

<i>Title:</i> NEON User Guide to Root Sampling Tower Plots (NEON.DP1.10067)	<i>Date:</i> 11/04/2019
<i>Author:</i> Samuel Simkin	<i>Revision:</i> B

## NEON USER GUIDE TO ROOT SAMPLING TOWER PLOTS (NEON.DP1.10067)

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## CHANGE RECORD

<b>REVISION</b>	<b>DATE</b>	<b>DESCRIPTION OF CHANGE</b>
A	04/18/2018	Initial Release
B	11/04/2019	Consolidation of 0-0.5 and 0.5-1 mm size classes, and discontinuation of sorting live vs. dead

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## 1 DESCRIPTION

### 1.1 Purpose

This document provides an overview of the data included in this NEON Level 1 data product, the quality controlled product generated from raw Level 0 data, and associated metadata. In the NEON data products framework, the raw data collected in the field, for example the dry weights of root samples from a single collection event, are considered the lowest level (Level 0). Raw data that have been quality checked via the steps detailed herein, as well as simple metrics that emerge from the raw data are considered Level 1 data products.

The text herein provides a discussion of measurement theory and implementation, data product provenance, quality assurance and control methods used, and approximations and/or assumptions made during L1 data creation.

### 1.2 Scope

This document describes the steps needed to generate the L1 data product, Root Sampling Tower Plots (NEON.DP1.10067.001), and associated metadata from input data. This document also provides details relevant to the publication of the data products via the NEON data portal, with additional detail available in the file, NEON Data Variables for Root Sampling Tower Plots (NEON.DP1.10067.001) (AD[05]), provided in the download package for this data product.

This document describes the process for ingesting and performing automated quality assurance and control procedures on the data collected in the field pertaining to TOS Protocol and Procedure: Core Sampling for Plant Belowground Biomass (AD[06]). The raw data that are processed in this document are detailed in the file, NEON Raw Data Validation for Root Sampling Tower Plots (NEON.DP0.10067.001) (AD[04]), provided in the download package for this data product. Please note that raw data products (denoted by 'DP0') may not always have the same numbers (e.g., '10033') as the corresponding L1 data product.

## 2 RELATED DOCUMENTS AND ACRONYMS

### 2.1 Associated Documents

AD[01]	NEON.DOC.000001	NEON Observatory Design (NOD) Requirements
AD[02]	NEON.DOC.000913	TOS Science Design for Spatial Sampling
AD[03]	NEON.DOC.000914	TOS Science Design for Plant Biomass, Productivity, and Leaf Area Index
AD[04]	NEON.DOC.001925	NEON Raw Data Validation for Root Sampling Tower Plots (NEON.DP0.10067.001)
AD[05]	NEON.DOC.rootsamp	NEON Data Variables for Root Sampling Tower Plots (NEON.DP1.10067.001)
AD[06]	NEON.DOC.014038	TOS Protocol and Procedure: Core Sampling for Plant Belowground Biomass
AD[07]	NEON.DOC.000008	NEON Acronym List
AD[08]	NEON.DOC.000243	NEON Glossary of Terms
AD[09]	NEON.DOC.002652	NEON Level 1, Level 2 and Level 3 Data Products Catalog
AD[10]	OS_Generic_Transitions.pdf	NEON Algorithm Theoretical Basis Document: OS Generic Transitions
AD[11]	Nicl Language.pdf	NEON's Ingest Conversion Language (NICL) specifications

### 3 DATA PRODUCT DESCRIPTION

The Root Sampling Tower Plots Data Product (NEON.DP1.10067.001) enables estimation of the amount of plant belowground biomass  $\leq 10$  mm diameter within the same landsurface area from which NEON Tower eddy covariance data are derived. At many sites this will also be the dominant vegetation type(s). NEON uses a 3-inch outside diameter (6.65 cm inside diameter) soil corer for belowground biomass sampling, with samples collected to a maximum depth of 30 cm, and this sampling depth is consistent with that used for soil biogeochemistry and microbe sampling. Within each 3 m x 0.5 m “cell” selected for belowground biomass sampling, two 30 cm cores are collected. Within each core, NEON sorts roots and root fragments  $\geq 1$  cm length to two rootStatus classes (live or dead) and the following sizeCategory bins: diameter  $\leq 0.5$  mm,  $0.5$  mm  $<$  diameter  $\leq 1$  mm,  $1$  mm  $<$  diameter  $\leq 2$  mm, and  $2$  mm  $<$  diameter  $\leq 10$  mm. When sufficient mass is available, dried, ground root samples are analyzed for %C, %N,  $^{13}\text{C}$  and  $^{15}\text{N}$  (NEON.DP1.10102.001), and additional sample is committed to the NEON Archive and is available upon request. Products resulting from this sampling include root biomass by sizeCategory and rootStatus per core.

Root fragments  $< 1$  cm length may comprise a significant portion of total plant belowground biomass, and for 20 randomly selected cores per sampling event per site, NEON employs a dilution sampling technique to quantify total root fragment mass (Koteen and Baldocchi 2013). Products resulting from this sampling include root fragment biomass per core (but not per siteCategory and rootStatus).

For details on the sampling protocol, see the TOS Protocol and Procedure: Core Sampling for Plant Belowground Biomass (AD[06]).

#### 3.1 Spatial Sampling Design

At each terrestrial NEON site, roots are sampled from all base plots that fall in the tower airshed (‘Tower Plots’, Figure 1), with the goal of estimating plant belowground biomass ( $\leq 10$  mm diameter) within the same landsurface area where NEON Tower eddy covariance data are derived. This equates to either 20 or 30 plots depending on the stature of site vegetation. Belowground biomass sampling does not occur in Distributed base plots.

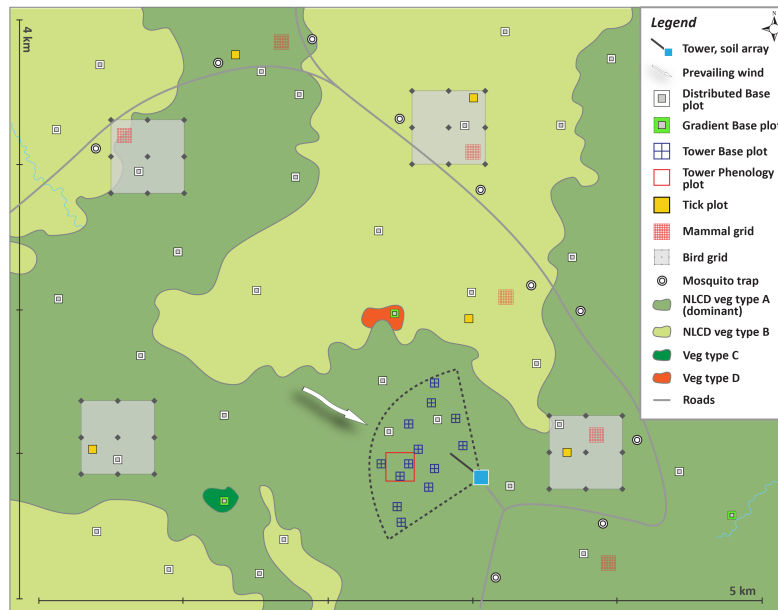


Figure 1: Representation of a NEON site with Tower and Distributed Plots; note that the actual Tower Plot number sampled ( $n=20$  or  $30$ ) is not accurately represented in the schematic.

In each Tower plot, one or two cells are randomly chosen for root coring, depending on plot size, and in a given root sampling year, the same cells are also used for aboveground Herbaceous Biomass sampling (NEON.DP1.10023.001). Sampling cell locations are randomized in advance, and once sampled, cells are removed from consideration for future sampling. See AD[03] for further details.

In 20m x 20m Tower Plots in short-stature vegetation, two soil cores are sampled from one cell per bout. In 40m x 40m Tower Plots installed in tall-stature vegetation, soil core sampling occurs in two randomly selected 20m x 20m subplots (out of four), and two soil cores are sampled from one cell per subplot per bout. This strategy means that at sites with thirty 20m x 20m Tower Plots, there will be  $n=60$  soil cores collected per bout, and at sites with twenty 40m x 40m Tower Plots, there will be  $n=80$  soil cores collected per bout (Figure 2).

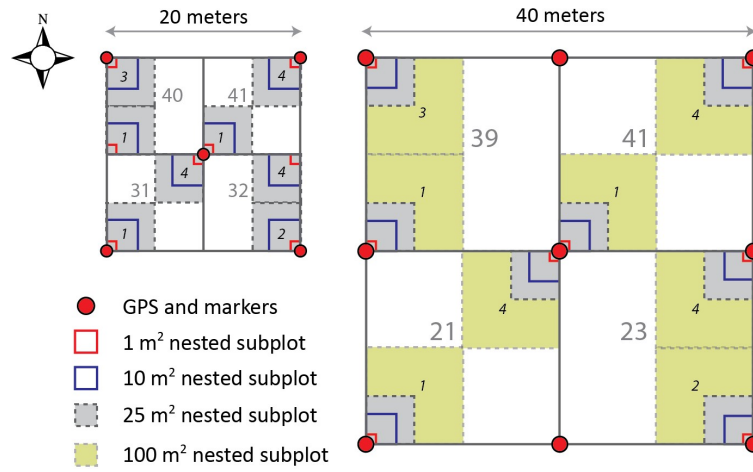


Figure 2: Illustration of two NEON plot sizes used for belowground biomass soil core sampling. Grey numbers indicate subplotIDs, and soil core sampling is only dependent on subplots for 40m x 40m plots. Italic black numbers show the location of nested subplots that are used for percent cover and diversity measurements. Soil core sampling is prohibited within 1 m<sup>2</sup> and 10 m<sup>2</sup> nested subplots.

Prior to driving the corer into the ground, crowns, corms, rhizomes, and other perennial belowground parts that are not roots are removed from the top 3 cm of soil and discarded. In some ecosystems, these non-root belowground plant parts may constitute a significant portion of the belowground biomass; however, the NEON protocol is focused on measuring fine root biomass. A soil core is taken to 30 cm maximum depth from both the northern and southern end of the clip cell (Figure 3).



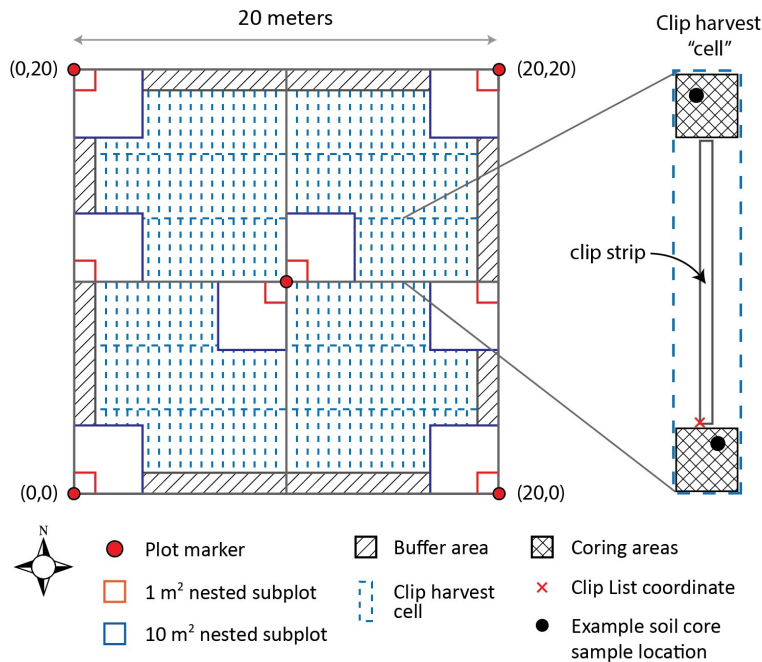


Figure 3: Example layout of NEON Tower Plot showing the locations of 3 m x 0.5 m cells used for belowground biomass soil core sampling (left). Within a cell selected for soil core sampling, one core is collected from each of the areas to the North and South of the clip-strip used for Herbaceous Biomass sampling (right).

### 3.2 Temporal Sampling Design

Belowground biomass soil cores are collected once every five years. It is theoretically desirable to perform belowground biomass core sampling when the root crop is at peak biomass. However, peak belowground biomass does not necessarily correspond with peak aboveground biomass, and in some ecosystems, does not vary in a predictable manner within a growing season from year to year (Milchunas and Lauenroth 2001). Combined with the fact that belowground biomass timecourse data are unavailable for the majority of NEON sites, the timing of belowground biomass soil core sampling is guided by these two factors, listed in order of importance: 1) Date of peak biomass herbaceous clip harvest: Perform belowground biomass soil coring either immediately before, during, or immediately after the herbaceous clip harvest associated with the greatest aboveground peak biomass. 2) Soil hardness: At some sites, peak herbaceous biomass occurs during hot, dry parts of the year when soils are extremely hard and veritably impenetrable due to high clay content (e.g. D10 CPER). At sites where these conditions occur, the timing of soil core sampling may be moved to earlier in the growing season when soil moisture is more conducive to core sampling. In addition to the above primary timing criteria, sampling must be timed to avoid standing water in potential soil core locations. If a plot is partially submerged but still accessible for terrestrial sampling, cells that contain standing water must be rejected for soil core sampling, and a new clip cell location must be chosen.

### 3.3 Variables Reported

All variables reported from the field or laboratory technician (L0 data) are listed in the file, NEON Raw Data Validation for Root Sampling Tower Plots (NEON.DP0.10067.001) (AD[04]). All variables reported in the published data (L1 data) are also provided separately in the file, NEON Data Variables for Root Sampling Tower Plots (NEON.DP1.10067.001) (AD[05]).

NEON TOS spatial data employs the World Geodetic System 1984 (WGS84) for its fundamental reference datum and GEOID09 for its reference gravitational ellipsoid. Latitudes and longitudes are denoted in decimal notation to six decimal places, with longitudes indicated as negative west of the Greenwich meridian.

Some variables described in this document may be for NEON internal use only and will not appear in downloaded data.

### 3.4 Spatial Resolution and Extent

The finest spatial resolution at which Root Sampling Tower Plots will be tracked is per soil core within a cell (two cores per cell) within the designated subplots of Tower Plots at each NEON terrestrial site. The number of soil cores per NEON site is normally 60 (when 20m x 20m plots are sampled) or 80 (when 40m x 40m plots are sampled).

Spatial hierarchy:

Tower Plots ( $\geq 1600 \text{ m}^2$ ): sampleID (ID of individual core within a clip cell) → clipID → subplotID → plotID → siteID → domainID

Tower Plots ( $400 \text{ m}^2$ ): sampleID (ID of individual core within a clip cell) → clipID → plotID → siteID → domainID

The basic spatial data included in the data download include the latitude, longitude, and elevation of the centroid of the plot where sampling occurred, plus associated uncertainty due to GPS error and plot width. Shapefiles of all NEON Terrestrial Observation System sampling locations can be found in the Document Library: <http://data.neonscience.org/documents>.

To derive a more precise estimate of the location of each soil core sample, there are two options:

1. Use the `def.calc.geo.os` function from the `geoNEON` package, available here: <https://github.com/NEONScience/NEON-geolocation>, or
2. Follow these steps to perform the same calculation:
  - a. The `namedLocation` field in the data is the named location of the plot; more precise geographic data require the named location of the subplotID in which cores were collected.
  - b. Construct the named location of the desired pointID for each record in `bbc_percore` by concatenating the fields for `namedLocation` and `subplotID` as:
    - i. `subplotID location = namedLocation + ' ' + subplotID`
    - ii. Example: `subplotID location = 'HARV_052.basePlot.bbc' + ' ' + 41 = HARV_052.basePlot.bbc.41`
  - c. Use the API (<http://data.neonscience.org/data-api>; e.g. [http://data.neonscience.org/api/v0/locations/HARV\\_052.basePlot.hbp.41](http://data.neonscience.org/api/v0/locations/HARV_052.basePlot.hbp.41)) to query for `elevation` ("locationElevation"), `easting` ("locationUtmEasting"), `northing` ("locationUtmNorthing"), `coordinateUncertainty` ("Value for Coordinate uncertainty"), `elevationUncertainty` ("Value for Elevation uncertainty"), and `utmZone` ("locationUtmZone") as inputs to the next step.

- d. Isolate the `clipCellNumber` where the soil core was collected - i.e., the last 3 digits of the `clipID`.
- e. Use the clip cell lookup table, available here: [http://data.neonscience.org/api/v0/documents/clipCellNumber\\_lookup](http://data.neonscience.org/api/v0/documents/clipCellNumber_lookup) (clicking on link will initiate download), to find the offsets for each `clipCellNumber` and subplot (`=pointID`), and use the offsets to adjust the UTM values downloaded in step 2.
- f. Increase `coordinateUncertainty` by an appropriate amount to account for error introduced by navigating within plots (suggest 1 m). Additional error may be introduced due to tape stretching to navigate to locations within plots.

### 3.5 Temporal Resolution and Extent

The finest temporal resolution that Root sampling tower plots data are tracked is a collect date. Root Sampling Tower Plots data are collected once every five years at each NEON core and relocatable site. The NEON Data Portal currently provides data in monthly files for query and download efficiency.

### 3.6 Associated Data Streams

Root Sampling Tower Plots data are spatially linked to the Herbaceous clip harvest (NEON.DP1.10023) data product, as these samples are collected from the same clip cell in a given Tower Plot in the same year, ideally with the Root Sampling Tower Plots sampling occurring either shortly before or after the Herbaceous clip harvest sampling. The Root Sampling Tower Plots data product is also directly linked to the Root Chemical Properties (NEON.DP1.10102) and Root Stable Isotopes (NEON.DP1.10099) data products by the variable **cnSampleID**. Archive samples, where there is sufficient sample material, are linked to this product by variable **bgcArchiveID**. Finally, additional belowground plant biomass data are available in the Root Sampling (Megapit) data product (NEON.DP1.10066), which is generated one time per site during initial NEON site characterization.

### 3.7 Product Instances

At each terrestrial NEON site, one or two cells will be sampled from 20-30 plots. For each core sample collected, roots will be sorted into up to four size categories, and roots within a size category are pooled across cores within a cell for analysis. Thus, on average, NEON will generate 120-160 unique root chemistry and isotope data points per site per sampling year. Because root samples are collected every 5 y from a given site, approximately 8-10 terrestrial NEON sites per year will be sampled for belowground biomass. Thus, we expect between 960-1600 data records per year.

### 3.8 Data Relationships

The Root sampling tower plots data product is comprised of samples collected within the same cell IDs as those used to generate the Herbaceous Clip Harvest data product (NEON.DP1.10023). In addition, the TOS Protocol and Procedure: Core Sampling for Plant Belowground Biomass (AD[06]) dictates that each core collected is associated with a unique **sampleID**. The roots in each unique `sizeCategory` x `rootStatus` combination are then assigned a unique **subsampleID**. Live subsamples are then pooled for the two cores collected from the same cell, creating a **poolSampleID**, and pooled root samples are prepared for chemical and isotopic analyses, yielding a **cnSampleID**. This means that each record in the `bbc_chemistryPooling` table may have zero or one child records, and each of these child records may then appear from zero to two times in the Root Chemical Properties (NEON.DP1.10102)

and Root Stable Isotopes (NEON.DP1.10099) data products. Duplicates and/or missing data may exist where protocol and/or data entry aberrations have occurred; users should check data carefully for anomalies before joining tables.

bbc\_percore.csv → Two records (i.e., unique **sampleIDs**) expected per **clipID**.

bbc\_rootmass.csv → Up to eight child records (one per **subsampleID**; i.e., 4 sizeCategories x 2 rootStatus classes) are expected per **sampleID**.

bbc\_dilution.csv → One **dilutionSampleID** expected per each of n=20 randomly selected **sampleIDs**, and 10 child **dilutionSubsampleID** records expected per **dilutionSampleID**.

bbc\_chemistryPooling.csv → Up to four records (**cnSampleID**) per **clipID**.

For each root biomass collection event, dried ground root material from each unique **cnSampleID** is submitted for external laboratory analyses for the Root Chemical Properties (NEON.DP1.10102) and Root Stable Isotopes (NEON.DP1.10099) data products. If any sample material remains after laboratory analyses, root material is retained for the archive, and assigned a **bgcArchiveID**.

### 3.9 Special Considerations

#### 3.9.1 Live-Dead Sorting

There is a high degree of certainty for the total root biomass in a given size class. However, the discrimination between live and dead root biomass via visual sorting had some uncertainty since we didn't confirm live and dead categories with an independent method such as staining. Consequently, we discontinued sorting root biomass into live and dead categories (recorded in field "rootStatus") on 2019-05-06. Before 2019-05-06, roots were sorted to 'live' and 'dead' status with the inherent confidence issues described above; after 2019-05-06, all roots have rootStatus = 'mixed' and the mass values reported are the total fine root biomass from both live and dead roots with no sorting attempted.

#### 3.9.2 Size Category sorting

We consolidated the 0-0.5 and 0.5-1 mm size classes into a single 0-1 mm size class on 2019-05-06. This should result in substantial labor savings, and still preserve functionally important separation of smaller 'absorptive' roots from larger 'transport' roots (see McCormack et al. 2015). A 1 mm cutoff for sorting the finest roots will yield valuable information about the biomass of roots within these two functional classes and will broadly apply across both forested and grassland ecosystems.

## 4 DATA QUALITY

### 4.1 Data Entry Constraint and Validation

Many quality control measures are implemented at the point of data entry within a mobile data entry application or web user interface (UI). For example, data formats are constrained and data values controlled through the provision of list-of-value options, which reduce the number of processing steps necessary to prepare the raw data for publication. An additional set of constraints are implemented during the process of ingest into the

NEON database. The product-specific data constraint and validation requirements built into data entry applications and database ingest are described in the document NEON Raw Data Validation for Root Sampling Tower Plots (NEON.DP0.10067.001), provided with every download of this data product. Data entry constraints are described in NiCl syntax in the validation file provided with every data download, and the NiCl language is described in NEON's Ingest Conversion Language (NICL) specifications (AD[11]).

## 4.2 Automated Data Processing Steps

Following data entry into a mobile application or web user interface, the steps used to process the data through to publication on the NEON Data Portal are detailed in the NEON Algorithm Theoretical Basis Document: OS Generic Transitions (AD[10]).

## 4.3 Data Revision

All data are provisional until a numbered version is released; the first release of a static version of NEON data, annotated with a globally unique identifier, is planned to take place in 2020. During the provisional period, QA/QC is an active process, as opposed to a discrete activity performed once, and records are updated on a rolling basis as a result of scheduled tests or feedback from data users. The Change Log section of the data product readme, provided with every data download, contains a history of major known errors and revisions.

## 4.4 Quality Flagging

The **dataQF** field in each data record is a quality flag for known errors applying to the record.

## 5 REFERENCES

Koteen, L. E., and D. D. Baldocchi. 2013. A randomization method for efficiently and accurately processing fine roots, and separating them from debris, in the laboratory. *Plant and Soil* 363:383-398.

McCormack, M. L., I. A. Dickie, D. M. Eissenstat, T. J. Fahey, C. W. Fernandez, D. Guo, H-S. Helmisaari, E. A. Hobbie, C. M. Iversen, R. B. Jackson, J. Leppalammi-Kujansuu, R. J. Norby, R. P. Phillips, K. S. Pregitzer, S. G. Pritchard, B. Rewald, and M. Zadworny, 2015. Redefining fine roots improves understanding of below-ground contributions to terrestrial biosphere processes. *New Phytologist* 207: 505-518.

Milchunas, D. G., and W. K. Lauenroth. 2001. Belowground primary production by carbon isotope decay and longterm root biomass dynamics. *Ecosystems* 4:139-150.