

8 Join PesticideUseData to KernAg-CDFA shapefile

The purpose of this Rmarkdown file is to join pesticide use data to Kern County Agriculture-CDFA shapefile so we can compare pesticide use across conventional and organic fields

```
library(tidyverse)
library(rgdal)
library(sf)

# Avoid scientific notation in output dataframes
options(scipen = 9999)

# Specify years of interest
years = 2017

# Specify buffer width being analyzed -- Buffer widths were originally implemented in the Kern Agriculture-CDFA shapefile
buf_width = c(50)

# Read in Pesticide Data
pest_data_raw <- read_csv("../R_input/CSV/PesticideUse/KernOrgCollapse1317.csv")

# Filter pesticide data for 2017
for(i in years){

  tmp <- filter(pest_data_raw, year==i)

  assign(paste0("pest_data_", i), tmp)
}

# Read in joined KernAg_CDFA shape file with appropriate buffer and convert to spatial dataframe
for(i in years){
  for(j in buf_width){

    tmp <- readOGR(paste0("../R_output/spatial/KernAg_CDFA_join/2017/buffer", j, "/All_KernAg_CDFA_join", i),
                  st_as_sf())

    assign(paste0("kern_ag_", i, "_B", j), tmp)
  }
}

## OGR data source with driver: ESRI Shapefile
## Source: "/Users/clairepowers/Desktop/Organics_Final/Working/R_files/R_output/spatial/KernAg_CDFA_join/2017/buffer100/All_KernAg_CDFA_join2017_B100.shp"
## with 11729 features
## It has 11 fields

# Rename PMT_SITE to 'permitsite' for each match in the following join() function
colnames(kern_ag_2017_B50)[3] = "permitsite"
# colnames(kern_ag_2017_B100)[3] = "permitsite"

# Join the two on permitsite and keep only the rows that had matches
kern_ag_pest_2017_B50 <- inner_join(kern_ag_2017_B50, pest_data_2017)
```

```

## Joining, by = "permitsite"

## Warning: Column `permitsite` joining factor and character vector, coercing
## into character vector

# kern_ag_pest_2017_B100 <- inner_join(kern_ag_2017_B100,pest_data_2017)

# Compare the number of CDFA organic fields before and after join
n_org_b4_join_B50 = sum(kern_ag_2017_B50$CDFA, na.rm = T) # 491
n_org_after_join_B50 = sum(kern_ag_pest_2017_B50$CDFA, na.rm = T) # 333

# n_org_b4_join_B100 = sum(kern_ag_2017_B100$CDFA, na.rm = T) # 537
# n_org_after_join_B100 = sum(kern_ag_pest_2017_B100$CDFA, na.rm = T) # 342

kern_ag_pest_2017_B50_shp = as(kern_ag_pest_2017_B50,"Spatial")
# kern_ag_pest_2017_B100_shp = as(kern_ag_pest_2017_B100,"Spatial")

dir.create(paste0("../R_output/spatial/KernAg_CDFA_pest/",years,"/B50"),
           recursive = TRUE)

## Warning in dir.create(paste0("../R_output/spatial/KernAg_CDFA_pest/",
## years, : '../R_output/spatial/KernAg_CDFA_pest/2017/B50' already exists

# dir.create(paste0("../R_output/spatial/KernAg_CDFA_pest/",years,"/buffer100"),
#            recursive = TRUE)

writeOGR(kern_ag_pest_2017_B50_shp,
         paste0("../R_output/spatial/KernAg_CDFA_pest/",years,"/B50"),
         paste0("KernAg_CDFA_Pest",years,"_B50"),
         driver = "ESRI Shapefile",
         overwrite_layer = TRUE)

## Warning in writeOGR(kern_ag_pest_2017_B50_shp, paste0("../R_output/spatial/
## KernAg_CDFA_pest/", : Field names abbreviated for ESRI Shapefile driver

# writeOGR(kern_ag_pest_2017_B100_shp,
#          paste0("../R_output/spatial/KernAg_CDFA_pest/",years,"/buffer100"),
#          paste0("KernAg_CDFA_Pest",years,"_B100"),
#          driver = "ESRI Shapefile",
#          overwrite_layer = TRUE)

```