The College Of WILLIAM & MARY

Recommendations for 2017 MBI Template Revisions
Vegetation Sampling Protocol

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This language is to be considered for insertion into "Exhibit J: Monitoring Requirements" of the 2017 MBI Template (USACE and DEQ 2017). It is recommended that these methods be described up front in the document and then referenced as the "Stratified-Random Sampling Protocol" (SRS Protocol) in subsequent sections where plot-based vegetation monitoring will be required.

USACE/DEQ Vegetation Stratified Random Sampling (SRS) Protocol for Compensatory Mitigation in Virginia

1. Woody Species Sampling: Woody species, including planted and volunteer trees and shrubs, shall be identified to species level and documented within sample plots by measuring stem density (stems per unit area) and stem area at groundline (SAG) (see description below). Woody species sampling plots shall be circular in dimension and measure 1076 ft^2 (100 m^2), which is equivalent to a circle with a radius of 18.5 ft (5.6 m). This plot size equates to 0.025 or 1/40th of an acre, which provides a multiplier of 40x for stem density conversion to per acre values (which is equivalent to 0.01 or 1/100th of a hectare, thus 100x conversion for stems per hectare).

   Woody species sampling plots shall be established within forested or scrub-shrub planting zones on the site using a stratified-random sampling design following the steps below:

   a. "Stratify" the site into cover types by planting zone or proposed habitat. Each cover type will be considered one "sample area" (e.g., forested planting zone, scrub-shrub planting zone, etc.). Note that sample areas can be composited from non-contiguous planting zones (as long as the proposed habitat is relatively homogeneous across the site).

b. Within each sample area, establish a baseline along one edge. Subdivide the baseline into equal segments (a second "stratification"). The segments may be any size but should be spaced in a manner that will allow the minimum number of plots to be sampled (see below).
c. Within each segment, locate a single random point along the baseline. Random points are determined using a random numbers generator and setting the minimum value at 1 and the maximum value at the overall width of the segment.
d. From the random baseline point, established a sampling transect perpendicular to the baseline and extending across the width of the sample area.
e. Along each transect within each segment, determine the locations of sampling plots using the same randomization procedure described above but taking the overall transect length as the maximum value for the random numbers generator. The number of plots per transect will vary depending on the overall length of each transect and the total minimum number of plots required for the site (see below).

Note: Most GIS applications (e.g., ArcGIS) include a randomization option that allows users to assign random points within a defined sample area or subdivision of a sample area. Using this type of approach, investigators can complete a desktop assignment of random plots within a selected area prior to fieldwork. This information can be incorporated into a data collection platform using mobile technology coupled with sub-meter GPS receivers, which can then be used to wayfind to the exact location of each point while sampling. This type of approach allows investigators to accommodate a stratified-random sampling design while alleviating the need to lay out baselines and transects. The GIS randomization option is particularly well-suited to sample areas comprised of non-contiguous zones.

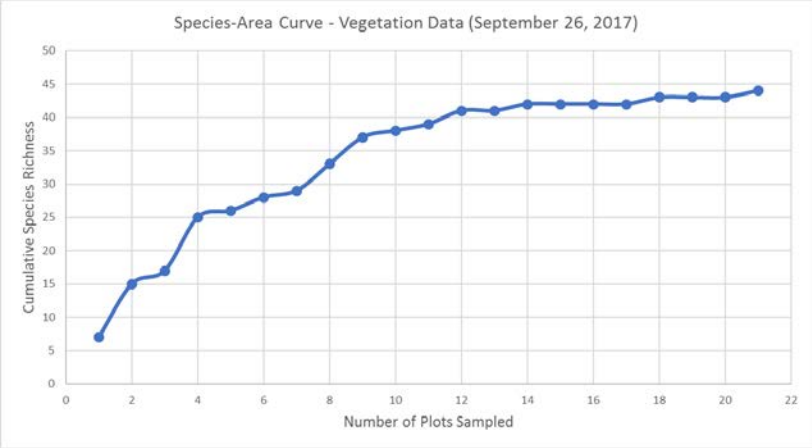
Minimum Plot Number: At a minimum, the total cover of woody sampling plots should make up at least 2% of the sample area (where "sample area" corresponds to relatively homogeneous planting zones such as "forested" or "scrub-shrub" as described above). A minimum number of plots shall be sampled within each sample area using the guidelines in Table 1 below. Once sampling has been completed, sample adequacy shall be evaluated using a species-area curve as described below.

Table 1. Minimum Number of Woody Sampling Plots (based on 2% of total sample area)

Sample Area (ac.)	Number of Plots	Sample Area (ac.)	Number of Plots
1-5	**4***	28	**23**
6	**5**	29	**23**
7	**6**	30	**24**
8	**6**	31	**25**
9	**7**	32	**26**
10	**8**	33	**27**
11	**9**	34	**28**
12	**10**	35	**28**
13	**11**	36	**29**
14	**11**	37	**30**
15	**12**	38	**31**
16	**13**	39	**32**
17	**14**	40	**32**
18	**15**	41	**33**
19	**15**	42	**34**
20	**16**	43	**35**
21	**17**	44	**36**
22	**18**	45	**36**
23	**19**	46	**37**
24	**19**	47	**38**
25	**20**	48	**39**
26	**21**	49	**40**
27	**22**	50+	**add 1 plot per 2ac.**

* Note: In order to ensure a sufficiency of SUs to calculate meaningful averages for observations in smaller planting zones or community types, a minimum of 4 woody sampling plots is recommended for sample areas 1-5ac. in size.

Sample Adequacy: Once the minimum number of plots has been sampled, a species-area curve shall be constructed plotting cumulative species richness on the Y-axis and total number of plots on the X-axis. If the curve "levels off" to the right, then the sample is adequate (see example). If the curve does not level off, one plot per transect shall be added using the stratified-random approach described above [e.g., if there are five total transects, then five total plots (one per transect) are added in the next sampling deployment]. Once these new plots have been sampled, species-area data from the additional plots shall be added to the curve and inspected to determine if an adequate sample size has been achieved. This process shall be repeated until the curve levels off.



Example of a species-area curve in which cumulative species richness is plotted against total number of plots sampled. The curve "levels off" near the middle of the sample, suggesting that the sample effort is adequate for the sample area.

SAG and Stem Density: SAG shall be expressed as the sum of the cross-sectional areas of all woody stems measured at groundline within plots, which can be converted to summary values based on the plot-to-acre (or plot-to-hectare) conversion above. Groundline shall be defined as the base of stem immediately above ground level or above noticeable root swelling or buttressing. To determine plot-based SAG, diameter at groundline shall be measured on each woody stem using calipers for smaller individuals or a DBH tape for larger trees. By recording individual stem diameters for each species within plots, both SAG and stem density can be calculated or interpreted from the data and expressed as an aggregate value (total SAG and stems per unit area) as well as SAG and density by species.

SAG by individual is calculated using the equation for the area of a circle: $\pi * r^2$, where r=radius (or diameter/2).

2. Herbaceous Species Sampling: Within emergent planting zones, herbaceous species shall be measured by estimating percent cover for each species within sample plots. Herbaceous plots shall be square sampling frames with inside dimensions of 3.3x3.3 ft (1x1 m), which is equivalent to an area of 10.8 ft^2 (1 m^2). Within emergent planting

zones, a minimum of 5 herbaceous plots per acre shall be sampled using a stratified-random sampling design as described above. Sample adequacy shall be evaluated using a species-area curve, also in the manner described above. If the sample is determined to be inadequate, plots will be added as described above until the species-area curve levels off.

Cover Classes: For estimating herbaceous species cover, it is recommended that cover classes be used, taking the midpoints of the classes for data analysis. The following cover classes are recommended (midpoints in parentheses, rounded to nearest whole integer):

Class 1:	0-1% (1%)
Class 2:	1-5% (3%)
Class 3:	5-25% (15%)
Class 4:	25-50% (38%)
Class 5:	50-75% (63%)
Class 6:	75-95% (85%)
Class 7:	95-100% (98%)