

CDW Tally Analysis: D05

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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 <- "D05"
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_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

## 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)

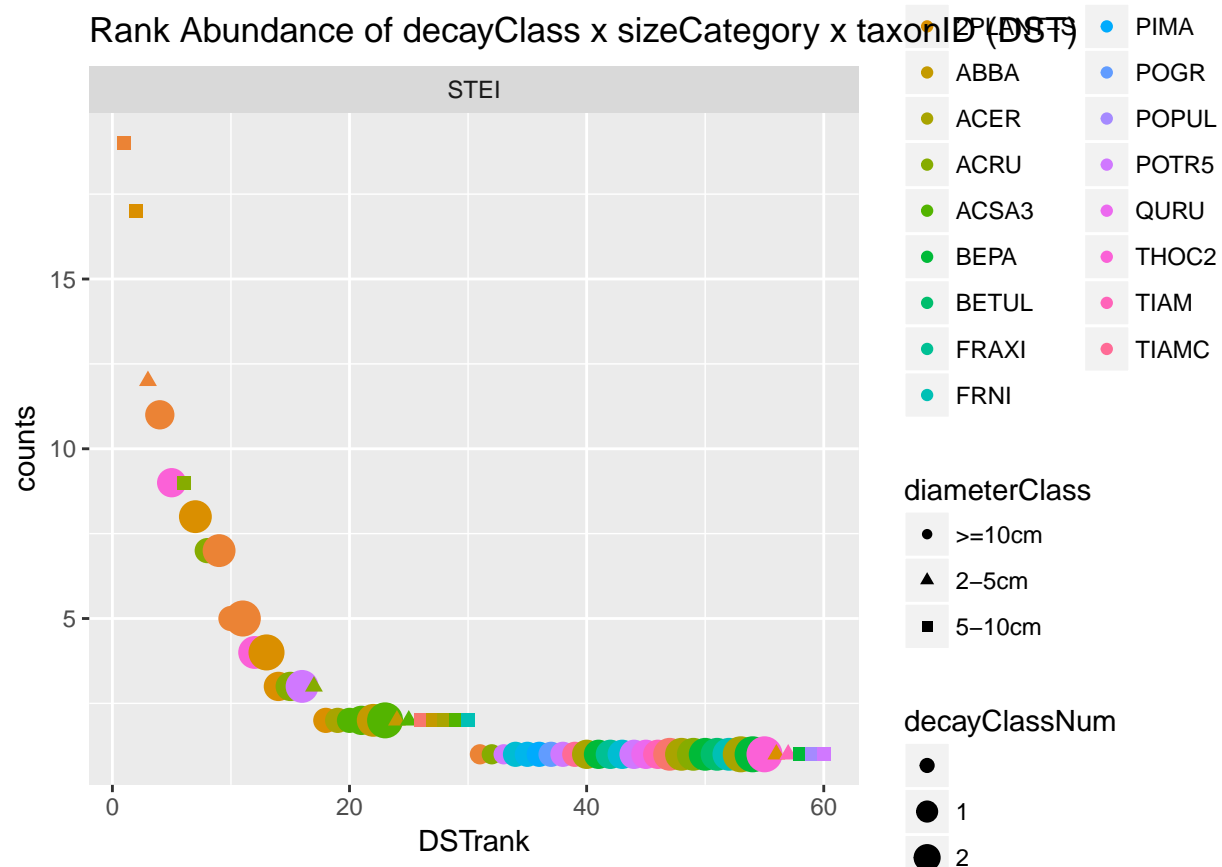
## write file
write.csv(cdw, file = paste(outpath, paste0("merged_", domain, "_cdw_rawdata.csv", sep=""), sep = "/"))
```

siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
STEI	2PLANT-H		5-10cm	19	185	10.27	10.27
STEI	2PLANT-S		5-10cm	17	185	9.19	19.46
STEI	2PLANT-H		2-5cm	12	185	6.49	25.95

siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
STEI	2PLANT-H	3	>=10cm	11	185	5.95	31.90
STEI	THOC2	3	>=10cm	9	185	4.86	36.76
STEI	ACRU		5-10cm	9	185	4.86	41.62
STEI	2PLANT-S	4	>=10cm	8	185	4.32	45.94
STEI	ACRU	2	>=10cm	7	185	3.78	49.72
STEI	2PLANT-H	4	>=10cm	7	185	3.78	53.50
STEI	2PLANT-H	2	>=10cm	5	185	2.70	56.20
STEI	2PLANT-H	5	>=10cm	5	185	2.70	58.90
STEI	THOC2	4	>=10cm	4	185	2.16	61.06
STEI	2PLANT-S	5	>=10cm	4	185	2.16	63.22
STEI	2PLANT-S	3	>=10cm	3	185	1.62	64.84
STEI	ACRU	3	>=10cm	3	185	1.62	66.46
STEI	POTR5	4	>=10cm	3	185	1.62	68.08
STEI	ACRU		2-5cm	3	185	1.62	69.70
STEI	2PLANT-S	2	>=10cm	2	185	1.08	70.78
STEI	ACER	2	>=10cm	2	185	1.08	71.86
STEI	ACSA3	2	>=10cm	2	185	1.08	72.94
STEI	ACSA3	3	>=10cm	2	185	1.08	74.02
STEI	ABBA	4	>=10cm	2	185	1.08	75.10
STEI	ACSA3	5	>=10cm	2	185	1.08	76.18
STEI	ABBA		2-5cm	2	185	1.08	77.26
STEI	ACSA3		2-5cm	2	185	1.08	78.34
STEI	2PLANT		5-10cm	2	185	1.08	79.42
STEI	ABBA		5-10cm	2	185	1.08	80.50
STEI	ACER		5-10cm	2	185	1.08	81.58
STEI	ACSA3		5-10cm	2	185	1.08	82.66
STEI	FRNI		5-10cm	2	185	1.08	83.74
STEI	2PLANT-H	1	>=10cm	1	185	0.54	84.28
STEI	ACRU	1	>=10cm	1	185	0.54	84.82
STEI	POTR5	1	>=10cm	1	185	0.54	85.36
STEI	FRPE	2	>=10cm	1	185	0.54	85.90
STEI	PICEA	2	>=10cm	1	185	0.54	86.44
STEI	PIMA	2	>=10cm	1	185	0.54	86.98
STEI	POGR	2	>=10cm	1	185	0.54	87.52
STEI	POTR5	2	>=10cm	1	185	0.54	88.06
STEI	TIAMC	2	>=10cm	1	185	0.54	88.60
STEI	ACER	3	>=10cm	1	185	0.54	89.14
STEI	BEPA	3	>=10cm	1	185	0.54	89.68
STEI	FRAXI	3	>=10cm	1	185	0.54	90.22
STEI	FRPE	3	>=10cm	1	185	0.54	90.76
STEI	POTR5	3	>=10cm	1	185	0.54	91.30
STEI	QURU	3	>=10cm	1	185	0.54	91.84
STEI	TIAM	3	>=10cm	1	185	0.54	92.38
STEI	2PLANT	4	>=10cm	1	185	0.54	92.92
STEI	ACER	4	>=10cm	1	185	0.54	93.46
STEI	ACRU	4	>=10cm	1	185	0.54	94.00
STEI	BEPA	4	>=10cm	1	185	0.54	94.54
STEI	BETUL	4	>=10cm	1	185	0.54	95.08
STEI	FRNI	4	>=10cm	1	185	0.54	95.62
STEI	ACER	5	>=10cm	1	185	0.54	96.16
STEI	BEPA	5	>=10cm	1	185	0.54	96.70
STEI	THOC2	5	>=10cm	1	185	0.54	97.24

siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
STEI	2PLANT-S		2-5cm	1	185	0.54	97.78
STEI	TIAM		2-5cm	1	185	0.54	98.32
STEI	BEPA		5-10cm	1	185	0.54	98.86
STEI	POPUL		5-10cm	1	185	0.54	99.40
STEI	POTR5		5-10cm	1	185	0.54	99.94

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 <- "D05"
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## 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)
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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 = "/"))

#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
```