CDW Tally Analysis: D03 JERC

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

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

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

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

## 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, yearboutbegan, eventid, volumefactor, sampli
                lidsazimuth, targettaxapresent, logdistance, logmaxdiameter, minorlogdiameter, logid, lo
                scientificname, decayclass) %>%
```

```
  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 = "/
```
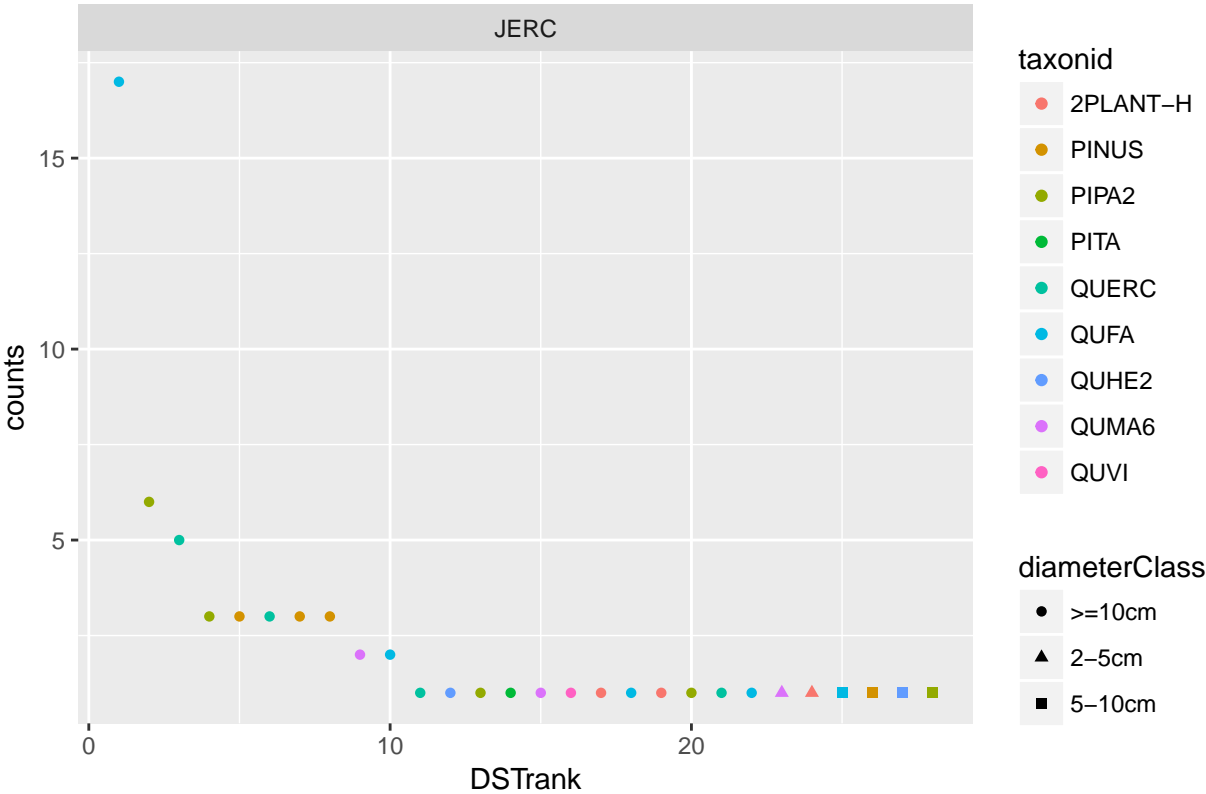
siteid	taxonid	decayClassNum	diameterClass	counts	totalLogs	relativeAbundance	cumulativeAbundance
JERC	QUFA	1	>=10cm	17	65	26.15	26.15
JERC	PIPA2	3	>=10cm	6	65	9.23	35.38
JERC	QUERC	3	>=10cm	5	65	7.69	43.07
JERC	PIPA2	1	>=10cm	3	65	4.62	47.69
JERC	PINUS	2	>=10cm	3	65	4.62	52.31
JERC	QUERC	2	>=10cm	3	65	4.62	56.93
JERC	PINUS	3	>=10cm	3	65	4.62	61.55
JERC	PINUS	4	>=10cm	3	65	4.62	66.17
JERC	QUMA6	1	>=10cm	2	65	3.08	69.25
JERC	QUFA	2	>=10cm	2	65	3.08	72.33
JERC	QUERC	1	>=10cm	1	65	1.54	73.87
JERC	QUHE2	1	>=10cm	1	65	1.54	75.41
JERC	PIPA2	2	>=10cm	1	65	1.54	76.95
JERC	PITA	2	>=10cm	1	65	1.54	78.49
JERC	QUMA6	2	>=10cm	1	65	1.54	80.03
JERC	QUVI	2	>=10cm	1	65	1.54	81.57
JERC	2PLANT-H	3	>=10cm	1	65	1.54	83.11
JERC	QUFA	3	>=10cm	1	65	1.54	84.65
JERC	2PLANT-H	4	>=10cm	1	65	1.54	86.19
JERC	PIPA2	4	>=10cm	1	65	1.54	87.73
JERC	QUERC	4	>=10cm	1	65	1.54	89.27
JERC	QUFA	4	>=10cm	1	65	1.54	90.81
JERC	QUMA6	1	2-5cm	1	65	1.54	92.35
JERC	2PLANT-H	2	2-5cm	1	65	1.54	93.89
JERC	QUFA	1	5-10cm	1	65	1.54	95.43
JERC	PINUS	2	5-10cm	1	65	1.54	96.97
JERC	QUHE2	3	5-10cm	1	65	1.54	98.51
JERC	PIPA2	4	5-10cm	1	65	1.54	100.05

Rank Abundance of decayClass x sizeCategory x taxonID (DST)

Code