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

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Photo by: J. Scott Altenbach
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Today's Presentation

- Introduction/Background
- Methods
- Results
- Discussion

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

Background/Introduction:

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.)

Credit: Ryan von Linden/NY DEC
https://www.whitenosesyndrome.org/static-page/what-is-white-nose-syndrome

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.**

Credit: Ryan von Linden/NY DEC
https://www.whitenosesyndrome.org/static-page/what-is-white-nose-syndrome

Seasonal Cycles:

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

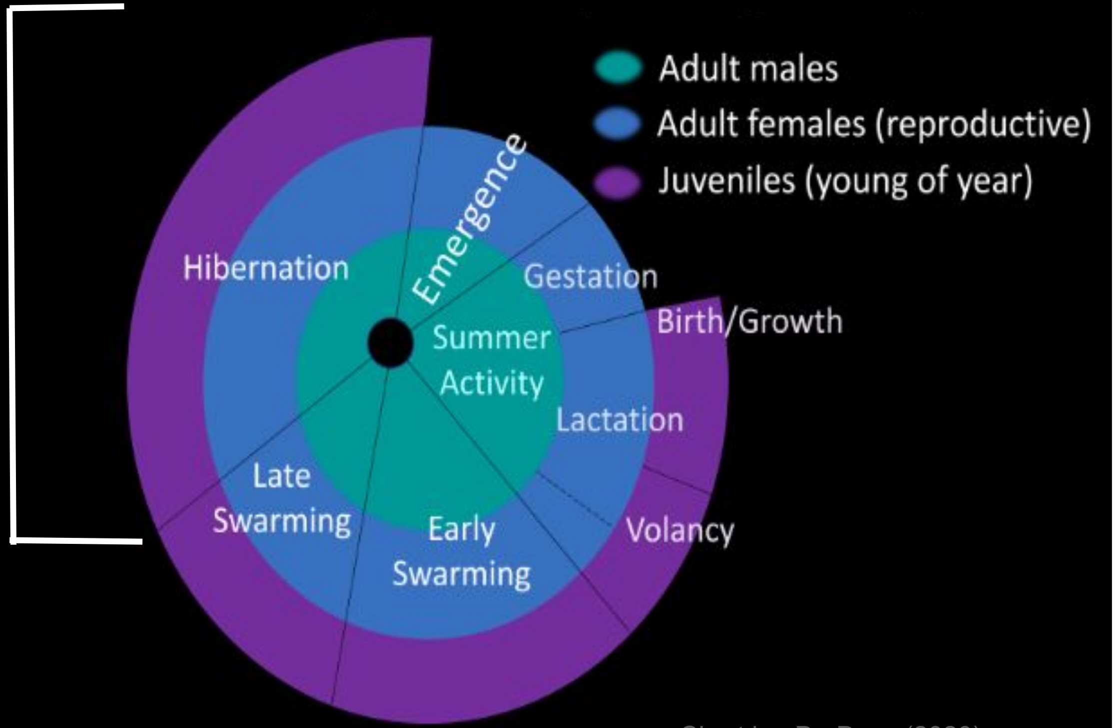


Chart by: Dr. Davy (2020)

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.

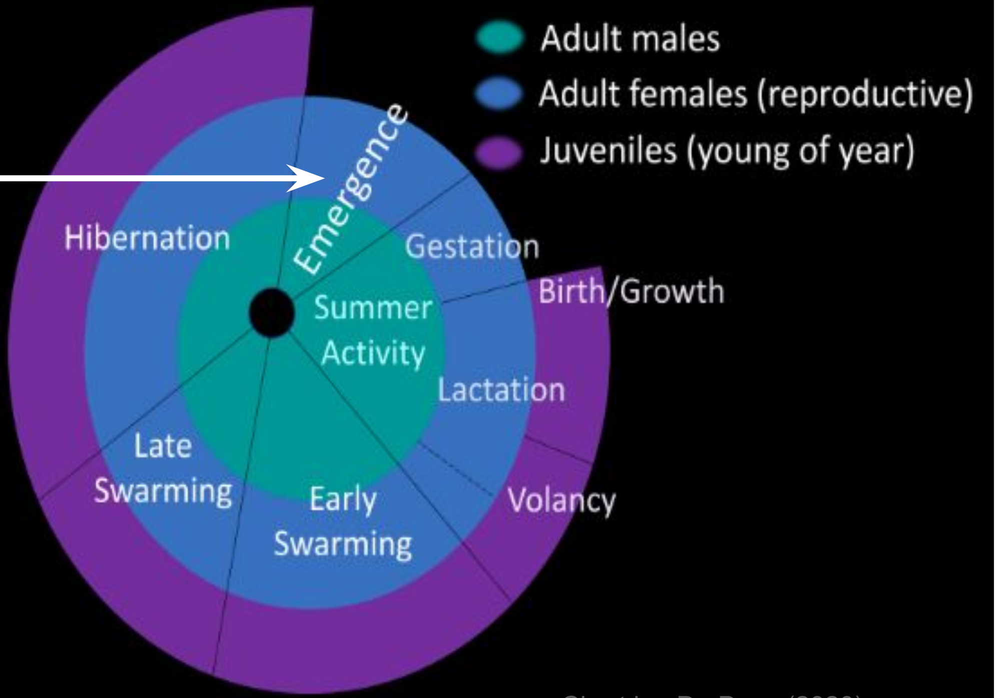
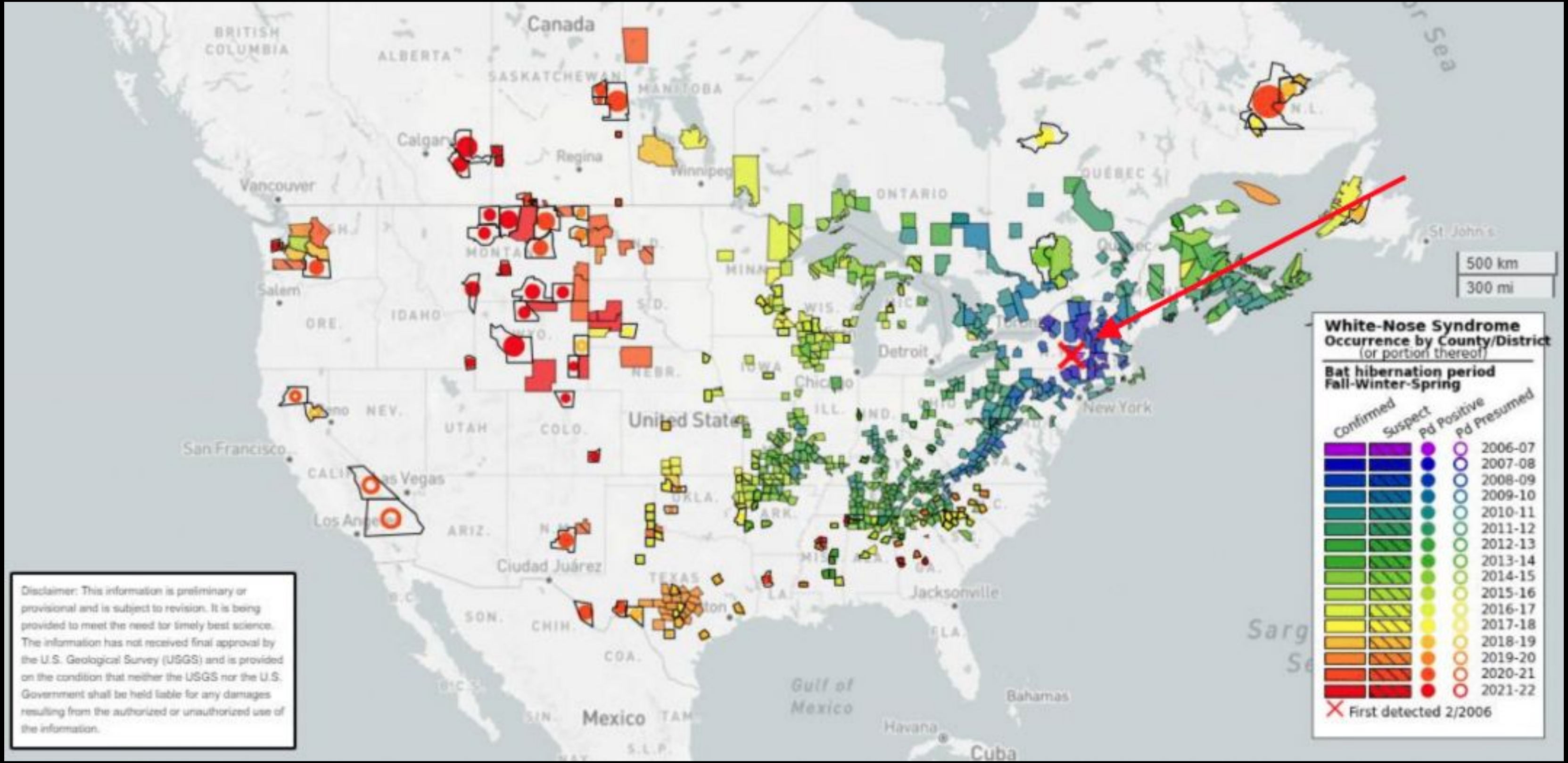


Chart by: Dr. Davy (2020)

Bats of Ontario – local hibernators

Photos: Charles Francis / Brock and Sherri Fentor

Spread of Fungus/Disease Over Time



Methodology:
Process/Methods

Image by Sherri & Brock Fenton
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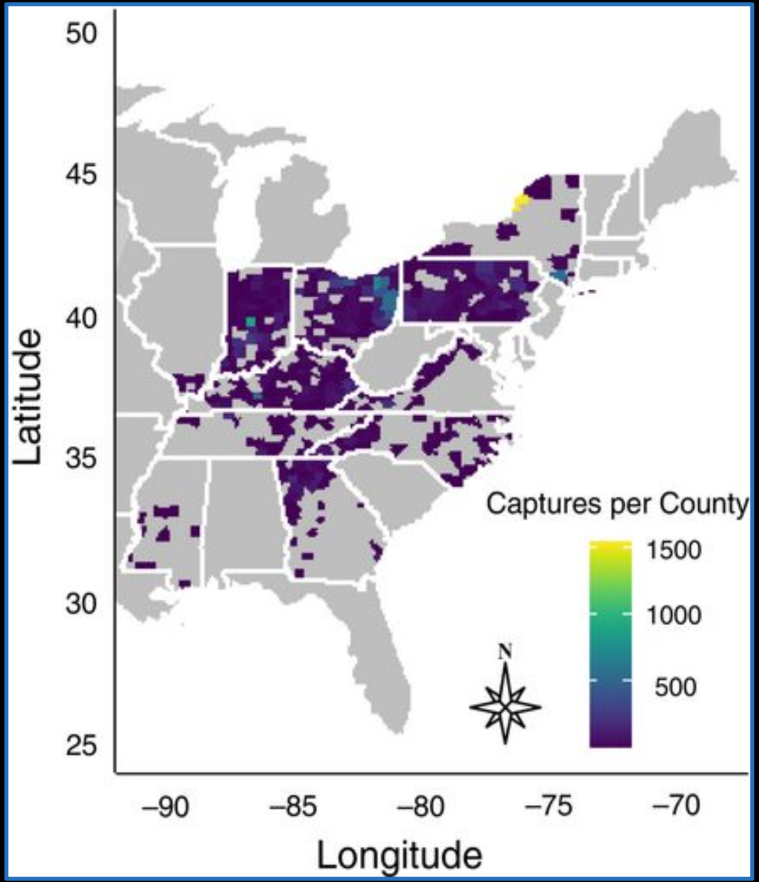
About Our Data:

- 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.
- Simplified to pre/post-invasion, pregnant/non-pregnant
- 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

Photo by: J. Scott Altenbach

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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

Photo by: J. Scott Altenbach

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Model Section: Gamma vs Normal distribution

- Original study fit linear mixed models with normal distributions
- **Gamma distribution** AIC = 155189
- **Normal distribution** AIC = 156321
- Gamma distribution more appropriate than normal **(lower AIC)**

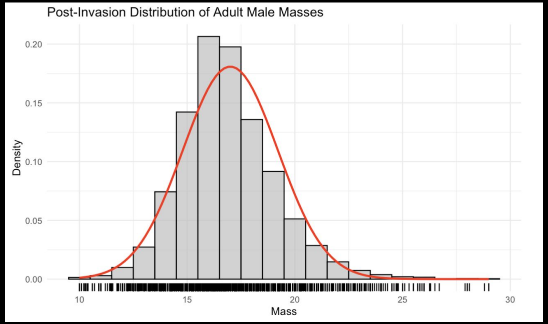

Figure x: *Distribution modeled using a **normal distribution** for Post-Invasion Adult Male Masses.*

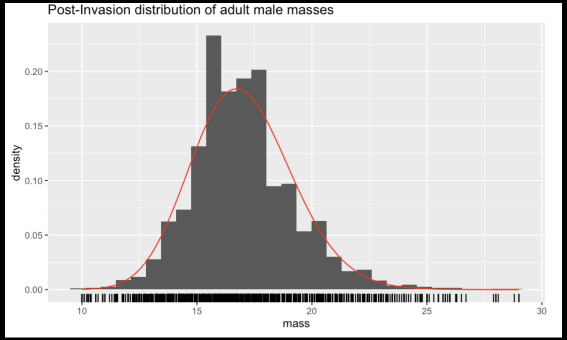

Figure x: *Distribution modeled using a **gamma distribution** for Post-Invasion Adult Male Masses.*

Methods of Analysis:

- 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

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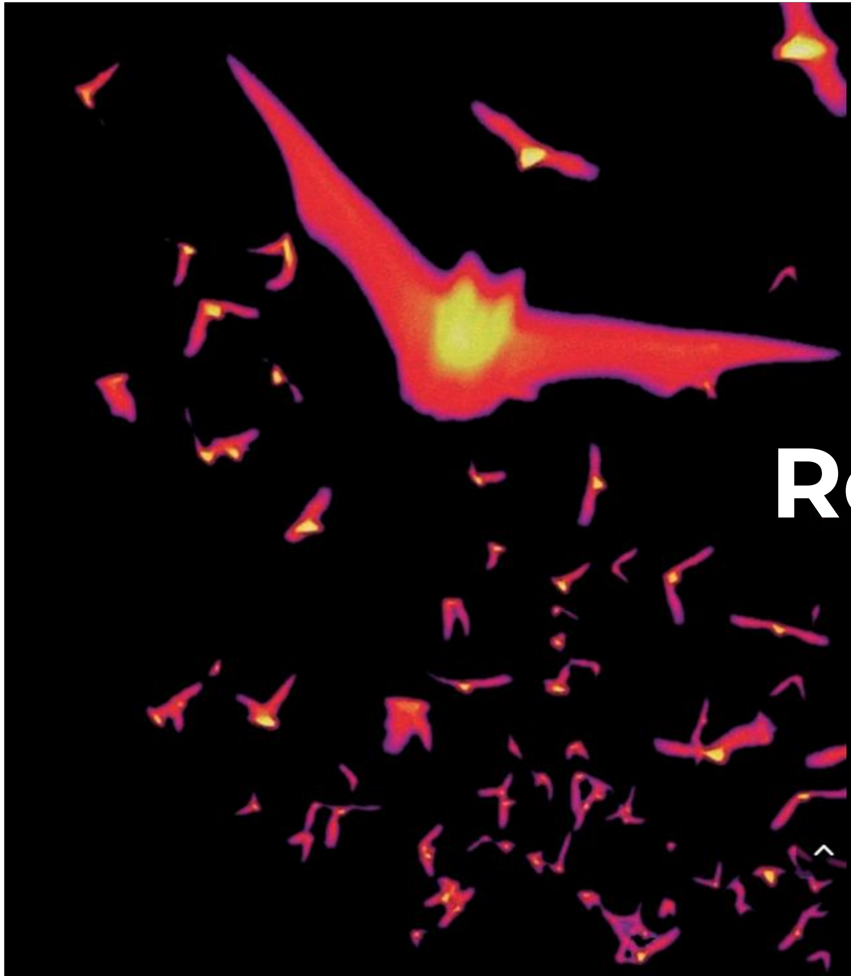

Results/Discussion

https://www.animalcapturewildlifecontrol.com/blog/big-brown-bats-101-understanding-our-nocturnal-neighbors/

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.**

Image by Traer Scott
https://socialbat.org/videos

Results: Gamma GLMM with Random Effects

```
 Family: Gamma  ( log )
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    30484

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.7955 -0.6163 -0.0102  0.5994  6.4132

Random effects:
 Groups    Name        Variance Std.Dev.
 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_groupPre-Invasion                          0.015950   0.004951    3.222  0.00128 **
sexmale                                           -0.138996   0.001839  -75.570  < 2e-16 ***
pregnancy_statusPregnant                           0.151456   0.003565   42.486  < 2e-16 ***
agejuvenile                                       -0.194312   0.002675  -72.630  < 2e-16 ***
disease_groupPre-Invasion:sexmale                 -0.001418   0.005010   -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
```

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

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:
  - age juvenile:

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

Results: Interaction Plot

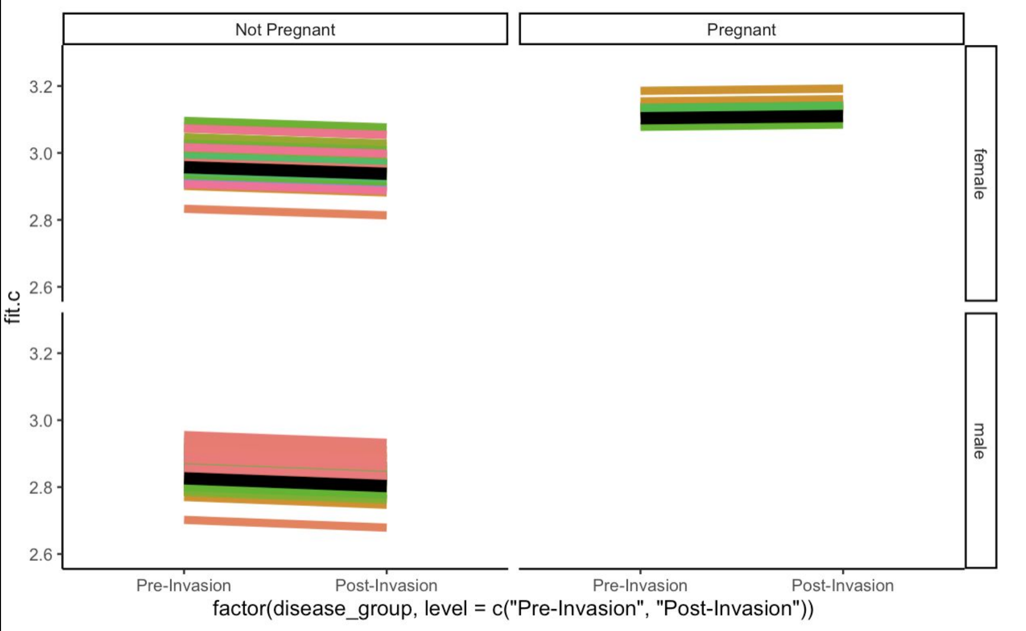

Figure x: Predicted log-mass by disease group, sex, and pregnancy status.

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.

Discussion:

- Research by Cheng et al. (2019), indicated that higher fat stores could reduce WNS mortality by 58%–70%. These results suggest that differences in fat storage and infection dynamics have reduced the impacts of WNS in many populations.
- Gamma GLMM is suited for the many variables accounted for in this study, where disease introduction (by year), sex, and reproductive status, highlight the ecological implications of understanding bat mass dynamics across geographic regions during invasion periods.

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Thank you!
Questions?

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