This metadata file describes five datasets and three R script files to repeat the analyses for the paper, “Continued preference for suboptimal habitat reduces bat survival with white-nose syndrome”, published in *Nature Communications*. We conducted all analyses using R version 4.0.2 and RStudio Version 1.3.1073.

**Authors:** Skylar R. Hopkins1,2\*, Joseph R. Hoyt1, J. Paul White3, Heather M. Kaarakka3, Jennifer A. Redell3, John E. DePue4, William H. Scullon5, A. Marm Kilpatrick6, and Kate E. Langwig1

**Affiliations**

1. Department of Biological Sciences, Virginia Tech, Blacksburg, VA 24060, USA; skylar.hopkins@vt.edu (\*corresponding author)
2. Department of Applied Ecology, North Carolina State University, Raleigh, NC, USA
3. Wisconsin Department of Natural Resources, Bureau of Natural Heritage Conservation, Madison, WI 53703, USA
4. Michigan Department of Natural Resources, Baraga, MI 49870, USA
5. Michigan Department of Natural Resources, Norway, MI 49908, USA
6. Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, CA 95060, USA

**STUDY DESIGN:**

From 2013 to 2020, we surveyed 22 hibernacula in Michigan and Wisconsin twice per year: once in early hibernation (November) and once in late hibernation (March). We surveyed 12 hibernacula before invasion (before the fungus had been established in a site for one year), during invasion (1-2 years since the fungus was first detected), and after invasion (>2 years after first detection), and we surveyed the 10 other hibernacula during at least one of the three invasion periods. Bats counted in the 12 long-term sites were included in our analysis of how bat temperature distributions in November shifted from pre- to post-invasion (Distribution Shift Analysis). After counting bats, we sampled up to 25 bats per site per survey, stratified by section, to quantify individual fungal loads and early hibernation roosting temperatures. If these sampled bats could be reached to safely remove them briefly from their roosts, we also banded them. All banded bats that were infected during early hibernation were included in our recapture analysis, where we determined whether bat recapture probabilities were affected by early hibernation roosting temperatures and early fungal loads (Fungal Load Change Analysis). All recaptured bats that were infected during early hibernation were included in our fungal load change analysis, where we determined whether over winter increases in fungal loads were affected by early hibernation roosting temperatures (Recapture Analysis). Note that only a few bats were infected and banded during Year 0, the year that the fungus was first detected at a given site, which we consider to occur within the pre-invasion period. All sample sizes in the figure represent the number of bats sampled during early hibernation. The figure below is Fig. S1 from the paper that contains these analyses.

****

**R Script Files**

**FungalLoadChangeAnalysis.R**

This R script loads three data files:

* The swab and temperature data from all bats swabbed in all sites in all years: **Cleaned MYLU Swab Data for Ecotraps Analysis.csv**
* The swab and temperature data for all banded bats: **Cleaned MYLU Band Data for Ecotraps Analysis.csv**
* The swab and temperature data or only bats that were banded and infected in during a fall survey: **Cleaned Inf MYLU Band Recap Data for Ecotraps Analysis.csv**

These data are used to determine whether changes in fungal loads from November to March were affected by November roosting temperatures and/or fungal loads. We use simple correlation tests and a Logan-10 growth curve, fit in a Bayesian framework, to explore these relationships. The Bayesian analysis uses weakly informative priors which allow for any possible curve shape, as shown by the simulation included at the end of the script. This script also makes Figure 2 from the paper.

**RecaptureAnalysis.R**

This R script loads three data files:

* The swab and temperature data from all bats swabbed in all sites in all years: **Cleaned MYLU Swab Data for Ecotraps Analysis.csv**
* The swab and temperature data for all banded bats: **Cleaned MYLU Band Data for Ecotraps Analysis.csv**
* The swab and temperature data or only bats that were banded and infected in during a fall survey: **Cleaned Inf MYLU Band Recap Data for Ecotraps Analysis.csv**

Using these data, the script runs the logistic regression for the recapture analysis, performs 5-fold cross-validation on 1000 random divisions of our dataset, and then calculates the average Area Under the Curve (AUC) for the resulting 1000 Receiver Operating Characteristic (ROC) curves. This script also makes the logistic regression and partial residuals figures.

**DistributionShiftAnalysis.R:**

This R script loads four data files:

* The swab and temperature data from all bats swabbed in the 12 sites that were sampled during all three invasion periods: **DistributionShiftAnalysis\_CleanedMYLUSwabData.csv**
* The swab and temperature data for all banded bats: **Cleaned MYLU Band Data for Ecotraps Analysis.csv**
* The swab and temperature data or only bats that were banded and infected in during a fall survey: **Cleaned Inf MYLU Band Recap Data for Ecotraps Analysis.csv**
* The count data for the 12 sitesthat were sampled during all three invasion periods: **DistributionShiftAnalysis\_CleanedCountData.csv**

These data are used to calculate how the average estimated November roosting temperature changed from pre-invasion to invasion to post-invasion and then to make a figure illustrating how these distribution shifts across invasion periods correspond to the temperature distributions of banded bats that were and were not recaptured.

**Data Files**

**DistributionShiftAnalysis\_CleanedMYLUSwabData.csv**

*Overview:* This CSV file contains cleaned *M. lucifugus* swab and temperature data for the 12 sites that were surveyed during all three invasion periods. The rows in this dataset are individual banded and unbanded bats and information regarding their location (site and section), roosting temperature, fungal loads as measured by qPCR, date sampled, etc. This csv file is similar to Cleaned MYLU Swab Data for Ecotraps Analysis.csv, below, but it includes only sampled bats from the 12 sites used in the Distribution Shift Analysis, and there is a section2 column where the section names have been matched to the section2 names used in the count data dataset (DistributionShiftAnalysis\_CleanedCountData.csv).

*Description of columns:*

*swab\_id*: The individual identification label given to each fungal swab, where a single standardized swab is used to quantify the fungal load on a single bat.

*gdL:* The fungal load on the bat in ng DNA, as quantified by qPCR. NAs indicate bats that were not infected and thus did not have measurable fungal loads.

*site*: The name of the site where the bat was sampled, anonymized to protect the locations of sensitive bat species.

*date*: The date that the bat was sampled in mm/dd/yy format.

*state:* The state where the hibernaculum/bat was sampled: Michigan or Wisconsin.

*section*: The name of the room/section within the hibernaculum where the bat was sampled. The corrected names that match the count data are in the *section2* column.

*temp*: The temperature (°C) of the substrate directly adjacent to the bat (<1 cm; the “roosting temperature”) as measured by a Fluke 62 MAX IR laser thermometer.

*month*: The month that the bat was sampled. 1 is January, 2 is February, etc.

*season*: The season during which the bat was sampled. Early hibernation (November) is indicated by “hiber\_earl” and late hibernation (March) is indicated by “hiber\_late”.

*band*: The unique band identification number for each banded bat. Note that not all bats in the dataset were banded. NA is used to indicate bands without bands.

*band2*: A second band identification number for a subset of banded bats that had two bands.

*pdate*: The date that the bat was sampled with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

*y:* The year that the bat was sampled.

*wyear*: The working year that the bat was sampled. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020).

*yoa*: The year that the fungus was first detected in the hibernaculum where the bat was sampled.

ysw: The number of years since the fungus was first detected in the hibernaculum where the bat was sampled, where *ysw* = *wyear* – *ysw*.

*section2*: The corrected name of the room/section within the hibernaculum where the bat was sampled. The corrected names match the section2 column from the count data.

**DistributionShiftAnalysis\_CleanedCountData.csv**

*Overview:* This CSV file contains cleaned *M. lucifugus* count data from the 12 hibernacula surveyed in all three invasion periods (pre-invasion, invasion, and post-invasion). The rows in this dataset are individual sections/rooms within hibernacula, with information about when the section was surveyed and how many *M. lucifugus* were sampled*.* These data were used in the Distribution Shift Analysis, and the section names have been matched to the section names used in the sampled bat data (DistributionShiftAnalysis\_CleanedMYLUSwabData.csv).

*Description of columns:*

*y:* The year that the section was surveyed.

*ysw*: The number of years since the fungus was first detected in the hibernaculum where the section was surveyed.

*site*: The name of the site, anonymized to protect the locations of sensitive bat species.

*section2*: The corrected name of the room/section within the hibernaculum. Some hibernacula have multiple sections and some are just a single room/section, called “ALL”.

*wyear*: The working year that the section was surveyed. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020).

*pdate*: The date that the section was surveyed with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

clustersize: The total number of bats counted in the section during the survey, which is the sum of all the individual bats and clusters of bats in the section. Zeros indicate where a survey was conducted and no bats were found in the section.

**Cleaned MYLU Swab Data for Ecotraps Analysis.csv**

*Overview:* This CSV file contains cleaned *M. lucifugus* swab and temperature data for all 22 sites. The rows in this dataset are individual banded and unbanded bats and information regarding their location (site and section), roosting temperature, fungal loads as measured by qPCR, date sampled, etc. This csv file is similar to DistributionShiftAnalysis\_CleanedMYLUSwabData.csv, but it all sampled bats, and there is no section2 column.

*Description of columns:*

*swab\_id*: The individual identification label given to each fungal swab, where a single standardized swab is used to quantify the fungal load on a single bat.

*gdL:* The fungal load on the bat in ng DNA, as quantified by qPCR. NAs indicate bats that were not infected and thus did not have measurable fungal loads.

*site*: The name of the site where the bat was sampled, anonymized to protect the locations of sensitive bat species.

*date*: The date that the bat was sampled in mm/dd/yy format.

*state:* The state where the hibernaculum/bat was sampled: Michigan or Wisconsin.

*section*: The name of the room/section within the hibernaculum where the bat was sampled. The corrected names that match the count data are in the *section2* column.

*temp*: The temperature (°C) of the substrate directly adjacent to the bat (<1 cm; the “roosting temperature”) as measured by a Fluke 62 MAX IR laser thermometer.

*month*: The month that the bat was sampled. 1 is January, 2 is February, etc.

*season*: The season during which the bat was sampled. Early hibernation (November) is indicated by “hiber\_earl” and late hibernation (March) is indicated by “hiber\_late”.

*band*: The unique band identification number for each banded bat. Note that not all bats in the dataset were banded. NA is used to indicate bands without bands.

*band2*: A second band identification number for a subset of banded bats that had two bands.

*pdate*: The date that the bat was sampled with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

*y:* The year that the bat was sampled.

*wyear*: The working year that the bat was sampled. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020).

*yoa*: The year that the fungus was first detected in the hibernaculum where the bat was sampled.

ysw: The number of years since the fungus was first detected in the hibernaculum where the bat was sampled, where *ysw* = *wyear* – *ysw*.

**Cleaned MYLU Band Data for Ecotraps Analysis.csv**

*Overview:* This CSV file contains cleaned *M. lucifugus* swab and temperature data for all banded bats from all 22 sites. The rows in this dataset are individual banded bats and information regarding their location (site and section), roosting temperature, fungal loads as measured by qPCR, date sampled, etc. This csv file is similar to Cleaned MYLU Swab Data for Ecotraps Analysis.csv, but it includes only banded bats. There are also some additional columns indicated whether the bat was recaptured or not.

*Description of columns:*

*swab\_id*: The individual identification label given to each fungal swab, where a single standardized swab is used to quantify the fungal load on a single bat.

*gdL:* The fungal load on the bat in ng DNA, as quantified by qPCR. NAs indicate bats that were not infected and thus did not have measurable fungal loads.

*site*: The name of the site where the bat was sampled, anonymized to protect the locations of sensitive bat species.

*date*: The date that the bat was sampled in mm/dd/yy format.

*state:* The state where the hibernaculum/bat was sampled: Michigan or Wisconsin.

*section*: The name of the room/section within the hibernaculum where the bat was sampled. The corrected names that match the count data are in the *section2* column.

*temp*: The temperature (°C) of the substrate directly adjacent to the bat (<1 cm; the “roosting temperature”) as measured by a Fluke 62 MAX IR laser thermometer.

*month*: The month that the bat was sampled. 1 is January, 2 is February, etc.

*season*: The season during which the bat was sampled. Early hibernation (November) is indicated by “hiber\_earl” and late hibernation (March) is indicated by “hiber\_late”.

*band*: The unique band identification number for each banded bat. Note that not all bats in the dataset were banded. NA is used to indicate bands without bands.

*band2*: A second band identification number for a subset of banded bats that had two bands.

*pdate*: The date that the bat was sampled with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

*y:* The year that the bat was sampled.

*wyear*: The working year that the bat was sampled. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020).

*yoa*: The year that the fungus was first detected in the hibernaculum where the bat was sampled.

*ysw*: The number of years since the fungus was first detected in the hibernaculum where the bat was sampled, where *ysw* = *wyear* – *ysw*.

*InitialCaptureYN*: Whether this sample represents the first time a bat was captured/banded in our dataset or not. 1 indicates that this was the first capture and 0 indicates that this was not the first recapture.

*YearBand*: This column simply pastes together the *wyear* and *band* columns to create a unique ID for each bat during each year. For example, 2016.AAA137 is bat AAA137 during the 2016 working year.

*NRecaps*: The number of times that this bat with this band was recaptured in our dataset.

*RecapturedSameYearYN*: Whether this bat was recaptured during the same working year (i.e., sited in both November and March) or not. 1 indicates that this bat was recaptured and 0 indicates that this bat was not recapture.

*EverRecapturedYN*: Whether this bat was recaptured during any year (i.e., sited in November 2016 and later in November 2018) or not. 1 indicates that this bat was recaptured and 0 indicates that this bat was not recapture. Note that only 5% of bats that were not recaptured within a working year were later recaptured in a different here, so this column is nearly identical to *RecapturedSameYearYN*.

**Cleaned Inf MYLU Band Recap Data for Ecotraps Analysis.csv**

*Overview:* This CSV file contains cleaned *M. lucifugus* swab and temperature data for all banded bats that were infected during a November survey from all 22 sites. The rows in this dataset are individual banded bats and information regarding their location (site and section), roosting temperature, fungal loads as measured by qPCR, date sampled, etc. The .x columns are data taken during the November survey and the .y columns are data taken during the March survey, if the bat was recaptured. NAs in the .y columns indicate that a bat banded/sampled in November was not recaptured in March of the same year.

*YearBand*: This column simply pastes together the *wyear* and *band* columns to create a unique ID for each bat during each year. For example, 2016.AAA137 is bat AAA137 during the 2016 working year.

*swab\_id.x*: The individual identification label given to each fungal swab, where a single standardized swab is used to quantify the fungal load on a single bat. This column gives the swab ID for the swab taken in November, whereas *swab\_id.y* gives the swab ID for the swab taken in March, if the bat was swabbed in March.

*earlygdL*: The fungal load on the bat in November in ng DNA, as quantified by qPCR. NAs indicate bats that were not infected and thus did not have measurable fungal loads.

*site.x*: The name of the site where the bat was sampled in November, anonymized to protect the locations of sensitive bat species. Bats never changed sites between November and March, so this column is identical to *site.y.*

*date.x*: The date that the bat was sampled during early hibernation in mm/dd/yy format.

*state.x*: The state where the hibernaculum/bat was sampled in November: Michigan or Wisconsin. Bats never changed sites between November and March, so this column is identical to *state.y.*

*section.x*: The name of the room/section within the hibernaculum where the bat was sampled in November.

*earlytemp*: The temperature (°C) of the substrate directly adjacent to the bat (<1 cm; the “roosting temperature”) as measured by a Fluke 62 MAX IR laser thermometer in November.

*month.x*: The month that the bat was sampled during early hibernation. 1 is January, 2 is February, etc.

*season.x*: The season that the bat was sampled. All entries are “hiber\_earl” because the .x columns all describe early hibernation data.

*band.x*: The unique band identification number for each bat. This column is the same as *band.y*.

*band2.x*: A second band identification number for a subset of banded bats that had two bands. This column is the same as *band2.y*.

*y.x*: The calendar year that the bat was sampled in November. This differs from *y.y* because bats sampled in the fall of one year (e.g., Nov. 2018) would be sampled again in the spring of the next calendar year (e.g., Mar. 2019).

*wyear.x*: The working year that the bat was sampled. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020). This column is identical to *wyear.y*.

*yoa.x*: The year that the fungus was first detected in the hibernaculum where the bat was sampled. This column is identical to *yoa.y*.

*pdate.x*: The date that the bat was sampled in November with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

*ysw.x*: The number of years since the fungus was first detected in the hibernaculum where the bat was sampled, where *ysw* = *wyear* – *ysw*. This column is identical to *ysw.y*.

*InitialCaptureYN.x*: Whether this sample represents the first time a bat was captured/banded in our dataset or not. 1 indicates that this was the first capture and 0 indicates that this was not the first recapture.

*NRecaps.x*: The number of times that this bat with this band was recaptured in our dataset. This column is identical to *NRecaps.y*.

*RecapturedSameYearYN.x*: Whether this bat was recaptured during the same working year (i.e., sited in both November and March) or not. 1 indicates recapture and 0 indicates no recapture.

*EverRecapturedYN.x*: Whether this bat was recaptured during any year (i.e., sited in November 2016 and later in November 2018) or not. 1 indicates that this bat was recaptured and 0 indicates that this bat was not recaptured. Note that only 5% of bats that were not recaptured within a working year were later recaptured in a different here, so this column is nearly identical to *RecapturedSameYearYN.x*.

*swab\_id.y*: The individual identification label given to each fungal swab, where a single standardized swab is used to quantify the fungal load on a single bat. This column gives the swab ID for the swab taken in March, whereas *swab\_id.x* gives the swab ID for the swab taken in November.

*lategdL*: The fungal load on the bat in March in ng DNA, as quantified by qPCR. NAs indicate bats that were not infected and thus did not have measurable fungal loads.

*site.y*: The name of the site where the bat was sampled in March, anonymized to protect the locations of sensitive bat species. Bats never changed sites between November and March, so this column is identical to *site.x.*

*date.y*: The date that the bat was sampled during late hibernation in mm/dd/yy format.

*state.y*: The state where the hibernaculum/bat was sampled in March: Michigan or Wisconsin. Bats never changed sites between November and March, so this column is identical to *state.x.*

*section.y*: The name of the room/section within the hibernaculum where the bat was sampled in March.

*latetemp*: The temperature (°C) of the substrate directly adjacent to the bat (<1 cm; the “roosting temperature”) as measured by a Fluke 62 MAX IR laser thermometer in March.

*month.y*: The month that the bat was sampled during late hibernation. 1 is January, 2 is February, etc.

*season.y*: The season that the bat was sampled. All entries are “hiber\_late” because the .y columns all describe late hibernation data.

*band.y*: The unique band identification number for each bat. This column is the same as *band.x*.

*band2.y*: A second band identification number for a subset of banded bats that had two bands. This column is the same as *band2.y*.

*y.y*: The calendar year that the bat was sampled in March. This differs from *y.x* because bats sampled in the fall of one year (e.g., Nov. 2018) would be sampled again in the spring of the next calendar year (e.g., Mar. 2019).

*wyear.y*: The working year that the bat was sampled. Because winters cross two years (e.g., Fall 2019 and Spring 2020), winters are numbered by the year during the spring survey (e.g., Fall 2019 surveys occurred in wyear 2020). This column is identical to *wyear.x*.

*yoa.y*: The year that the fungus was first detected in the hibernaculum where the bat was sampled. This column is identical to *yoa.x*.

*pdate.y*: The date that the bat was sampled in March with regards to winter periods. Because winters cross two years (e.g., Fall 2019 and Spring 2020), the pdate was created to sort dates within a period between fall months (<13) and spring months (>13), where January dates are 13.

*ysw.y*: The number of years since the fungus was first detected in the hibernaculum where the bat was sampled, where *ysw* = *wyear* – *ysw*. This column is identical to *ysw.x*.

*InitialCaptureYN.y*: Whether this sample represents the first time a bat was captured/banded in our dataset or not. Because this dataset only includes bats banded/sampled in November, all bats sampled in March would have been previously sampled, so this column will always be a 0 (not a first capture) or an NA (not sampled/recaptured).

*NRecaps.y*: The number of times that this bat with this band was recaptured in our dataset. This column is identical to *NRecaps.x*.

*RecapturedSameYearYN.y*: Whether this bat was recaptured during the same working year (i.e., sited in both November and March) or not. This column will either have a 1, indicating a recapture, or an NA, because the bat was not recaptured.

*EverRecapturedYN.y*: Whether this bat was recaptured during any year (i.e., sited in November 2016 and later in November 2018) or not. 1 indicates that this bat was recaptured and 0 indicates that this bat was not recaptured. Note that only 5% of bats that were not recaptured within a working year were later recaptured in a different here, so this column is nearly identical to *RecapturedSameYearYN.y*.

*logearlyloads*: The log10 transformed *earlygdL*, where a small constant (0.0001) was added to all *earlygdL* values before log10 transforming.

loglateloads: The log10 transformed *lategdL*, where a small constant (0.0001) was added to all *lategdL* values before log10 transforming.

*YSWBins*: The invasion period during which the sample was taken. Pre-invasion includes all years up to an including the first year that the fungus was first detected at a site (*ysw*=0). Invasion includes *ysw*=1 and *ysw*=2. Post-invasion is >2 years after the fungus was first detected at a site.