Big Brown Bat (Eptesicus fuscus) Post **Hibernation Mass Changes During White-Nose Syndrome** Invasion

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https://georgiabiodiversity.org/portal/profile?es_id=21048&group=bats_

Today's Presentation

Introduction/Background

- Methods
- Results
- Discussion



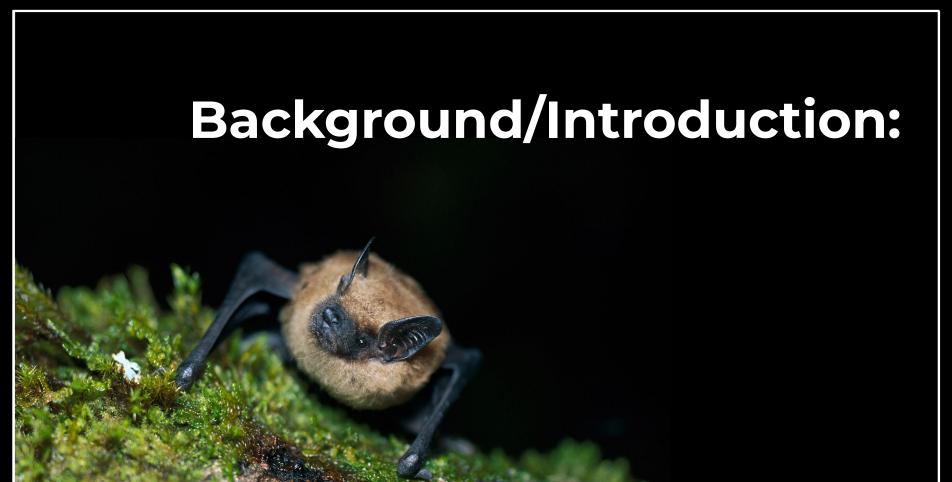


Image by Michael Durham: https://www.batcon.org/bat/eptesicus-fuscus/

What is White Nose Syndrome?

- White Nose Syndrome (WNS) is a disease impacting hibernating bat species caused by the fungal pathogen:
 - Pseudogymnoascus destructans (Pd)
- Pd grows in temperatures between 12-16°C, allowing Pd to thrive in bat winter hibernacula conditions
- as Heterothermic mammals, bat species are vulnerable to WNS when they undergo periods of suppressed immune functioning during torpor/hibernation.



Little Brown Bat with WNS fungus (New York, Oct. 2008.)

WNS and Mass Changes



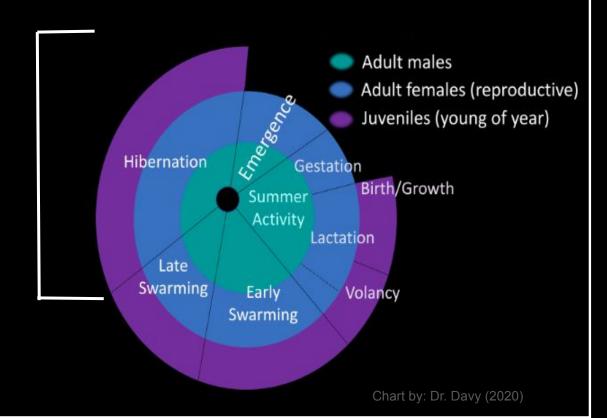
Little Brown Bat with WNS fungus (New York, Oct. 2008.)

- Pd impacts the epithelial tissues of the bats, leaving an uncomfortable white fuzz and fissions on their muzzles and wings (pictured).
- The arousal of Pd infection wakes them up and prematurely burns their brown fat and water, leading to associated losses in mass.

Seasonal Cycles:



Little Brown Bat with WNS fungus (New York, Oct. 2008.)



Seasonal Cycles:

Pd exposure has physiological carry-over effects in the mass of recovered individuals, where:

Energy expenditure of Pd immune responses/stress decreases available energy for emergent seasonal behaviors such as migration to summer hibernacula and initiation of reproduction; w/ differing energy necessities between adult and juvenile male and female bats.

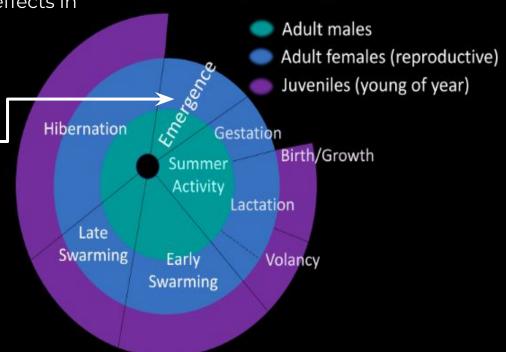
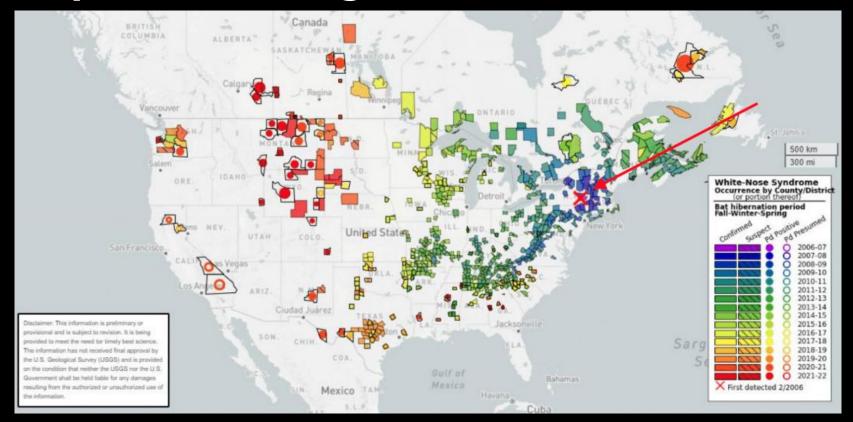


Chart by: Dr. Davy (2020)

Bats of Ontario – local hibernators



Spread of Fungus/Disease Over Time



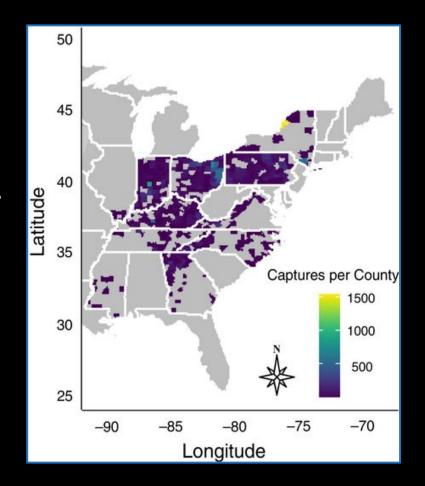
Methodology: Process/Methods



Image by Sherri & Brock Fenton https://norfolknaturalist.ca/2023

About Our Data:

- Big brown bat (EPFU) captured & recorded from 1990-2010
- 30,497 individual records across 3,797 unique capture sites across eastern United States
- Age, sex, reproductive status, mass, forearm length, etc.
- Focus on mass (more directly impacted by WNS)



Process:

- Attempt 1
 - Gamma distribution. Attempted to find MLE, where parameters are maximized (shape, scale)
 - Mean = shape * scale
 - Variance = shape * scale^2
 - CI: lower shape * lower scale upper shape * upper scale
- Attempt 2
 - Try to model using different types of distributions
- Attempt 3
 - GLMMs using gamma distribution



Model Section: Gamma vs Normal distribution

- Gamma distribution AIC = 155189
- Normal distribution AIC = 156321
- Gamma distribution more appropriate than normal (lower AIC)

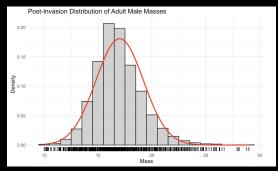


Figure x: Distribution modeled using a normal distribution for Post-Invasion Adult Male Masses.

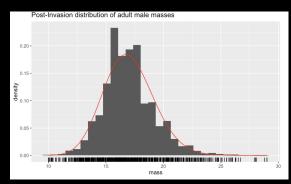


Figure x: Distribution modeled using a **gamma distribution** for Post-Invasion Adult Male Masses.

Hypotheses:

- Null hypothesis
 - Age and sex are not correlated with the effect of *Pd* on mass of EPFU
- Alternative hypothesis
 - Age and sex are correlated with the effect of Pd on mass of EPFU
- Prediction:
 - Mass and mass variation fitted on a
 Gamma distribution will decrease over
 Pd exposure time



Methods of Analysis:

- Original study fit linear mixed models with normal distributions
- Generalized Linear Mixed Model using Gamma distribution → glmer()
- Link function: "log"
 - multiplicative effects → additive on log scale
 - better than others
- Trying different fixed and random effects, looking at coefficients for effects on mass
- Elevation as a fixed effect → unable to obtain elevation data





Comparison of Random Effects

Random Effects Tested:

- 1. **Model 1**: Random intercept for year
- 2. **Model 2**: Random intercept for site_mask.
- 3. **Model 3**: Random intercept for state

Model	Random Effect	AIC
Model 1	year	138844.5
Model 2	site_mask	132567.2
Model 3	state	137431.1

Figure x: Model Comparison: Site_mask model fits bat mass data best.

Model 2 (Random Effect: site_mask) has the lowest AIC, indicating it provides the best fit for the data.



Results: Gamma GLMM with Random Effects

```
Formula: mass ~ disease_group * sex * pregnancy_status * age + (1 | site_mask)
   Data: data new
     AIC
             BIC logLik deviance df.resid
132567.2 132667.1 -66271.6 132543.2
Scaled residuals:
            10 Median
-4.7955 -0.6163 -0.0102 0.5994 6.4132
Random effects:
                      Variance Std.Dev.
 Groups
          Name
 site_mask (Intercept) 0.003297 0.05742
 Residual
                      0.013525 0.11630
Number of obs: 30496, groups: site_mask, 3797
Fixed effects:
                                                   Estimate Std. Error t value Pr(>|z|)
(Intercept)
                                                   2.967439
                                                             0.002390 1241.774 < 2e-16 ***
disease_aroupPre-Invasion
                                                             0.004951
                                                   0.015950
                                                                         3.222 0.00128 **
sexmale
                                                  -0.138996
                                                             0.001839 -75.570 < 2e-16 ***
pregnancy_statusPregnant
                                                   0.151456
                                                             0.003565 42.486 < 2e-16 ***
                                                             0.002675 -72.630 < 2e-16 ***
agejuvenile
                                                  -0.194312
disease_groupPre-Invasion:sexmale
                                                             0.005010
                                                  -0.001418
                                                                        -0.283 0.77723
disease_groupPre-Invasion:pregnancy_statusPregnant -0.028060
                                                             0.009989
                                                                        -2.809 0.00497 **
disease_groupPre-Invasion:agejuvenile
                                                   0.021801
                                                             0.007604
                                                                         2.867 0.00415 **
sexmale:agejuvenile
                                                   0.072712
                                                             0.003635
                                                                        20.005 < 2e-16 ***
disease_groupPre-Invasion:sexmale:agejuvenile
                                                   0.003845 0.010337
                                                                         0.372 0.70988
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data Overview

- Focus: Pre- and Post-Invasion Bat Mass Differences with different fixed effects
- Predictors: disease_group, sex, pregnancy_status, age
- Random Effects: site_mask
- Key Fixed Effects:
 - disease_group Pre-Invasion:
 - pregnancy_status Pregnant:
 - o age juvenile:

GLMM captures the skewed distribution of bat mass better than LMM.

Figure x: GLMM Summary: Key predictors and variances for bat mass.

Family: Gamma (loa)

Results: Interaction Plot

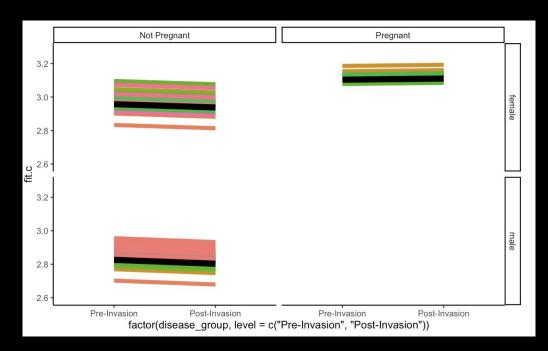


Figure x: Predicted log-mass by disease group, sex, and pregnancy status.

Key Takeaways

 Gamma GLMM captures positively skewed mass data for pregnant bats.

 Significant predictors include disease_group, pregnancy_status, and age.

 Random effect for site_mask accounts for spatial variability.

Conclusion:

- Alt hypothesis/prediction accepted:
 - Age and sex are correlated with the effect of *Pd* on mass of EPFU, with the Gamma as the best fit to account for the skewed distribution of mass compared to the Normal Distribution (i.e. for pregnant status)
- Gamma GLMM highlights the ecological implications of WNS, where disease introduction (by year), sex, and reproductive status, highlight the understanding of bat mass dynamics across geographic regions during invasion periods.



Literature Cited:

- Adams, A. M., Trujillo, L. A., Campbell, C. J., Akre, K. L., Arroyo-Cabrales, J., Burns, L., Coleman, J. T. H., Dixon, R. D., Francis, C. M., Gamba-Rios, M., Kuczynska, V., McIntire, A., Medellín, R. A., Morris, K. M., Ortega, J., Reichard, J. D., Reichert, B., Segers, J. L., Whitby, M. D., & Frick, W. F. (2024). The state of the bats in North America. Annals of the New York Academy of Sciences, 1541(1), 115–128. https://doi.org/10.1111/nyas.15225
- Davy, C. M., Mastromonaco, G. F., Riley, J. L., Baxter-Gilbert, J. H., Mayberry, H., & Willis, C. K. R. (2017). Conservation Implications of Physiological Carry-Over Effects in Bats Recovering from White-Nose Syndrome. *Conservation Biology*, *31*(3), 615–624. https://doi.org/10.1111/cobi.12841
- lamba, K. (2022). Data analysis of flea beetle (Psylliodes chrysocephala L.): Comparing three (3) distribution families of generalized linear model. *Journal of Entomology and Zoology Studies*, *10*(1), 388-394.
- Simonis, M. C., Hartzler, L. K., Turner, G. G., Scafini, M. R., Johnson, J. S., & Rúa, M. A. (2023). Long-term Exposure to an Invasive Fungal Pathogen Decreases *Eptesicus fuscus* Body Mass with Increasing Latitude. *Ecosphere*, *14*(2), e4426. https://doi.org/10.1002/ecs2.4426

Thank you! Questions?

