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Web address for GitHub repository

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```

## [1] "C:/Users/rscho/OneDrive/Documents/MEM Courses/Sem2/ENV 872/McCollum_Schoenecker_
## Warning: package 'tidyverse' was built under R version 4.1.2
## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.2      v dplyr  1.0.6
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   2.0.2      v forcats 0.5.1
## Warning: package 'ggplot2' was built under R version 4.1.1
## Warning: package 'readr' was built under R version 4.1.1
## Warning: package 'purrr' was built under R version 4.1.1
## Warning: package 'forcats' was built under R version 4.1.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## Warning: package 'lubridate' was built under R version 4.1.2
##
## Attaching package: 'lubridate'
##
## The following objects are masked from 'package:base':
##
##   date, intersect, setdiff, union
## Warning: package 'sf' was built under R version 4.1.2
## Linking to GEOS 3.9.1, GDAL 3.2.1, PROJ 7.2.1; sf_use_s2() is TRUE
## Warning: package 'trend' was built under R version 4.1.2
## Warning: package 'zoo' was built under R version 4.1.1
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##   as.Date, as.Date.numeric
## Warning: package 'Kendall' was built under R version 4.1.2
## Warning: package 'tseries' was built under R version 4.1.2
## Registered S3 method overwritten by 'quantmod':
##   method             from
##   as.zoo.data.frame zoo

```

```
## Reading layer `cb_2018_us_county_20m' from data source
##   `C:\Users\rscho\OneDrive\Documents\MEM Courses\Sem2\ENV 872\McCollum_Schoenecker_EN
##   using driver `ESRI Shapefile'
## Simple feature collection with 3220 features and 9 fields
## Geometry type: MULTIPOLYGON
## Dimension:      XY
## Bounding box:   xmin: -179.1743 ymin: 17.91377 xmax: 179.7739 ymax: 71.35256
## Geodetic CRS:   NAD83
```

1 Rationale and Research Questions

According to a 2019 study by Rosenberg et al, North America's bird population has declined by 30% over the last fifty years. Many drivers are causing this steep decline, including the encroachment of human development into natural spaces as well as climate change. While this loss has occurred across habitat guilds and among both rare and common species, it also has important implications for the diversity of North America's bird population as some species near extinction (Rosenberg et al 2019). Additionally, the phenomenon of urbanization itself often supports a less diverse population of generalist species as opposed to habitat specialists (Callaghan et al 2019). This reduction of biodiversity has negative consequences for the resiliency of natural ecosystems, as well as various ecosystem services (Şekercioğlu et al 2004).

The Research Triangle region of central North Carolina is made up of some of the largest cities in the state, including Raleigh, Durham, and Cary. This region is characterized by mixed woodlands that support bird diversity (Minor and Urban 2010), and is currently experiencing rapid development (Doran and Golden 2016). In order to investigate changes in the diversity of the Research Triangle's population during the past decade (2010-2020), we accessed open source eBird data from the three main counties that make up the region (Durham, Orange, and Wake counties) and analyzed them with time series methodology. In this analysis, we hoped to answer the following questions:

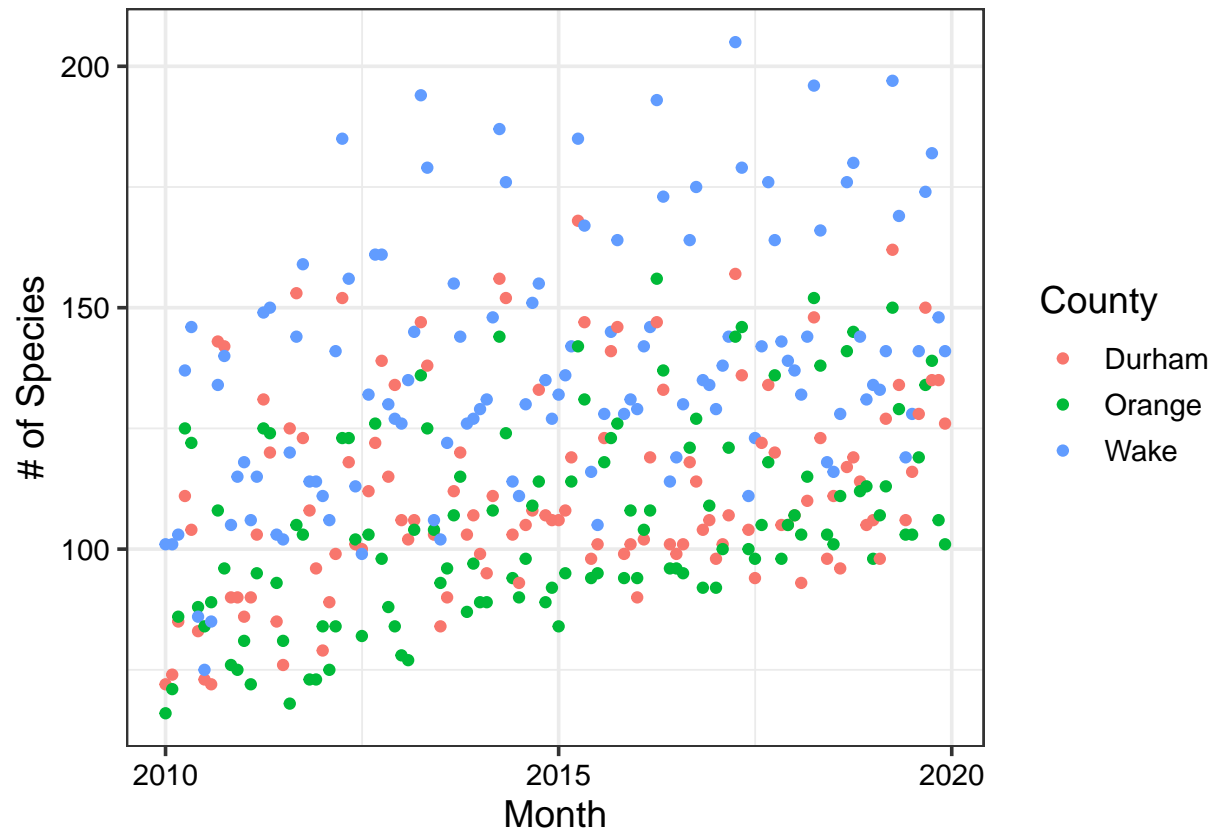
1. How did the diversity of the Research Triangle's bird population change over the 2010s?
 - 1a. Is this change consistent across the three main counties in the Research Triangle (Durham, Wake, and Orange)?
 - 1b. Was there a clear trend in the presence of species of concern across the decade?
2. How did the popularity of eBird change in the Research Triangle over the 2010s?

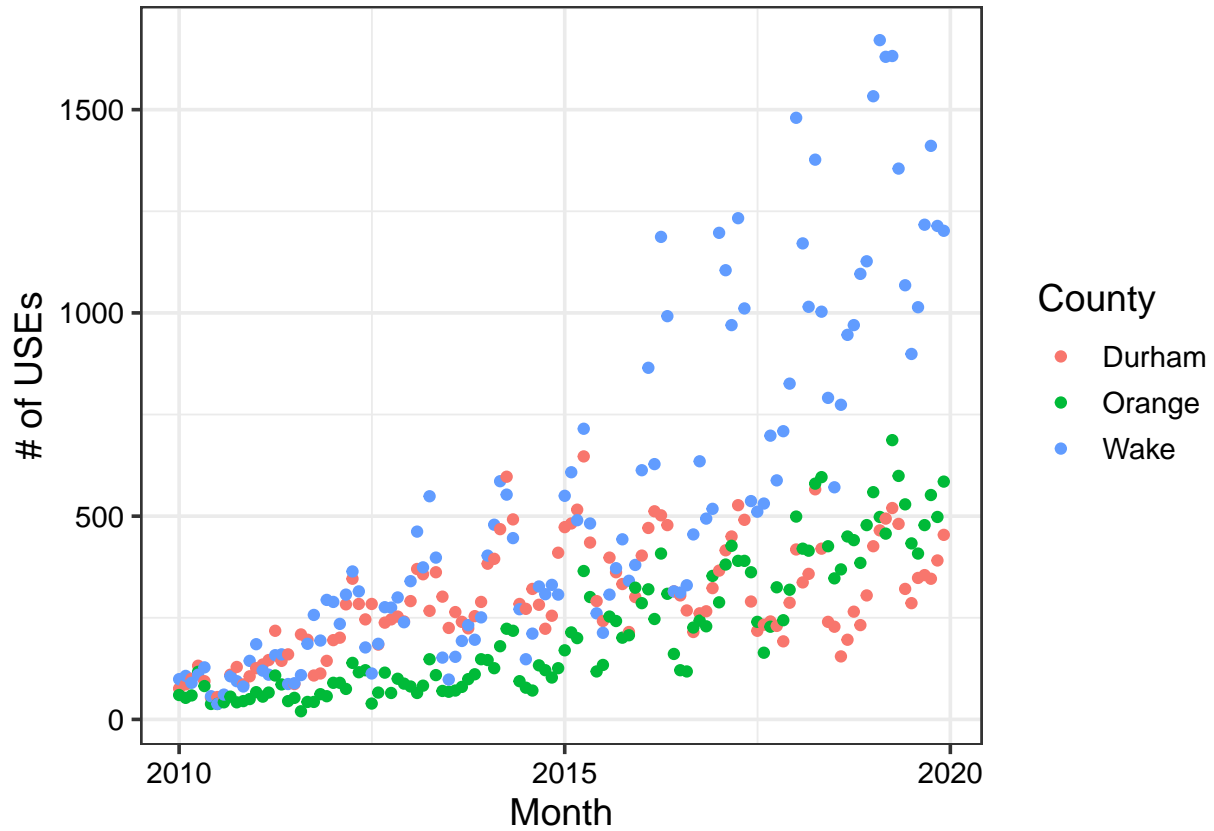
2 Dataset Information

eBird is an open-source citizen science website created by the Cornell University Lab of Ornithology which allows the public to upload their own bird observation data collected from around the world (eBird 2022). The site has become incredibly popular with both amateur birders and scientific researchers since its creation. We downloaded bird observation data from the site for Durham, Orange, and Wake counties collected between January 2010 and December 2019. The data includes many variables including the common and scientific names of each bird species and observation data, time, and geographic coordinates. However, several variables in the dataset were not of use to us, so we selected 12 variables from the original set to create new, tidy datasets for each county (Table 1). This wrangling was performed with v. 4.1 of the R programming language (R Core Team 2021) as well as the tidyverse package (Wickham et al 2019).

Using the tidy data, we created tables for each county summarizing the number of unique species observed, or species richness, within each month of the decade. We used this metric as the indicator for bird diversity. We also created summary tables that showed the total number of unique sampling events uploaded for each month of the decade for each county. We used this metric as the indicator for the popularity of eBird.

```
## `summarise()` has grouped output by 'COUNTY'. You can override using the `.groups` ar
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```

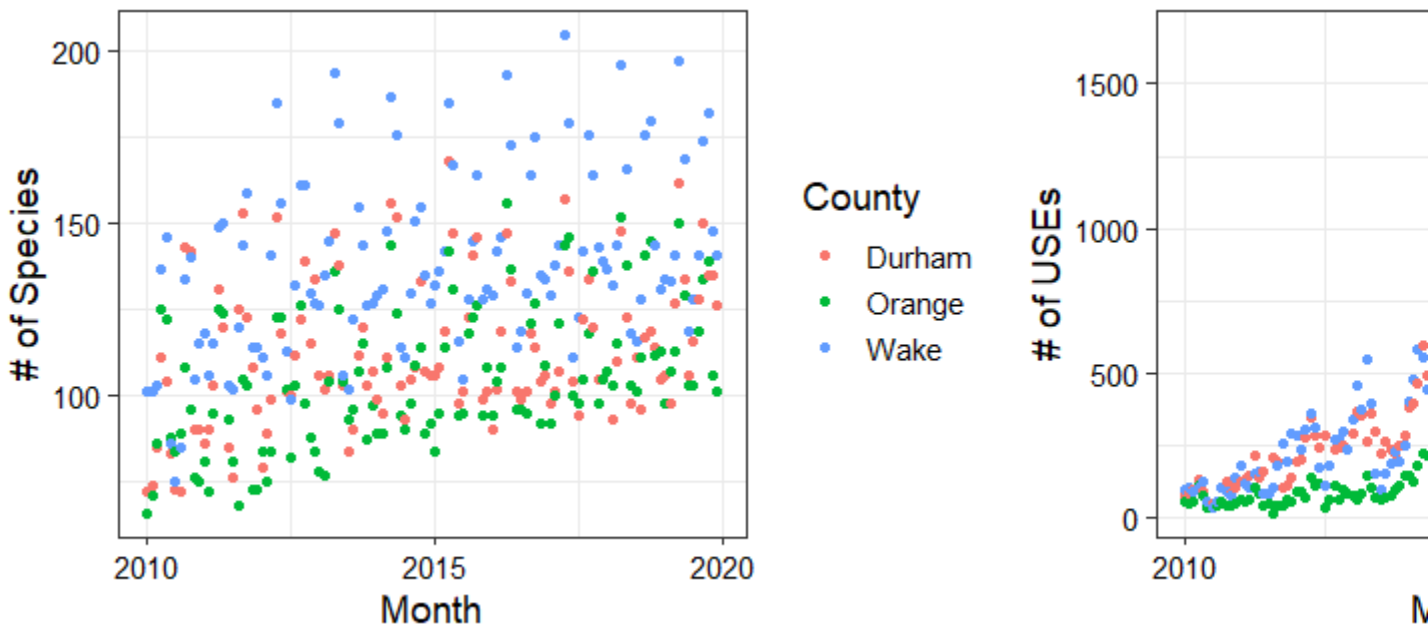




In order to perform our analysis related to species of concern in the Research Triangle, we also used a dataset provided by the North Carolina Wildlife Resources Commission (NCWRC) detailing Species of Greatest Conservation Need (SGCN) in the state (NCWRC 2020). SGCN are determined by the NCWRC based on any policies concerning threatened or endangered species, risks related to the type of habitat they use, as well as other indicators of concern. The raw data included information on all SGCN identified in North Carolina, but through wrangling we filtered in order to create a vector that only included SGCN that were birds (Table 2). By cross-referencing this vector with the eBird data, we were able to calculate how many SGCN were observed in each county during each year of the decade.

3 Exploratory Analysis

For our first step in analyzing our data, we created simple plots of species richness (Figure 1) and unique sampling events (Figure 2) across the decade to see if any clear trends could be identified. While all three counties exhibited possible positive trends in species richness, these were not entirely clear and required further analysis. There was a stronger positive trend in unique sample events that was visible for all three counties, but we also wanted to analyze this trend more precisely.



Since the eBird data included latitude and longitude for every observation, the other component of our exploratory analysis included visualizing the location of each observation geospatially (Figure 3). This plot shows that the distribution of sampling locations was not evenly distributed across the region and that observations were concentrated around the urban centers of each county (Durham, Chapel Hill, and Raleigh).

```
Durham.total <- rbind(Durham.1, Durham.2)
Orange.total <- rbind(Orange.1, Orange.2)
Wake.total <- rbind(Wake.1, Wake.2, Wake.3)
```

```
Durham.sf <- Durham.total %>%
  group_by(LOCALITY.ID, LONGITUDE, LATITUDE) %>%
  summarize(spp_total = length(unique(COMMON.NAME))) %>%
  st_as_sf(coords = c("LONGITUDE", "LATITUDE"), crs = 4326)
```

`summarise()` has grouped output by 'LOCALITY.ID', 'LONGITUDE'. You can override using `ungroup()`

```
Orange.sf <- Orange.total %>%
  group_by(LOCALITY.ID, LONGITUDE, LATITUDE) %>%
  summarize(spp_total = length(unique(COMMON.NAME))) %>%
  st_as_sf(coords = c("LONGITUDE", "LATITUDE"), crs = 4326)
```

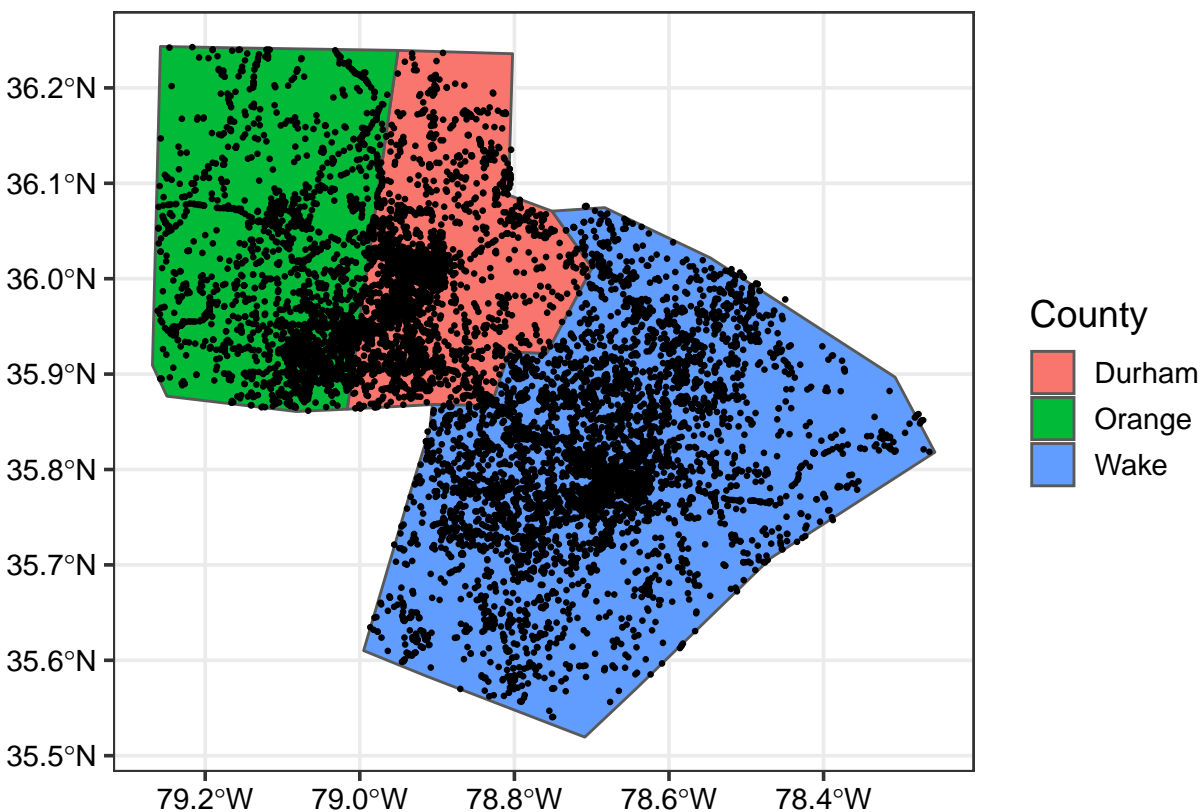
```
st_as_sf(coords = c("LONGITUDE", "LATITUDE"), crs = 4326)
```

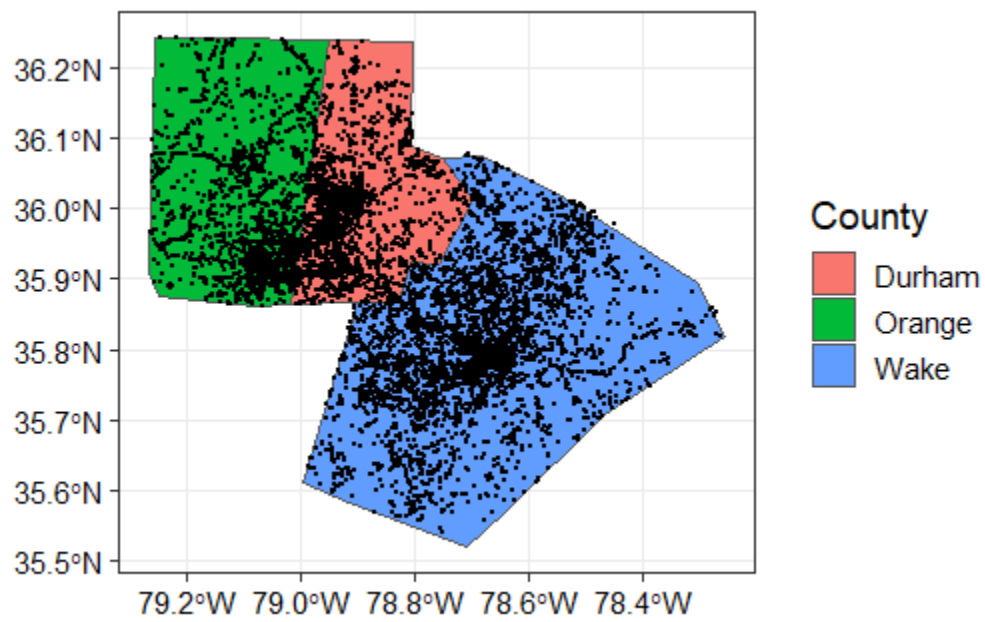
`summarise()` has grouped output by 'LOCALITY.ID', 'LONGITUDE'. You can override using `ungroup()`

```
Wake.sf <- Wake.total %>%  
  group_by(LOCALITY.ID, LONGITUDE, LATITUDE) %>%  
  summarize(spp_total = length(unique(COMMON.NAME))) %>%  
  st_as_sf(coords = c("LONGITUDE", "LATITUDE"), crs = 4326)
```

`summarise()` has grouped output by 'LOCALITY.ID', 'LONGITUDE'. You can override using `ungroup()`

```
counties_sf <- st_transform(counties_sf, crs = 4326)  
  
ggplot() + geom_sf(data = counties_sf, aes(fill = NAME)) +  
  geom_sf(data = Durham.sf, size = 0.5) +  
  geom_sf(data = Orange.sf, size = 0.5) +  
  geom_sf(data = Wake.sf, size = 0.5) + labs(fill = "County")
```





4 Analysis

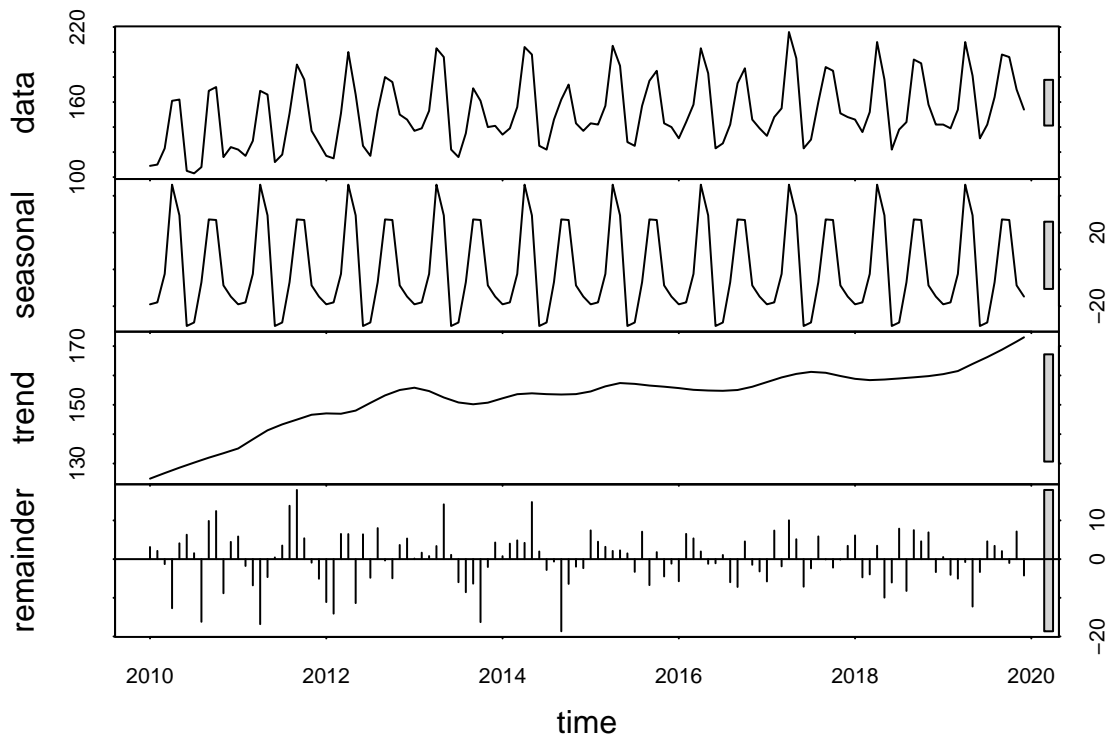
4.1 Question 1: How did the diversity of the Research Triangle's bird population change during the 2010s?

A time series analysis of species richness across all three counties combined showed both a seasonal trend as well as a strong positive monotonic trend (Figure 4). The seasonal trend likely correlates with the spring and fall migration seasons when more species would be present in the area. A seasonal Mann-Kendall test supported our identification of a significant positive trend in species richness across the time period (score = 195, tau = 0.366, $p < 0.001$).

```
total.1 <- rbind(Durham.1, Orange.1, Wake.1)
total.2 <- rbind(Durham.2, Orange.2)
total.2 <- rbind(total.2, Wake.2, Wake.3)
total.data <- rbind(total.1, total.2)

spp.counts.total <- total.data %>%
  group_by(MY) %>%
  summarize(spp_total = length(unique(COMMON.NAME)))

# Species richness by month
Total.ts <- ts(spp.counts.total$spp_total, start = c(2010,1), frequency = 12)
Total.decomp <- stl(Total.ts, s.window = "periodic")
plot(Total.decomp)
```



```
Total.spp.trend <- Kendall::SeasonalMannKendall(Total.ts)
Total.spp.trend
```

```
## tau = 0.563, 2-sided pvalue =5.9952e-15
```

```
summary(Total.spp.trend)
```

```
## Score = 301 , Var(Score) = 1488.333
```

```
## denominator = 534.4285
```

```
## tau = 0.563, 2-sided pvalue =5.9952e-15
```

4.2 Question 1a: Is this trend consistent across all three main counties in the region (Durham, Orange, and Wake)?

Individual time series analysis for each county also exhibited seasonality as well as positive monotonic trends (Figures 5a-c). The pattern and rate of this positive trend was slightly different among the counties, however. While species richness saw a steeper increase earlier in the decade in Wake County, there was a more gradual increase throughout the period in Orange County, and Durham County saw a steeper increase in more recent years. Seasonal Mann-Kendall tests produced significant results for Durham (score = 172, $\tau = 0.322$, $p < 0.001$), Orange (score = 381, $\tau = 0.710$, $p < 0.001$), and Wake counties (score = 345, $\tau = 0.650$, $p < 0.001$).

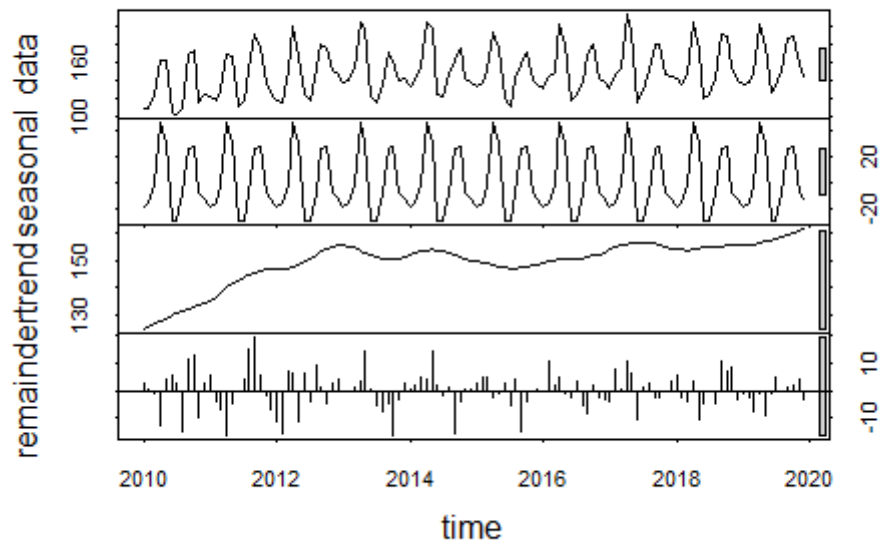
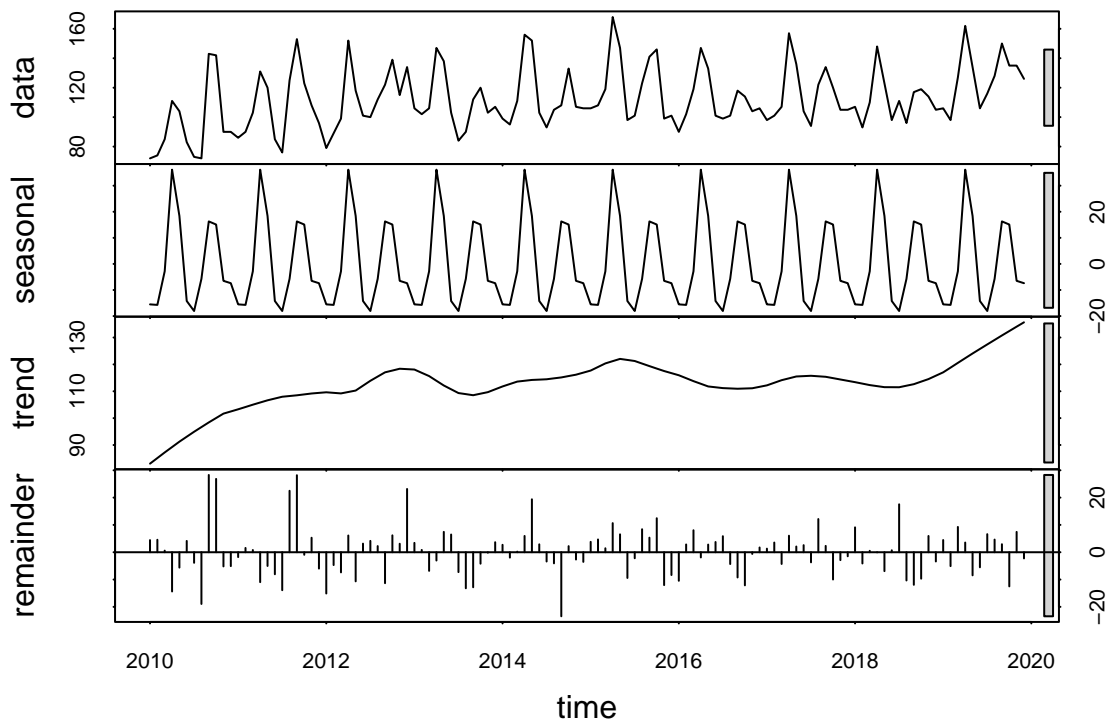


Figure 1: Figure 4. Time series decomposition for species richness aggregated across all three counties from 2010 to 2019.

```
# DURHAM
Durham.ts <- ts(spp.counts.Durham$spp_total, start = c(2010,1), frequency = 12)
Durham.decomp <- stl(Durham.ts, s.window = "periodic")
plot(Durham.decomp)
```



```
Durham.spp.trend <- Kendall::SeasonalMannKendall(Durham.ts)
Durham.spp.trend
```

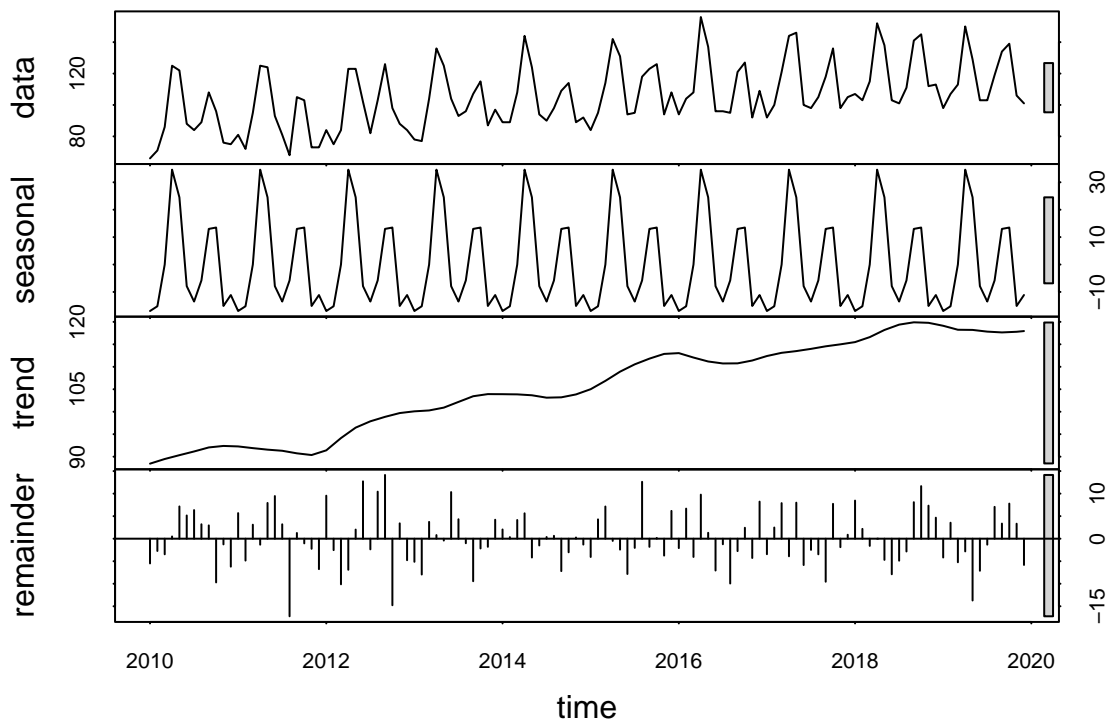
```
## tau = 0.322, 2-sided pvalue =8.2001e-06
```

```
summary(Durham.spp.trend)
```

```
## Score = 172 , Var(Score) = 1487.333
## denominator = 533.9257
## tau = 0.322, 2-sided pvalue =8.2001e-06
```

```
# ORANGE
```

```
Orange.ts <- ts(spp.counts.Orange$spp_total, start = c(2010,1), frequency = 12)
Orange.decomp <- stl(Orange.ts, s.window = "periodic")
plot(Orange.decomp)
```

```
Orange.spp.trend <- Kendall::SeasonalMannKendall(Orange.ts)
Orange.spp.trend
```

```
## tau = 0.71, 2-sided pvalue =< 2.22e-16
```

```
summary(Orange.spp.trend)
```

```
## Score = 381 , Var(Score) = 1493
```

```
## denominator = 536.4688
```

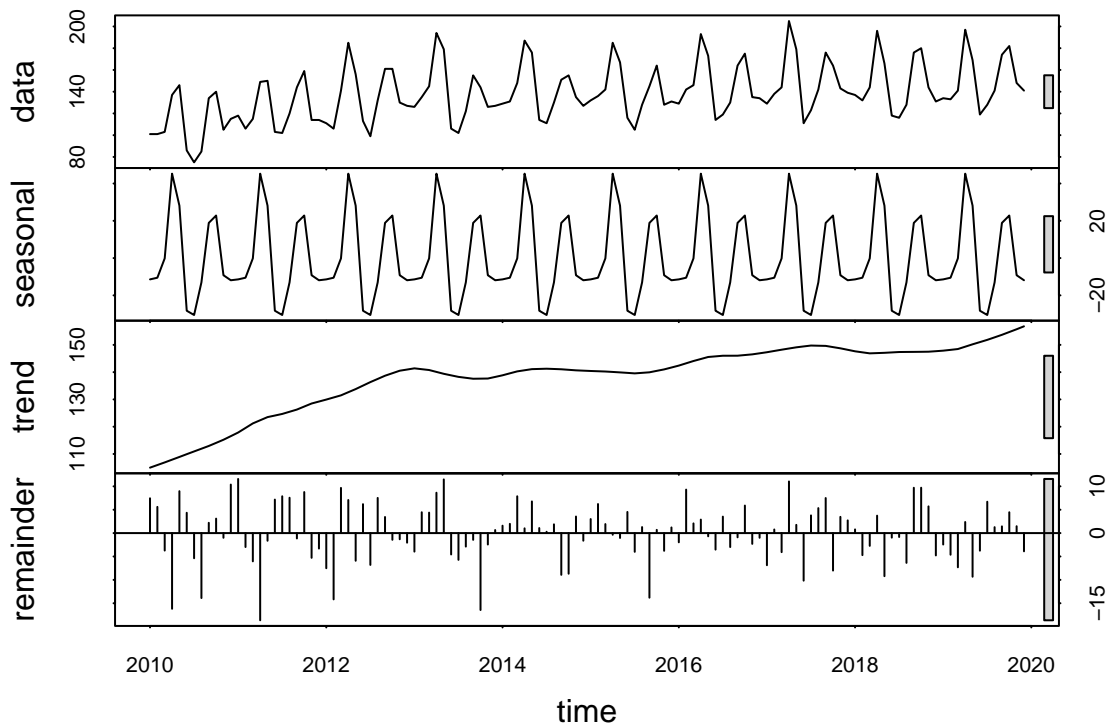
```
## tau = 0.71, 2-sided pvalue =< 2.22e-16
```

```
# WAKE
```

```
Wake.ts <- ts(spp.counts.Wake$spp_total, start = c(2010,1), frequency = 12)
```

```
Wake.decomp <- stl(Wake.ts, s.window = "periodic")
```

```
plot(Wake.decomp)
```

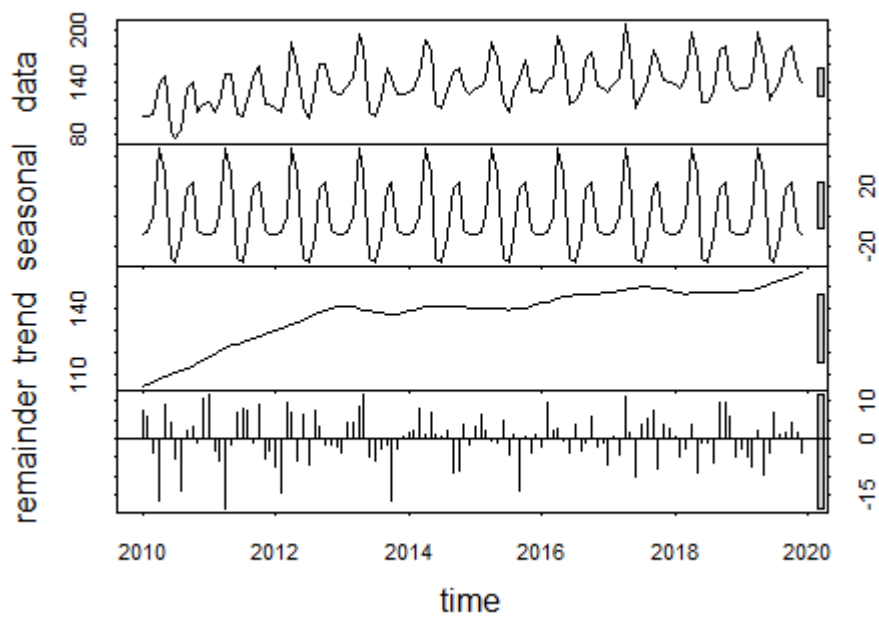
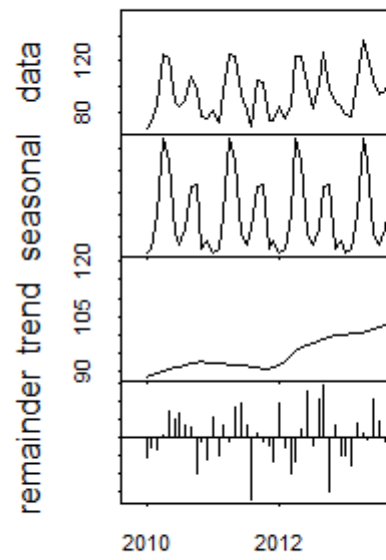
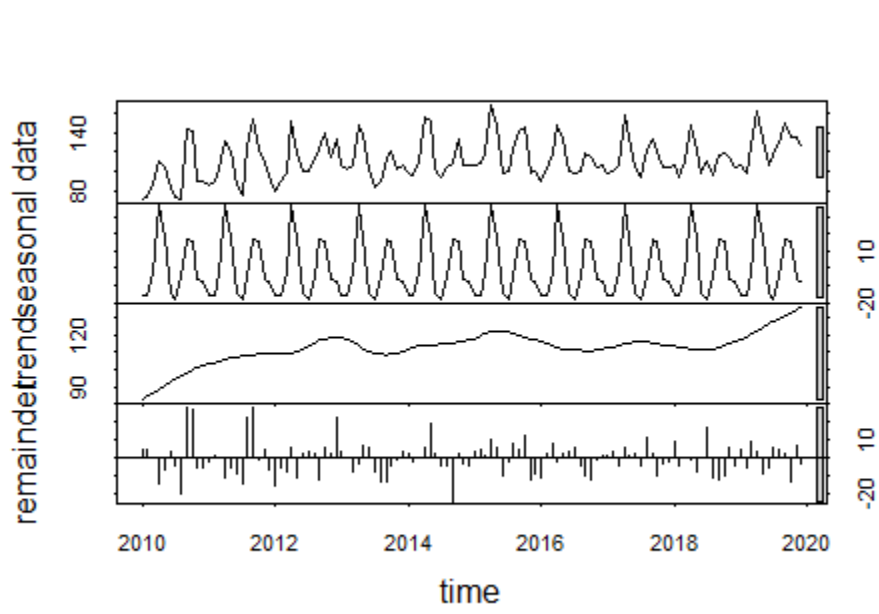


```
Wake.spp.trend <- Kendall::SeasonalMannKendall(Wake.ts)
Wake.spp.trend
```

```
## tau = 0.65, 2-sided pvalue =< 2.22e-16
```

```
summary(Wake.spp.trend)
```

```
## Score = 345 , Var(Score) = 1479.667
## denominator = 530.3824
## tau = 0.65, 2-sided pvalue =< 2.22e-16
```



4.3 Question 1b: Was there a clear trend in the presence of species of concern across the decade?

For each of the three counties, the number of SGCN observed in the final year of the period (2019) was noticeably higher than the number observed in the first year of the period (2010; Figure 6). However, none of the counties exhibited a constant increase in SGCN count across the entire decade, suggesting that further analysis is necessary to fully understand the trend in these data.

```
Durham.total <- Durham.total %>%
  mutate(SGCN = ifelse(COMMON.NAME %in% SGCN_bird_list, "Y", "N"))

Durham.SGCN <- unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y"])

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2010]))
## [1] 34

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2011]))
## [1] 50

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2012]))
## [1] 40

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2013]))
## [1] 35

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2014]))
## [1] 36

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2015]))
## [1] 43

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2016]))
## [1] 35

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2017]))
## [1] 40

length(unique(Durham.total$COMMON.NAME[Durham.total$SGCN == "Y" & Durham.total$YEAR == 2018]))
## [1] 43
```

```
## [1] 47
```

```
Du.SGCN.counts <- c(34, 50, 40, 35, 36, 43, 35, 40, 43, 47)
Du.SGCN.years <- c(2010:2019)
Du.SGCN.by.year <- cbind(Du.SGCN.years, Du.SGCN.counts)
colnames(Du.SGCN.by.year) <- c("Year", "SGCN_total")
# write.csv(Du.SGCN.by.year, "./Data/Processed/Durham_SGCNcounts.csv")
```

```
Du.SGCN <- read.csv("./Data/Processed/Durham_SGCNcounts.csv")
```

```
Orange.total <- Orange.total %>%
  mutate(SGCN = ifelse(COMMON.NAME %in% SGCN_bird_list, "Y", "N"))
```

```
Orange.SGCN <- unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y"])
```

```
# The not as elegant way since pipe isn't working...
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2010]))
```

```
## [1] 26
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2011]))
```

```
## [1] 23
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2012]))
```

```
## [1] 25
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2013]))
```

```
## [1] 29
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2014]))
```

```
## [1] 31
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2015]))
```

```
## [1] 33
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2016]))
```

```
## [1] 32
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2017]))
```

```
## [1] 32
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2018]))
```

```
## [1] 33
```

```
length(unique(Orange.total$COMMON.NAME[Orange.total$SGCN == "Y" & Orange.total$YEAR == 2010]))
```

```
## [1] 31
```

```
Or.SGCN.counts <- c(26, 23, 25, 29, 31, 33, 32, 32, 33, 31)
```

```
Or.SGCN.years <- c(2010:2019)
```

```
Or.SGCN.by.year <- cbind(Or.SGCN.years, Or.SGCN.counts)
```

```
colnames(Or.SGCN.by.year) <- c("Year", "SGCN_total")
```

```
# write.csv(Or.SGCN.by.year, "./Data/Processed/Orange_SGCNcounts.csv")
```

```
Or.SGCN <- read.csv("./Data/Processed/Orange_SGCNcounts.csv")
```

```
Wake.total <- Wake.total %>%
```

```
  mutate(SGCN = ifelse(COMMON.NAME %in% SGCN_bird_list, "Y", "N"))
```

```
Wake.SGCN <- unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y"])
```

```
# The not as elegant way since pipe isn't working...
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2010]))
```

```
## [1] 38
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2011]))
```

```
## [1] 42
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2012]))
```

```
## [1] 46
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2013]))
```

```
## [1] 49
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2014]))
```

```
## [1] 43
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2015]))
```

```
## [1] 48
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2016]))
```

```
## [1] 49
```

```
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2017]))
```

```

## [1] 45
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2018]))

## [1] 48
length(unique(Wake.total$COMMON.NAME[Wake.total$SGCN == "Y" & Wake.total$YEAR == 2019]))

## [1] 50
Wa.SGCN.counts <- c(38, 42, 46, 49, 43, 48, 49, 45, 48, 50)
Wa.SGCN.years <- c(2010:2019)
Wa.SGCN.by.year <- cbind(Wa.SGCN.years, Wa.SGCN.counts)
colnames(Wa.SGCN.by.year) <- c("Year", "SGCN_total")
# write.csv(Wa.SGCN.by.year, "./Data/Processed/Wake_SGCNcounts.csv")

Wa.SGCN <- read.csv("./Data/Processed/Wake_SGCNcounts.csv")

# Aggregating SGCN counts for all three counties
SGCN.total <- cbind(Du.SGCN[,2:3], Or.SGCN[,3], Wa.SGCN[,3])
colnames(SGCN.total) <- c("Year", "Durham", "Orange", "Wake")
SGCN.total <- pivot_longer(SGCN.total, cols = c("Durham", "Orange", "Wake"),
                           names_to = "County")

ggplot(SGCN.total) + geom_point(aes(x = Year, y = value, col = County)) +
  geom_line(aes(x = Year, y = value, col = County)) +
  scale_x_discrete(name = "Year", limits = c(2010, 2012, 2014, 2016, 2018)) +
  ylab("# of SGCN")

## Warning: Continuous limits supplied to discrete scale.
## Did you mean `limits = factor(...)` or `scale_*_continuous()`?

```

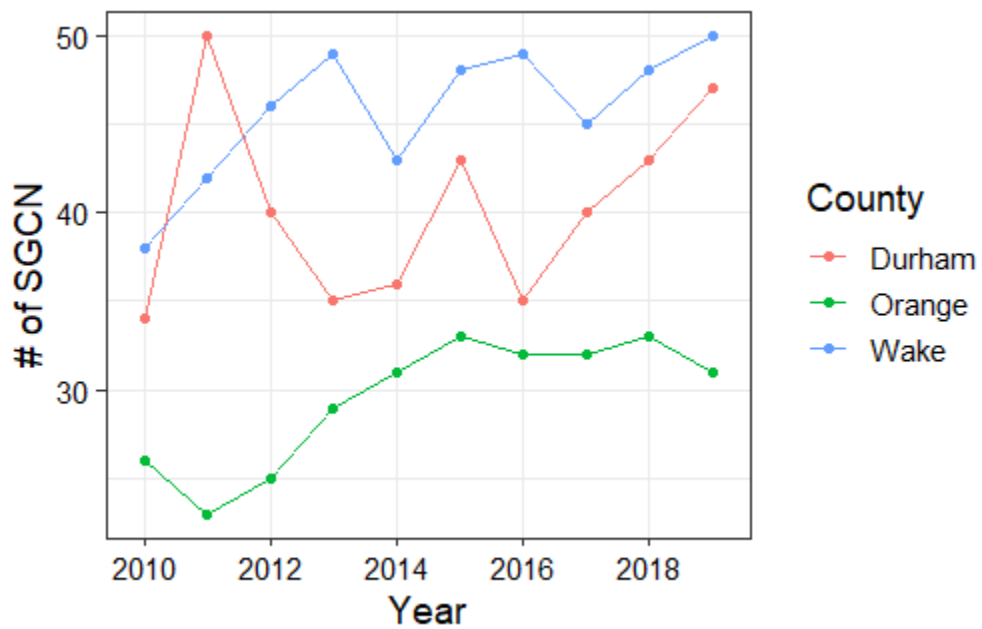
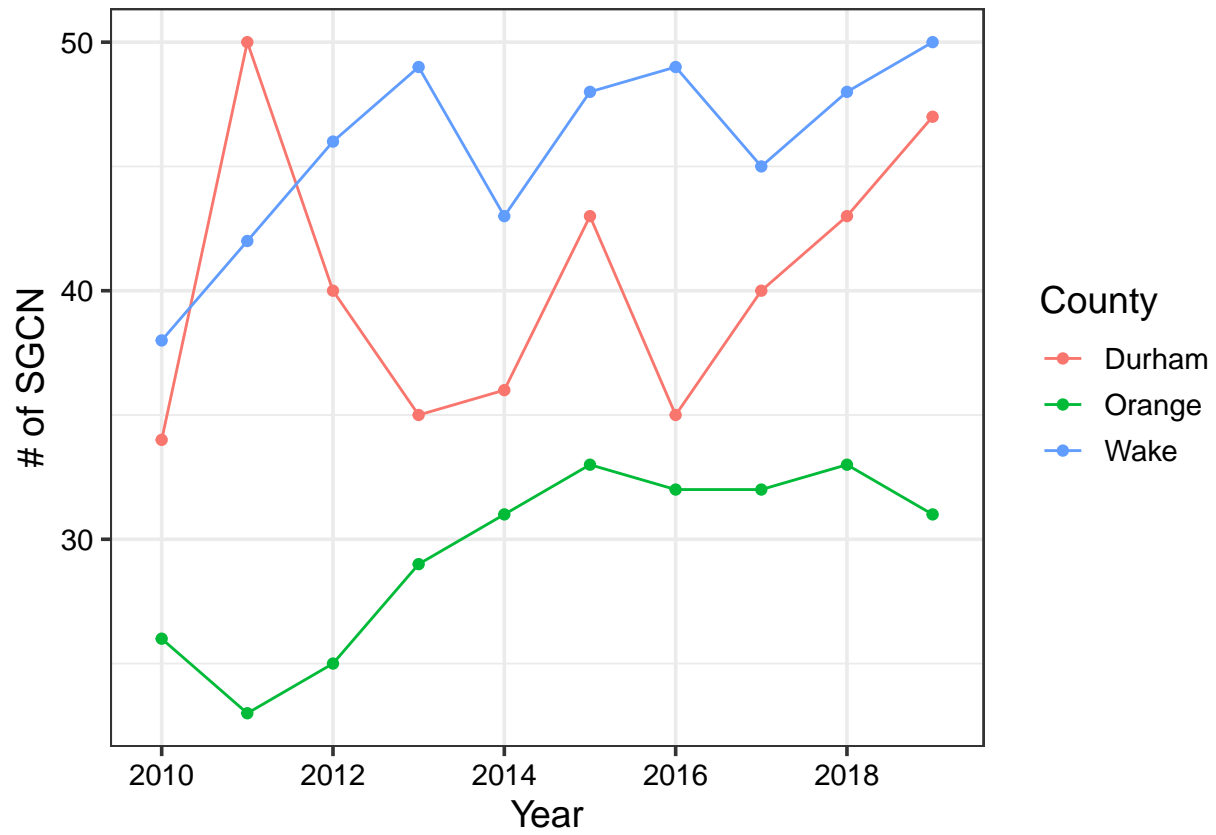


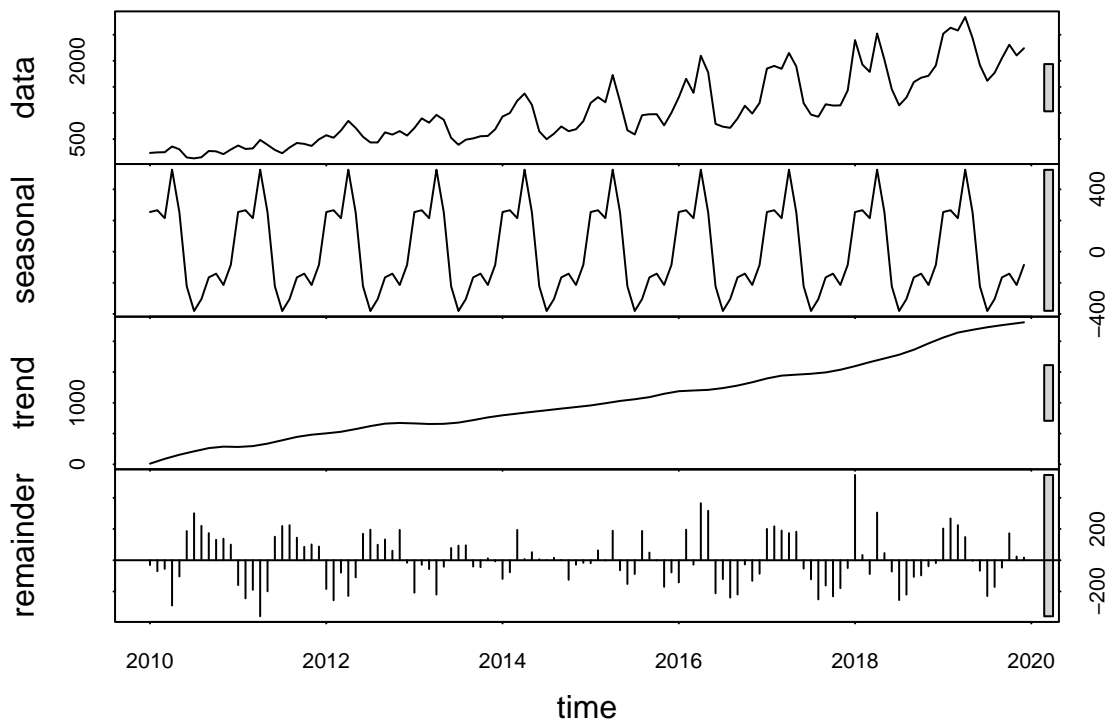
Figure 2: Figure 6. Number of SGCN observed in each county for each year of the study period.

4.4 Question 2: How did the popularity of eBird change in the Research Triangle across the 2010s?

A time series analysis of unique sampling events across all three counties combined showed both a seasonal trend as well as a strong positive monotonic trend (Figure 7). The seasonal trend in this time series is likely related to a higher frequency in birding activity during the spring migration and summer breeding season when weather conditions are pleasant. Our visual assessment of the decomposition was supported by a seasonal Mann-Kendall test that showed a significant positive trend in species richness across the period (score = 520, tau = 0.963, $p < 0.001$). This trend was also consistent within each county (Figures 8a-c). Additionally, seasonal Mann-Kendall tests showed that this monotonic trend was significant for Durham (score = 283, tau = 0.525, $p < 0.001$), Orange (score = 495, tau = 0.918, $p < 0.001$), and Wake counties (score = 514, tau = 0.952, $p < 0.001$).

```
total.event.counts <- read.csv("./Data/Processed/Total_EventCounts.csv")
total.event.counts <- total.event.counts %>%
  group_by(MY) %>%
  summarize(total_events = sum(value))

# Unique sampling events by month
Total.event.ts <- ts(total.event.counts$total_events, start = c(2010,1), frequency = 12)
Total.event.decomp <- stl(Total.event.ts, s.window = "periodic")
plot(Total.event.decomp)
```



```
Total.event.trend <- Kendall::SeasonalMannKendall(Total.event.ts)
Total.event.trend
```

```
## tau = 0.963, 2-sided pvalue =< 2.22e-16
```

```
summary(Total.event.trend)
```

```
## Score = 520 , Var(Score) = 1500
```

```
## denominator = 540
```

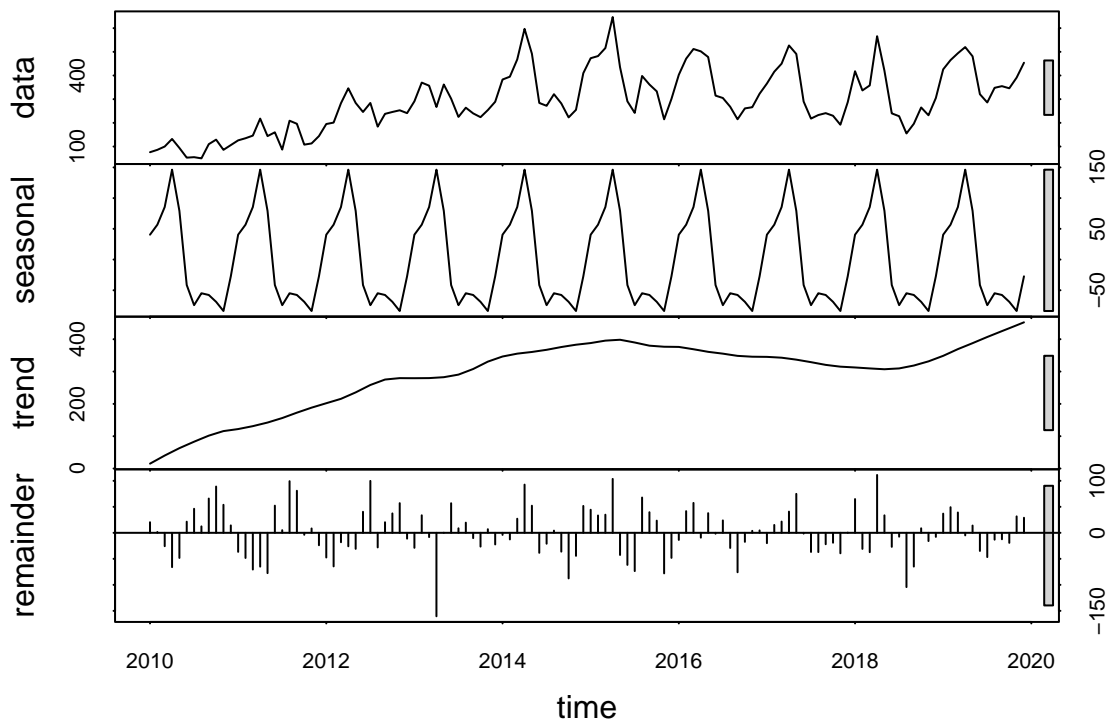
```
## tau = 0.963, 2-sided pvalue =< 2.22e-16
```

```
# DURHAM
```

```
Durham.event.ts <- ts(event.counts.Durham$event_total, start = c(2010,1), frequency = 12)
```

```
Durham.event.decomp <- stl(Durham.event.ts, s.window = "periodic")
```

```
plot(Durham.event.decomp)
```



```
Durham.event.trend <- Kendall::SeasonalMannKendall(Durham.event.ts)
Durham.event.trend
```

```
## tau = 0.525, 2-sided pvalue =2.6823e-13
```

```
summary(Durham.event.trend)
```

```
## Score = 283 , Var(Score) = 1499
```

```
## denominator = 539.4972
```

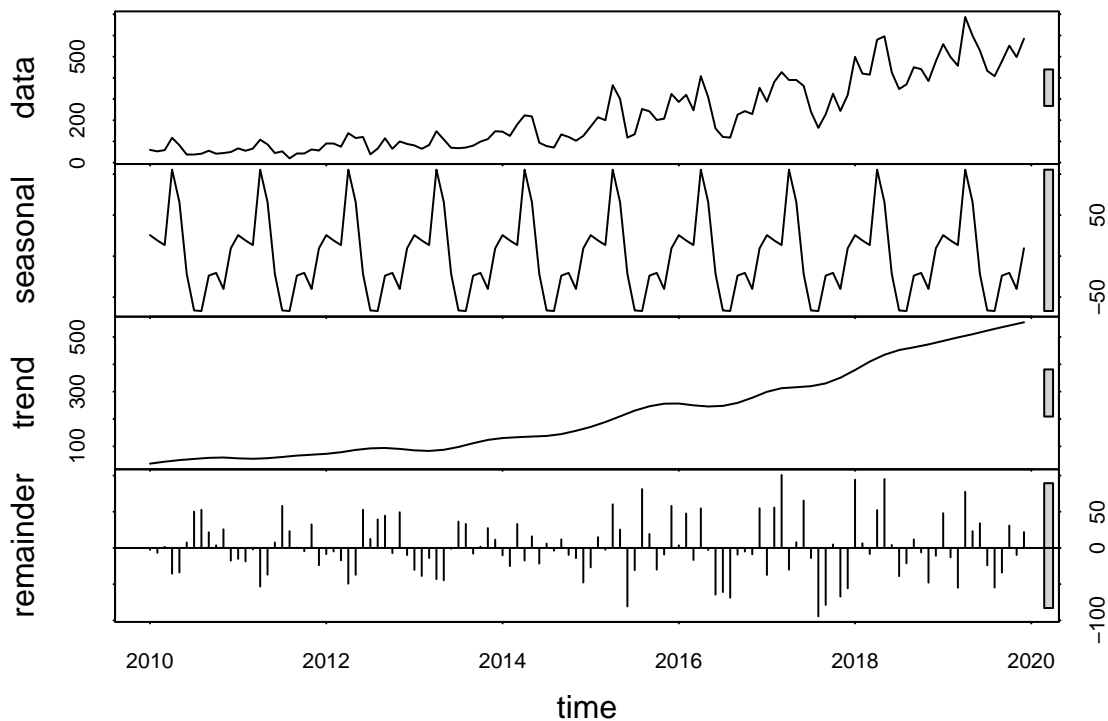
```
## tau = 0.525, 2-sided pvalue =2.6823e-13
```

```
# ORANGE
```

```
Orange.event.ts <- ts(event.counts.Orange$event_total, start = c(2010,1), frequency = 12)
```

```
Orange.event.decomp <- stl(Orange.event.ts, s.window = "periodic")
```

```
plot(Orange.event.decomp)
```



```
Orange.event.trend <- Kendall::SeasonalMannKendall(Orange.event.ts)
Orange.event.trend
```

```
## tau = 0.918, 2-sided pvalue =< 2.22e-16
```

```
summary(Orange.event.trend)
```

```
## Score = 495 , Var(Score) = 1499
```

```
## denominator = 539.4972
```

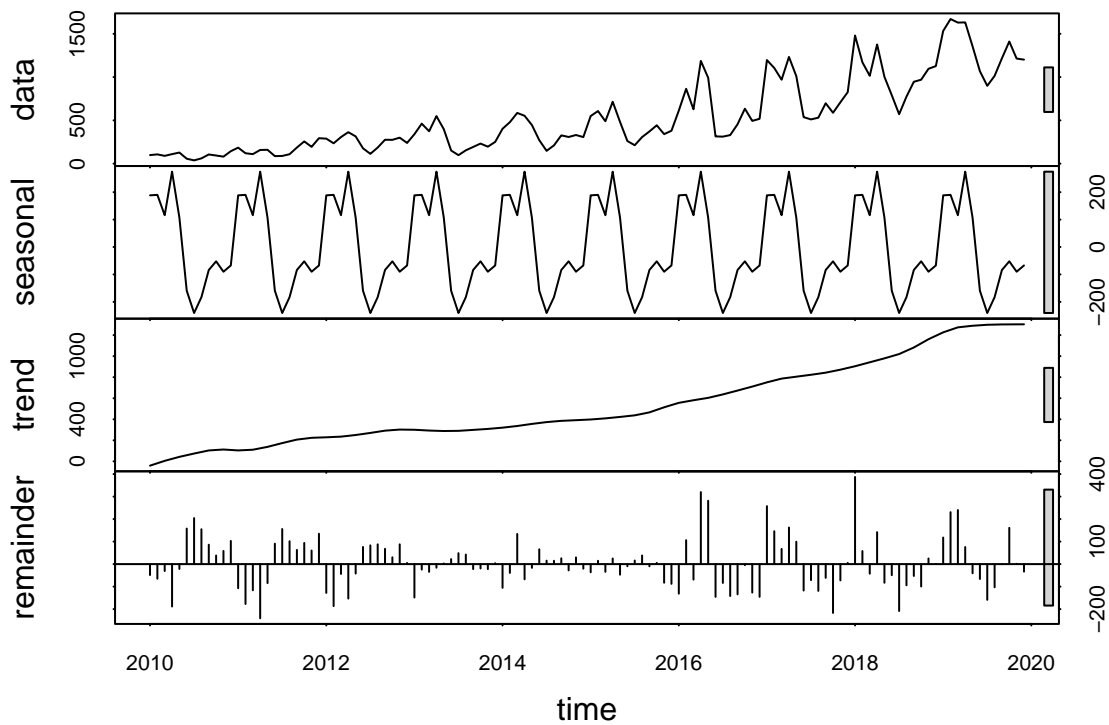
```
## tau = 0.918, 2-sided pvalue =< 2.22e-16
```

```
# WAKE
```

```
Wake.event.ts <- ts(event.counts.Wake$event_total, start = c(2010,1), frequency = 12)
```

```
Wake.event.decomp <- stl(Wake.event.ts, s.window = "periodic")
```

```
plot(Wake.event.decomp)
```



```
Wake.event.trend <- Kendall::SeasonalMannKendall(Wake.event.ts)
Wake.event.trend
```

```
## tau = 0.952, 2-sided pvalue =< 2.22e-16
```

```
summary(Wake.event.trend)
```

```
## Score = 514 , Var(Score) = 1500
## denominator = 540
## tau = 0.952, 2-sided pvalue =< 2.22e-16
```

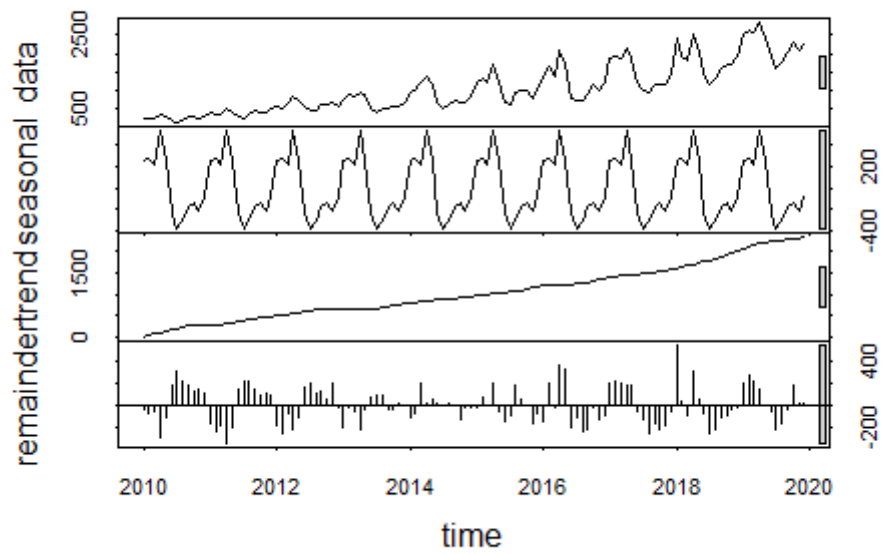
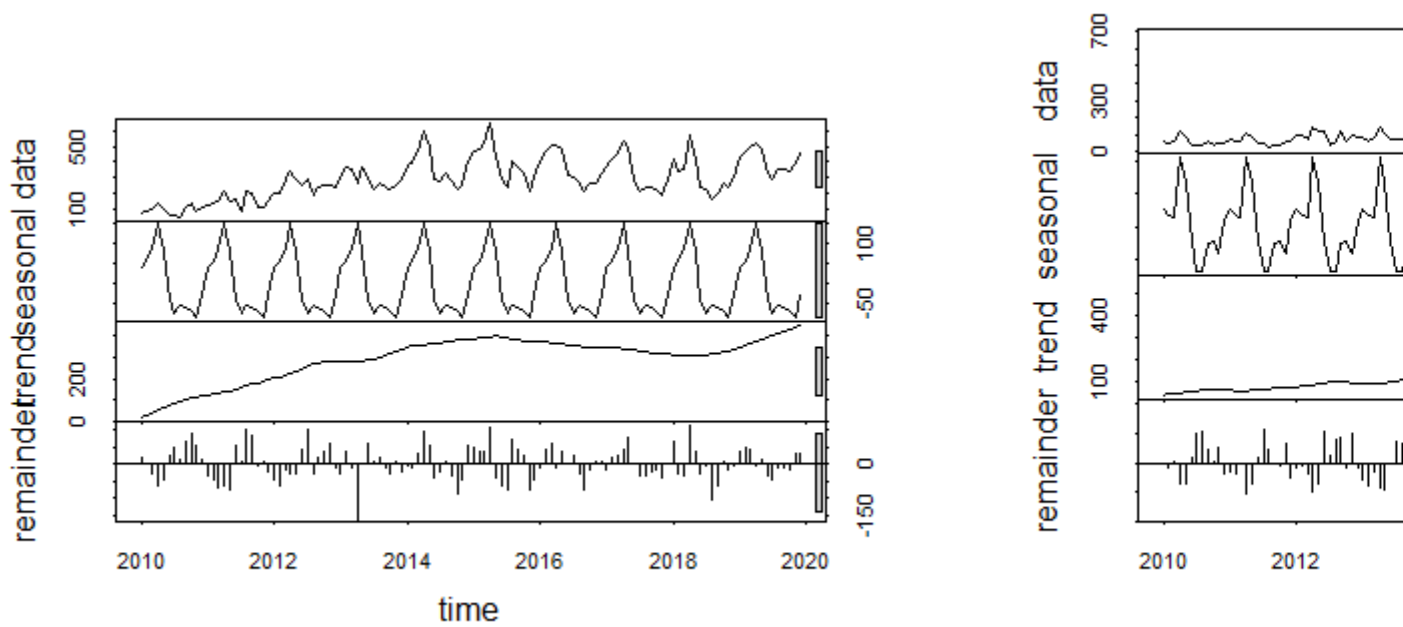
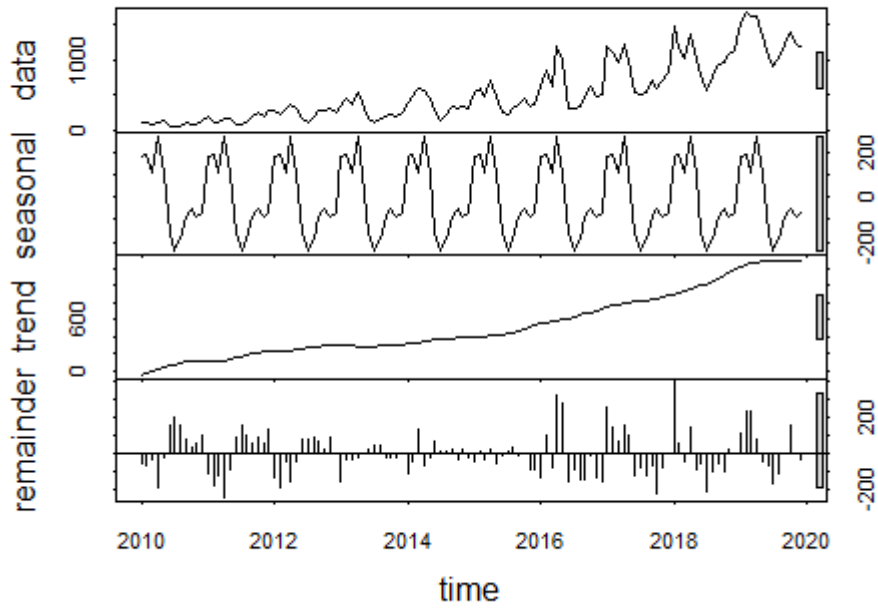


Figure 3: Figure 7. Time series decomposition for event count aggregated across all three counties from 2010 to 2019.





In order to complete these time series analyses in R, we utilized the `zoo` (Zeileis and Grothendeick 2005) and `tseries` (Trapletti and Hornik 2021) packages to construct the time series objects and the `trend` (Pohlert 2020) and `Kendall` (McLeod 2011) packages to perform the seasonal Mann-Kendall tests.

5 Summary and Conclusions

According to our analysis of eBird data, species richness and diversity increased in the Research Triangle between 2010 and 2019. This conclusion does not support our initial hypothesis that diversity of the Research Triangle’s bird population would have decreased due to human development. However, our other analyses invite the possibility that this increase in species richness may be a product of confounding variables.

Our time series analysis of unique sampling events across the decade showed that eBird popularity drastically increased from 2010 to 2019. If more people survey birds and upload their data, logically, this will lead to more species being observed. Therefore, based on our analyses it is not possible to say whether species richness increased, or how much of this increase was caused by changes in eBird usage. The conclusion that species richness increased is also not supported by the results of our SGCN analysis, which did not show any clear trend over time. If species diversity were increasing, it would be likely that the number of SGCN observed in the Research Triangle was also increasing. Because of this, we cannot make any definitive statements answering the question of how bird diversity in the Research Triangle changed during the 2010s.

Despite our lack of conclusive results, researching changes in bird populations across North America is incredibly important considering past literature that has shown the risks they face. In terms of future work related to this study, using a more consistent data source such as the US Geological Survey Breeding Bird Survey (USGS BBS), which is collected along pre-specified 25mi transects once a year, could help illustrate the changes we were looking for without the confounding variables brought on by the nature of open-source data. That being said, citizen science and datahubs such as eBird are still very valuable for conservation research and bolstering interest in environmental protection among the wider public.

6 References

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