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

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Photo by: J. Scott Altenbach
https://georgiabiodiversity.org/portal/profile?es_id=21048&group=bats

# 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; *Pd* thrives in bat winter hibernacula conditions
- as *Heterothermic mammals*: bat species are vulnerable during torpor/hibernation w suppressed immune functioning.

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.)

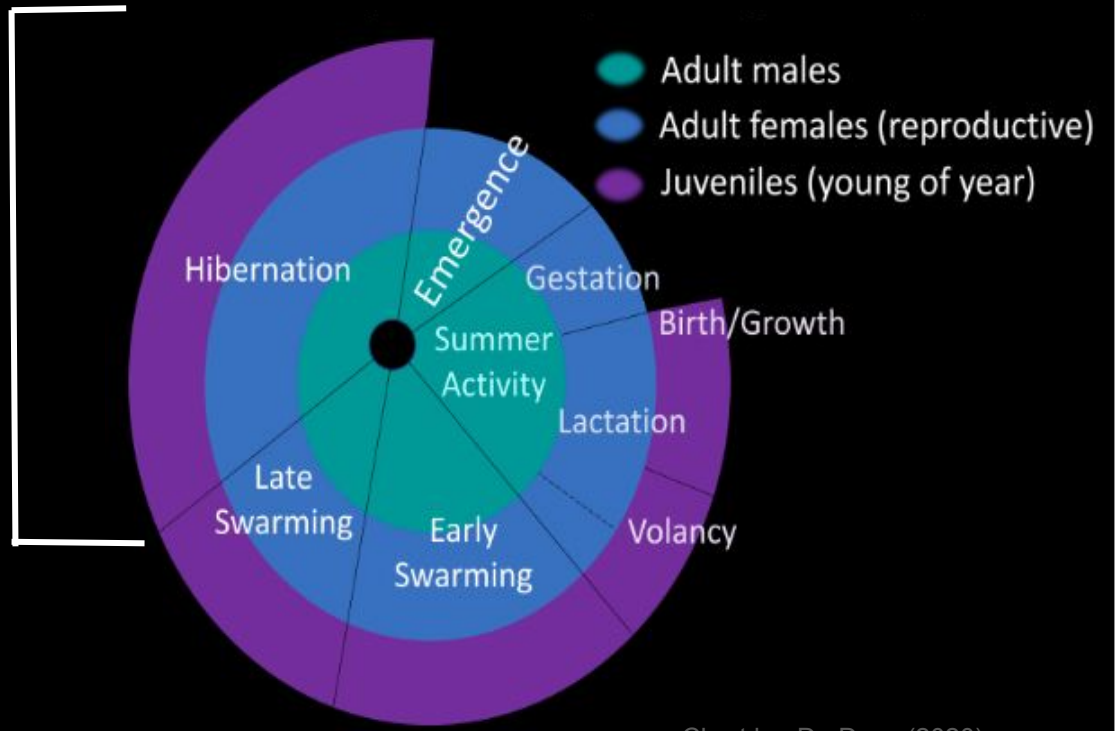



Chart by: Dr. Davy (2020)

# Seasonal Cycles:

Pd exposure has 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.

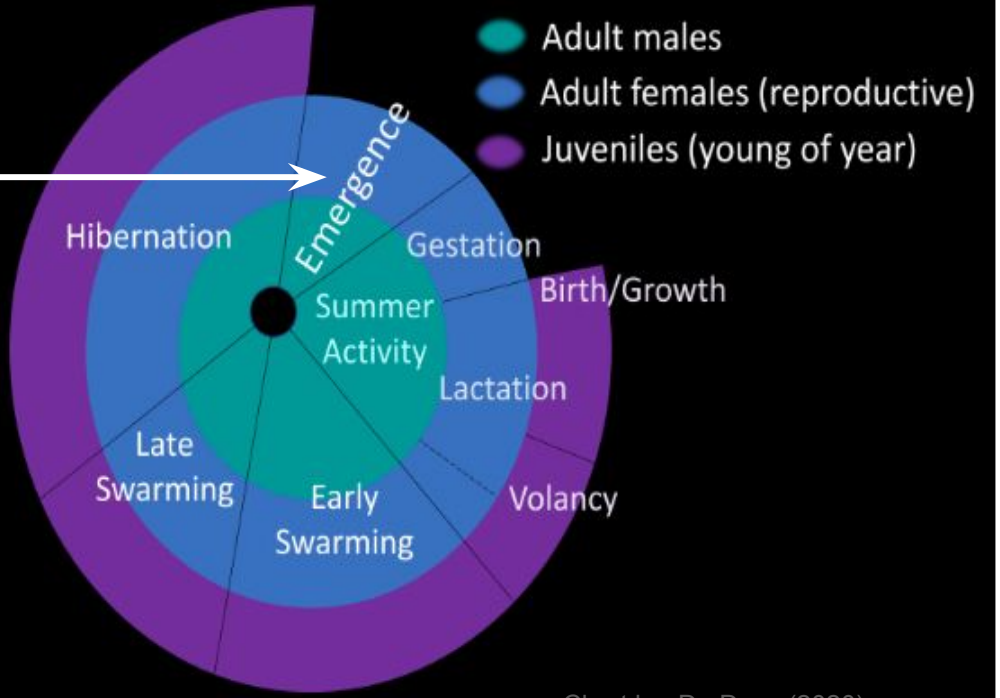
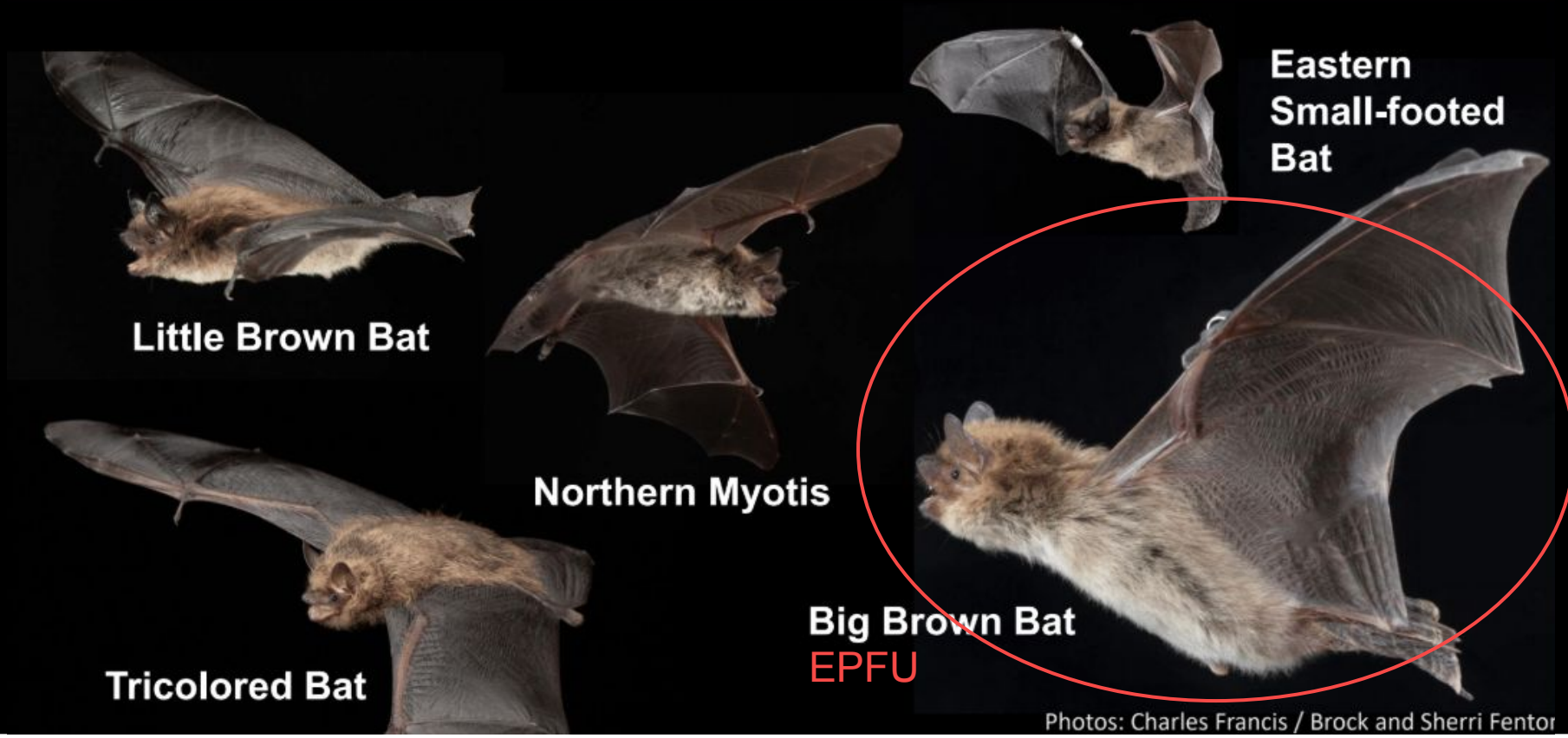
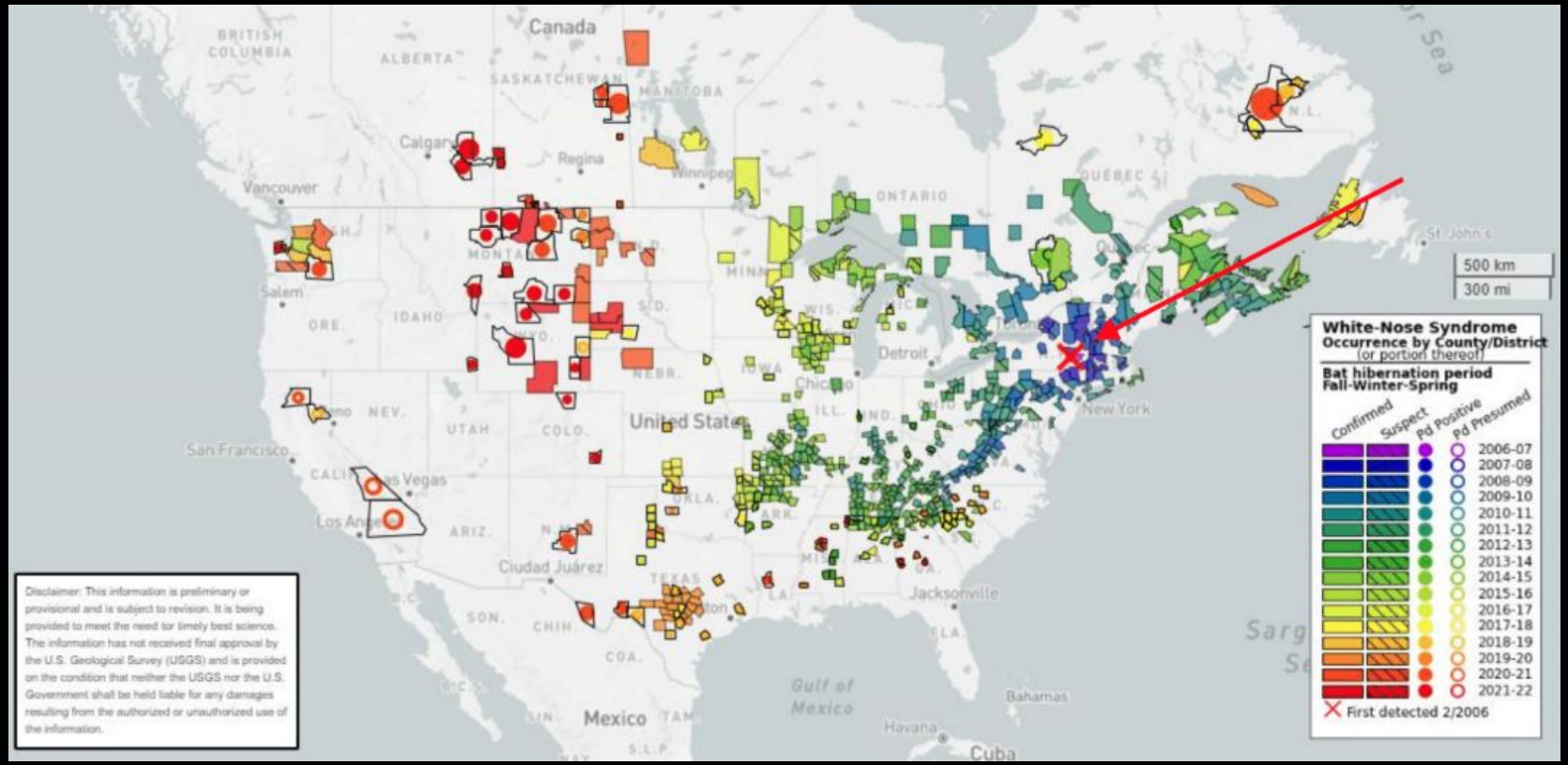



Chart by: Dr. Davy (2020)

# Bats of Ontario – local hibernators



# Spread of Fungus/Disease Over Time

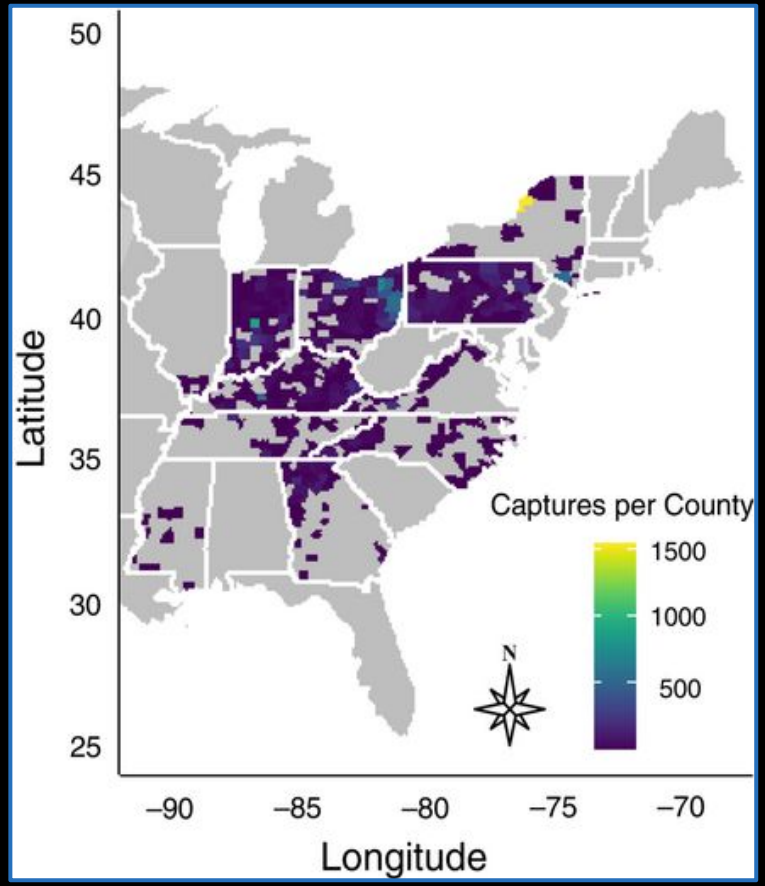


# **Methodology:**
# Process/Methods

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

# About Our Data:

- Big brown bat (EPFU) captured & recorded from 1990-2010 by Simonis et al., (2023)
- 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

**Photo by: J. Scott Altenbach**
https://georgiabiodiversity.org/portal/profile?es_id=21048&group=bats

# 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
- Generalized Linear Mixed Model using Gamma distribution → glmer()
- **Gamma distribution** AIC = 155189
- **Normal distribution** AIC = 156321
- Gamma distribution more appropriate than normal **(lower AIC)**

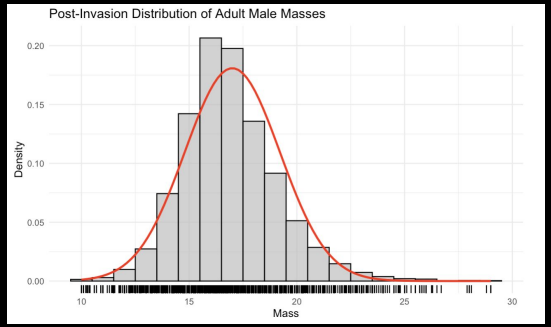


***Figure x**: Distribution modeled using a **normal distribution** for Post-Invasion Adult Male Masses.*

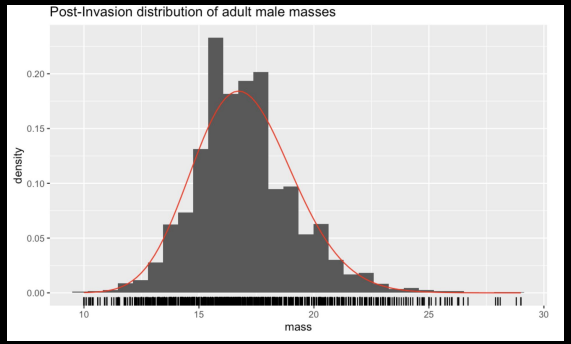


***Figure x**: Distribution modeled using a **gamma distribution** for Post-Invasion Adult Male Masses.*

# Methods of Analysis:

- 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 data

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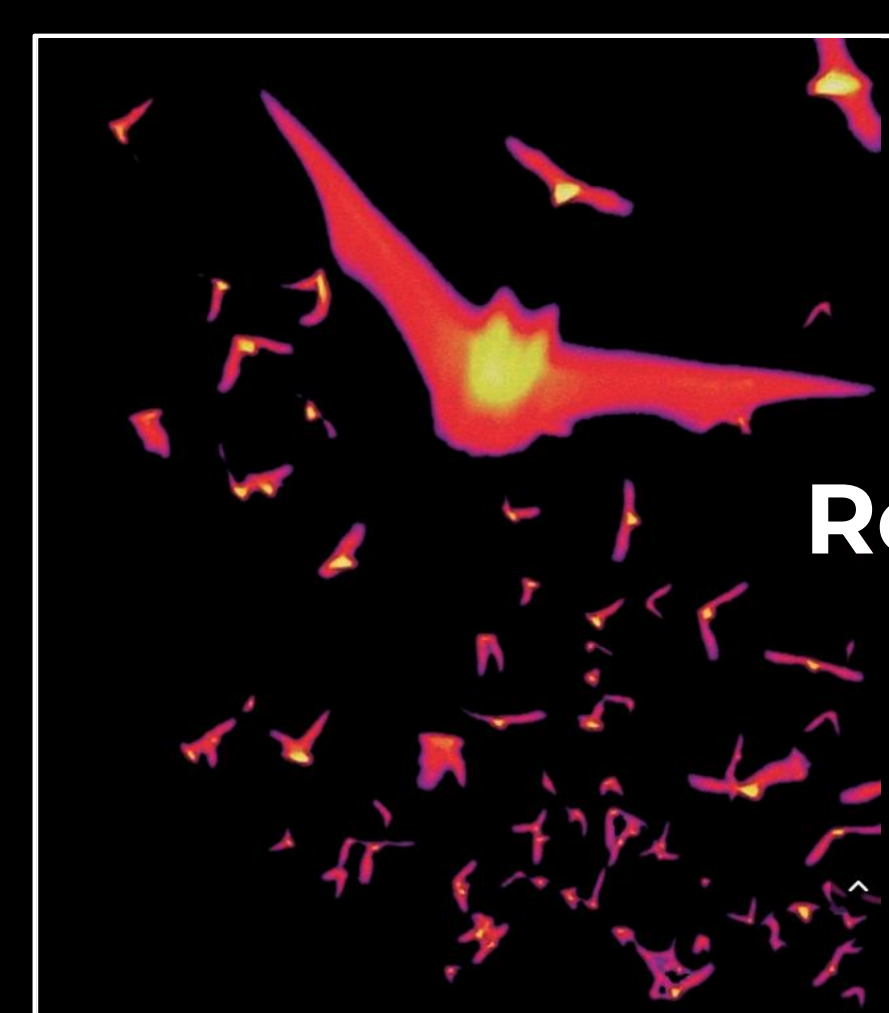

# Results/Discussion

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

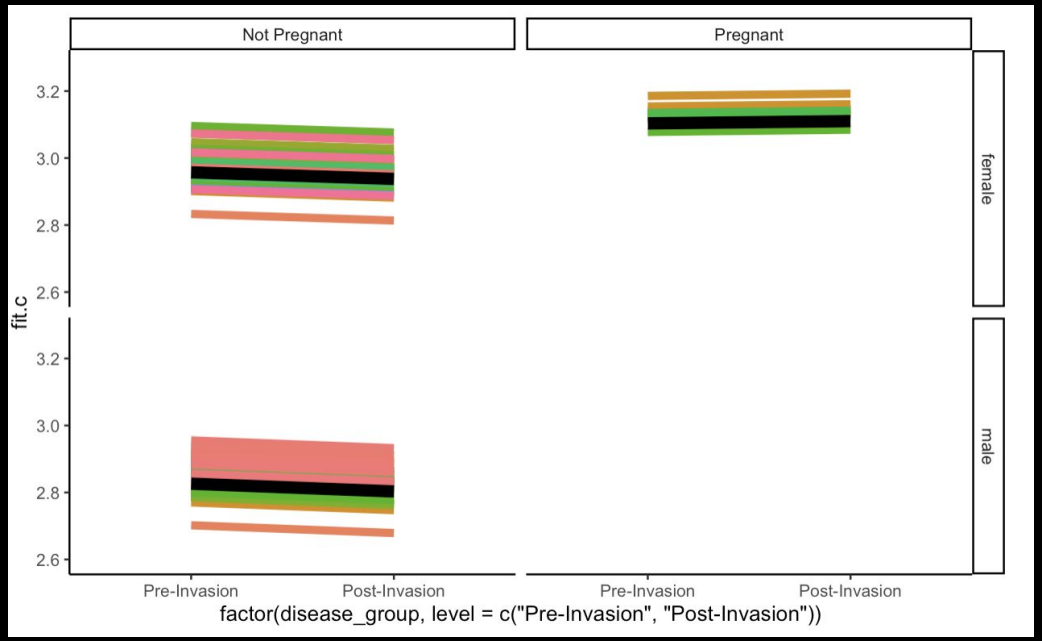


*Figure x: Predicted log-mass by disease group, sex, and pregnancy status.*

**Key Takeaways**

- **Gamma GLMM** captures positively skewed mass data.
- 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 accounts for 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:


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https://socialbat.org/videos

# Thank you!
# Questions?


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