

CDW Tally Analysis: D03 DSNY

Courtney Meier, Cody Flagg

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

## Define paths and other inputs
domain <- "D03"
site <- "DSNY"

# 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"))

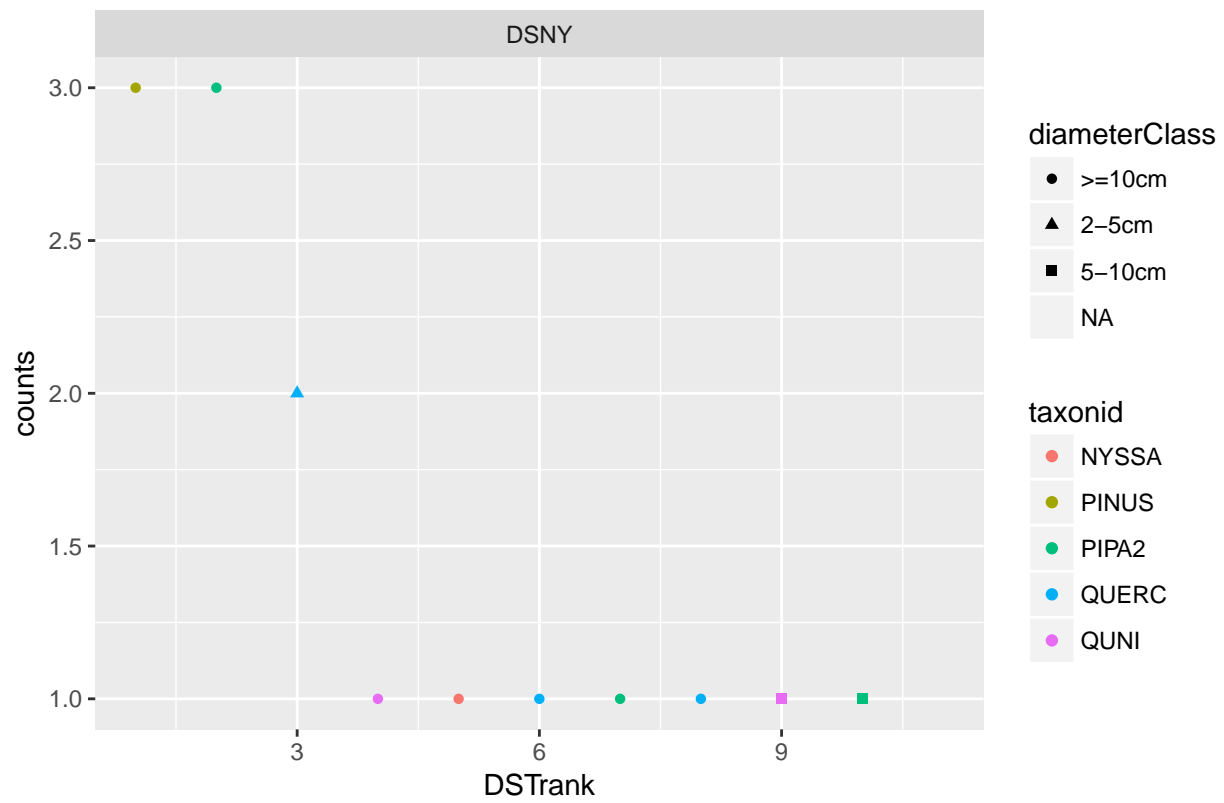
## Simplify decayclass to numeric value wrapped inside sapply(decayClassNum, "[", 1) e.g. 'return first
cdw$decayClassNum <- sapply(stringr::str_split(cdw$decayclass, pattern = " "), "[", 1)

## 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	D
DSNY	PINUS	3	>=10cm	3	16	18.75	18.75	
DSNY	PIPA2	3	>=10cm	3	16	18.75	37.50	
DSNY	QUERC	2	2-5cm	2	16	12.50	50.00	
DSNY	QUNI	2	>=10cm	1	16	6.25	56.25	
DSNY	NYSSA	4	>=10cm	1	16	6.25	62.50	
DSNY	QUERC	4	>=10cm	1	16	6.25	68.75	
DSNY	PIPA2	5	>=10cm	1	16	6.25	75.00	
DSNY	QUERC	5	>=10cm	1	16	6.25	81.25	
DSNY	QUNI	2	5-10cm	1	16	6.25	87.50	
DSNY	PIPA2	3	5-10cm	1	16	6.25	93.75	
DSNY	QUERC	3	NA	1	16	6.25	100.00	

```
## Warning: Removed 1 rows containing missing values (geom_point).
```

Rank Abundance of decayClass x sizeCategory x taxonID (DST)



Code