

# CDW Tally Analysis: D11

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```
## Windows paths
# inpath <- "C:/Users/cflagg/Documents/GitHub/neonPlantSampling/cdw_tally_analysis/D07/"
# outpath <- inpath

## macOS inputs
inpath <- "~/Documents/workDocuments/gitRepositories/neonPlantSampling/cdw_tally_analysis/fulcrumData_2"
domain <- "D11"
outpath <- paste("~/Documents/workDocuments/gitRepositories/neonPlantSampling/cdw_tally_analysis/", domain)

## import libraries
library(plyr)
library(dplyr)
library(ggplot2)

## import data
parent_cdw <- read.csv(paste(inpath,"tos_coarse_downed_wood_tally_prod.csv",sep=""), header=TRUE)
child_cdw <- read.csv(paste(inpath,"tos_coarse_downed_wood_tally_prod_per_plot_azimuth_log.csv",sep=""))

## filter out parent fields that are unneeded
parent_cdw_fil <- dplyr::select(parent_cdw,
                                fulcrum_id, domainid, siteid, plotid_parent, tallydate, volumefactor, parti
## filter out child fields that are unneeded
child_cdw_fil <- dplyr::select(child_cdw,
                                fulcrum_parent_id, lidsazimuth, logdiameter, taxonid, decayclass, logid_ingest
## join parent to child via parent::fulcrum_id to child::fulcrum_parent_id
cdw <- merge(x = parent_cdw_fil, y = child_cdw_fil, by.x = "fulcrum_id", by.y = "fulcrum_parent_id", all
## filter to the selected domain only
cdw <- dplyr::filter(cdw, domainid == domain)

## create diameter class factor
cdw$diameterClass <- ifelse(cdw$logdiameter >= 10, '>=10cm',
                            ifelse(cdw$logdiameter <5, "2-5cm", "5-10cm"))

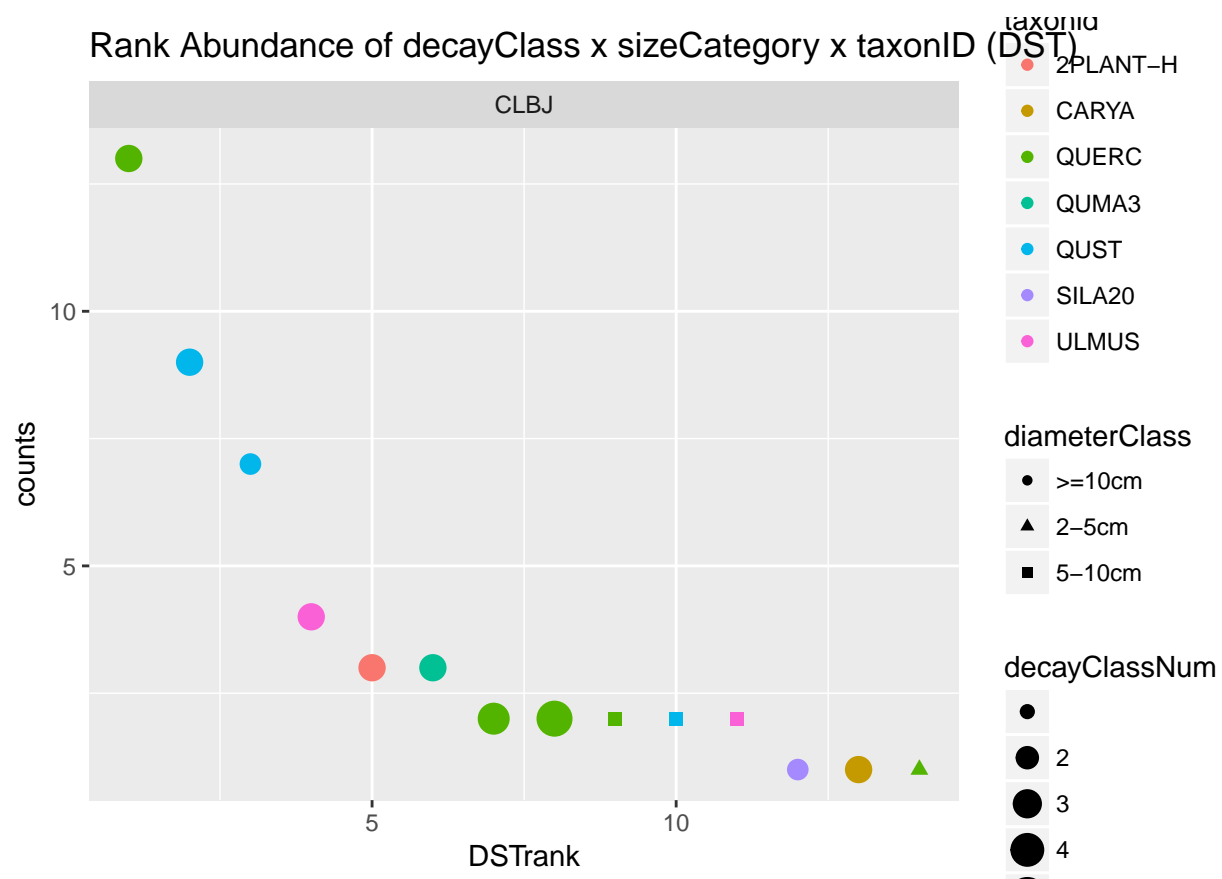
## simplify decayclass to numeric value wrapped inside sapply(decayClassNum, "[", 1) e.g. 'return first
cdw$decayClassNum <- sapply(stringr::str_split(cdw$decayclass, pattern = " "), "[", 1)

## write file
write.csv(cdw, file = paste(outpath, paste0("merged_",domain,"_cdw_rawdata.csv", sep=""), sep = "/"))
```

| siteid | taxonid | decayClassNum | diameterClass | counts | totalLogs | relativeAbundance | cumulativeAbundance |
|--------|---------|---------------|---------------|--------|-----------|-------------------|---------------------|
| CLBJ   | QUERC   | 3             | >=10cm        | 13     | 52        | 25.00             | 25.00               |
| CLBJ   | QUST    | 3             | >=10cm        | 9      | 52        | 17.31             | 42.31               |
| CLBJ   | QUST    | 2             | >=10cm        | 7      | 52        | 13.46             | 55.77               |

| siteid | taxonid  | decayClassNum | diameterClass | counts | totalLogs | relativeAbundance | cumulativeAbundance |
|--------|----------|---------------|---------------|--------|-----------|-------------------|---------------------|
| CLBJ   | ULMUS    | 3             | >=10cm        | 4      | 52        | 7.69              | 63.46               |
| CLBJ   | 2PLANT-H | 3             | >=10cm        | 3      | 52        | 5.77              | 69.23               |
| CLBJ   | QUMA3    | 3             | >=10cm        | 3      | 52        | 5.77              | 75.00               |
| CLBJ   | QUERC    | 4             | >=10cm        | 2      | 52        | 3.85              | 78.85               |
| CLBJ   | QUERC    | 5             | >=10cm        | 2      | 52        | 3.85              | 82.70               |
| CLBJ   | QUERC    |               | 5-10cm        | 2      | 52        | 3.85              | 86.55               |
| CLBJ   | QUST     |               | 5-10cm        | 2      | 52        | 3.85              | 90.40               |
| CLBJ   | ULMUS    |               | 5-10cm        | 2      | 52        | 3.85              | 94.25               |
| CLBJ   | SILA20   | 2             | >=10cm        | 1      | 52        | 1.92              | 96.17               |
| CLBJ   | CARYA    | 3             | >=10cm        | 1      | 52        | 1.92              | 98.09               |
| CLBJ   | QUERC    |               | 2-5cm         | 1      | 52        | 1.92              | 100.01              |

## Warning: Using size for a discrete variable is not advised.



## Code

```
## Windows paths
# inpath <- "C:/Users/cflagg/Documents/GitHub/neonPlantSampling/cdw_tally_analysis/D07/"
# outpath <- inpath

## macOS inputs
inpath <- "~/Documents/workDocuments/gitRepositories/neonPlantSampling/cdw_tally_analysis/fulcrumData_2020"
domain <- "D11"
```

```

outpath <- paste("~/Documents/workDocuments/gitRepositories/neonPlantSampling/cdw_tally_analysis/", domainid)

## import libraries
library(plyr)
library(dplyr)
library(ggplot2)

## import data
parent_cdw <- read.csv(paste(inpath, "tos_coarse_downed_wood_tally_prod.csv", sep=""), header=TRUE)
child_cdw <- read.csv(paste(inpath, "tos_coarse_downed_wood_tally_prod_per_plot_azimuth_log.csv", sep=""))

## filter out parent fields that are unneeded
parent_cdw_fil <- dplyr::select(parent_cdw,
                                fulcrum_id, domainid, siteid, plotid_parent, tallydate, volume_factor, partid)
## filter out child fields that are unneeded
child_cdw_fil <- dplyr::select(child_cdw,
                                fulcrum_parent_id, lidsazimuth, logdiameter, taxonid, decayclass, logid_inge)

## join parent to child via parent::fulcrum_id to child::fulcrum_parent_id
cdw <- merge(x = parent_cdw_fil, y = child_cdw_fil, by.x = "fulcrum_id", by.y = "fulcrum_parent_id", all=TRUE)

## filter to the selected domain only
cdw <- dplyr::filter(cdw, domainid == domain)

## create diameter class factor
cdw$diameterClass <- ifelse(cdw$logdiameter >= 10, '>=10cm',
                           ifelse(cdw$logdiameter < 5, "2-5cm", "5-10cm"))

## simplify decayclass to numeric value wrapped inside sapply(decayClassNum, "[", 1) e.g. 'return first'
cdw$decayClassNum <- sapply(stringr::str_split(cdw$decayclass, pattern = " "), "[", 1)

## write file
write.csv(cdw, file = paste(outpath, paste0("merged_", domainid, "_cdw_rawdata.csv", sep=""), sep = "/"))

#names(cdw)

## table 1 -- count of taxonIDs, report top 10?
## order ascending output by totalTaxa length() will count length of a vector

## Filter out 'blank' transects where TTP = NO
cdw_fil <- dplyr::filter(cdw, targettaxapresent == "Y")
t1 <- ddply(cdw_fil, ~siteid+taxonid+decayClassNum+diameterClass, summarize, counts = length(taxonid))

# an alternative to ddply call, returns similar result but output column name is defaulted
# plyr::count(cdw, c("siteid", "taxonid", "decayClassNum", "diameterClass"))

## Sort rows by siteID then by descending number of counts
t1 <- dplyr::arrange(t1, siteid, desc(counts), diameterClass, decayClassNum, taxonid)

## Calculate relative abundances
t1$totalLogs <- nrow(cdw_fil)
t1$relativeAbundance <- round((t1$counts/t1$totalLogs)*100, 2)
t1$cumulativeAbundance <- round(cumsum(t1$relativeAbundance), 2)

```

```

## determine raw ranking by count of DST combo within siteid
t1 <- plyr::ddply(t1, ~siteid, mutate, DStrank = as.numeric(paste(1:length(counts))), DSTcombo = paste0
t2 <- ddply(cdw, ~siteid+taxonid, summarize, counts = length(taxonid))

## Determine required sample size per DST combo, and cumulative sample size
t1$sampledDiskNum <- ifelse(t1$diameterClass == ">=10cm", 10,5)
t1$cumulativeDiskNum <- cumsum(t1$sampledDiskNum)

## species abundance/total abundance
ggplot(data = t1, aes(x = DStrank, y = counts, color = taxonid, shape = diameterClass, size = decayClass))

```