

# Analyzing passerine response to restoration on Lagoon Island, UCSB

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## Introduction: Description of Data and Project

Efforts to remove invasive grasses and restore coastal sage scrub and oak woodlands are widespread throughout California. The goal of most of these restoration projects is to improve and restore ecosystem structure and functioning under the assumption that doing so will support populations of native wildlife (Gardali et al., 2006). Unfortunately, the impact of these restoration projects on local species populations is often unknown (Brawn et al., 2006). This makes it challenging to assess whether a restoration initiative has been successful. Restoration projects benefit from studies that evaluate the impacts of restoration efforts on local wildlife populations because findings from these studies can inform strategies to refine future restoration efforts (Ruiz-Jaen et al., 2005). Furthermore, providing tangible evidence of restoration success can be beneficial for securing funding for future restoration initiatives.

The Cheadle Center for Biodiversity and Ecological Restoration (CCBER) has conducted oak woodland and coastal sage scrub restoration activities on Lagoon Island on the campus of the University of California, Santa Barbara intermittently since 2005. Research has suggested that restoration activities in small patches of habitat, such as those on Lagoon Island, can increase reproductive success and breeding density of savannah and woodland birds (Brawn et al., 2006). In this analysis, we evaluate the impact of restoration efforts on Lagoon Island for two species of local songbirds: Song Sparrows and the California Towhee.

## Main Findings

- Population growth rate for Song Sparrows on Lagoon Island was positive for the 5 years following to native plant restoration, but negative for the subsequent 5 years, suggesting a possible short term benefit resulting from the restoration
- California Towhee populations remained somewhat stable, with a slightly negative growth rate post-restoration
- Overall, our statistical testing did not reveal that there was a significant difference between the growth rates of local Song Sparrow and California Towhee populations and the growth rates of the larger state populations. We are therefore not able to confidently attribute any trends we find in the local population to specific management actions, as they may simply reflect overall statewide trends for both these species.

## A. Data Cleaning

### CCBER

```

birds_all$species <- factor(birds_all$species)

###keeping original data - this is the one you need for modelling. this code just cleans up the month c

birds_all_clean <- birds_all %>%
  mutate(
    date = paste(day, month, year),
    date = dmy(date)
  ) %>%
  dplyr::select(-month, -day) %>%
  mutate(
    month = month(date, label = TRUE)
  ) %>%
  drop_na(month) %>%
  filter(year != 2017) %>%
  as.data.frame()

####wrangling data for nice graphs

#break out and then parse dates - this will make graphing nicer
data_long <- melt(birds_all,
  # ID variables - all the variables to keep but not split apart on
  id.vars=c("day", "month", "year", "species"),
  # The source columns
  measure.vars=c("lagoon_island_zone_summary"),
  # Name of the destination column that will identify the original
  # column that the measurement came from
  variable.name="location",
  value.name="count"
) %>%
  mutate(
    species = str_to_lower(species),
    date = paste(day, month, year),
    date = dmy(date)
  ) %>%
  dplyr::select(-month, -day) %>%
  mutate(
    month = month(date, label = FALSE)
  ) %>%
  mutate(species = case_when(
    species %in% "western scrub-jay" ~ "california scrub-jay",
    TRUE ~ species
  ))

#further wrangling if we want each line to represent one bird, also change the name of the scrub jay to
data_tidy<- uncount(data_long, weights = count) %>%
  mutate(species = str_to_lower(species)) %>%
  mutate(species = case_when(
    species %in% "western scrub-jay" ~ "california scrub-jay",
    TRUE ~ species
  ))

```

```

#filter by the species we are interested in, and up to 2016 since that is what best matches the bbs

#tidy version (missing zero counts)
bird_species_tidy <- data_tidy %>%
  filter(species == "california scrub-jay" | species == "common yellowthroat" | species == "song sparrow")

#version with counts
bird_species_count <- data_long %>%
  filter(species == "california scrub-jay" | species == "common yellowthroat" | species == "song sparrow")

```

## Breeding Bird Survey

```

#change the id codes into species names
bbs_clean <- bbs_all %>%
  mutate(
    species = case_when(
      aou %in% 5190 ~ "house finch",
      aou %in% 5540 ~ "white-crowned sparrow",
      aou %in% 5810 ~ "song sparrow",
      aou %in% 5911 ~ "california towhee",
      aou %in% 6810 ~ "common yellowthroat",
      aou %in% 7190 ~ "bewick's wren",
      aou %in% 7510 ~ "blue-gray gnatcatcher",
      aou %in% 4812 ~ "california scrub jay"
    )
  ) %>%
  select(-aou, -country)

```

## Summary graphs - CCBER

```

#create dfs that summarize yearly and monthly totals
bird_summary_year <- bird_species_tidy %>%
  select(-location) %>%
  #filter(species != "house finch") %>%
  filter(year != 2017) %>%
  group_by(year, species) %>%
  summarize(
    count = length(species)
  )

bird_summary_month_yr <- bird_species_tidy %>%
  select(-location) %>%
  group_by(month, year, species) %>%
  summarize(
    count = length(species)
  )

#change to sparrow bewicks only
sparrow_towhee_only <- bird_species_tidy %>%
  select(-location) %>%
  filter(species == "song sparrow" | species == "california towhee") %>%

```

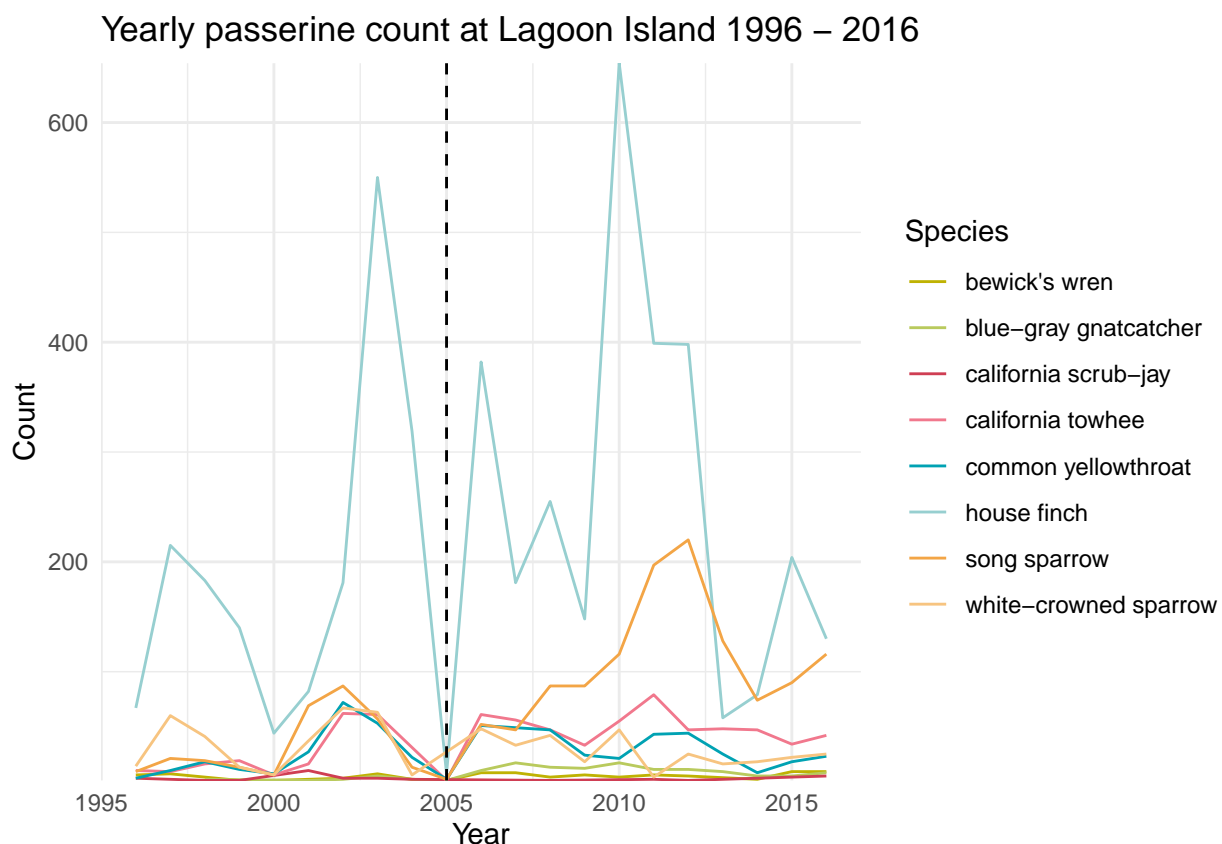
```

group_by(year, species) %>%
  summarize(
    count = length(species)
  )

#yearly abundance graph with all the birds
yearly_abundance_graph <- ggplot(bird_summary_year, aes(x = year, y = count, group = species))+
  geom_line(aes(color = species))+
  theme_minimal()+
  labs(x = "Year", y = "Count", title = "Yearly passerine count at Lagoon Island 1996 - 2016", color = "species")+
  scale_y_continuous(expand = c(0,0))+
  geom_vline(xintercept = 2005, linetype = "dashed")+
  scale_color_paletteer_d("ggthemes::Summer")

yearly_abundance_graph

```



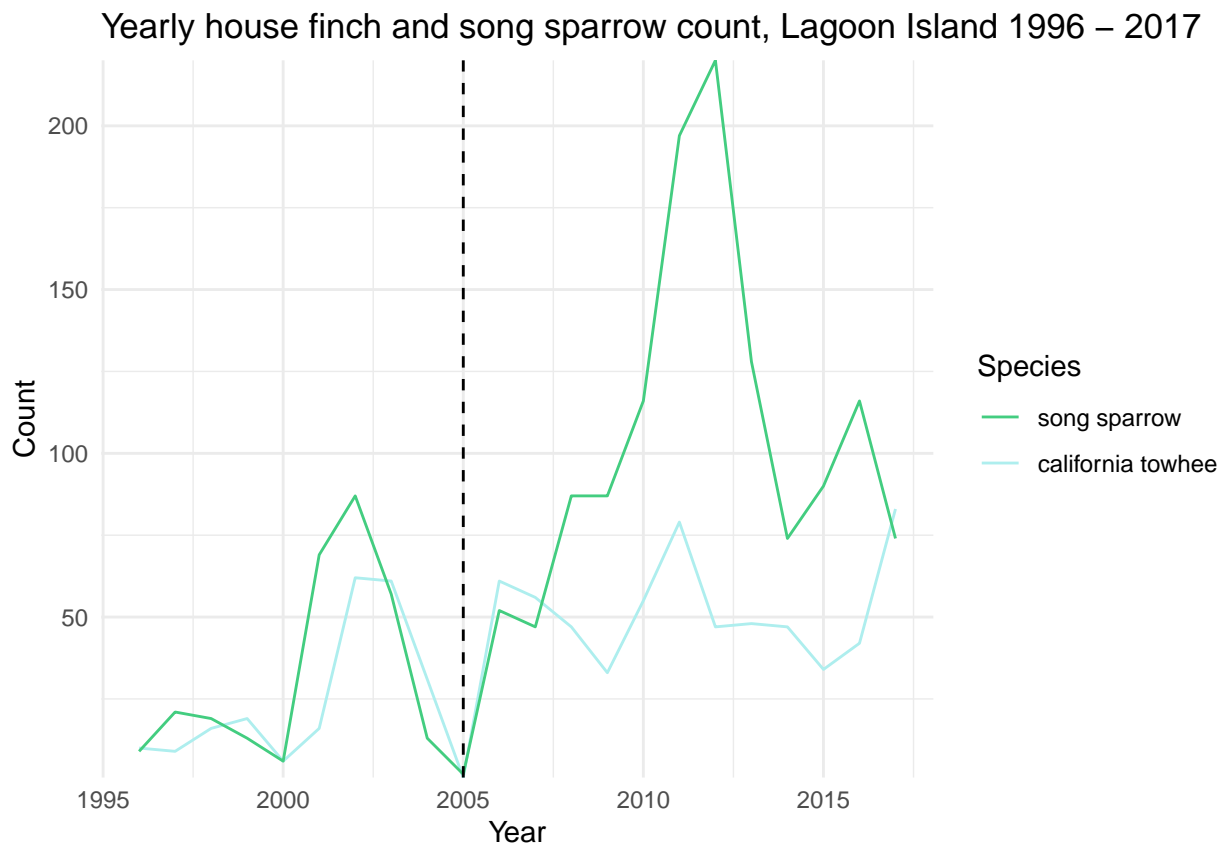
```

ggsave("count_all_yr.png", width = 6, height = 3, units = "in")

#just sparrow and finch
sparrow_towhee_gg <- ggplot(sparrow_towhee_only, aes(x = year, y = count, group = species)) +
  geom_line(aes(color = species))+
  theme_minimal()+
  labs(x = "Year", y = "Count", title = "Yearly house finch and song sparrow count, Lagoon Island 1996 - 2016", color = "species")+
  scale_y_continuous(expand = c(0,0))+
  geom_vline(xintercept = 2005, linetype = "dashed")+
  scale_color_manual(breaks = c("song sparrow", "california towhee"), values = c("paleturquoise2", "seagreen4"))

```

```
sparrow_towhee_gg
```



## Analysis: Song Sparrow

### CCBER data

#### Model

We fit a GAM on our observation data, and then used that to predict yearly abundance, in July, for the species.

```
#go back to data read in `birds_all_clean` - pre major wrangling  
#pick a species
```

```
birds_ssparrow <- birds_all_clean %>%  
  filter(species == "Song Sparrow")
```

```
#run GAM on CCBER data
```

```
ccber_ssparrow_model <- mgcv::gam(lagoon_island_zone_summary ~ s(year) + month, family = poisson, data = birds_ssparrow)  
  
summary(ccber_ssparrow_model)
```

```
#create new data frame to use with the model  
newd <- data.frame(year = 1996:2016, month = "Jul")
```

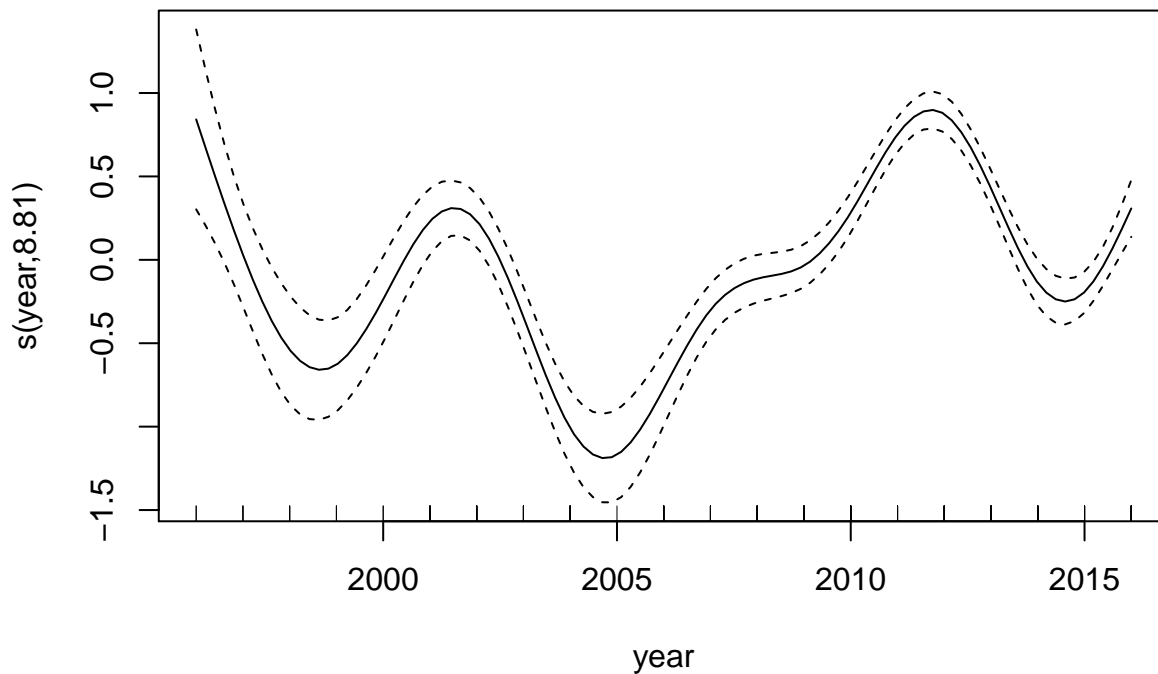
```
#predict abundance using new data, type predict shows actual abundance instead of log

ssparrow_predict <- predict.gam(ccber_ssparrow_model, newd, type="response")

ssparrow_predict

#notes /issues
#didn't month because I couldn't figure it out
#how can we ask the models for integers

plot(ccber_ssparrow_model)
```



```
ssparrow_test <- lm(lagoon_island_zone_summary~year+ month, data = birds_ssparrow)

#summary(ssparrow_test)
```

Tidy model and visualize

```
ccber_ssparrow_tidy <- broom::tidy(ccber_ssparrow_model) #this didn't end up being necessary

#we want the actual counts per year for song sparrows, so use the `birds_summary_year` df

ssparrow_by_year <- bird_summary_month_yr %>%
  filter(species == "song sparrow") %>%
  filter(month == 7) %>%
  filter(year != 2017)

#we need data for 1996 - 2000, going to create a dataframe with count = 0

month <- rep(7,7)
year <- c(1996, 1997, 1998, 1999, 2000, 2004, 2005)
species <- c("song sparrow", "song sparrow", "song sparrow", "song sparrow", "song sparrow", "song sparrow", "song sparrow")
count <- rep(0,7)
```

```

#make into dataframe
missing_ss <- data.frame(month, year, species, count)

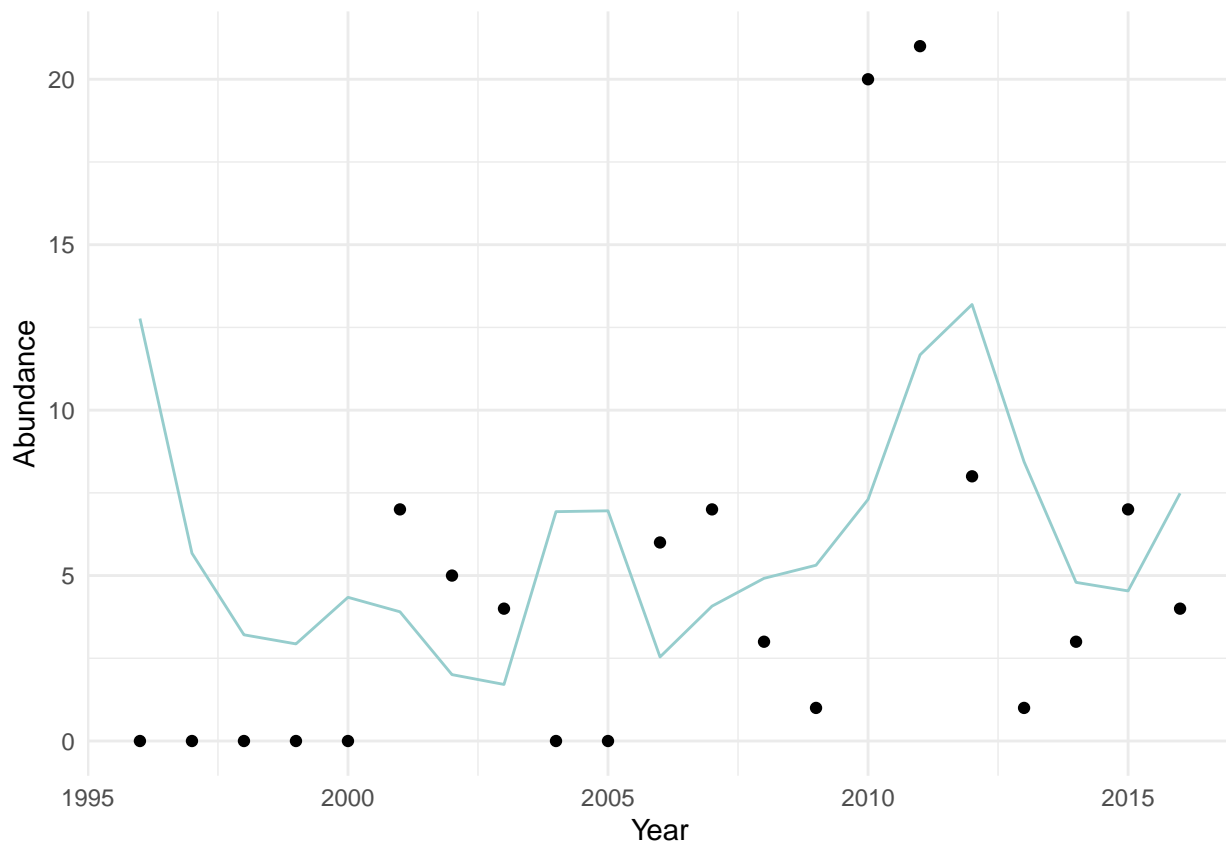
ssparrow_jul <- bind_rows(missing_ss, ssparrow_by_year)

#bind obs and predictions
ssparrow_complete <- data.frame(ssparrow_jul, ssparrow_predict)

ssparrow <- ggplot(data = ssparrow_complete, aes(x = year, y = count)) +
  geom_point()+
  geom_line(aes(x = year, y = ssparrow_predict), color = "paleturquoise3") +
  theme_minimal()+
  labs(x = "Year", y = "Abundance")

ssparrow

```



```

#ggsave("count_v_predict.png", width = 6, height = 3, units = "in")

```

### Calculate growth rates

```

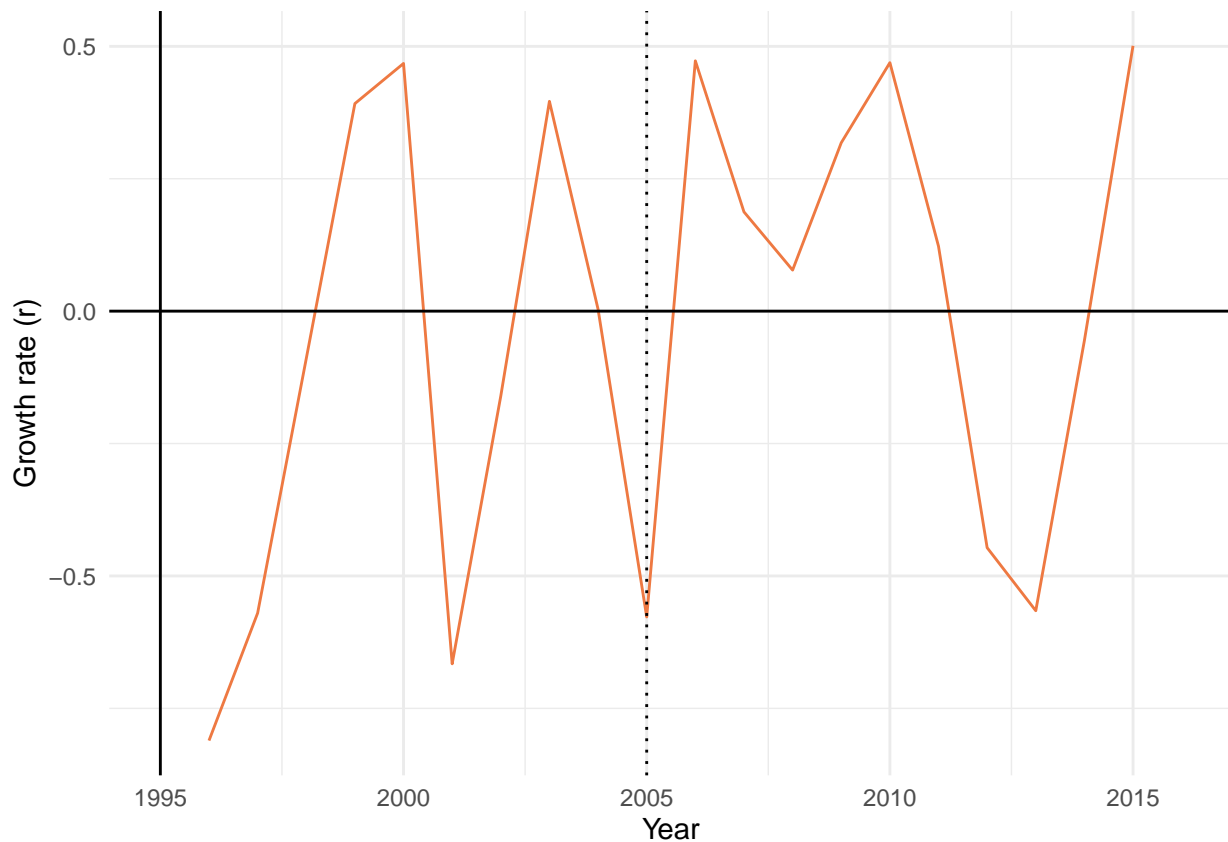
#create a new column in sparrows complete that calculates r based on the year before using the log equation
ssparrow_gr <- ssparrow_complete %>%
  mutate(
    r = log(lead(ssparrow_predict)/ssparrow_predict)
  )

```

*#graph - what should we test?*

```
ssparrow_r <- ggplot(ssparrow_gr, aes(x = year, y = r))+  
  geom_line(color = "sienna2")+  
  theme_minimal()+  
  geom_hline(yintercept = 0)+  
  geom_vline(xintercept = 1995)+  
  geom_vline(xintercept = 2005, linetype = "dotted")+  
  labs(x = "Year", y = "Growth rate (r)")
```

ssparrow\_r



```
ggsave("ssparrow_gr_ccber.png", width = 6, height = 3, units = "in")
```

*#find averages - I didn't make a new data frame for each test I just changed the names and re-ran this*

```
ss_ccber_before <- ssparrow_gr %>%  
  filter(year < 2006) %>%  
  filter(year != 2016)
```

```
ss_avg_bef_ccber <- mean(ss_ccber_before$r) #this always stays the same  
sd_bef <- sd(ss_ccber_before$r) # feed in a vector  
se_bef <- sd_bef/sqrt(nrow(ss_ccber_before)) #calculate se
```

```
ss_ccber_after <- ssparrow_gr %>%
```



```

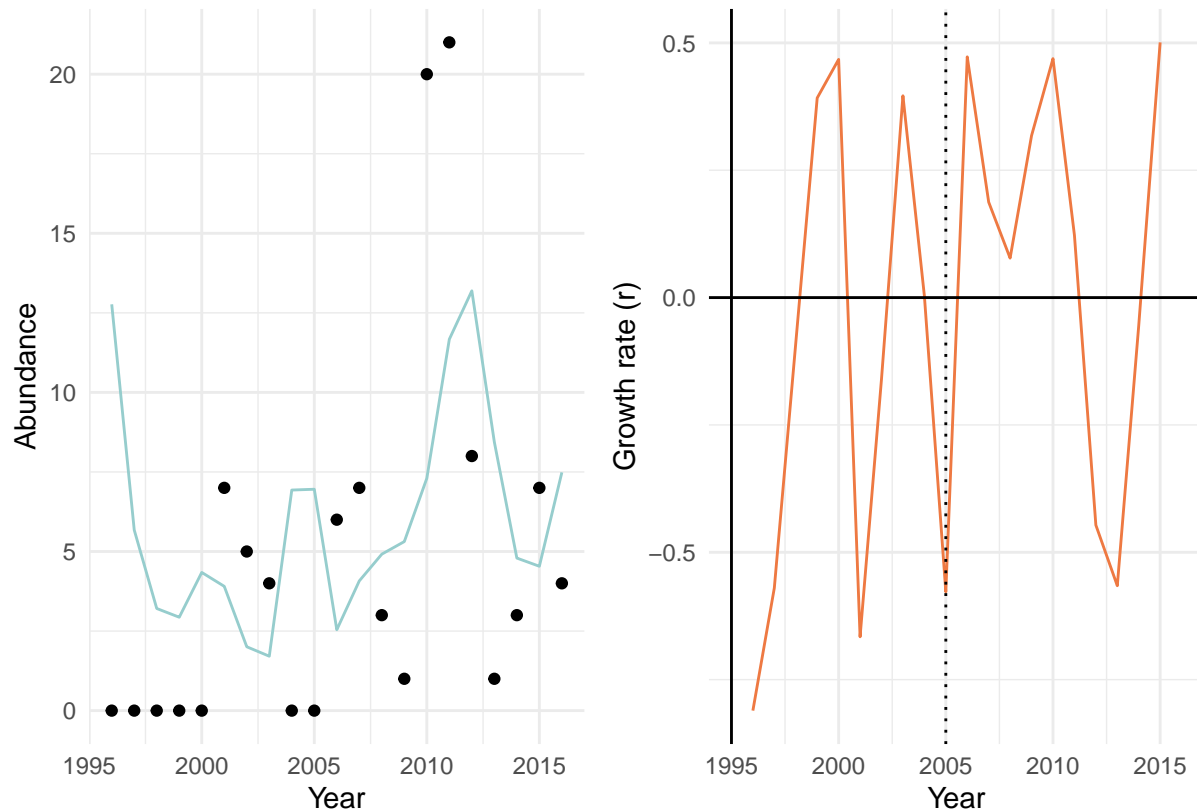
filter(year > 2010) %>%
filter(year != 2016)

ss_avg_after_5 <- mean(ss_ccber_after$r)
sd_after_5<- sd(ss_ccber_after$r) # feed in a vector
se_after_5<- sd_bef/sqrt(nrow(ss_ccber_after))

```

Combine graphs using patchwork - just for fun

```
ssparrow + ssparrow_r
```



## Breeding Bird Survey

We repeated the process above with data from the breeding bird survey. This will allow us to compare our findings from Lagoon Island to trends in the overall populations, helping us better understand if any changes we see are indeed a result of restoration or are reflecting a larger trend.

### Model

```

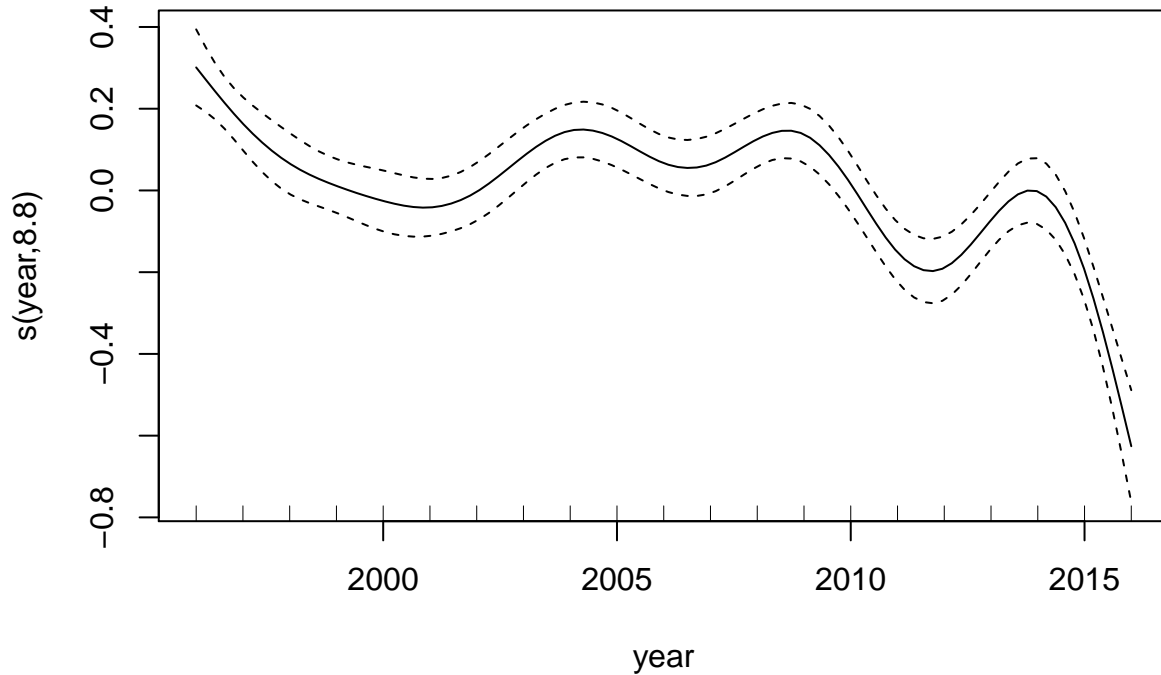
#filter out song sparrow

bbs_ssparrow <- bbs_clean %>%
  filter(species == "song sparrow") %>%
  group_by(year) %>%
  summarize(
    species_total = sum(species_total)
  )

#run GAM

```

```
bbs_ssparrow_model <- mgcv::gam(species_total ~ s(year), family = poisson, data = bbs_ssparrow)
summary(bbs_ssparrow_model)
plot(bbs_ssparrow_model)
```



```
#create new data frame for predictions
newd_bbs <- data.frame(year = 1996:2016)

#predict abundance using new data

ssparrow_predict_bbs <- predict.gam(bbs_ssparrow_model, newd_bbs, type="response")

ssparrow_predict_bbs
```

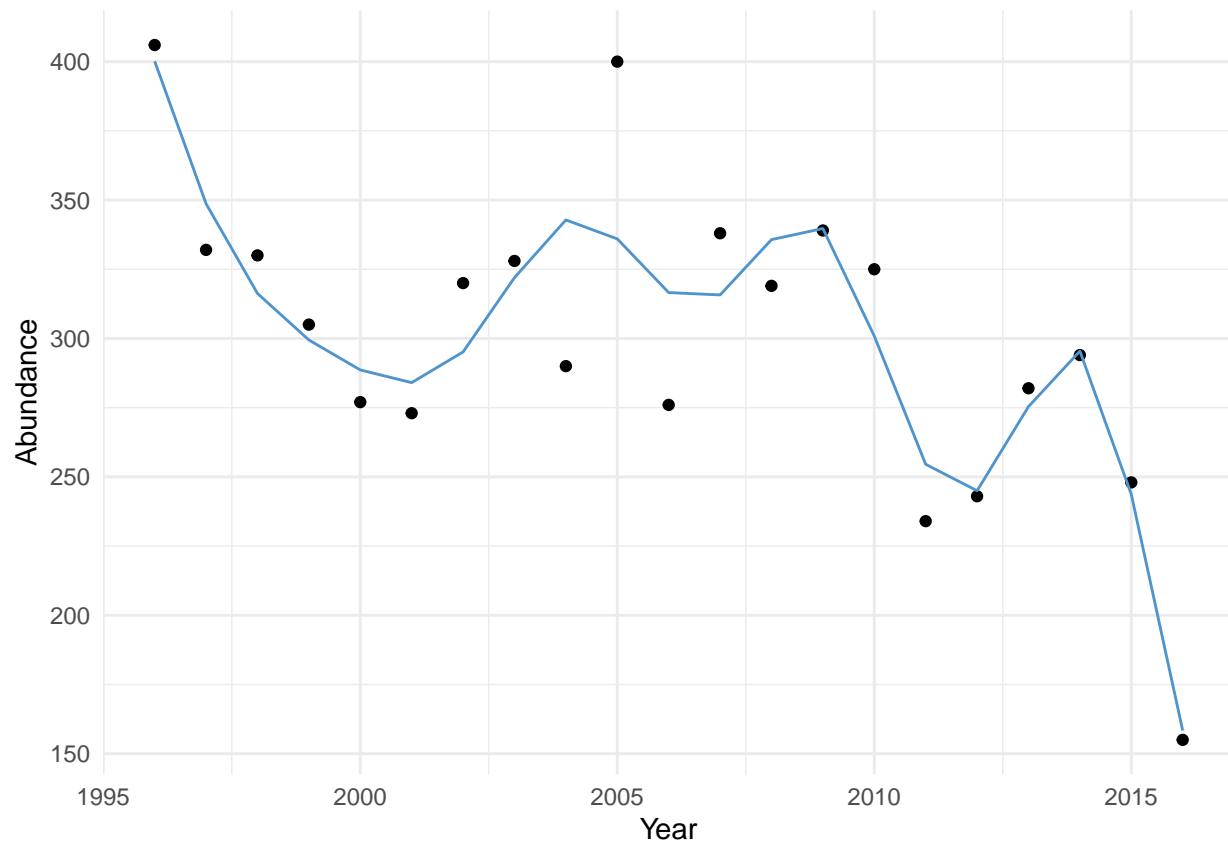
Join observations and predictions

```
ssparrow_complete_bbs <- data.frame(bbs_ssparrow, ssparrow_predict_bbs)

ssparrow_gr_bbs <- ssparrow_complete_bbs %>%
  mutate(
    r = log(lead(ssparrow_predict_bbs)/ssparrow_predict_bbs)
  )
```

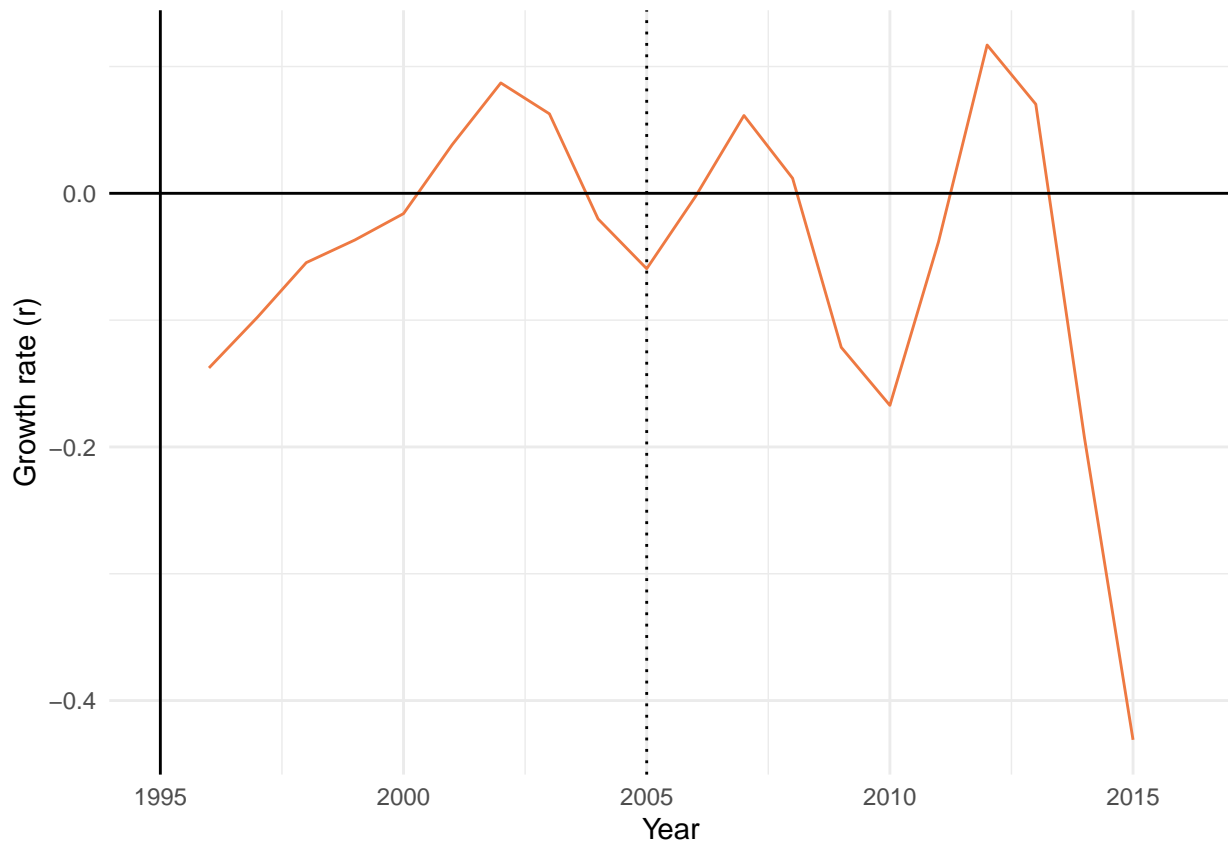
```
#note - this graph of the model prediction + observation for BBS is all the data because it is compiled
ssparrow_bbs <- ggplot(data = ssparrow_complete_bbs, aes(x = year, y = species_total)) +
  geom_point()+
  geom_line(aes(x = year, y = ssparrow_predict_bbs), color = "steelblue3") +
  theme_minimal()+
  labs(x = "Year", y = "Abundance")

ssparrow_bbs
```



```
ggsave("count_v_predict_bbs.png", width = 6, height = 3, units = "in")
```

```
ssparrow_bbs_r <- ggplot(ssparrow_gr_bbs, aes(x = year, y = r))+  
  geom_line(color = "sienna2")+  
  theme_minimal()+  
  geom_hline(yintercept = 0)+  
  geom_vline(xintercept = 1995)+  
  geom_vline(xintercept = 2005, linetype = "dotted")+  
  labs(x = "Year", y = "Growth rate (r)")  
  
ssparrow_bbs_r
```



```
ggsave("ssparrow_bbs_growthrate.png", width = 6, height = 3, units = "in")
```

### Calculate growth rates

```
#df
ss_bbs_before <- ssparrow_gr_bbs %>%
  filter(year < 2006) %>%
  filter(year != 2016)
#numbers
ss_bbs_bef <- mean(ss_bbs_before$r)
sd_bbs_bef<- sd(ss_bbs_before$r) # feed in a vector
se_bbs_bef <- sd_bef/sqrt(nrow(ss_bbs_before)) #calculate se

#df
ss_bbs_after <- ssparrow_gr_bbs %>%
  filter(year > 2010) %>%
  filter(year != 2016)
#numbers
ss_bbs_after_5 <- mean(ss_bbs_after$r)
sd_bbs_after_5<- sd(ss_bbs_after$r) # feed in a vector
se_bbs_after_5 <- sd_bef/sqrt(nrow(ss_bbs_after))
```

### Test if difference between growth rates for CCBER and BBS is significant

*#three tests: before, after 2005, after 2010.*

```
t.test(ss_ccber_before$r, ss_bbs_before$r, conf.level = 0.95, paired = TRUE)
```

```
##
## Paired t-test
##
## data: ss_ccber_before$r and ss_bbs_before$r
## t = -0.90234, df = 9, p-value = 0.3904
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.4840278 0.2079918
## sample estimates:
## mean of the differences
## -0.138018

t.test(ss_ccber_after$r, ss_bbs_after$r, conf.level = 0.95, paired = TRUE)

##
## Paired t-test
##
## data: ss_ccber_after$r and ss_bbs_after$r
## t = 0.021413, df = 4, p-value = 0.9839
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.7877922 0.8000379
## sample estimates:
## mean of the differences
## 0.006122855
```

## Analysis: California towhee

We repeated the process for a second species, the California Towhee. Again, we used observation data to estimate local abundances and growth rates, and compared that to background data for California Towhee's across the state of California from the breeding bird survey.

### CCBER

#### Model

```
#Go back to data read in `birds_all_clean` - pre major wrangling
#Pick a species - California towhee

birds_ctowhee <- birds_all_clean %>%
  filter(species == "California Towhee")

#Run GAM on CCBER data

ccber_ctowhee_model <- mgcv::gam(lagoon_island_zone_summary ~ s(year) + month, family = poisson, data =
summary(ccber_ctowhee_model)

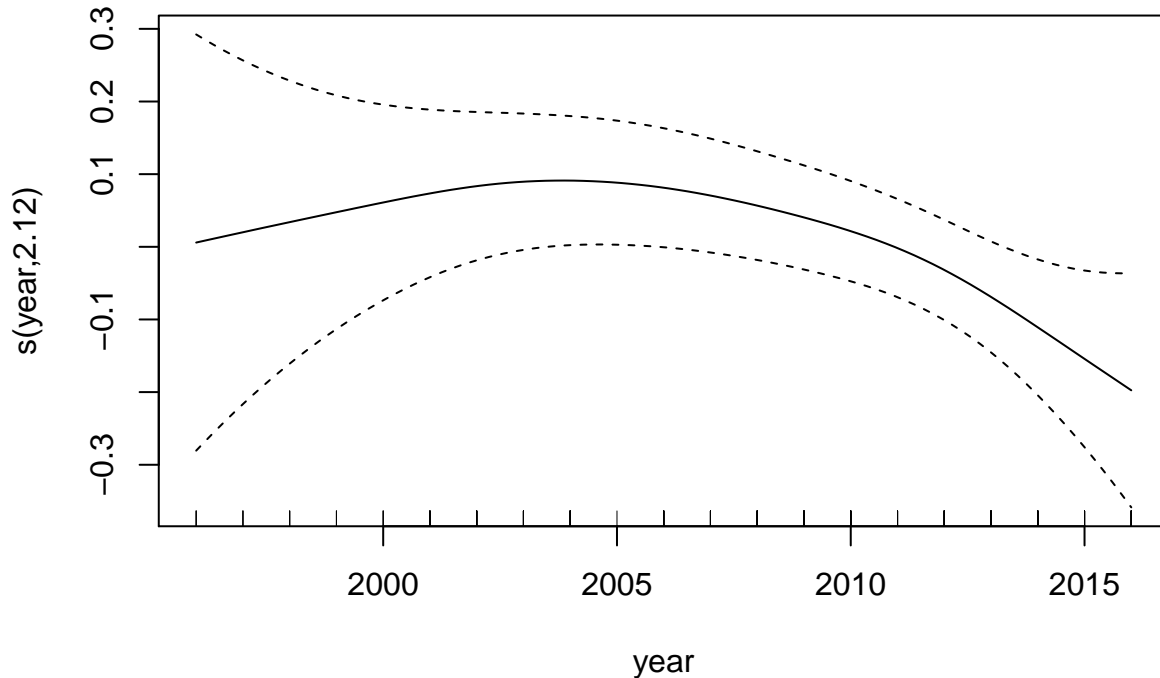
#create new data frame to use with the model
newd <- data.frame(year = 1996:2016, month = "Jul")

#predict abundance using new data, type predict shows actual abundance instead of log

ctowhee_predict <- predict.gam(ccber_ctowhee_model, newd, type="response")
```

```
ctowhee_predict
```

```
plot(ccber_ctowhee_model)
```



```
ctowhee_test <- lm(lagoon_island_zone_summary~year+ month, data = birds_ctowhee)
summary(ctowhee_test)
```

### Tidy model and visualize

```
ccber_ctowhee_tidy <- broom::tidy(ccber_ctowhee_model) #this didn't end up being necessary
```

```
#we want the actual counts per year for towhees, so use the `birds_summary_year` df
```

```
ctowhee_by_year <- bird_summary_month_yr %>%
  filter(species == "california towhee") %>%
  filter(month == 7) %>%
  filter(year != 2017)
```

```
#we need data for 1996, 97, 98, 00, 01, and 05 going to create a dataframe with count = 0
```

```
#this process needs to be adjusted for every species since the missing years will be different for each
```

```
month <- rep(6,6)
```

```
year <- c(1996, 1997, 1998, 2000, 2001, 2005)
```

```
species <- c("california towhee", "california towhee", "california towhee", "california towhee", "california towhee", "california towhee")
```

```
count <- rep(0,6)
```

```
#make into dataframe
```

```
missing_ct <- data.frame(month, year, species, count)
```

```
ctowhee_jul <- bind_rows(missing_ct, ctowhee_by_year)
```

```
#bind obs and predictions
```

```
ctowhee_complete <- data.frame(ctowhee_jul, ctowhee_predict)
```

```
ctowhee <- ggplot(data = ctowhee_complete, aes(x = year, y = count)) +
```

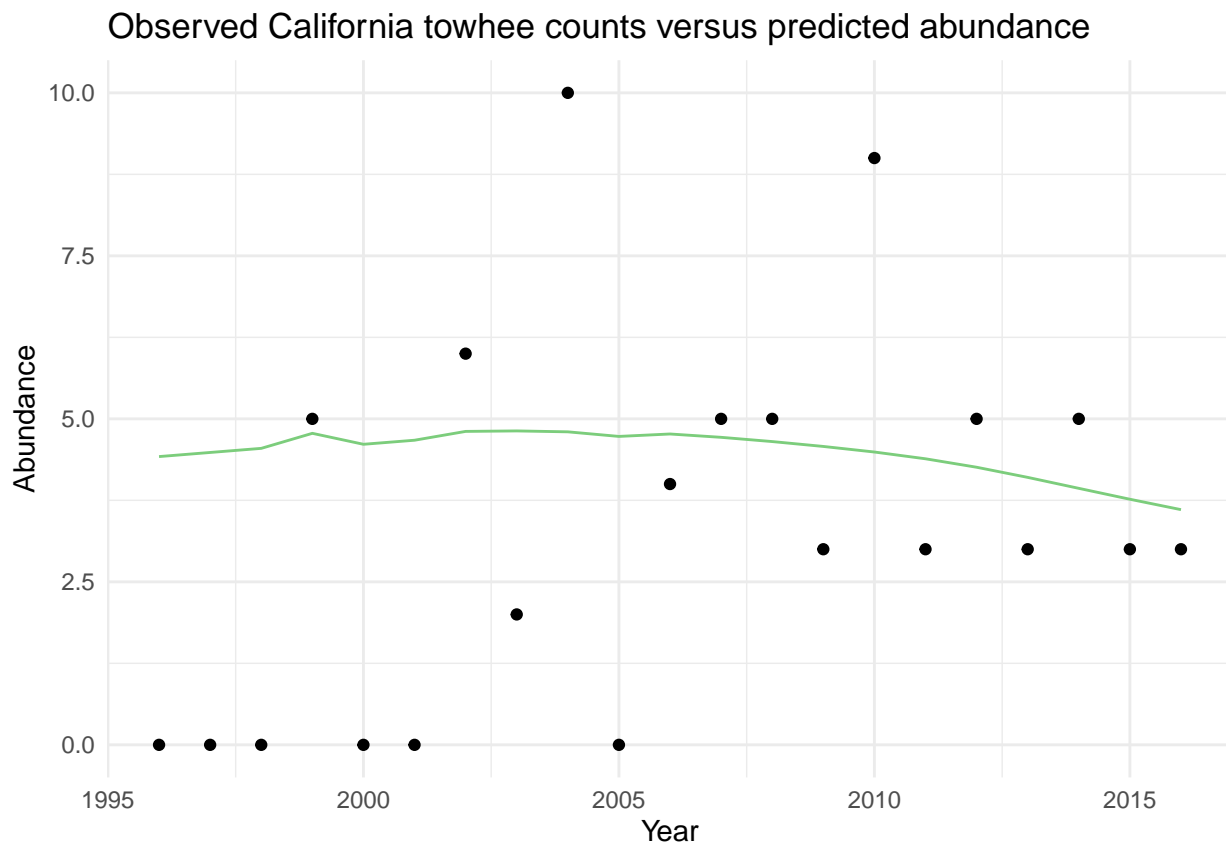
```
  geom_point() +
```

```
  geom_line(aes(x = year, y = ctowhee_predict), color = "palegreen3") +
```

```
  theme_minimal() +
```

```
  labs(x = "Year", y = "Abundance", title="Observed California towhee counts versus predicted abundance")
```

```
ctowhee
```



```
ggsave("count_v_predict.png", width = 6, height = 3, units = "in")
```

### Calculate growth rates

```
#create a new column in ctowhee complete that calculates r based on the year before using the log equation
```

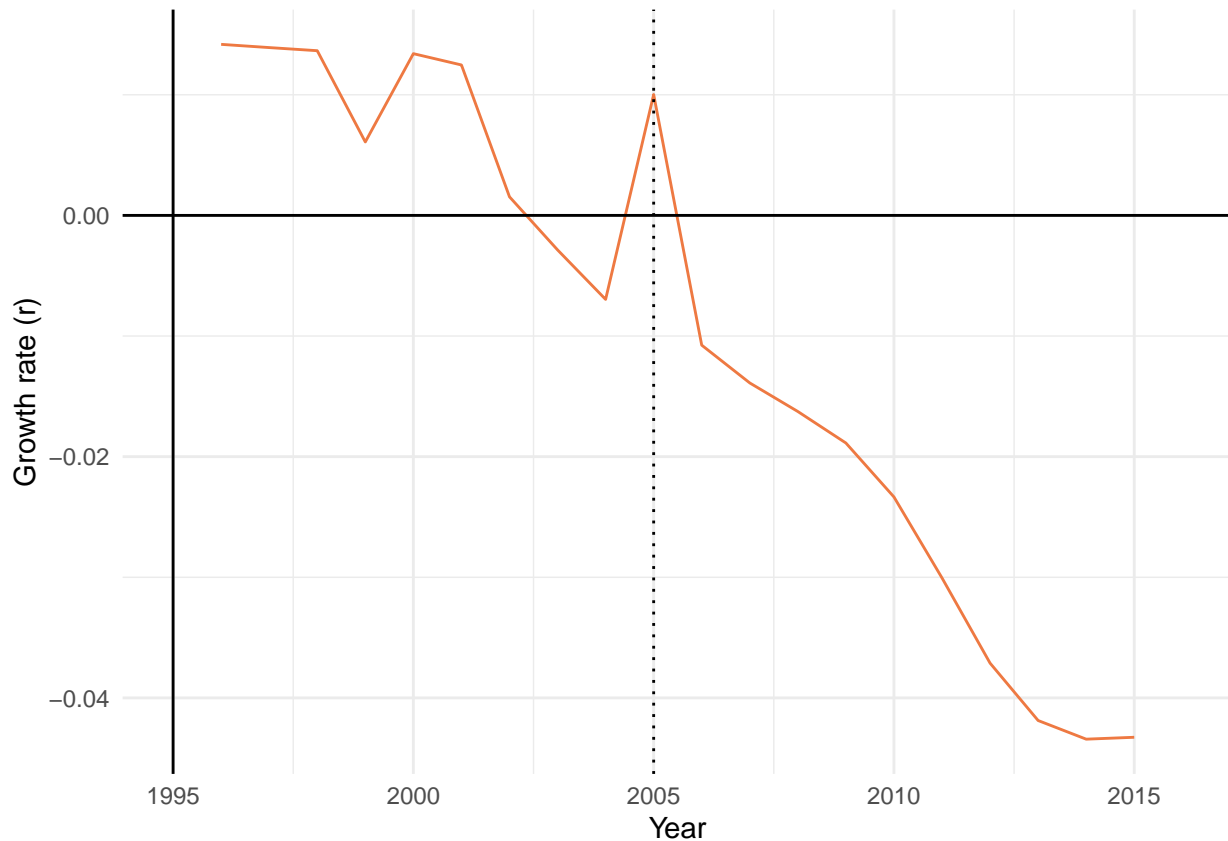
```
ctowhee_gr <- ctowhee_complete %>%  
  mutate(  
    r = log(lead(ctowhee_predict)/ctowhee_predict)  
  )
```

```
#graph - what should we test?
```

```
ctowhee_r <- ggplot(ctowhee_gr, aes(x = year, y = r)) +  
  geom_line(color = "sienna2") +
```

```
theme_minimal()+
geom_hline(yintercept = 0)+
geom_vline(xintercept = 1995)+
geom_vline(xintercept = 2005, linetype = "dotted")+
labs(x = "Year", y = "Growth rate (r)")
```

ctowhee\_r



```
ggsave("ctowhee_gr_ccber.png", width = 6, height = 3, units = "in")
```

*#find averages - I didn't make a new data frame for each test I just changed the names and re-ran this*

```
ct_ccber_before <- ctowhee_gr %>%
  filter(year < 2006) %>%
  filter(year != 2016)
```

```
ct_avg_bef_ccber <- mean(ct_ccber_before$r) #this always stays the same
sd_bef <- sd(ct_ccber_before$r) # feed in a vector
se_bef <- sd_bef/sqrt(nrow(ct_ccber_before)) #calculate se
```

```
ct_ccber_after <- ctowhee_gr %>%
  filter(year > 2005) %>%
  filter(year != 2016)
```

*#redo for 5 and 10 years after restoration*



```

ct_avg_after_5 <- mean(ct_ccber_after$r)
sd_after_5<- sd(ct_ccber_after$r) # feed in a vector
se_after_5<- sd_bef/sqrt(nrow(ct_ccber_after))

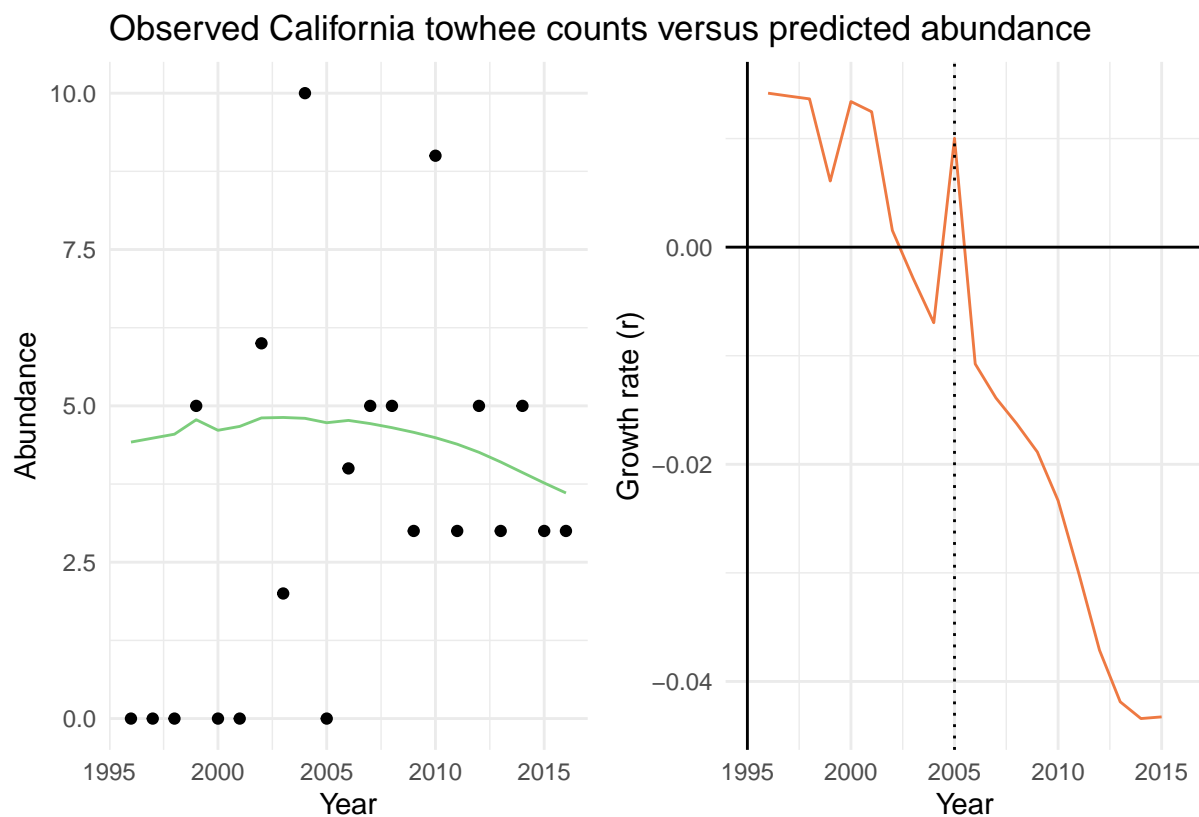
ct_ccber_after_10 <- ctowhee_gr %>%
  filter(year > 2010) %>%
  filter(year != 2016)

ct_avg_after_10 <- mean(ct_ccber_after_10$r)
sd_after_10<- sd(ct_ccber_after_10$r) # feed in a vector
se_after_10<- sd_bef/sqrt(nrow(ct_ccber_after_10))

```

Combine graphs using patchwork - this is more for knitting

```
ctowhee + ctowhee_r
```



```
# May want to change y-axis scale
```

BBS

Model

```
#filter out song sparrow
```

```

bbs_ctowhee <- bbs_clean %>%
  filter(species == "california towhee") %>%
  group_by(year) %>%
  summarize(

```

```

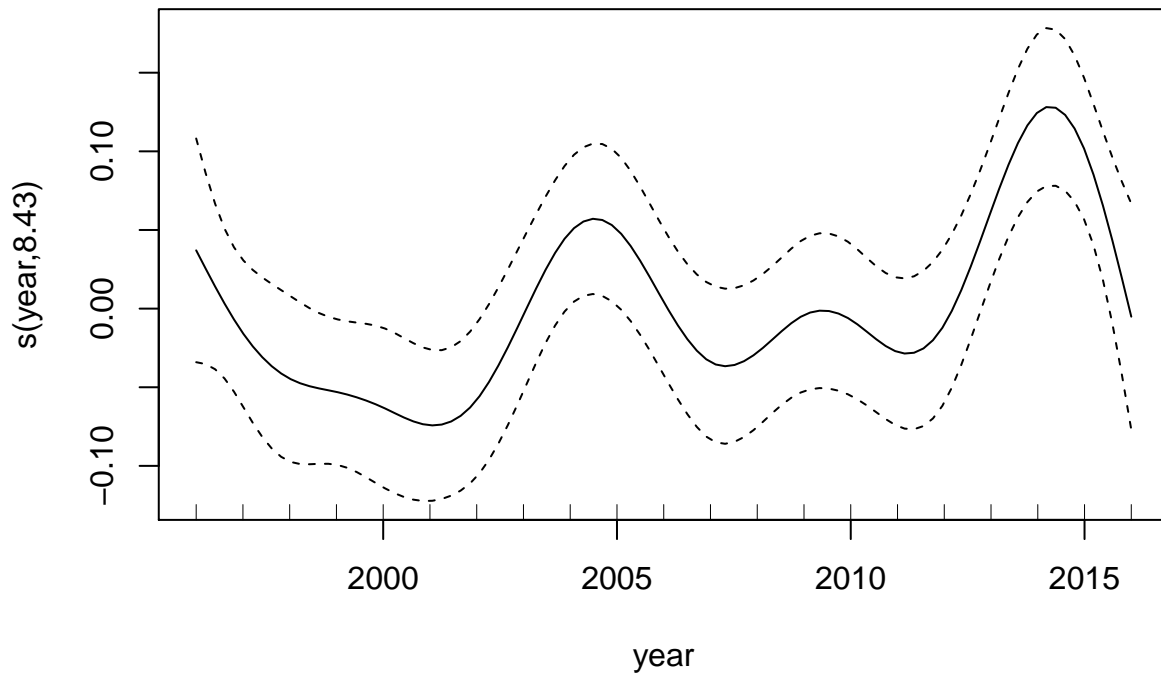
    species_total = sum(species_total)
  )

#run GAM
bbs_ctowhee_model <- mgcv::gam(species_total ~ s(year), family = poisson, data = bbs_ctowhee)

summary(bbs_ctowhee_model)

plot(bbs_ctowhee_model)

```



```

#create new data frame for predictions
newd_ctowhee_bbs <- data.frame(year = 1996:2016)

#predict abundance using new data

ctowhee_predict_bbs <- predict.gam(bbs_ctowhee_model, newd_ctowhee_bbs, type="response")

ctowhee_predict_bbs

```

### Join observations and predictions

```

ctowhee_complete_bbs <- data.frame(bbs_ctowhee, ctowhee_predict_bbs)

ctowhee_gr_bbs <- ctowhee_complete_bbs %>%
  mutate(
    r = log(lead(ctowhee_predict_bbs)/ctowhee_predict_bbs)
  )

```

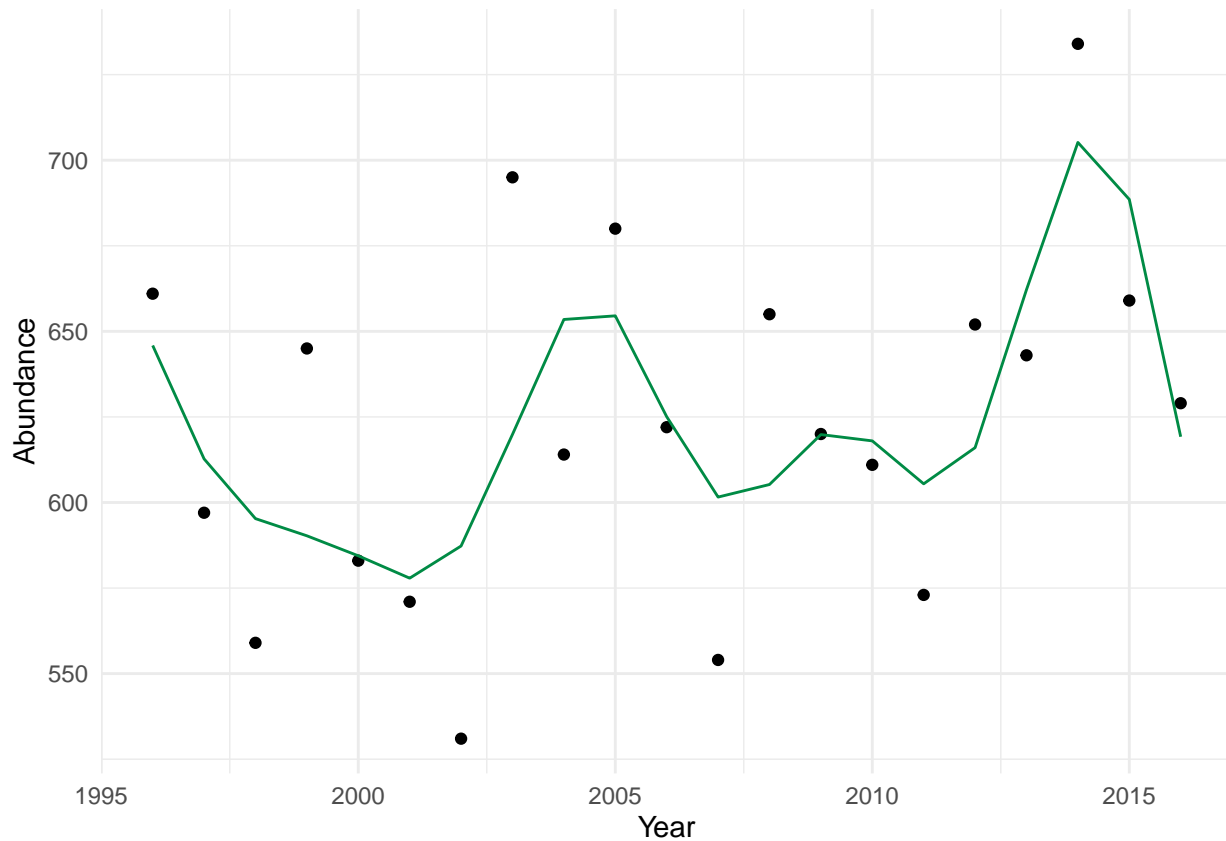
```

#note - this graph of the model prediction + observation for BBS is all the data because it is compiled
ctowhee_bbs <- ggplot(data = ctowhee_complete_bbs, aes(x = year, y = species_total)) +
  geom_point() +
  geom_line(aes(x = year, y = ctowhee_predict_bbs), color = "springgreen4") +
  theme_minimal() +

```

```
labs(x = "Year", y = "Abundance")
```

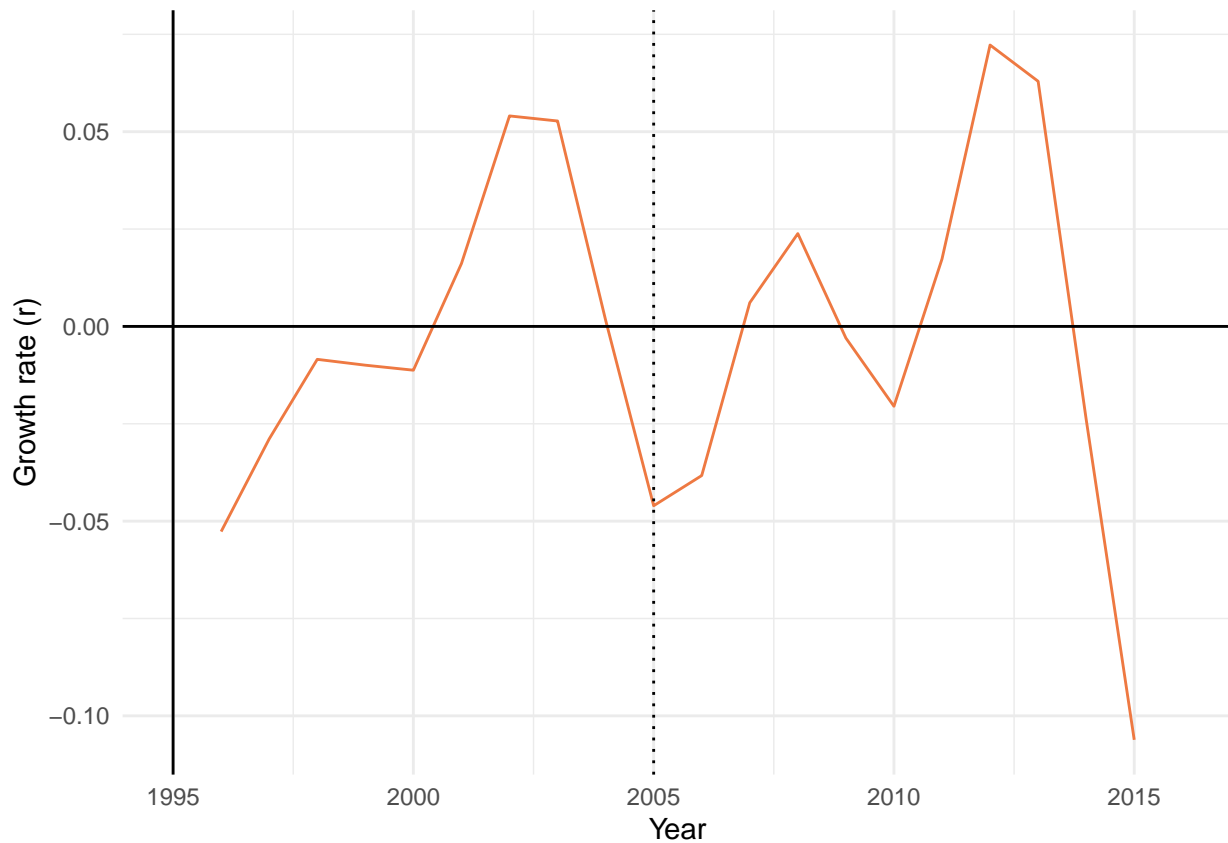
ctowhee\_bbs



```
ggsave("count_v_predict_bbs.png", width = 6, height = 3, units = "in")
```

```
ctowhee_bbs_r <- ggplot(ctowhee_gr_bbs, aes(x = year, y = r))+
  geom_line(color = "sienna2")+
  theme_minimal()+
  geom_hline(yintercept = 0)+
  geom_vline(xintercept = 1995)+
  geom_vline(xintercept = 2005, linetype = "dotted")+
  labs(x = "Year", y = "Growth rate (r)")
```

ctowhee\_bbs\_r



```
ggsave("ctowhee_bbs_growthrate.png", width = 6, height = 3, units = "in")
```

### Calculate growth rates

```
#df
ct_bbs_before <- ctowhee_gr_bbs %>%
  filter(year < 2006) %>%
  filter(year != 2016)

#numbers before restoration
ct_bbs_bef <- mean(ct_bbs_before$r)
sd_bbs_bef<- sd(ct_bbs_before$r) # feed in a vector
se_bbs_bef <- sd_bef/sqrt(nrow(ct_bbs_before)) #calculate se

#df
ct_bbs_after <- ctowhee_gr_bbs %>%
  filter(year > 2005) %>%
  filter(year != 2016)

#numbers 5 and 10 years after restoration

ct_bbs_after_5 <- mean(ct_bbs_after$r)
sd_bbs_after_5<- sd(ct_bbs_after$r) # feed in a vector
se_bbs_after_5 <- sd_bef/sqrt(nrow(ct_bbs_after))

ct_bbs_after_10 <- ctowhee_gr_bbs %>%
  filter(year > 2010) %>%
  filter(year != 2016)
```

```

ct_avg_bbs_after_10 <- mean(ct_bbs_after_10$r)
sd_bbs_after_10<- sd(ct_bbs_after_10$r) # feed in a vector
se_bbs_after_10 <- sd_bef/sqrt(nrow(ct_bbs_after_10))

#Make a dataframe with averages - try again later
#
# Dates <- c(2005, 2010,2015)
# Before <- c(ss_bbs_bef, ss_bbs_bef, ss_bbs_bef)
# After <- c(ss_bbs_after_5, ss_bbs_after_10, ss_bbs_after_15)
#
# average_table_bbs <- data.frame(Dates, Before, After)

```

Test if difference between growth rates for CCBER and BBS is significant for california towhee  
*#three tests: before, after 2005, after 2010.*

```

t.test(ct_ccber_before$r, ct_bbs_before$r, conf.level = 0.95, paired= TRUE)

t.test(ct_ccber_after$r,ct_bbs_after$r, conf.level = 0.95, paired = TRUE)

t.test(ct_ccber_after_10$r,ct_bbs_after_10$r, conf.level = 0.95, paired = TRUE)

```

## Results and Discussion

Our results for the Song Sparrow suggest that the 2005 restoration may have had an effect on the population growth rate early on. Before from 1996 – 2005 the average growth rate was negative, while the average growth rate from 2006 to 2016 was positive. However, leaving out the first 5 years after restoration, the average growth rate from 2010 to 2016 is negative. This suggests there was a positive spike in growth rate directly after 2005, with growth rates then declining later on. We wonder if perhaps the coastal sage restoration (2006) which involved removal of non-native grasses, may have made the habitat more suitable for Song Sparrows by increasing insect abundance, their main diet. However, prescribed burns, which occurred from 2006 – 2008, could have the opposite if they decreased insect abundances in the short term. These are just speculations – when comparing local growth rates to Song Sparrow trends for the entire state, we did not find any significant differences. There may be other factors affecting Song Sparrows at larger scales driving these trends, that our analysis cannot necessarily rule out.

Our findings for the California Towhee differ from that of the Song Sparrow. Our model predictions show a more or less stable population for California Towhees across all years, with a gradual decrease after 2005. The average growth rate for California Towhees from 2005-2017 is negative at Lagoon Island, while throughout the state the average growth rate fluctuates between positive and negative. However, there were no significant differences in average growth rate for this species at Lagoon Island versus across California. The restoration at Lagoon Island may not have necessarily benefited California Towhees in the short-term, but because there are no significant differences from statewide trends, this is difficult to conclude. Similar to the Song Sparrow, there may be other variables besides restoration that are affecting California Towhees on Lagoon Island.

## Limitations

While the measures of bird abundance used in this analysis provide useful information, this analysis is not without its limitations. The assumption that higher bird abundance signifies higher quality habitat is not necessarily true (Golet et al., 2003). In the future, collecting data on demographic rates could provide information about whether restored areas are supporting viable populations, which would be a better metric

of restoration success. (Gardali et al., 2006). Furthermore, little is known about what higher bird abundance indicates about the impacts of restoration on other taxonomic groups (Ruiz-Jaen et al., 2005).

An additional limitation of this analysis is that it may be too early to determine the impacts of restoration on some bird populations. Research on the impacts of revegetation on birds in Northern California found that some species did not show up on revegetated plots until 10 years after plantings. This delay may impact the species in this study (Gardali et al., 2006).

Lastly, our model fitted to CCBER bird counts may have been skewed by missing data. We wanted to control for seasonality by including a categorical month variable, however not every year had data available for every month. The raw CCBER data did not clarify whether the missing data corresponded to zero counts or if it simply meant no one had performed the count that month. To create a data frame that our model could use to generate predictions for a given month (we used July), we had to include 0 counts for the missing years. Given that both species are quite common in this area, treating the missing data as missing birds may not be realistic, and could have skewed our predictions towards lower abundances than what they actually are.