This metadata file describes datasets and R files for the paper “Mobility and infectiousness in the spatial spread of an emerging pathogen”, published in *Journal of Animal Ecology*. We conducted all analyses using R version 4.0.2 and RStudio Version 1.3.1073.

Kate E. Langwig1\*, J. Paul White2, Katy L. Parise3, Heather M. Kaarakka2, Jennifer A. Redell2, John E. DePue4, William H. Scullon5, Jeffrey T. Foster3, A. Marm Kilpatrick6,Ψ, Joseph R. Hoyt1,Ψ

**Affiliations:**

*1 Department of Biological Sciences, Virginia Polytechnic Institute, Blacksburg, VA, 24060 USA*

*2 Wisconsin Department of Natural Resources, Madison, WI, 53703 USA*

*3 Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, AZ 86011, USA*

*4 Michigan Department of Natural Resources, Baraga, MI 49870, USA*

*5Michigan Department of Natural Resources, Norway, MI 49908, USA*

*6 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, CA 95064 USA*

\*Corresponding author: klangwig@gmail.com; Ψthese authors contributed equally

**Data Files**

**data.csv**

*Overview:* This CSV file contains aggregate data where each row is site and species combination sampled on a particular date in the year *P. destructans* was first detected at a site.

*Description of columns:*

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

*date:* The date the sample was collected

*species:* the species of bat sampled, as latin binomial 4 letter codes. The first two letters correspond to the first two of the genus and the second two letters correspond to the first two letter of the species.

*pdate:* pdate = month + (days/31), If month is less than 11, it is the month number +12. The purpose of this column to create a winter year that begins Nov 1 and goes through October 31.

wyear: the winter year when the data were collected, e.g. Nov 2015 - March 2016 is winter year 2016

ysw: year since WNS arrived; 0 = year of arrival

gd: prevalence of *P. destructans* from swab samples at a site on a particular species. 1 = 100% of individuals of a particular species sampled were positive for *P. destructans*

N: the number of individuals of that particular species sampled

lgdL: mean log10( *P. destructans* loads)

count: the number of bats counted in of that particular species during the trip

lambda: the proportional change in the count from the previous season (e.g. (March count/previous March count). A constant (+1) was added to every count to avoid division by 0.

season: whether the visit occured in early hibernation ('hiber\_earl', before January 1) or late hibernation ('hiber\_late, after January 1) .

se: binomial standard error bars of prevalence estimates

site\_prev: this is the prevalence of *P. destructans* calculated across all the total bats positive / total bats sampled. This value will be duplicated in every row the is the same site and date.

pdarr: whether Pd was detected during the visit or not

t: This column denotes whether Pd was first detected in the site in late hibernation (winter) or early hibernation (fall).

early.prev.prob: This is the average prevalence of *P. destructans* across a given species during early hibernation

weighted.average.early.num: N\*early.prev.prob; used for calculations for the expected average prevalence of *P. destructans* at a site based on the species community and average prevalence on a species during November.

**mw0.trim.csv**

*Overview:* This CSV file contains data where each row is a swab sample from an individual bat.

*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

*species:* the species of bat sampled, as latin binomial 4 letter codes. The first two letters correspond to the first two of the genus and the second two letters correspond to the first two letter of the species.

*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”.

lgdL: log10( *P. destructans* loads)

*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*.

t: This column denotes whether Pd was first detected in the site in late hibernation (winter) or early hibernation (fall).

pdate2: pdate-11

**preWNS.csv**

*Overview:* This CSV file contains the counts of bats of each species in the years before WNS was detected at a site. These were used for calculating overwinter movements of bats prior to the arrival of WNS.

*Description of columns:*

*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.

*species:* the species of bat sampled, as latin binomial 4 letter codes. The first two letters correspond to the first two of the genus and the second two letters correspond to the first two letter of the species.

*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.

*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).

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

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

*state:* The state where the hibernaculum/bat was sampled

count: the number of bats counted in of that particular species during the trip

lambda: the proportional change in the count from the previous season (e.g. (March count/previous March count). A constant (+1) was added to every count to avoid division by 0.

*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”.

*overwinter.lambda*: The proportional change between the March and November bat count

during the same winter year.

early.winter.count: This is count from the site in early hibernation copied into the same row as the count from late hibernation at a site.

overwinter.diff: count - early.winter.count

log.overwinter.lambda = log10(overwinter.labmda)

log.early.winter.count = log10(early.winter.count)

**site.dat**

*Overview:* This CSV file has a row for each unique site with covariates that were explored to determine their influence on the probability that *P. destructans* was detected in either early or late hibernation.

*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

detection: when Pd was first detected at a site

spec.num: The number of unique species at that site (aka richness)

total: The total number of bat counted at site

sum.mylu: The total number of Myotis lucifugus at the site

sum.myse: The total number of Myotis septentrionalis at the site

sum.epfu: The total number of Eptesicus fuscus at the site

sum.pesu: The total number of Perimyotis subflavus at the site

pd.arrival: 0 if Pd was first detected in late hibernation, 1 if Pd was first detected in the fall

mean.temp: average temperature from HOBO t/rh data loggers in the site. NA if loggers failed.

mean.rh: average humidity from HOBO t/rh data loggers in the site. NA if loggers failed.

mean.rh: average vapor pressure deficit from HOBO t/rh data loggers in the site. NA if loggers failed.

log.overwinter.lambda: The average proportional change between the March and November bat count prior to the arrival of WNS.

early.pdates: The pdate a sampling trip to the site occurred in early hibernation. NA if no bats were present.

**R Files**

**Langwig\_midwinter\_arrival\_ms\_rev.html / Langwig\_midwinter\_arrival\_ms\_rev.rmd**

This html file or R Markdown is an R Notebook and uses the above files to perform the analyses in the paper. It is annotated with specific analyses and output. This file is also an official appendix to the published paper.