and moderate changes, such as equipment updates or changes in methodology that do not impact analysis are incremented by tenths (e.g., 1.1, 1.2, 1.3, …, etc.). Whole number increments (e.g., 1.0, 2.0, 3.0, …, etc.) are reserved for major revisions. Of course, differentiating between what is moderate vs. major may not always be clear, but it is anticipated that with a little "common sense" and discussion protocol leads can adequately document and track revisions through time to the benefit of future data users. It should be noted that prior to 2020 all revisions were incremented by tenths.

Revision History Log

Version #	Date	Revised by	Changes
1.1	01/15/12	B. Moore and R. White	- Time allotted was changed from 45 to 55 minutes (*Note: unsure of the significance of this change as teams have never been on a time limit when recording data – bmoore 2/24/2020*) - Clarified that sampling window extends late April to late September with plot (park) revisits occurring same time each year within two weeks of initial sampling - Noted a large number of collections from 2011 were *Carex* and *Dichanthelium* lacking identifiable inflorescences. Pointed out it is ok to not spend large amount of time attempting to identify as the species within these genera will likely be lumped for analysis. - Additional tips to streamline collections process were provided.

			- Depth 1 (10 x 10 m) time constraint changed from 5 to 10 minutes (*As noted, previously botanists have never been on a time limit when recording data; in other words, this "limit" has been ignored – bmoore 2/24/2020*).
1.2	09/27/12	B. Moore and R. White	- Added step that if a collection for later identification is not useable/identifiable the checkmark in the collected column on the field data form should be changed to an X to indicate no further identification is planned or possible. - Emphasized the process for assigning species cover classes should be a relatively quick process in the field.

1.3	4/4/2018	C. Bledsoe and B. Moore	Note some edits were made prior to 2017 field season. However, these edits remained draft(?) and were rolled into an additional round of edits made prior to the 2018 season. In short, this version contains edits made prior to two seasons but only implemented (i.e. utilized by field crews) beginning in the 2018 season.
			- "Time allotted: 55 minutes" changed to Time estimate: 120 minutes" (*As noted earlier in this revision log, we are unsure of the significance of this change as teams have never been on a time limit when recording data – bmoore 2/24/2020*)
			- Opening paragraph references soils data. A note was added that as of 2018 soils data collection had not been initiated.
			- Added note that "if a sapling forks below 0.5 m measure each fork as a separate sapling."
			- Clarified that vines are not counted as a seedling or sapling
			- Added note that if an intensive corner is not sampled a note should be made in Plot Layout Notes
			- Emphasized importance of asking questions of more experienced crew members if any confusion about how data are to be collected or recorded
			- Removed statement that Depth 1 "must be completed in 10 minutes or less" (*As noted, previously botanists have never been on a time limit when recording data – bmoore 2/25/2020*).
			- Added text that there is no strict time limit for searching of residual species (depth 1). If it has been 2+ minutes since a species has been added than this might be an indicator that it is time to move on to the next module.
			- Removed sentence that cover class should be assigned quickly (completed in 10 minutes or less).
			- Added reminder to record cover classes for species overhanging, but not actually rooted in plot.
			- Added several notes/reminders regarding revists including:
			  o Avoid extra time spent going back to previous modules in an attempt to relocate all species from a previous sampling event.
			  o If a corner was not sampled in a previous sampling event for whatever reason (e.g., yellow jacket nest), it should still be sampled in the current sampling event.
			  o What to do if find <u>obvious</u> ID errors (from previous sampling event) on the preprinted species list for the current event. This included questions to consider

			when making this determination as to whether previous sampling event data should be modified. ○ Made note on what to do if early detection species observed in the plot ○ Re-emphasized that it is OK to not identify every taxon to species level as it is not always possible particularly for genera such as *Carex* and *Dichanthelium*. ○ Only quality specimens should be kept for vouchers
1.33	3/29/2020	B. Moore	- Added definition of (canopy) cover - Improved directions for documenting when one of the eight corners is not sampled - Added note discouraging the use of minimally experienced crew members as data recorders - Improved directions for establishing 10 m^2 subplots including adding a more robust method using incremented light duty chains as an alternative - Identified potential tasks that could be performed by extra or minimally trained field crew members - Added cover table with category ranges and some descriptors (Table 2) to aid in making determinations between classes - Moved Revision History to end of SOP and added more detailed list of changes made to date
1.34	8/10/2020	B. Moore	- Address grammatical changes and clarifying comments made by IMD regional program manager