

Preregistration

# Preregistration: Effects of white-nose syndrome (WNS) on bat community structure in Cypress Hills, Saskatchewan, Canada.

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## Study Information

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<b>Title</b>	Preregistration: Effects of white-nose syndrome (WNS) on bat community structure in Cypress Hills, Saskatchewan, Canada.
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<b>Description</b>	White-nose syndrome (WNS) is an infectious fungal disease caused by <i>Pseudogymnoascus destructans</i> targeting hibernating bats. First detected in New York City in the winter of 2006, it has since affected and killed more than 6 million hibernating bats in eastern North America Jachowski et al. (2014a). Notably, the disease
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has had a pronounced effect on the little brown bat, *Myotis lucifugus*, where it's predicted that regional population collapse and extirpation could occur as soon as within the next 16 years Frick et al. (2010). Other bat species responded variably: some studies show that silver-haired bat (*Lasionycteris noctivagans*) detection rates increased following WNS (Jachowski et al., 2014b; Nocera, Ford, Silvis, & Dobony, 2019a), while results for big brown bats (*Eptesicus fuscus*) are mixed, but most studies seem to show that their numbers increased following competitive relaxation from other declining bat species (Francel, Ford, Sparks, & Brack, 2012; Jachowski et al., 2014c; Morningstar, Robinson, Shokralla, & Hajibabaei, 2019; Nocera, Ford, Silvis, & Dobony, 2019b). Because WNS affects bat species differentially, community-level monitoring studies are needed to fully appreciate and mitigate consequences for community structure and ecosystem function Hoyt, Kilpatrick, & Langwig (2021). In 2021, the first instance of *P. destructans* with no bat mortality was reported from the Cypress Hills Interprovincial Park in Saskatchewan, Canada (Wilson pers. comm., Lausen-WCS Canada pers. comm.), indicating westward disease spread into central Canada. This study aims to inform local bat conservation efforts by compiling and comparing bat community data from before and after the introduction of WNS in Cypress Hills, in addition to constructing population projection models under WNS to predict species survivorship into the future.

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**Hypotheses** We expect to see white-nose syndrome affect bat species differently in the Cypress Hill region of Saskatchewan, Canada (See Figure 1).

**Directional:** Like other parts of eastern North America, we expect to see pronounced population **declines** in little brown bats (*Myotis lucifugus*).

**Directional:** We expect to see population **increases** in silver-haired bats (*Lasionycteris noctivagans*) and big brown bats (*Eptesicus fuscus*) due to reduced interspecific competition.

## Design Plan

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**Study type** **Observational Study.** Data is collected from study subjects that are not randomly assigned to a treatment. This includes surveys, natural experiments, and regression discontinuity designs.

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<b>Blinding</b>	No blinding is involved in this study.
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<b>Study design</b>	<p>Timing: The Bat Community in the Cypress Hills has been monitored since 1991, and we will continue to monitor the community until 2030. Monitoring will start around mid-June every year, depending upon permit permissions. Monitoring will finish in mid-August.</p> <p>Study sites: Researchers will place mist nets at various points along Battle Creek in the Cypress Hills West Block. We will choose these sites based on records from previous capture data. We will continue to return to these sites each year until 2030. We will also attempt to net at each site at similar dates each year.</p> <p>Field methods: We will raise 1-3 mist nets across Battle Creek at each net site. Number of nets will be chosen based on personnel, time, and previous net set-ups. Each mist net will be raised at last light and we will monitor net activity for three hours per night. Every hour we will record ambient temperature, cloud cover and wind speed. We will close nets if it is raining or wind speed is above 20 km/s.</p> <p>We will check the nets every 10 minutes for one hour after last light, and every 15 minutes for the two proceeding hours. If a bat is captured it will be extracted and moved away from the mist nets in order to reduce other bats being attracted to the distress call of the captured bat. We will take data on each captured bats species, age, sex, and mass. Bats will be released at most half an hour after capture.</p>
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<b>Randomization</b>	Not applicable
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## Sampling Plan

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<b>Existing data</b>	<p><b>Registration prior to analysis of the data.</b> As of the date of submission, the data exist and you have accessed it, though no analysis has been conducted related to the research plan (including calculation of summary statistics). A common situation for this scenario when a large dataset exists that is used for many different studies over time, or when a data set is randomly split into a sample for exploratory analyses, and the other section of data is reserved for later confirmatory data analysis.</p>
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<b>Explanation of existing data</b>	<p>Capture data from bats in the Cypress Hills has been collected since 1991, and so we have data for this project from 1991 until now. The existing data was collected by other researchers and was used for many different studies over time. These researchers left their raw data available for others to use. Currently, only one of the project members has seen the original data. However, they have only seen the data from 1991-1992, and the 2019 dataset and they have not conducted any prior analyses or investigations of it. The other project members have not seen any of the existing data yet. Furthermore, this project assesses community structure changes before and after the detection of White-nose syndrome in Saskatchewan until 2030. We will not analyze the data until after 2030.</p>
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<b>Data collection procedures</b>	<p>Monitoring will start around mid-June every year, depending upon permit permissions. Monitoring will finish in mid-August. We will monitor community structure using the capture data we collect from mist nets.</p> <p>We will set up 1-3 mist nets at one site each night. Nets will be set up across Battle Creek. Nets will be at least 1m tall, and wide enough to cover the width of the creek. Nets will be set up at transition sites where the flyway above Battle Creek transitions from a cluttered environment with lots of debris to open sky. Nets will also be placed over calm sections of water, without ripples.</p> <p>Each mist net will be raised at last light and we will monitor net activity for three hours per night. Every hour we will record ambient temperature, cloud cover and wind speed. We will close nets if it is raining or wind speed is above 20 km/s.</p> <p>We will check the nets every 10 minutes for one hour after last light, and every 15 minutes for the two proceeding hours. If a bat is captured it will be extracted and moved away from the mist nets in order to reduce other bats being attracted to the distress call of the captured bat. We will take data on each captured bats species, age, sex, and mass. Bats will be released at most half an hour after capture.</p> <p>We will continue to return to these sites each year until 2030. We will also attempt to net at each site at similar dates each year.</p>
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<b>Sample size</b>	Our target sample size is 4000 individuals. However, we do not have a pre-determined count and cannot control the number of bats we capture each year.
<b>Sample size rationale</b>	We do not have control over how many bats we will capture a night. We are assuming based anecdotal knowledge and previous experience that in three months we will capture 100-200 bats, and after forty years of data collection we will collect around 4000 bats.
<b>Stopping rule</b>	<p>Data collection will end each year in mid-August. The field station where researchers live during the field season is owned by the University of Regina, who use the station for an undergraduate class during the last week of August. The field station is closed after that, so data collection will stop mid-August</p> <p>The project overall will end in 2030. White-Nose Syndrome was first detected in Saskatchewan in 2021. Ending the project 10 years after WNS was first detected allows us to observe bat community structure at the start of the disease, directly after it should have killed the largest number of bats, and ten years later when it should have become endemic to the population.</p>
<b>Variables</b>	
<b>Manipulated variables</b>	<i>TK</i> I'm assuming 'raw' abundance records will be transformed to some measure of frequency/ratio or otherwise 'extrapolated' to some measure of abundance?
<b>Measured variables</b>	We are going to be measuring the population size of the bat species in the Cypress Hills before and after the detection of White-nose Syndrome. We will measure this by counting how many bats of each we catch in mist nets each year.
<b>Indices</b>	Enter your response here.

## Analysis Plan

It's hypothesized that the community would undergo similar changes as eastern coast populations. Following equations aim to describe changes in the size of populations of different bat species. Some coefficients should be estimated based on Saskatchewan bat community data from 1990-2021 (growth rate, carrying capacity and competition coefficients) and some from previous studies in east coast (transmission rate) populations and then predication can be made for Saskatchewan bat community.

$$N_{i,t+1} = N_{i,t}r_i(1 + \frac{K_i - N_{i,t} - \sum_{j=1}^n \alpha_{i,j}N_{j,t}}{K}) - I_{i,t}$$

Where:  $N_{i,t}$  is the population size of species i at time t  $r_i$  is the intrinsic growth rate of species i  $K_i$  is the carrying capacity for species i  $\alpha_{i,j}$  is the coefficient for competition effect of species j on species i.  $I_{i,t}$  is the number of individuals infected with WNS at time t. It's assumed that all of these individuals will dye before next time point. This parameter is calculated as follow:

$$I_{i,t+1} = d_i I_{i,t} \frac{N_{i,t}}{k_i}$$

Where  $d_i$  is the transmission rate of WNS in species i. It's assumed that transmission of diseases is density dependent.

Estimation of coefficients:  $r$ ,  $K$  and  $\alpha$ : They should be calculated based on the data gathered sofar (1991-2021) using genetic algorithm (or any other optimization method?).

$d$ : depends on the objective of study: 1- If we are going to make predictions for future dynamics of populations, previous studies should be used to estimate this parameter. It should be considered that  $d$  probably won't stay constant over time and evolutionary dynamics of host and parasite would affect it. 2- If we are going to estimate  $d$  in each of these populations after the end of study, similar method as other coefficients can be used.

Note that in both cases an initial number of infected individuals at year 2021 is required ( $I_{i,t=2021}$ ).

<b>Statistical models</b>	The model provides some predictions for population of different species at different time points and we can test our hypothesis using a chi-2 goodness of fit test. Besides, power analysis will be conducted using <b>pwr</b> package. A single test should be conducted for all for species over 2021-2030 period. If the test finds significant difference, then an exploratory test should be conducted (further details explained in next sections) to determine new values for the coefficients using the data from Saskatchewan bat community 2021-2030 using a genetic algorithm optimization method. Then it should be determined if the sample size can support the estimated effect size and again another round of power analysis should be conducted.
<b>Transformations</b>	Enter your response here.
<b>Inference criteria</b>	
<b>Data exclusion</b>	Enter your response here.
<b>Missing data</b>	We might expect bat records not to have a species identifier. As this is the data of interest these records will have to be removed as there is no feasible way to impute the missing data.
<b>Exploratory analyses (optional)</b>	If the test finds significant difference, then an exploratory test should be conducted to determine new values for the coefficients using the data from Saskatchewan bat community 2021-2030 using a genetic algorithm optimization method. Then it should be determined if the sample size can support the estimated effect size and again another round of power analysis should be conducted.

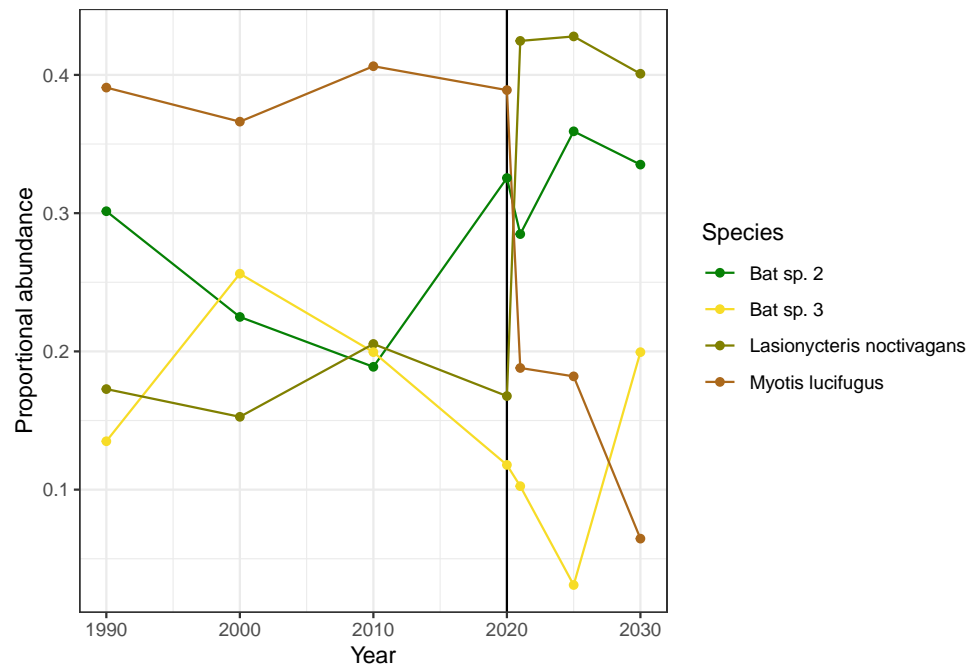


Figure 1: Expected changes in bat species frequencies after the introduction of white nose syndrome in 2019 the Cypress hill region of Saskatchewan Province.

## Other

## References

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