Linking Potentially Misclassified Healthy Food Access to Diabetes Prevalence

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WSDS 2025

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Coming Soon to Theaters

1. **Invited Talk**: Linking Potentially Misclassified Healthy Food Access to Diabetes Prevalence
   Women in Statistics and Data Science Conference - November 2025
   Slides

Today, we'll cover:

1. Motivation
2. Methods
3. Simulations
4. Case Study
5. Wrap Up

1

Motivation

Healthy Eating ➡️ Healthy Living

- A **healthy diet** is full of fruits, vegetables, whole grains, and other high-nutrient foods.
- A healthy diet increases the likelihood of good overall health and **decreases risk of preventable illness** (World Health Organization, 2019).
- Maintaining a healthy diet requires **consistent access to healthy food**, which may be hindered by physical or social barriers like geography or income.
- Review studies found **high prevalence of diabetes** in food-insecure households (Gucciardi et al., 2014).

Measuring Food Access 🍎

- Define a **neighborhood** of interest with a **radius**, a **centroid**, and possibly some **healthy food retailers**.
- We pick one of **three common methods** to quantify food access.

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density: 2

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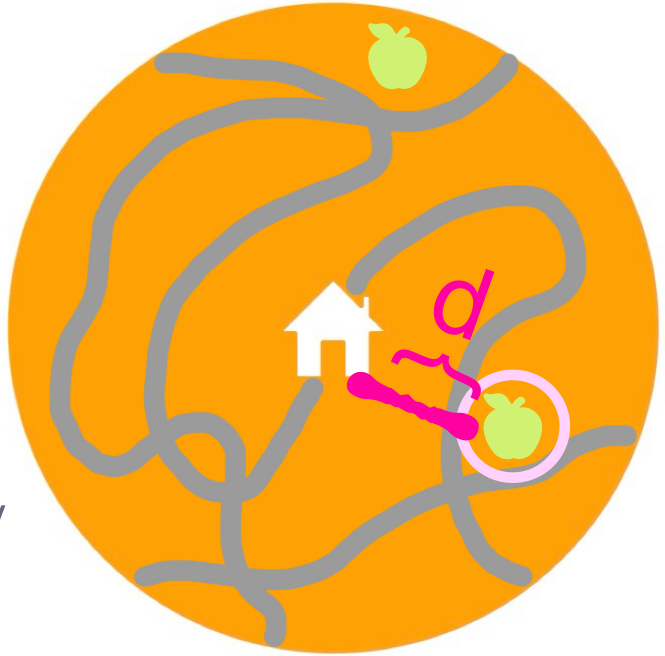

proximity: d

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indicator: 👍

Measuring Food Access 🍎

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Draw a straight line?

Measuring Food Access 🍎

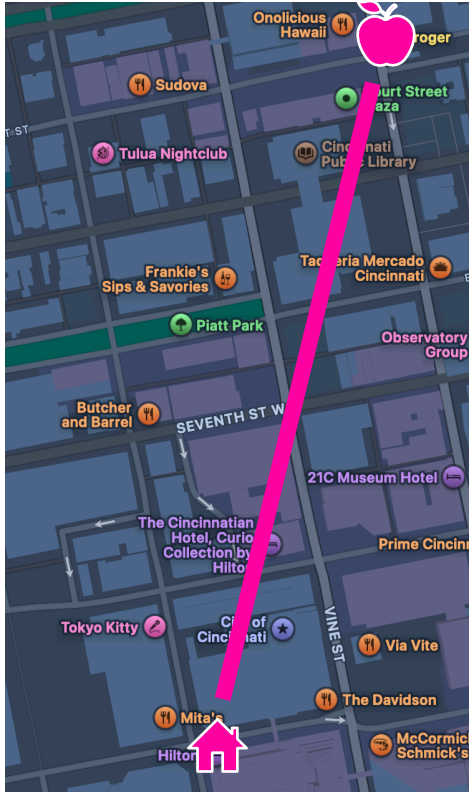
- All of these methods require some notion of **distance**!

Draw a straight line?

Follow the road?

Distance Computations

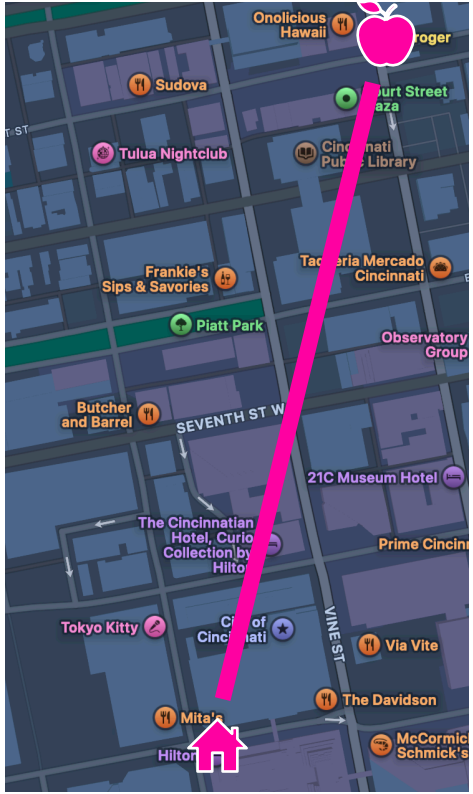
- The **Haversine distance** is a trigonometric function of latitude and longitude.
- It ignores physical obstacles, so it **underestimates** the true distance between two points and is considered **error-prone**.



0.4 miles

Distance Computations

- The **route-based** distance works around obstacles.
- It is **more accurate** than the Haversine distance, but it is **computationally and financially expensive**.
- These distances can be found with the **ggmap** package in R, which queries Google Maps.



0.7 miles

We're left with a data challenge!

- In a **perfect world**, we'd have the route-based access indicators for **every neighborhood** of interest.
- In **real life**, we have a cap on how many route-based distances we can get, so **not every neighborhood** has an available route-based access indicator.
- Luckily, we do have a (**potentially misclassified**) Haversine-based access indicator for **every neighborhood**. Sometimes, we have both!

2

Methods

For neighborhood i, we observe:

$$(Y_i, X_i, X_i^*, \mathbf{Z}_i)$$

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outcome, number of diabetes cases in the neighborhood

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error-prone but always available

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correct but only available if query indicator $Q_i = 1$

covariate vector (assumed to be error-free)

$\mathbf{Z}_i \in \mathbb{R}^k$

$$(Y_i, X_i, X_i^*, \mathbf{Z}_i)$$

exposure, representing the food access indicator for that neighborhood

$X_i \in \{0,1\}$

error-prone but always available

How do we query?

- Having X for **some** of the **N** neighborhoods is better than having it for none!
- **Two phase design** maximizes the utility of the available information.
- We **only** have X* for **N - n** neighborhoods, but we have **both** X* and X for **n** of them!
- X* is subject to **misclassification**, but X is subject to **missingness**.

We break down each queried observation.

$$P(Y_i, X_i, X_i^*, \mathbf{Z}_i) = P_\beta(Y_i \mid X_i, \mathbf{Z}_i) P_\eta(X_i \mid X_i^*, \mathbf{Z}_i) P(X_i^*, \mathbf{Z}_i)$$

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$$Y_i \mid X_i, \mathbf{Z}_i \sim \text{Poisson}(\beta_0 + \beta_1 X_i + \beta_2 \mathbf{Z}_i + \log(O_i))$$

$\exp(\beta_1)$ gives us the target association

outcome model

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$\exp(\beta_1)$ gives us the target association

outcome model

error model

$$X_i \mid X_i^*, \mathbf{Z}_i \sim \text{Bernoulli}(p_i)$$

$$p_i = \text{expit}(\eta_0 + \eta_1 X_i + \eta_2 \mathbf{Z}_i)$$

We break down each unqueried observation.

$$P(Y_i, X_i^*, \mathbf{Z}_i) = \sum_{x=0}^{1} P_\beta(Y_i \mid X_i = x, Z) P_\eta(X_i = x \mid \mathbf{Z}_i) P(X_i^*, \mathbf{Z}_i)$$

We break down each unqueried observation.

marginalize over X

$$P(Y_i, X_i^*, \mathbf{Z}_i) = \sum_{x=0}^{1} P_\beta(Y_i \mid X_i = x, Z) P_\eta(X_i = x \mid \mathbf{Z}_i) P(X_i^*, \mathbf{Z}_i)$$

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outcome model (same Poisson)

error model (same Bernoulli)

We stack the observations to build the likelihood.

$$\mathscr{L}_N(\beta, \eta) = \prod_{i=1}^{N} \{P(X_i, X_i^*, Y_i, \mathbf{Z}_i)\}^{Q_i} \{P(X_i^*, Y_i, \mathbf{Z}_i)\}^{1-Q_i}$$

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queried neighborhoods

We now compute an MLE.

- We **maximize** the likelihood function via an **EM algorithm** (Dempster et. al, 1977).
- We estimate **standard errors** via numerical differentiation.

3

Simulations

We follow this estimation procedure.

Generate:
1. Z
2. X* | Z
3. X | X*, Z
4. Y | X, Z

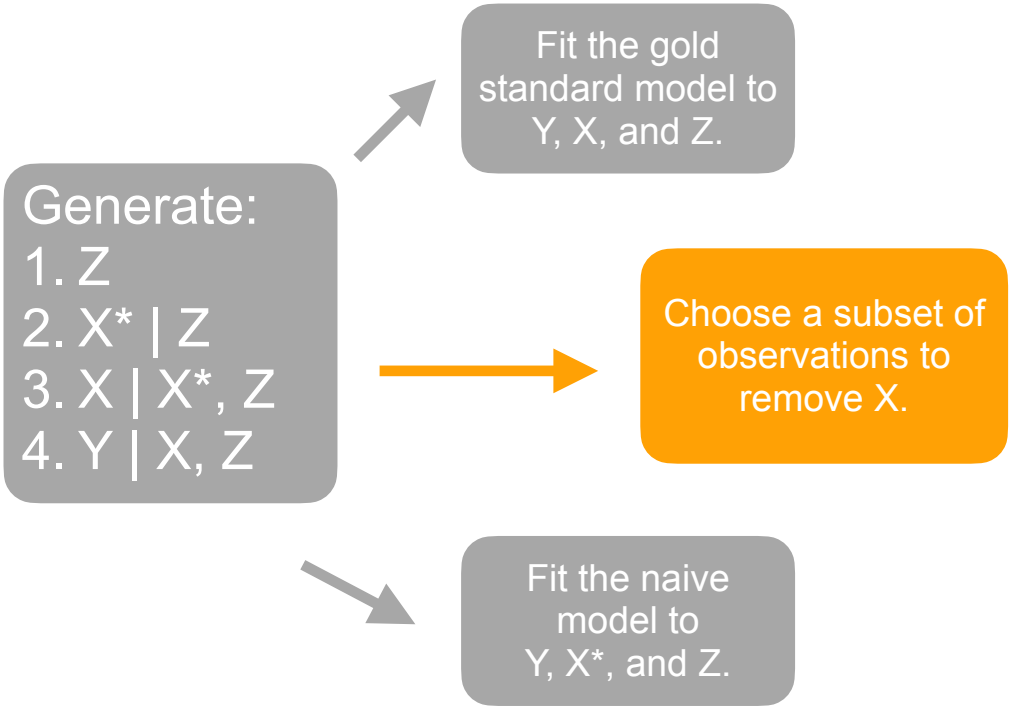
We follow this estimation procedure.

Generate:
1. Z
2. X* | Z
3. X | X*, Z
4. Y | X, Z

Fit the gold standard model to Y, X, and Z.

Fit the naive model to Y, X*, and Z.

We follow this estimation procedure.



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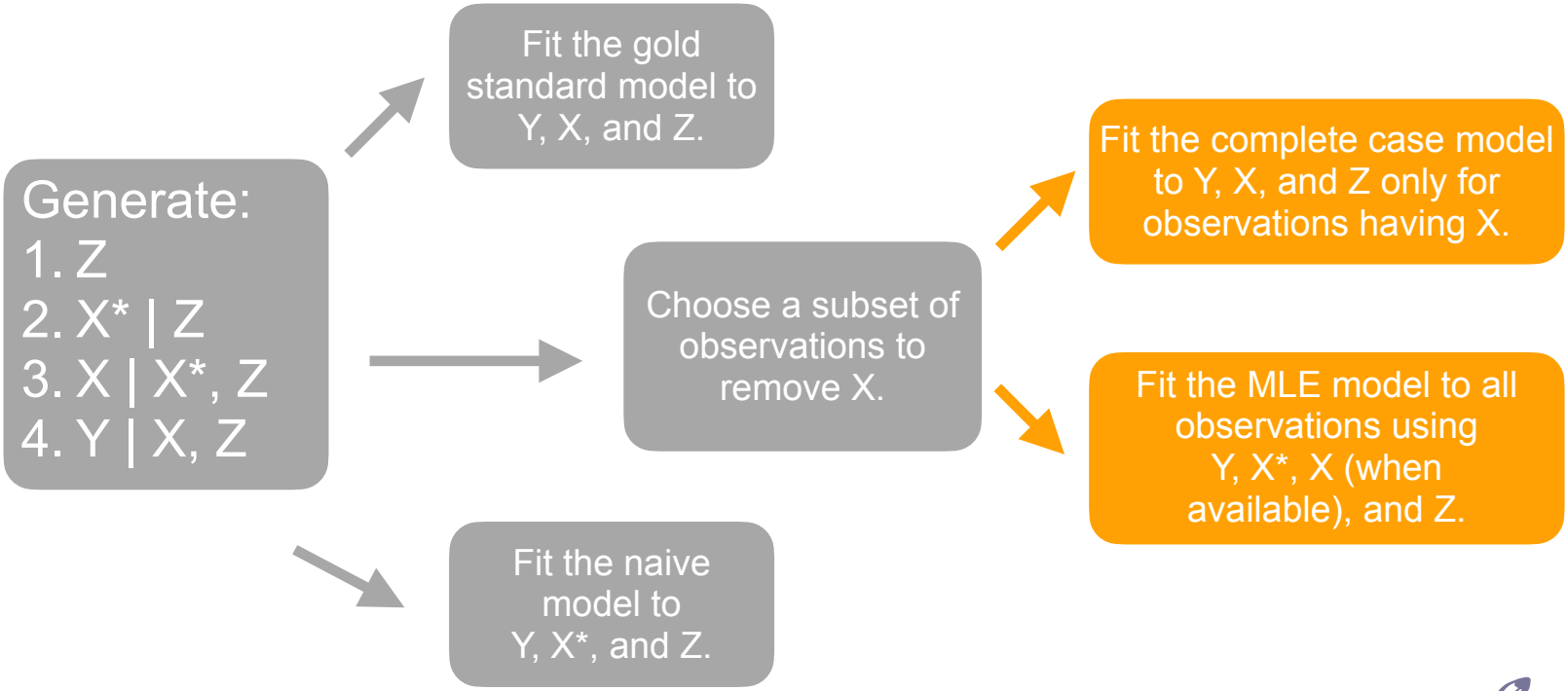
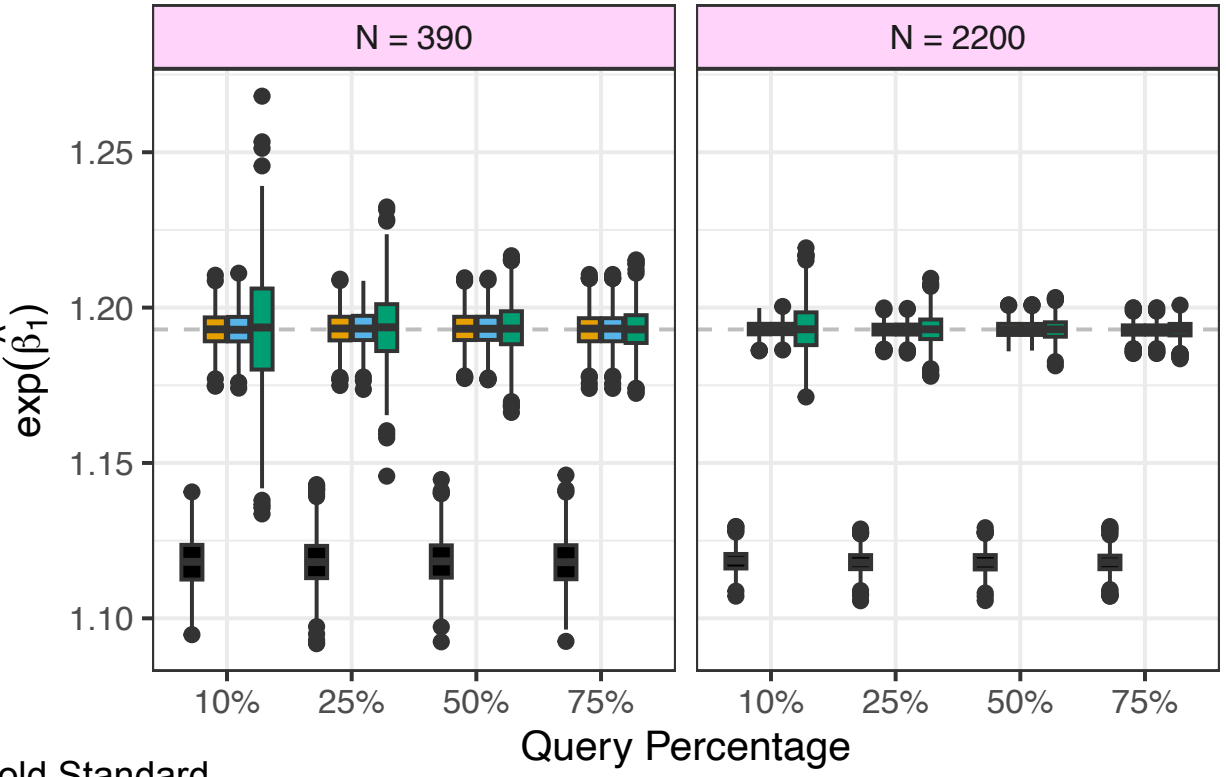


We focus on two variations.

- We're looking to estimate **exp(β_1)**, the **prevalence ratio**.
- Study 1: *What happens as we query fewer observations?* We'll fix everything but the **query proportion** and then repeat the study with more neighborhoods.
- Study 2: *What happens as the errors become more drastic?* We'll fix everything but the **positive predictive value** and then repeat the study with more neighborhoods.

What happens as we vary the query size?



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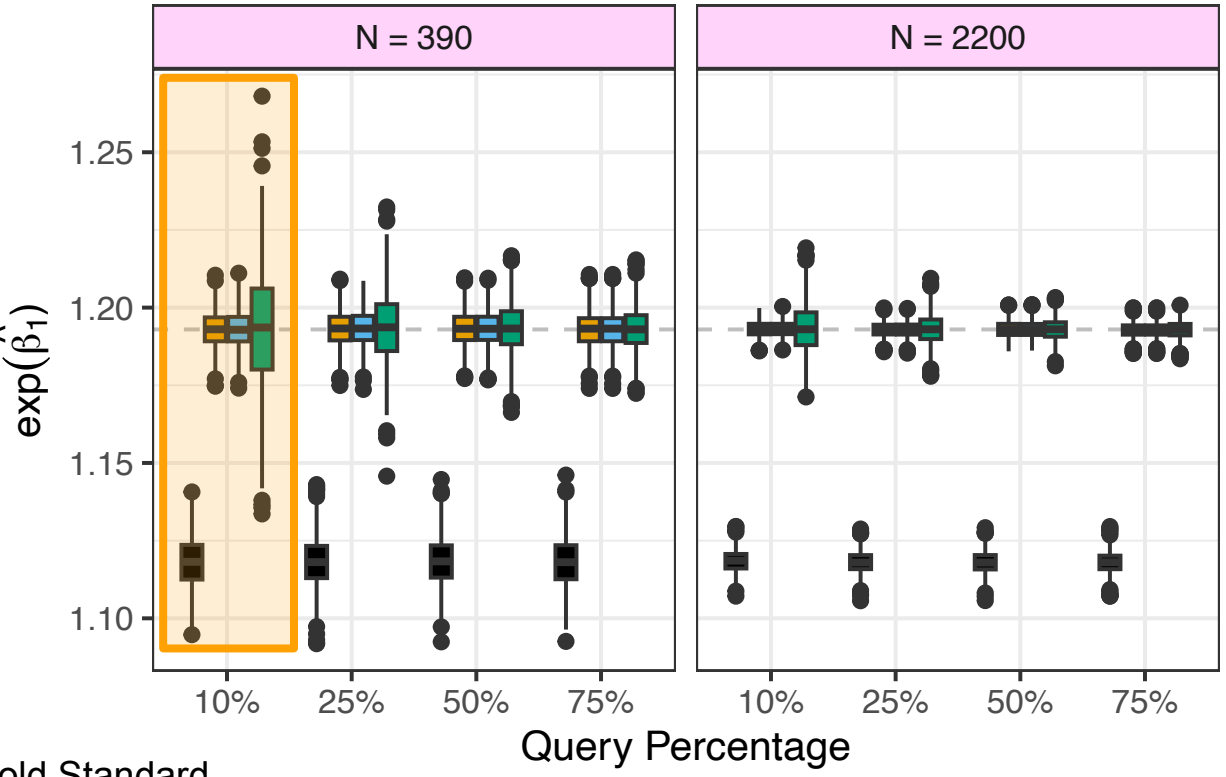

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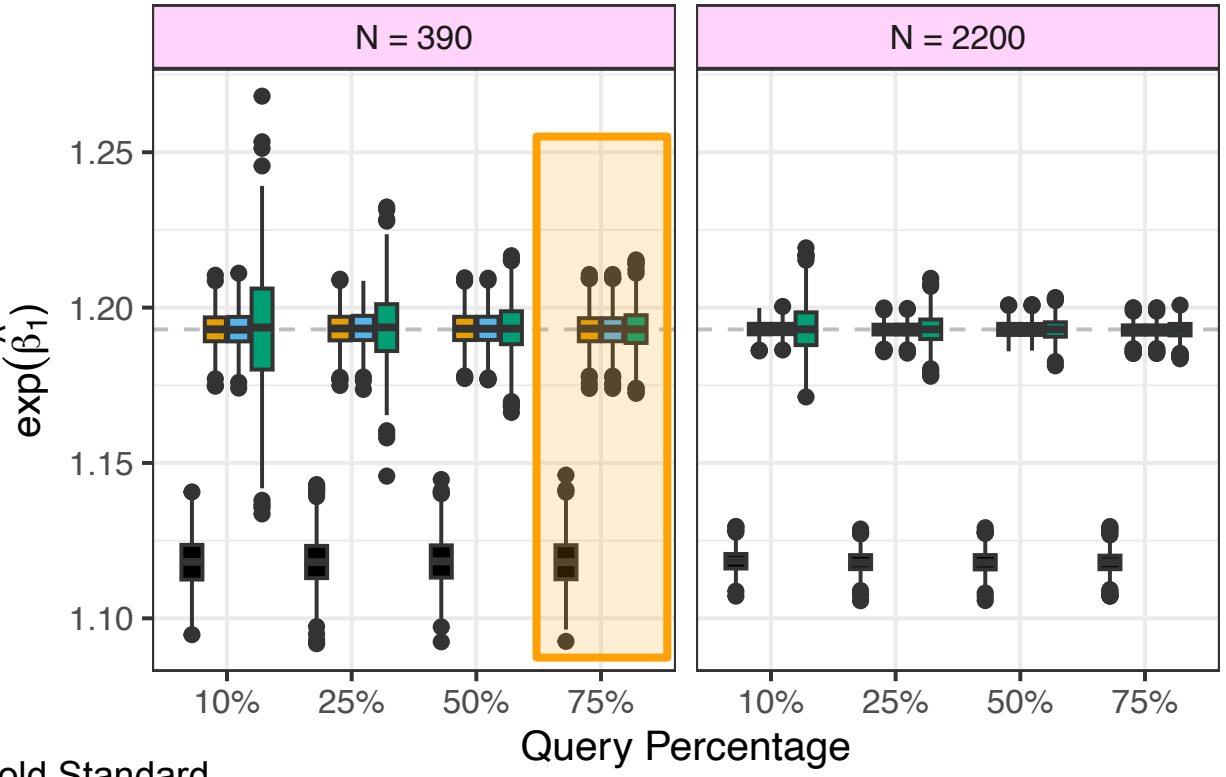

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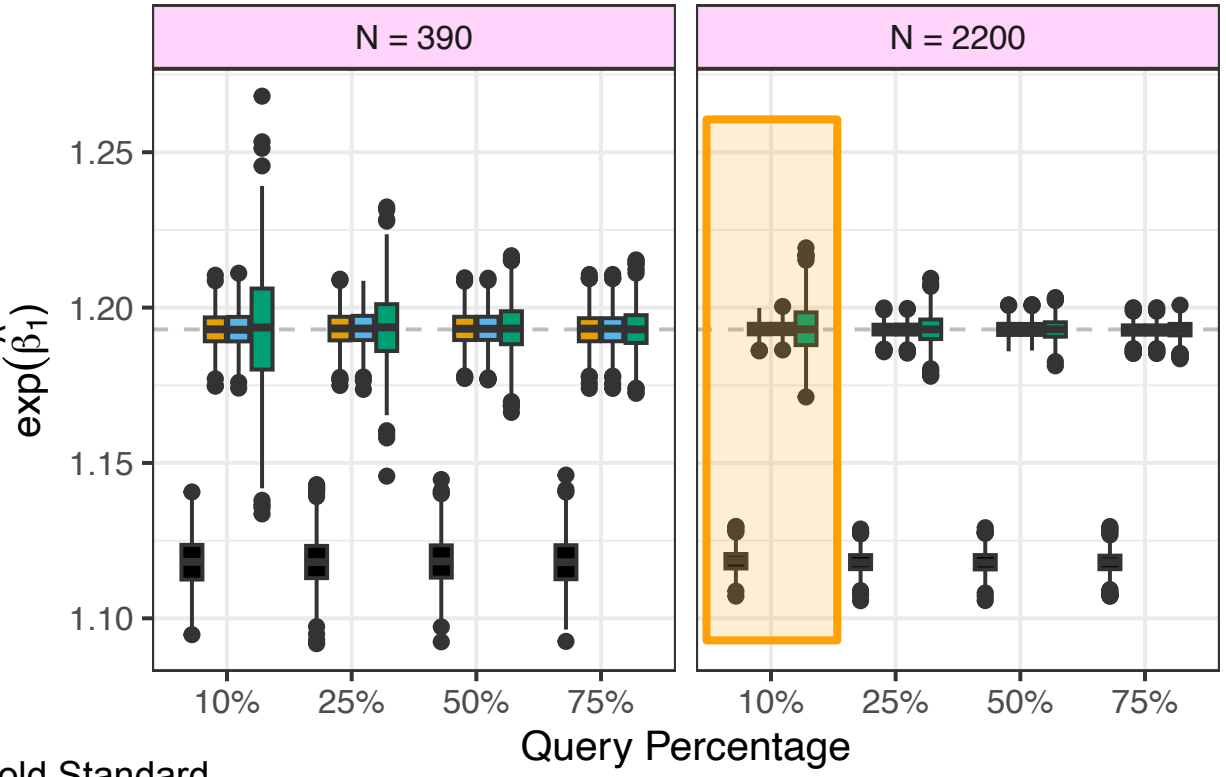

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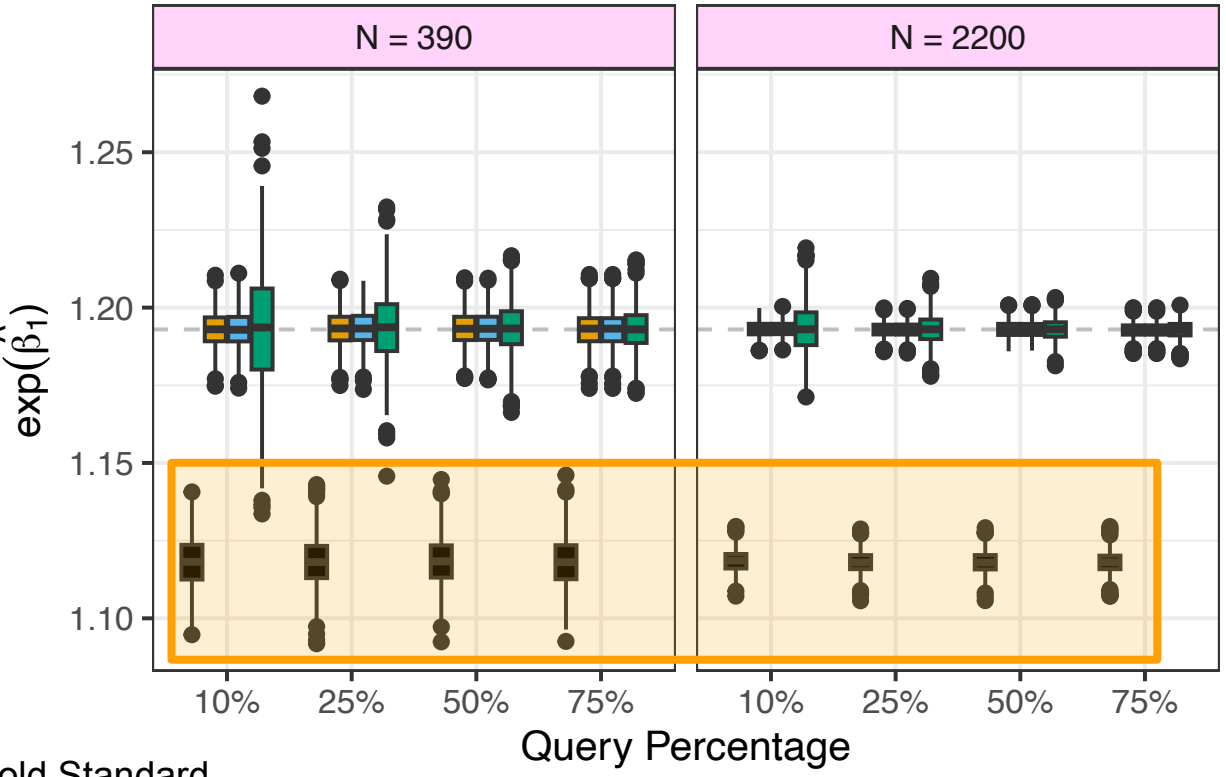
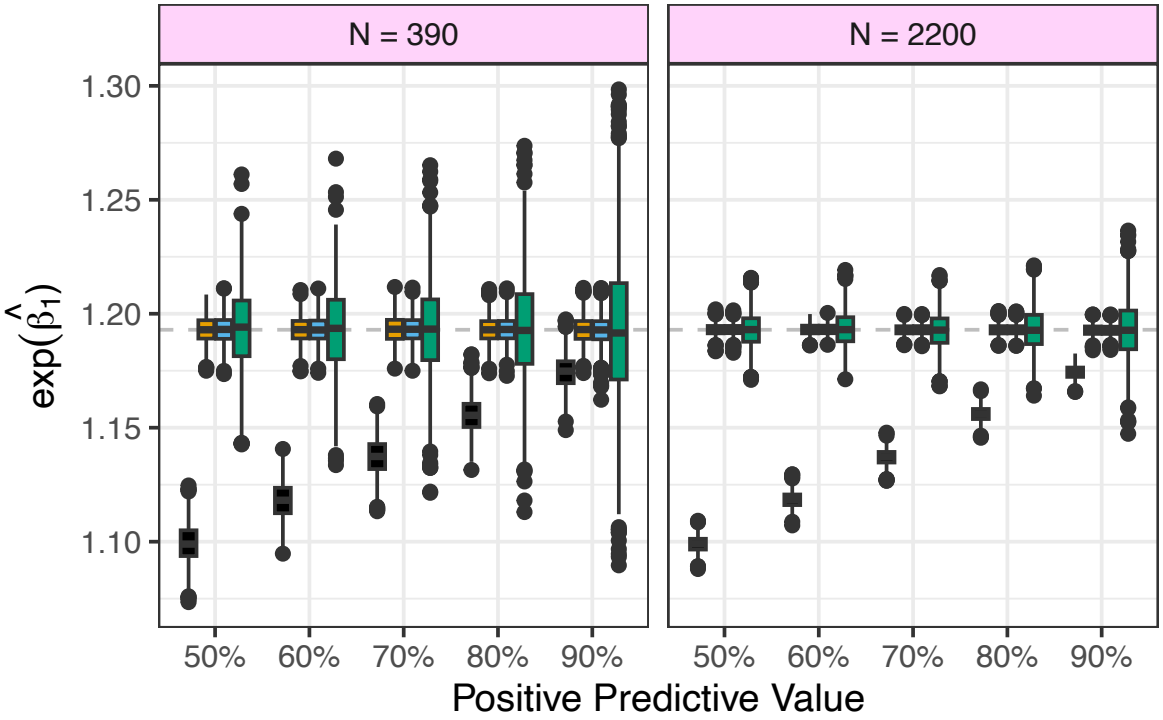


What happens as the errors get worse?



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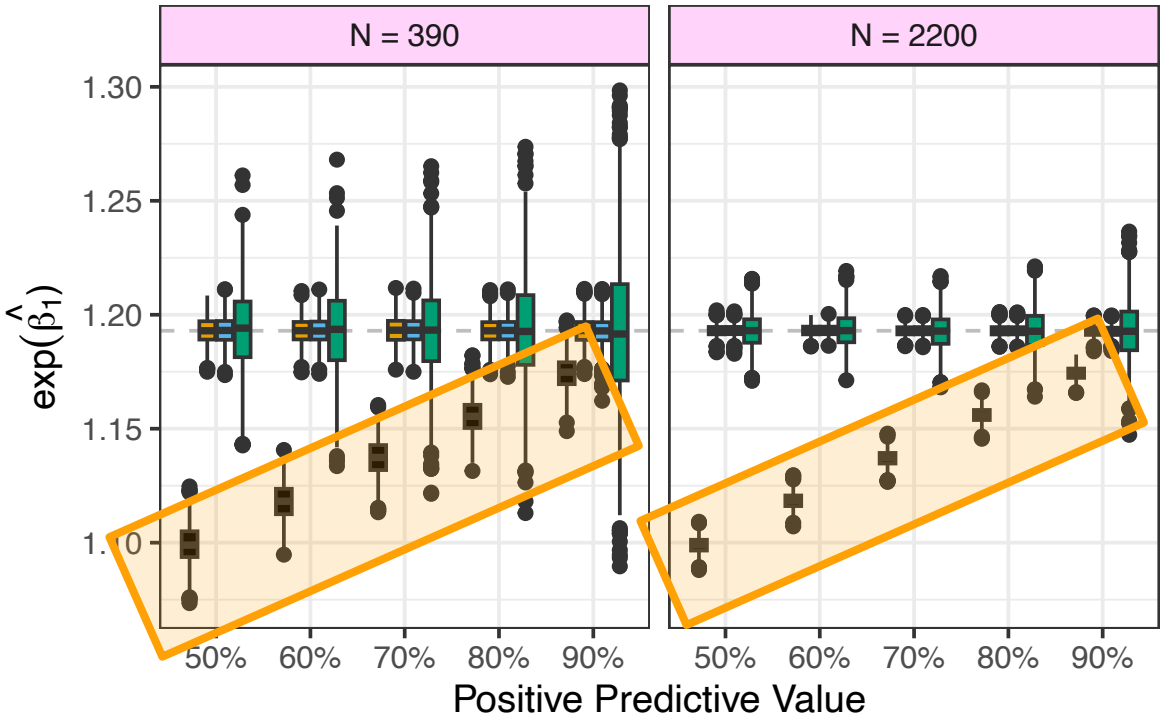

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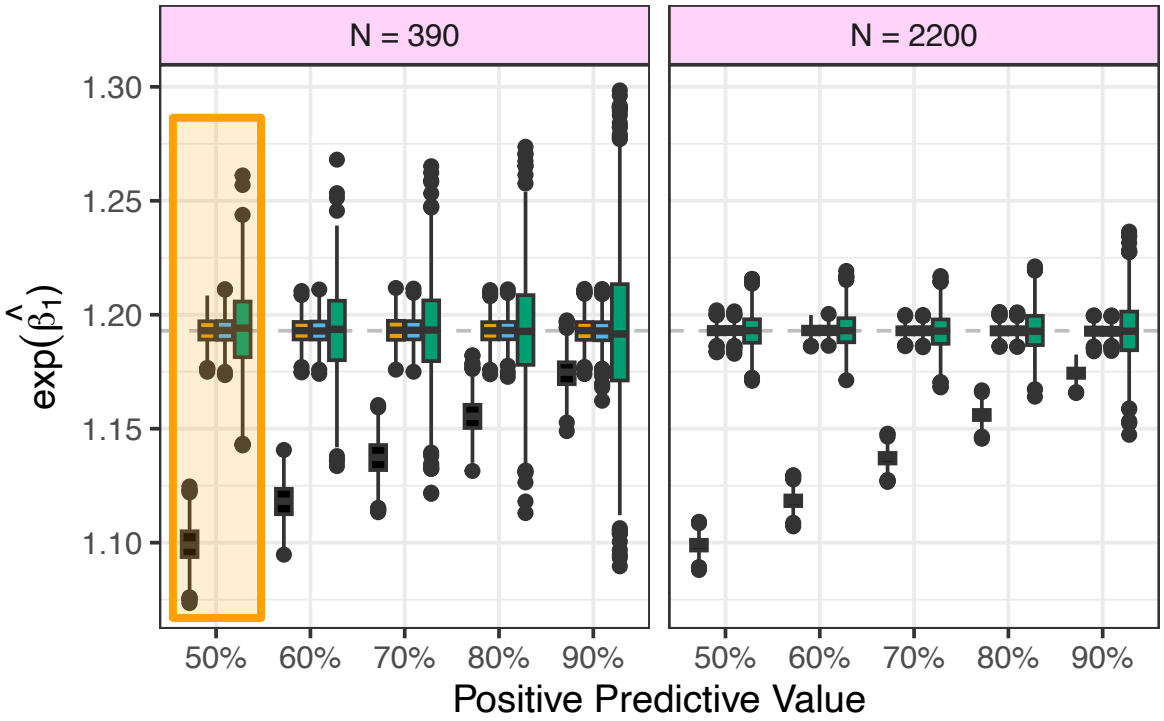

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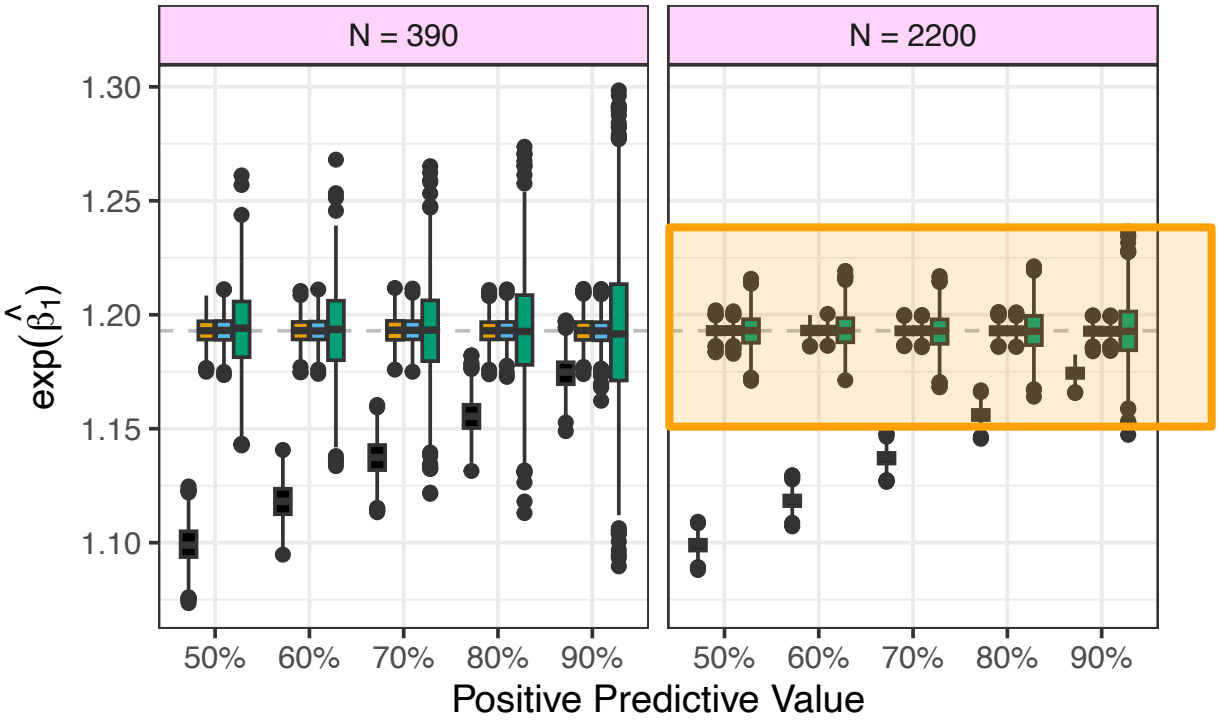


Takeaways

- The MLE **avoids the heavy bias** of the naive analysis and **improves on the efficiency** of the complete case analysis.
- Even as we increase the sample size enough to let asymptotic behavior take care of some of the **issues in the competitors**, the MLE still shows improved behavior.

4

Case Study

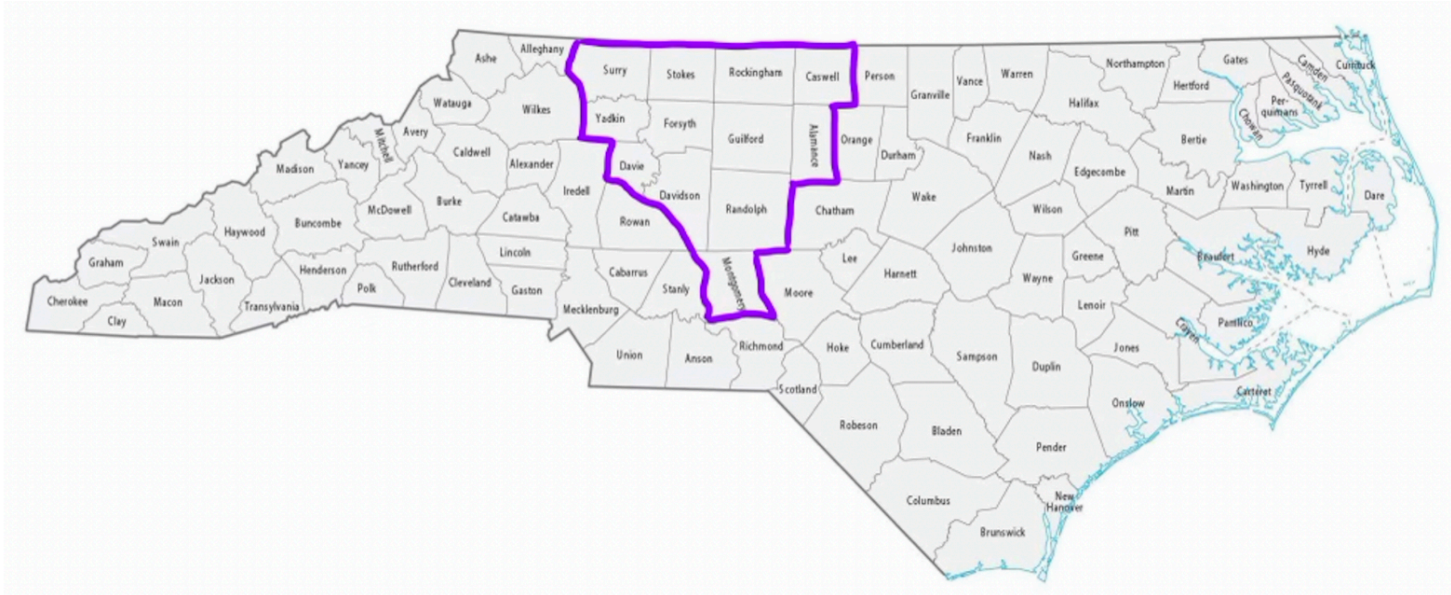
To reorient in context:

- Our original question was:

  “Can we sidestep the **misclassification and missingness issues** in our data and still accurately estimate an association between **access to healthy food** and **diabetes prevalence**?”

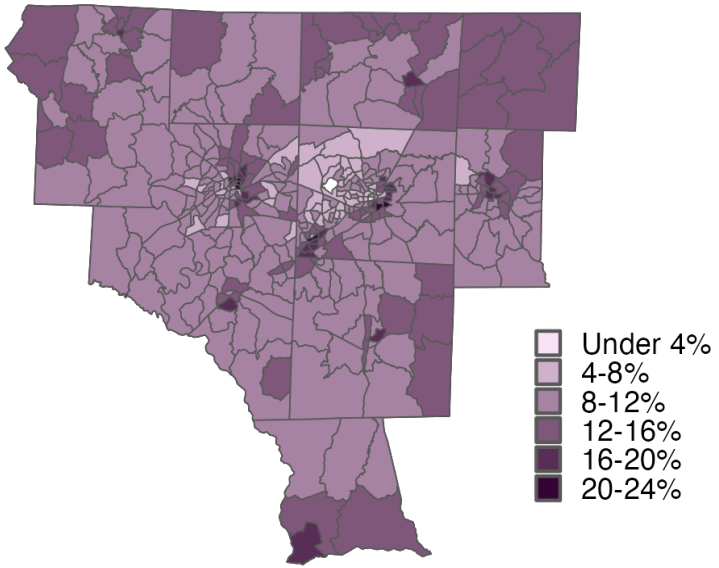
- We now apply our method to data from the **Piedmont Triad** in **North Carolina**.

What's the Piedmont Triad?



What does diabetes prevalence look like in the Triad?

- Prevalence in North Carolina was **12.4%** in 2021 (American Diabetes Association).
- Most tracts have between **8-12%** prevalence but this **varies** across the Triad.
- Tracts with **lower prevalences** tended to be smaller and **urban**.



From Lotspeich et. al 2025, we adapt:

- N = 387 census tract **population centers and sizes** from the 2010 census
- F = 701 **healthy food retailers** from the 2022 USDA SNAP retailer locator release
- Tract level **diabetes prevalences** from the 2022 CDC PLACES release
- Indicators of **metro status** for each neighborhood derived from the 2010 USDA RUCA code release

The outcome model just got a bit more specific.

$$\log\{\mathrm{E}_{\beta}(Y_i \mid X_i, M_i)\} = \beta_0 + \beta_1 X_i + \beta_2 M_i + \beta_3 X_i \times M_i + \log(O_i)$$

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the expected diabetes case count (Y_i) in a tract given its food access at that radius (X_i) and metro status (M_i)

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the (log) ratio of diabetes prevalence in a non-metro tract with food access at that radius compared to one without

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add these!

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the (log) ratio of diabetes prevalence in a metro tract with food access at that radius compared to one without

The outcome model just got a bit more specific.

add these!

the population offset

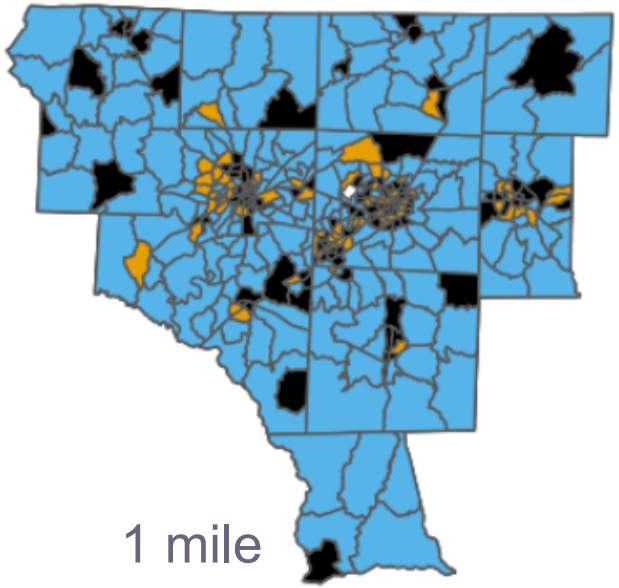
$$\log\{\mathrm{E}_{\beta}(Y_i \mid X_i, M_i)\} = \beta_0 + \beta_1 X_i + \beta_2 M_i + \beta_3 X_i \times M_i + \log(O_i)$$

the expected diabetes case count (Y_i) in a tract given its food access at that radius (X_i) and metro status (M_i)

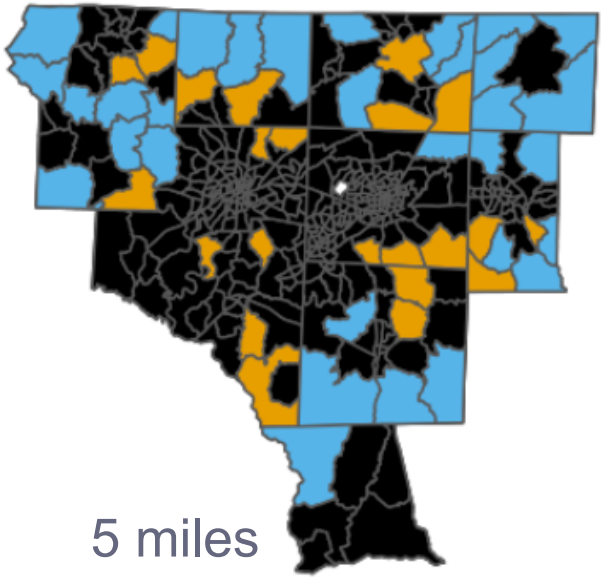
the (log) ratio of diabetes prevalence in a non-metro tract with food access at that radius compared to one without

the (log) ratio of diabetes prevalence in a metro tract with food access at that radius compared to one without

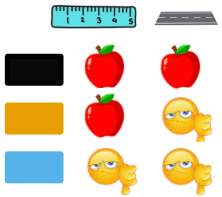
We can visualize food access at the tract level.



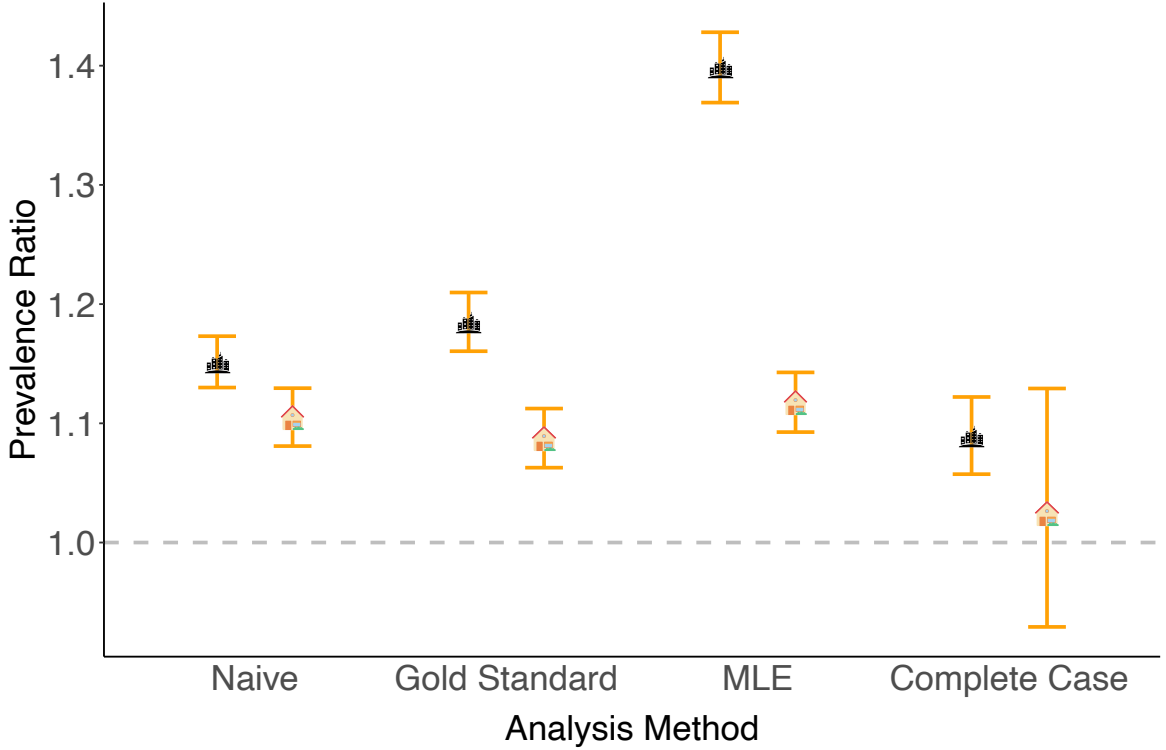
1 mile



5 miles

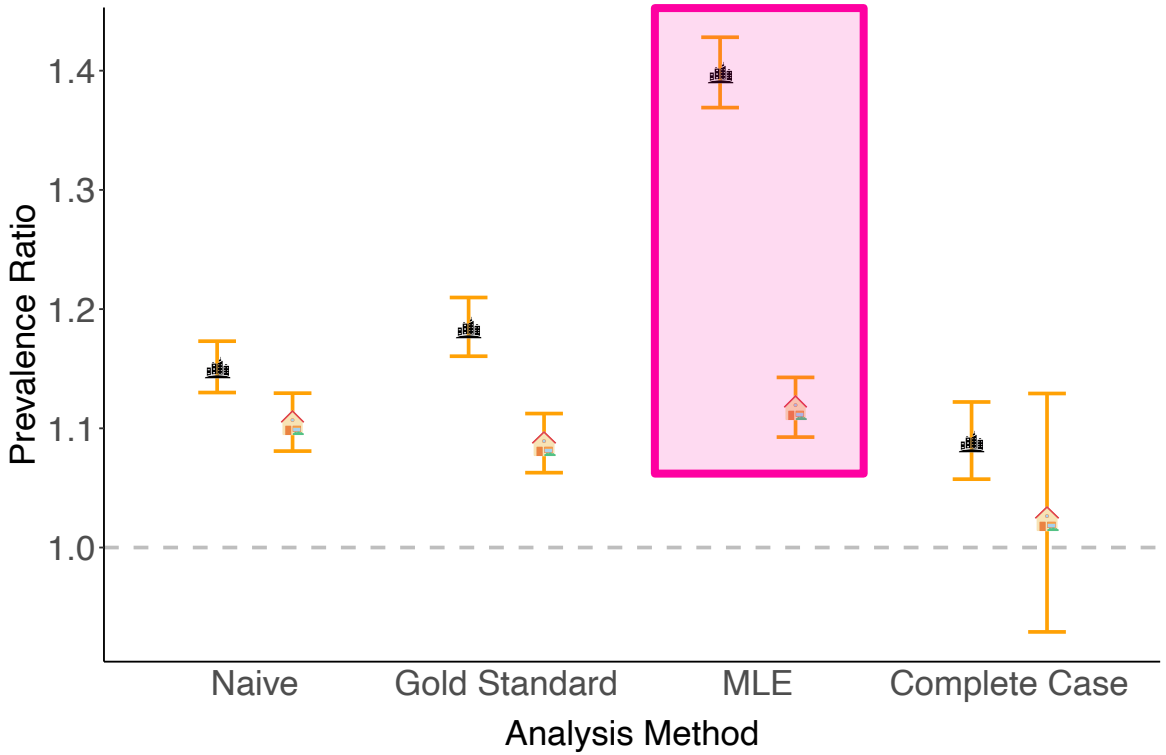


At the one mile radius:



Metro Tract
Non Metro Tract

At the one mile radius:



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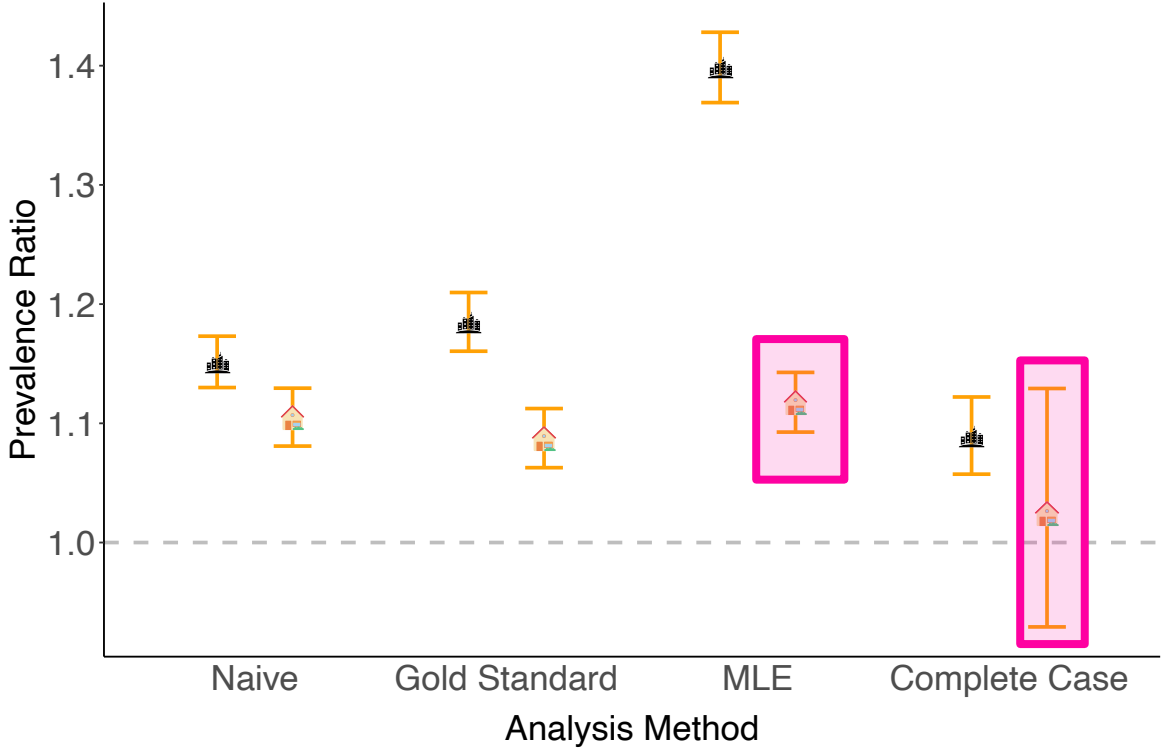
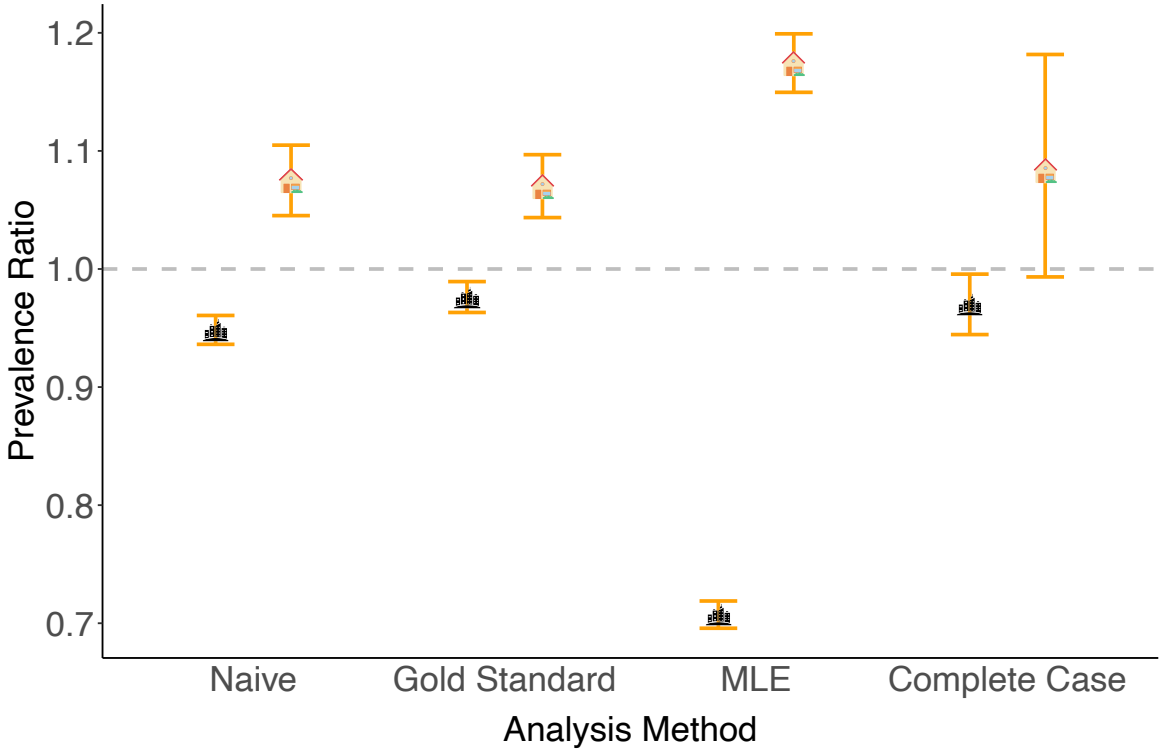


Metro Tract
Non Metro Tract

At the five mile radius:



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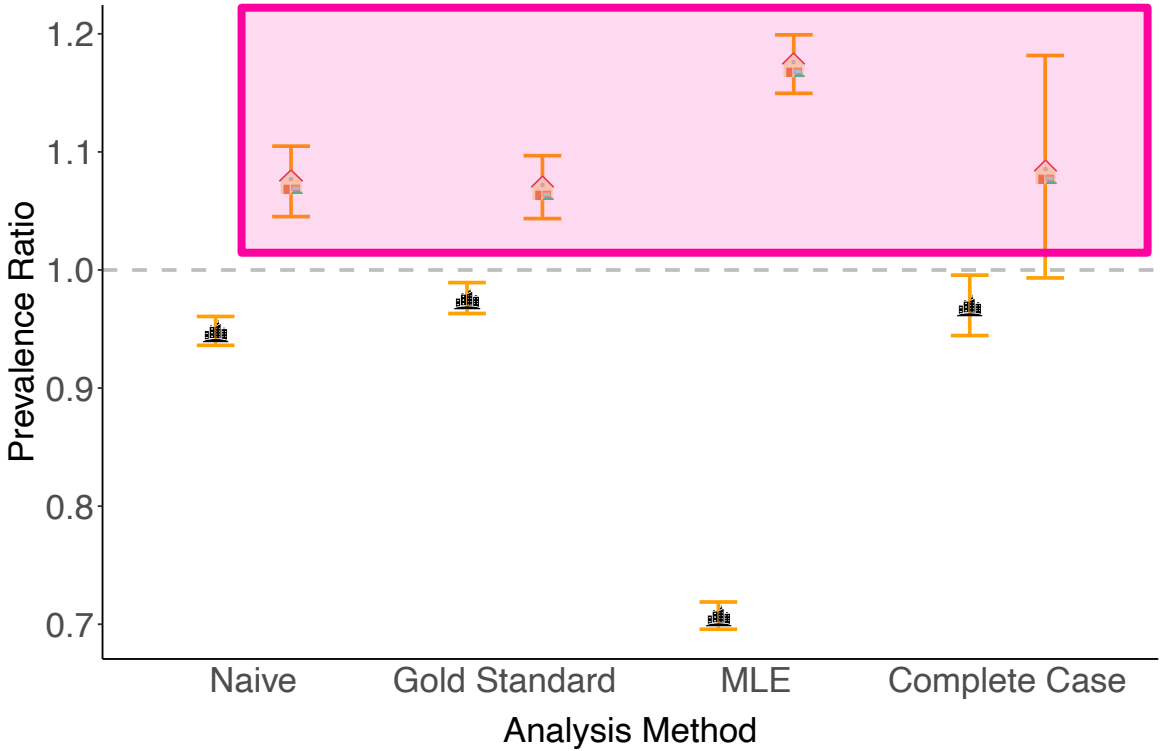

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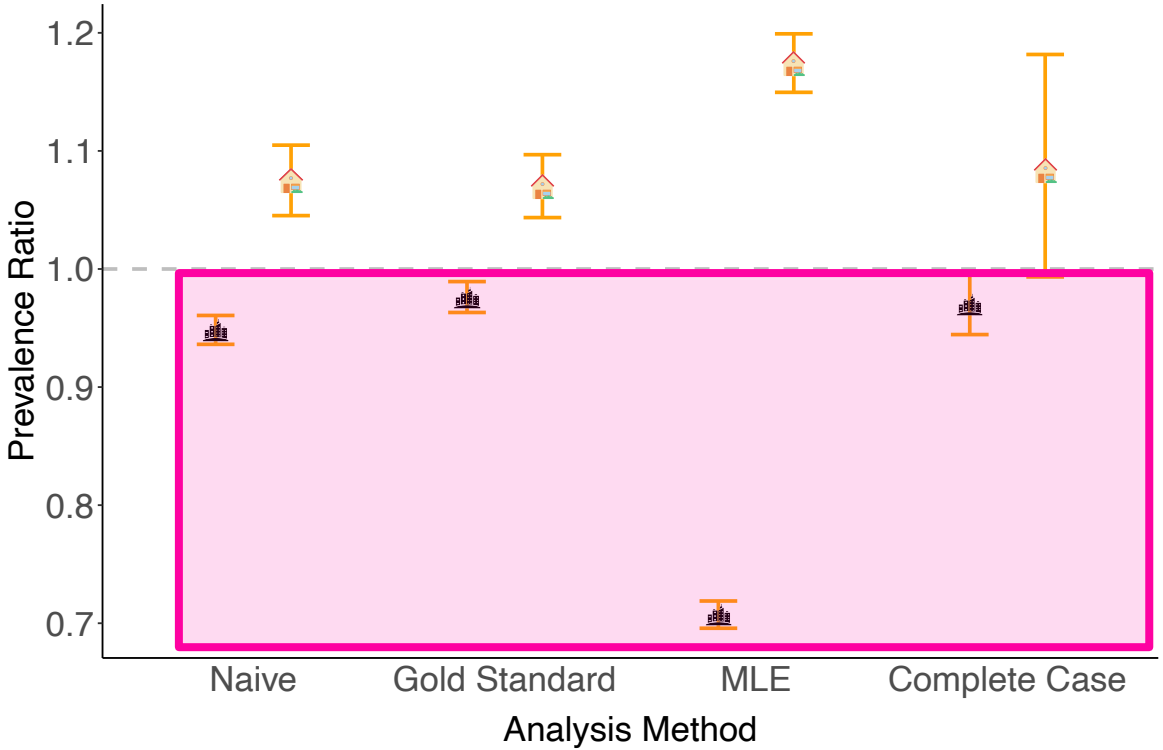

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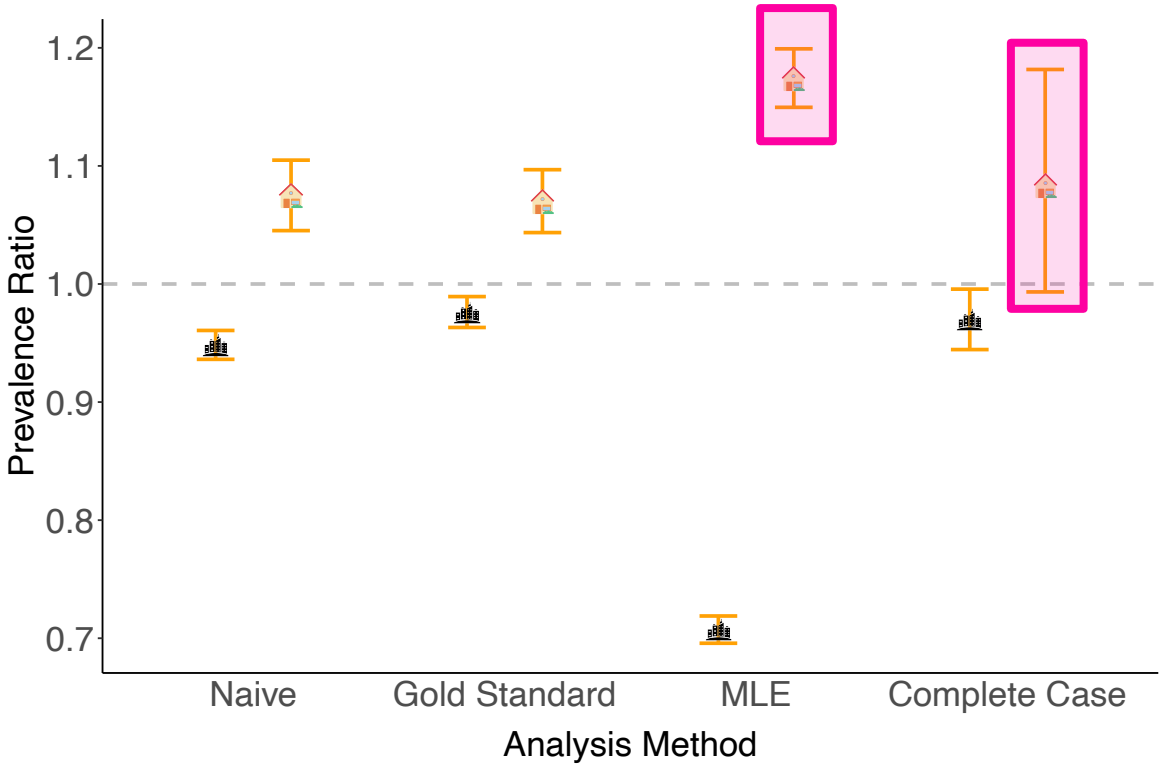


Metro Tract
Non Metro Tract

Takeaways

- Association patterns depend on the **radius**.
- Overall, tracts with **food access** within a mile counterintuitively saw **higher** diabetes prevalences.
- Overall, tracts with **food access** within five miles had diabetes patterns dictated by **metro status**.
- The MLE model usually reported **stronger** effects more **efficiently** than the complete case.

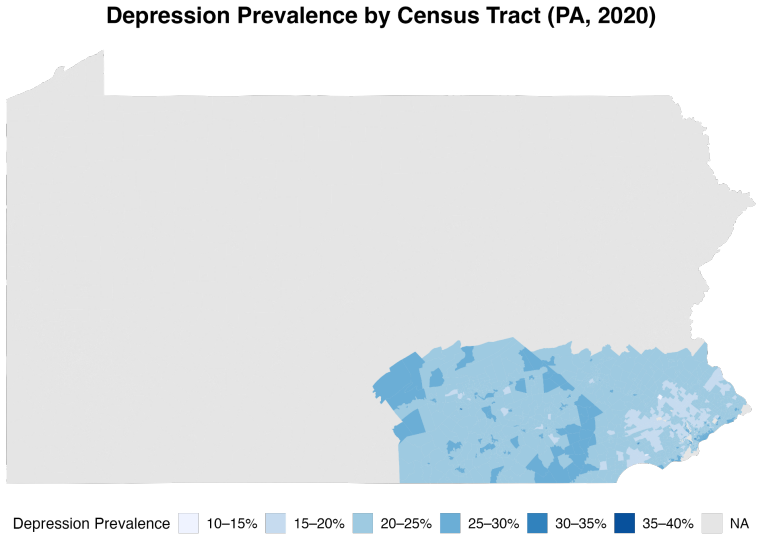
5

Wrap Up

Today, we:

- Derived a novel **maximum likelihood estimator** for Poisson regression with a **misclassified binary covariate** and a two phase validation design
- Implemented the method and its standard error estimator using an expectation-maximization algorithm in R
- Showcased its **asymptotic and small-sample advantages** via simulation studies
- Demonstrated its utility by estimating **diabetes prevalence** as a function of **food access and urbanicity** in North Carolina

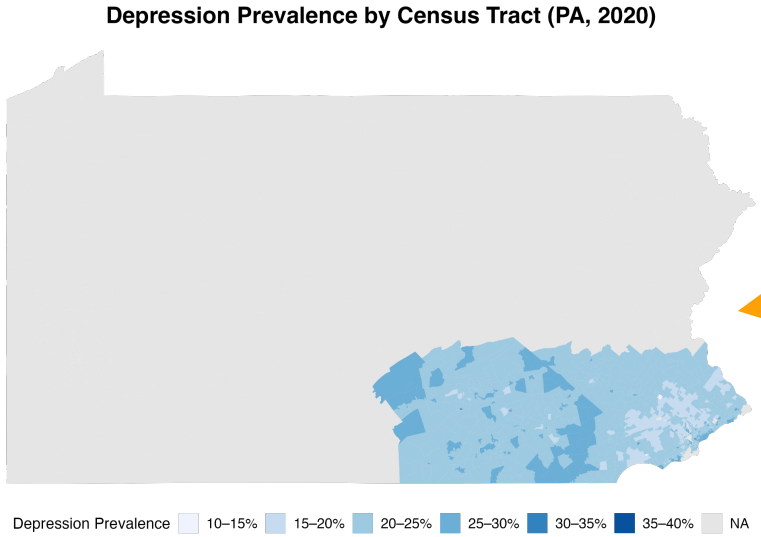
We can extend this framework!



$$X_i \in \{0,1\} \rightarrow X_i \in \mathbb{R}$$

Figure by Daniel Hoberman

We can extend this framework!

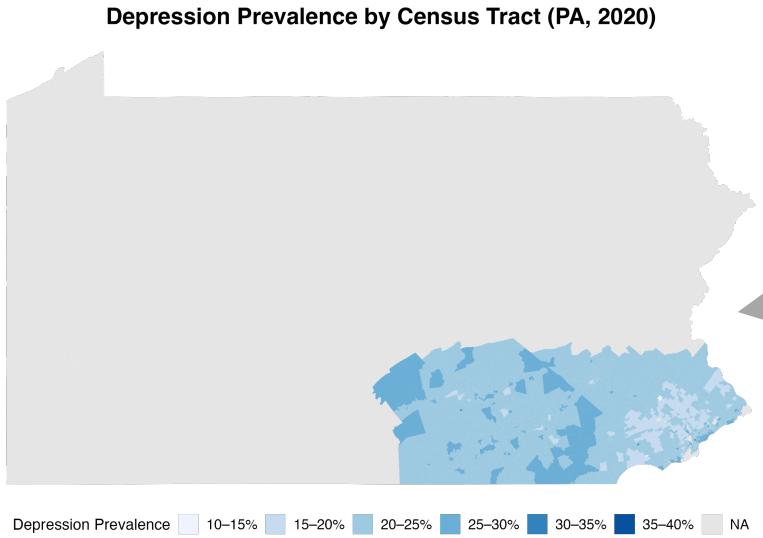


$$X_i \in \{0,1\} \rightarrow X_i \in \mathbb{R}$$

new communities and new context

Figure by Daniel Hoberman

We can extend this framework!



more flexible method settings

$$X_i \in \{0,1\} \rightarrow X_i \in \mathbb{R}$$

new communities and new context

Figure by Daniel Hoberman

Acknowledgements

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