Final report: Mohonk Preserve 2016 Butterfly Biodiversity survey.

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Contents

1 Executive summary

This research addressed two questions:

1. Are standardized butterfly traps an effective way to quantify the butterfly fauna of the Mohonk Preserve?
2. Has climate change impacted emergence time of the butterfly fauna of the Mohonk Preserve?

    1. During the late Spring and early Summer of 2016 I established transects for standardized butterfly traps at three locations on the Mohonk Preserve: **Spring Farm**, **White Oak**, and **Glory Hill**. These traps were baited with fermented bananas and monitored following a protocol established by Conservation International for fruit-feeding butterflies. This was the first application of this protocol in North America. Briefly, traps were baited and checked daily for three days and any butterflies present in the traps were identified, marked, and released. Other butterflies encountered in proximity to the traps were also identified and their abundances noted. Following a survey period, the traps were idle for two weeks and the trapping cycle resumed. After three trapping periods (nine survey days over six weeks) a total of three butterfly species were captured in the traps with no recaptures. I observed an additional 12 species of butterfly in significant abundances at the sites that were never observed in the traps. The low butterfly diversity observed in the traps strongly suggests that this method is not ideal to monitor butterfly biodiversity at the Mohonk Preserve.
    2. The Mohonk Preserve has collected weather data continuously for over 100 years and observed the first occurance of butterfly species for nearly as long. I was able to access the preserve's weather data for dates starting in 1896. I did observe flucuations in annual temperature and an overall trend of increasing temperatures at the Mohonk Preserve. I requested but was not given the corresponding butterfly observational data and could not investigate how this temperature increase affected the butterfly fauna of the Mohonk Preserve.

2 Introduction

2.1 Population size

Standardized trap sampling fruit-feeding nymphalid butterflies has been shown to be an effective means for understanding butterfly diversity in space and time, and for use in conservation efforts (DeVries and Walla 2001; Hill and Hamer 2004; Molleman et al. 2006; DeVries et al. 2012; Frietas et al. 2014). Conservation International, a world leader in assessing biodiversity, has produced a standard protocol to estimate butterfly biodiversity that can be employed anywhere in the world (DeVries et al, in press). The data generated by these trap studies will allow the estimation of population size as well as species richness turnover, which are important first steps in monitoring the health and viability of local species. Once determined, the Mohonk Preserve will be able to monitor these populations (perhaps incorporating citizen scientists) and detect changes in the preserve before they are visually evident (Agosti et al. 2000).

The Nymphalidae is the largest family of butterflies, and the fruit-feeding butterflies may comprise up to 50% of the nymphalid species richness in tropical forests (DeVries et al. 2012). Fruit-feeding nymphalids at the Mohonk preserve include members of the genera Nymphalis, Speyeria, Phyciodes, Vanessa, and Polygonia. One of the most salient characteristics of this group is that they can be sampled in a standardized manner to avoid human collector biases, thus facilitating comparisons of species richness, composition and abundance within and among habitat types. For these reasons, I propose focusing standardized sampling methods exclusively on fruit-feeding nymphalids, rather than on the entire butterfly community. There are many trap studies now being conducted. Most of these are, however, not directly comparable because they do not use consistent trap designs and protocols (see examples and citations in DeVries 1987, DeVries & Walla 2001, Batra 2006, Frietas et al. 2015). The sampling protocol provided here is based on more than 10 years of monthly sampling conducted in lowland forests at Garza Cocha, Sucumbios Province, Ecuador and the Tirimbina Biological Reserve Heredia Province, Costa Rica that have been demonstrated to be directly comparable (DeVries & Walla 2001, DeVries et al. 2012).

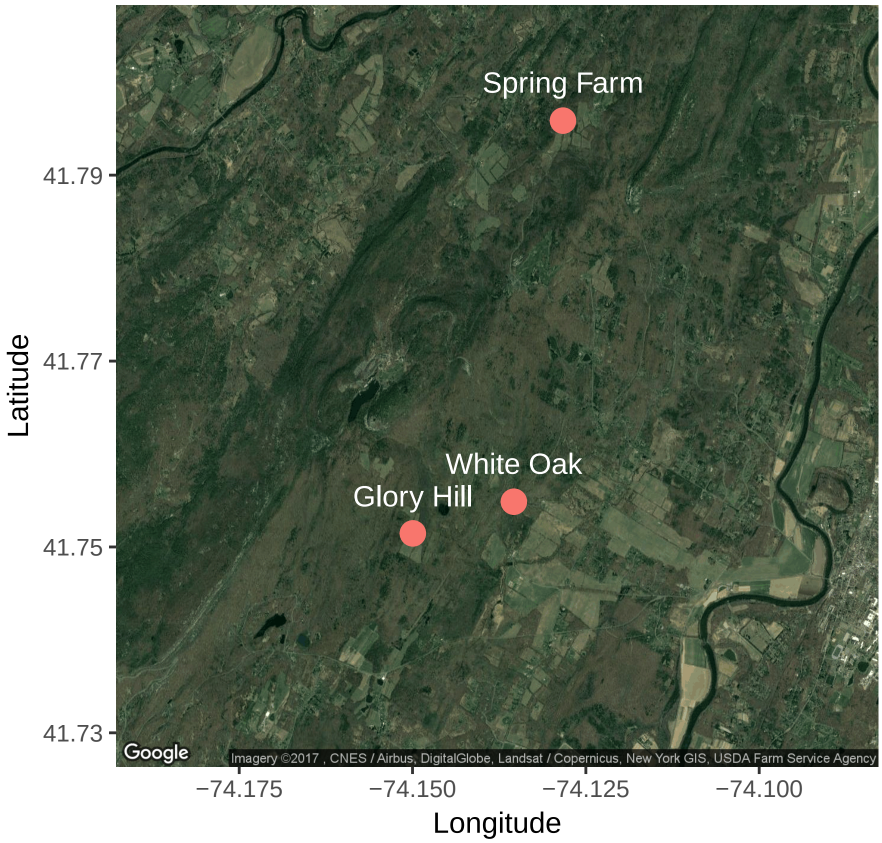
2.2 Global climate change

Global climate change is one of the most serious threats to biodiversity of natural and human ecosystems, affecting both the distribution of species and the timing of biological events (Amano et al. 2010). Since the 1980's mean annual temperature in the Northeastern United States has risen approximately 2°F. Some of this increase has occurred during the late winter and early spring seasons, resulting in a seasonal warm up 5-10 days earlier than was the case in 1980 (Andresen and Winkler 2009). Herbivorous insects, such as butterflies, must be synchronized with their host plants such that food resources are available to the insects at critical stages of development. If this symbiosis is disturbed, as has been predicted with global change, there may be limited resources available for developing larvae (Parmesan 2007). Using an approach similar to that of Cook et al. (2008), I will use the wealth of natural history observations available at the Mohonk Preserve, such as first occurrence records, to correlate emergence with existing weather data from the Mohonk Preserve. In addition to the data collected by Mohonk Preserve personnel, the American Museum of Natural History has numerous specimens in their collection, many dating back over 100 years, that have been collected in the surrounding region. The relationship between insect emergence and accumulated degree days (a measure of total heating) is well established and remains constant for particular species (Pedigo 2002). Significant warming has occurred in the Northeastern United States since 2002 (IPCC 2013), which was the most recent date that Cook et al. (2008) incorporated into their study. If warming has occurred at the Mohonk Preserve the calendar date of an event should occur earlier in the year and is detectable using common statistical models, such as time series analysis and eigenvalue decomposition (Barnett et al. 1999). I will then use projections of future climate change to examine how the butterfly community may respond to the predicted changes (Winkler et al. 2011).

3 Trap study

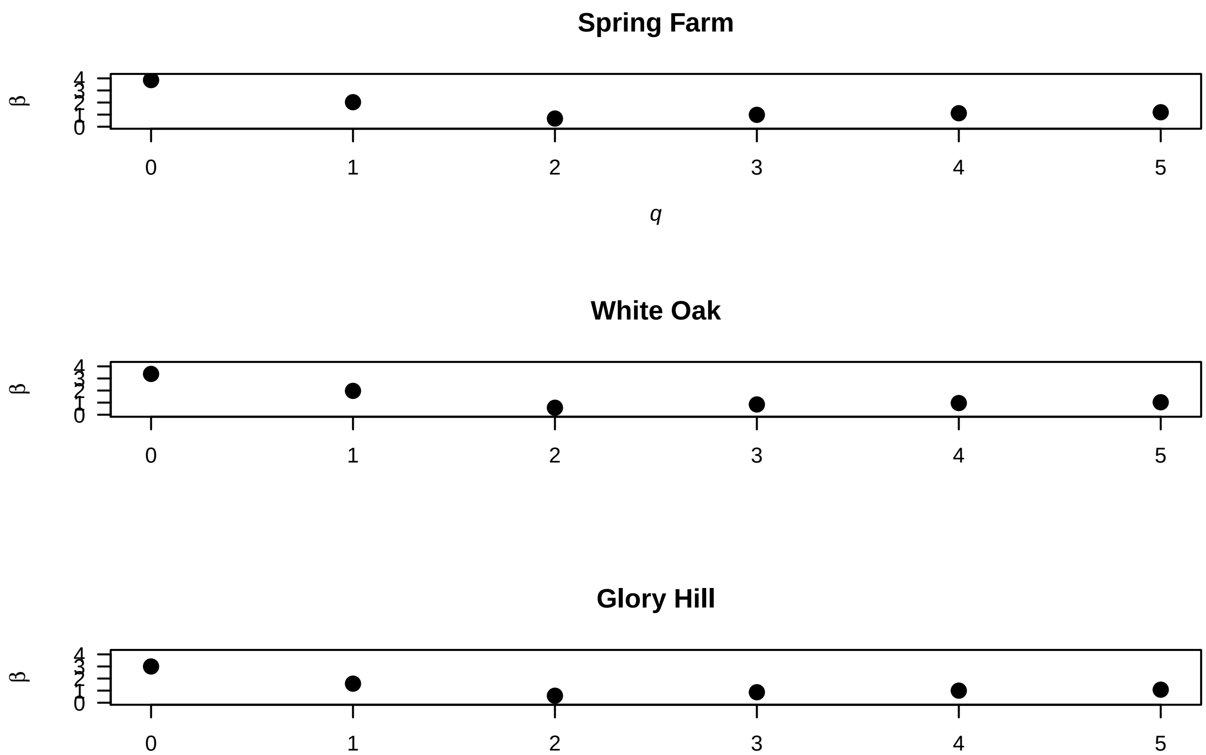
3.1 Locations

Transects were established at **Spring Farm**, **White Oak**, and **Glory Hill**.



3.2 Diversity

Diversity estimates



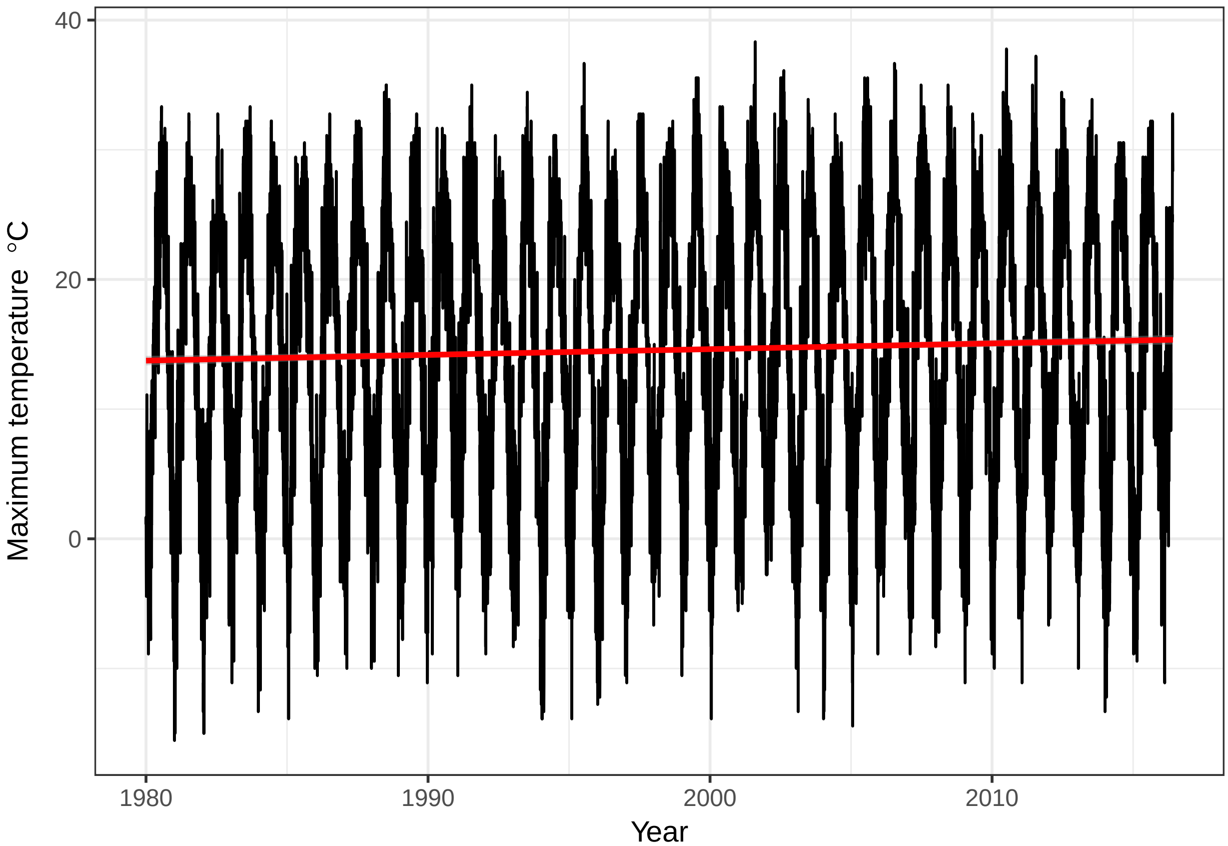
4 Climate change

weather <- ts(weather)

str(weather) head(weather) tail(weather) dim(weather) print(weather) frequency(weather) # one observation per day deltat(weather) # one observation per day

This is just linear. Need to look at when warming occurs by date.

```
ggplot(recent, aes(x = DATE, y = Max_Celsius)) +
    theme_bw() +
    geom_line() +
    ylab(expression("Maximum temperature " *~degree*C)) +
    xlab("Year") +
    stat_smooth(method = "lm", col = "red")
```



lm1 <- lm(Max_Celsius ~ DATE, data = recent) summary(lm1)

older <- weather %>% filter(DATE >= as.Date("1900-01-01")) dim(older)

This is just linear. Need to look at when warming occurs by date. ggplot(older, aes(x = DATE, y = Max_Celsius)) + theme_bw() + geom_line() + ylab(expression("Maximum temperature" ~*degree*C)) + xlab("Year") + stat_smooth(method = "auto", col = "red")

weather %>% filter()

m1 <- envcpt(data = recent$Max_Celsius)

Using the forecast package

fit1 <- auto.arima(recent$mean_C) checkresiduals(fit1) # The data are correlated head(USAccDeaths)

recent_month <- recent %>% separate(DATE, into = c("YEAR", "MONTH", "DAY"), convert = TRUE) %>% group_by(YEAR, MONTH) %>% summarize(MEAN_MONTH_C = mean(mean_C, na.rm = TRUE)) %>% mutate(MONTH2 = month.abb[MONTH]) %>% filter(YEAR <= 2015)

spread(key = MONTH2, value = MEAN_MONTH_C)

head(recent_month) tail(recent_month) dim(recent_month)

write.csv(recent_month,"Change/tsMohonk.csv", na = "NA")

tsMohonk <- read.csv("Change/tsMohonk.csv", header = TRUE, row.names = 1) str(recent_month) head(recent_month)

ts2 <- as.timeSeries(recent_month, row.names = row.names(recent_month), optional = TRUE, start = 1980, end = 2015, format = "%Y") str(ts2) dim(ts2)

row.names(ts2) <- c(1980:2015)

ts3 <- ts(ts2, start = 1980, end = 2015, freq = 1) str(ts3) row.names(ts3) <- c(1980:2015) str(ts3)

ts5 <- ts(tsMohonk, start = 1980, end = 2015, freq = 1) str(ts5) head(ts5) colnames(ts5) str(USAccDeaths)

ggseasonplot(ts5, polar = TRUE)

Back to ggplot2 ggplot(recent_month, aes(x = factor(MONTH), y = MEAN_MONTH_C), fill = factor(YEAR)) + scale_x_discrete(breaks = 1:12) + coord_polar() + geom_polygon(aes(group = factor(YEAR), color = factor(YEAR)), fill = NA, alpha = 1) + scale_color_manual(values = rev(SW_palette("Sabine", 37, type = "continuous"))) + ylab(expression("Mean monthly temp" $\sim degree$C)) + xlab("Month") + theme(legend.title = element_blank())

```
+
scale_shape_manual(labels = unique(recent_month$YEAR))
```

```
+
guides(color = guide_legend(overrive.aes = list(shape = 1)))
```

```
+
 +
scale_linetype(labels = unique(recent_month$YEAR))
```