

CDW Tally Analysis: D05 TREE

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```
## Load libraries
library(plyr)
library(dplyr)
library(ggplot2)
library(httr)

## Define paths and other inputs
domain <- "D05"
site <- "TREE"

# Define path for writing out files
if (file.exists("~/Documents/workDocuments")){
  outpath <- paste("~/Documents/workDocuments/gitRepositories/neonPlantSampling/cdw_tallyAnalysis/", domain, ".csv")
}

if (file.exists("~/Documents/neonScienceDocs")){
  outpath <- paste("~/Documents/neonScienceDocs/gitRepositories/neonPlantSampling/cdw_tallyAnalysis/", domain, ".csv")
}

## Define function for retrieving Fulcrum data
get_Fulcrum_data <- function(api_token, sql){
  require(httr)
  url = paste0("https://api.fulcrumapp.com/api/v2/query?token=",
    api_token, "&format=json", "&q=", sql, "&headers=true")
  request <- httr::GET(url, add_headers("X-ApiToken" = api_token,
    Accept = "application/json"))
  content <- jsonlite::fromJSON(httr::content(request, as = "text"))
  return(content$rows)
}

## Import data from Fulcrum
# Define Fulcrum API token
api_token = "3ab235047ec293b27f06f6819e81b291435f9c61282345ff1de9624f744034b4233a6fcd1b87c3c2"

# Define CDW Fulcrum query for domain
cdwQuery = paste(URLEncode('SELECT * FROM "(TOS) Coarse Downed Wood: Tally [PROD]" AS parent
  JOIN "(TOS) Coarse Downed Wood: Tally [PROD]/per_plot_azimuth_log" AS child'),
  URLEncode(paste0("ON (parent._record_id = child._parent_id)
  WHERE domainid LIKE'", domain, "'")), sep = "%20")

# Get CDW data from Fulcrum
cdw <- get_Fulcrum_data(api_token = api_token, sql = cdwQuery)

## Select desired fields from 'cdw' data frame, then select data for specified site only
cdw %>%
  dplyr::select(domainid, siteid, plotid_parent, tallydate, volumefactor_ingest, particle_count, lidsaz,
    taxonid, decayclass, logid_ingest, logdistance, loglength, acceptedtaxonid, target) %>%
  dplyr::filter(siteid==site) -> cdw
```

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

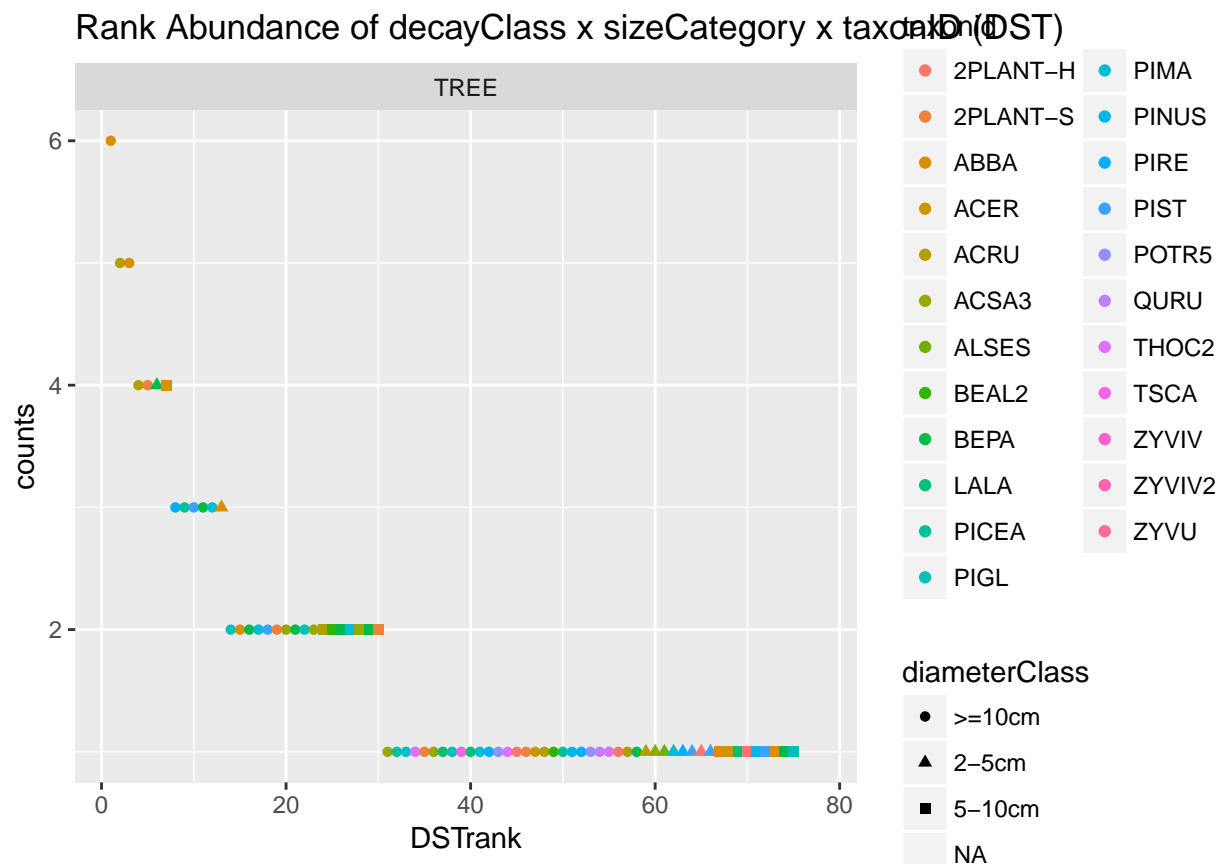
## Simplify decayclass to numeric value wrapped inside sapply(decayClassNum, "[", 1) e.g. 'return first
cdw$decayClassNum <- sapply(stringr::str_split(cdw$decayclass, pattern = " "), "[", 1)

## Write data file
write.csv(cdw, file = paste(outpath, paste(domain, site, "merged", "cdw_rawdata.csv", sep="_"), sep = "/
```

siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
TREE	ABBA	3	>=10cm	6	132	4.55	4.55
TREE	ACRU	2	>=10cm	5	132	3.79	8.34
TREE	ABBA	4	>=10cm	5	132	3.79	12.13
TREE	ACRU	3	>=10cm	4	132	3.03	15.16
TREE	2PLANT-S	5	>=10cm	4	132	3.03	18.19
TREE	BEPA	2	2-5cm	4	132	3.03	21.22
TREE	ABBA	3	5-10cm	4	132	3.03	24.25
TREE	PIRE	2	>=10cm	3	132	2.27	26.52
TREE	PICEA	3	>=10cm	3	132	2.27	28.79
TREE	PIST	3	>=10cm	3	132	2.27	31.06
TREE	BEPA	4	>=10cm	3	132	2.27	33.33
TREE	PIMA	4	>=10cm	3	132	2.27	35.60
TREE	ABBA	3	2-5cm	3	132	2.27	37.87
TREE	PIGL	1	>=10cm	2	132	1.52	39.39
TREE	ABBA	2	>=10cm	2	132	1.52	40.91
TREE	BEPA	2	>=10cm	2	132	1.52	42.43
TREE	PIMA	2	>=10cm	2	132	1.52	43.95
TREE	PIST	2	>=10cm	2	132	1.52	45.47
TREE	2PLANT-S	3	>=10cm	2	132	1.52	46.99
TREE	ACSA3	3	>=10cm	2	132	1.52	48.51
TREE	BEPA	3	>=10cm	2	132	1.52	50.03
TREE	PIGL	3	>=10cm	2	132	1.52	51.55
TREE	ACSA3	4	>=10cm	2	132	1.52	53.07
TREE	ACRU	2	5-10cm	2	132	1.52	54.59
TREE	BEAL2	2	5-10cm	2	132	1.52	56.11
TREE	BEPA	2	5-10cm	2	132	1.52	57.63
TREE	PIMA	2	5-10cm	2	132	1.52	59.15
TREE	ACSA3	3	5-10cm	2	132	1.52	60.67
TREE	BEPA	3	5-10cm	2	132	1.52	62.19
TREE	2PLANT-S	4	5-10cm	2	132	1.52	63.71
TREE	ACSA3	1	>=10cm	1	132	0.76	64.47
TREE	PICEA	1	>=10cm	1	132	0.76	65.23
TREE	PIMA	1	>=10cm	1	132	0.76	65.99
TREE	THOC2	1	>=10cm	1	132	0.76	66.75
TREE	2PLANT-S	2	>=10cm	1	132	0.76	67.51
TREE	ACSA3	2	>=10cm	1	132	0.76	68.27
TREE	LALA	2	>=10cm	1	132	0.76	69.03
TREE	PIGL	2	>=10cm	1	132	0.76	69.79
TREE	TSCA	2	>=10cm	1	132	0.76	70.55
TREE	LALA	3	>=10cm	1	132	0.76	71.31

siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
TREE	PIMA	3	>=10cm	1	132	0.76	72.07
TREE	PIRE	3	>=10cm	1	132	0.76	72.83
TREE	POTR5	3	>=10cm	1	132	0.76	73.59
TREE	THOC2	3	>=10cm	1	132	0.76	74.35
TREE	2PLANT-H	4	>=10cm	1	132	0.76	75.11
TREE	2PLANT-S	4	>=10cm	1	132	0.76	75.87
TREE	ACER	4	>=10cm	1	132	0.76	76.63
TREE	ACRU	4	>=10cm	1	132	0.76	77.39
TREE	BEAL2	4	>=10cm	1	132	0.76	78.15
TREE	PICEA	4	>=10cm	1	132	0.76	78.91
TREE	PINUS	4	>=10cm	1	132	0.76	79.67
TREE	PIRE	4	>=10cm	1	132	0.76	80.43
TREE	POTR5	4	>=10cm	1	132	0.76	81.19
TREE	QURU	4	>=10cm	1	132	0.76	81.95
TREE	THOC2	4	>=10cm	1	132	0.76	82.71
TREE	2PLANT-H	5	>=10cm	1	132	0.76	83.47
TREE	ACRU	5	>=10cm	1	132	0.76	84.23
TREE	BEPA	5	>=10cm	1	132	0.76	84.99
TREE	ACRU	2	2-5cm	1	132	0.76	85.75
TREE	ACSA3	2	2-5cm	1	132	0.76	86.51
TREE	ALSES	2	2-5cm	1	132	0.76	87.27
TREE	PIMA	2	2-5cm	1	132	0.76	88.03
TREE	PIRE	2	2-5cm	1	132	0.76	88.79
TREE	PIST	2	2-5cm	1	132	0.76	89.55
TREE	2PLANT-H	3	2-5cm	1	132	0.76	90.31
TREE	PIST	3	2-5cm	1	132	0.76	91.07
TREE	ABBA	2	5-10cm	1	132	0.76	91.83
TREE	ACER	2	5-10cm	1	132	0.76	92.59
TREE	LALA	2	5-10cm	1	132	0.76	93.35
TREE	2PLANT-H	3	5-10cm	1	132	0.76	94.11
TREE	PINUS	3	5-10cm	1	132	0.76	94.87
TREE	PIST	3	5-10cm	1	132	0.76	95.63
TREE	ABBA	4	5-10cm	1	132	0.76	96.39
TREE	BEPA	4	5-10cm	1	132	0.76	97.15
TREE	PIGL	4	5-10cm	1	132	0.76	97.91
TREE	ZYVIV	NA	NA	1	132	0.76	98.67
TREE	ZYVIV2	NA	NA	1	132	0.76	99.43
TREE	ZYVU	NA	NA	1	132	0.76	100.19

Warning: Removed 3 rows containing missing values (geom_point).



Code