CDW Tally Analysis: D17

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

##  Define paths and other inputs
domain <- "D17"
site <- "SJER"

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

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

## 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 = "6ce6d01c4ec984e68fcecbb04d96f71a229f1db388fe1acd90c1fb6ba77a1daf"

# Define CDW Fulcrum query for D17
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("ON (parent._record_id = child._record_id)
                        WHERE domainid LIKE 'D17'"), 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 SJER only
cdw %>%
  dplyr::select(domainid, siteid, plotid_parent, tallydate, volumefactor, particle_count, lidsazimuth, l
                    taxonid, decayclass, logid_ingest, logdistance, loglength, acceptedtaxonid, targett
  dplyr::filter(siteid=="SJER") -> cdw
```

```
## 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 data file
write.csv(cdw, file = paste(outpath, paste(domain, site, "merged","cdw_rawdata.csv", sep="_"), sep = "/
```
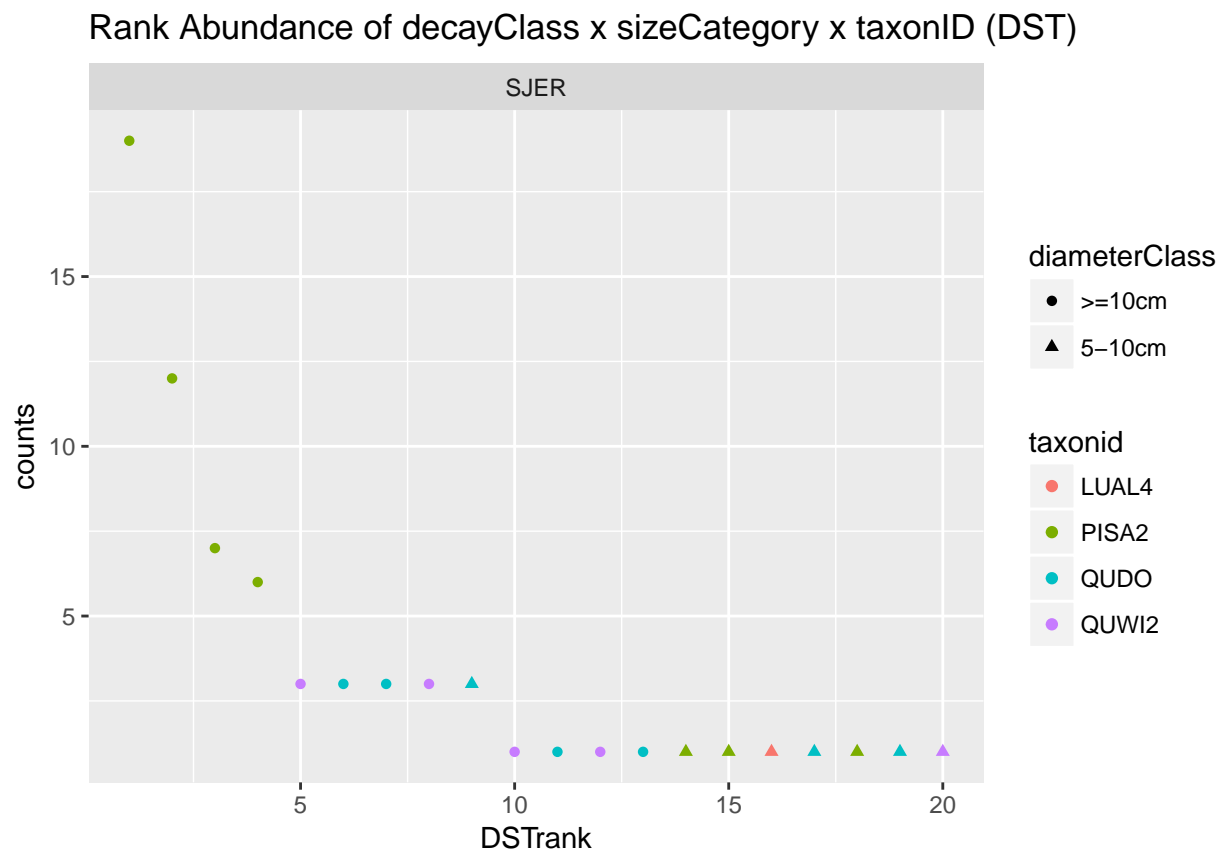
siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance	DS
SJER	PISA2	2	>=10cm	19	70	27.14	27.14	
SJER	PISA2	3	>=10cm	12	70	17.14	44.28	
SJER	PISA2	1	>=10cm	7	70	10.00	54.28	
SJER	PISA2	4	>=10cm	6	70	8.57	62.85	
SJER	QUWI2	2	>=10cm	3	70	4.29	67.14	
SJER	QUDO	3	>=10cm	3	70	4.29	71.43	
SJER	QUDO	4	>=10cm	3	70	4.29	75.72	
SJER	QUWI2	4	>=10cm	3	70	4.29	80.01	
SJER	QUDO	1	5-10cm	3	70	4.29	84.30	
SJER	QUWI2	1	>=10cm	1	70	1.43	85.73	
SJER	QUDO	2	>=10cm	1	70	1.43	87.16	
SJER	QUWI2	3	>=10cm	1	70	1.43	88.59	
SJER	QUDO	5	>=10cm	1	70	1.43	90.02	
SJER	PISA2	1	5-10cm	1	70	1.43	91.45	
SJER	PISA2	2	5-10cm	1	70	1.43	92.88	
SJER	LUAL4	3	5-10cm	1	70	1.43	94.31	
SJER	QUDO	4	5-10cm	1	70	1.43	95.74	
SJER	PISA2	NA	5-10cm	1	70	1.43	97.17	
SJER	QUDO	NA	5-10cm	1	70	1.43	98.60	
SJER	QUWI2	NA	5-10cm	1	70	1.43	100.03	

Rank Abundance of decayClass x sizeCategory x taxonID (DST)

Code