Adjusting for Covariate Misclassification to Quantify the Relationship Between Diabetes and Local Access to Healthy Food

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Roadmap

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

Healthy Eating ➡ **Healthy Living**

- A **healthy diet** is full of fruits, vegetables, whole grains, and other highnutrient 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).

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The **density** approach counts the number of healthy food retailers within a given radius.

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The **proximity** approach measures the distance* to the nearest healthy food retailer.

*more on that later

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- 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**.
- The Haversine distance in the image is **impassable**, as it crosses a pond.

Distance Computations

Figure: Haversine distance from Reynolda Manor House to a nearby Food Lion

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- The **route-based distance** works around obstacles.
- It is **more accurate** than the Haversine distance, but it is **computationally and financially expensive**.
- These distances are computed with the **ggmap** package in R, which accesses the Google Maps API.
- In our case study, these distances are **over a mile** longer than the Haversine distances for **1 in 5** neighborhoods!

Distance Computations

Figure: Route distance from Reynolda Manor House to a nearby Food Lion

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Guiding Questions

• Can we use a function of distance to healthy food retailers to

- **quantify food access** in the Piedmont Triad, even if this function is **subject to misclassification**?
- and missingness?

• Can we estimate the relationship between **food access** and **diabetes prevalence** in the presence of misclassifications

Methods

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- -

• X_r is an error-free binary explanatory variable for food access based on route-based distances and a radius r (e.g., $r = 1$ mile)

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- O is an offset, the population of the area

Model Notation

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-

Model Notation

• Outcome Model

-
-

$Y_i \mid X_{ri}, Z_i \sim \text{Poisson}(\lambda_i)$

$\lambda_i = \beta_0 + \beta_1 X_{ri} + \beta_2 Z_i$

Model Notation

• Outcome Model

-
-

$Y_i \mid X_{ri}, Z_i \sim \text{Poisson}(\lambda_i)$

exponentiate to get the prevalence ratio

• Error Model

- *Xri* ∣ *X** *ri*
-

Model Notation

• Outcome Model

-
- $\lambda_i = \beta_0$

$$
Y_i | X_{ri}, Z_i \sim \text{Poisson}(\lambda_i)
$$
\n
$$
\lambda_i = \beta_0 + \beta_1 X_{ri} + \beta_2 Z_i
$$
\n
$$
\text{exponentiate to get the}
$$
\n
$$
X_{ri} | X_{ri}^*, Z_i \sim \text{Bernoulli}(\pi_i)
$$

 $\pi_i = \exp(\eta_0 + \eta_1 X_{ri}^* + \eta_2 Z_{i})$

A Little More on Xr and X* r

- Let d be the route-based distance to the nearest healthy food retailer.
- Let h be the Haversine distance to the nearest healthy food retailer.
- Let r be the radius of interest.

 $X_r =$ X^* r =

- 1 if $d \le r$ $\left\{ \begin{array}{ll} 1 \text{ if } d \leq r \\ 0 \text{ if } d > r \end{array} \right.$ "Access" "No Access"
- 1 if $h \le r$ $\left\{ \begin{array}{ll} 1 \text{ if } h \leq r \\ 0 \text{ if } h > r \end{array} \right.$ "Error-Prone Access" "No Access"

Two-Phase Design

- Having **some correct** route-based distances is better than none.
- **Error-prone** Haversine distances are available for all N neighborhoods, and we can use them to create our indicator of food access X* ^r that is subject to **misclassification**.
- In addition to X* ^r, we **query** route-based distances to create our indicator X_r for n neighborhoods, where $n < N$.
- We now have a **missing data problem**, as (N - n) neighborhoods only have X_r^* .

Only n of Nneighborhoods have complete data.

Outcome Model Options

• Gold Standard

- Naive Analysis
- Complete Case Analysis
- Maximum Likelihood Estimation

The model achieves optimal bias and variance.

The model assumes we have all of the correct data available, but we do not.

Outcome Model Options

- Gold Standard
- **• Naive Analysis**
- Complete Case Analysis
- Maximum Likelihood Estimation

The model is easy to fit and utilizes information from the error-prone data for all of the neighborhoods.

The model is biased by a function of the sensitivity and specificity (Shaw et al., 2020).

Outcome Model Options

- Gold Standard
- Naive Analysis
- **• Complete Case Analysis**
- Maximum Likelihood Estimation

The model is unbiased, as it uses the error-free measurements.

The model does not take the unqueried data into account.

Outcome Model Options

- Gold Standard
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- Complete Case Analysis
- **• Maximum Likelihood Estimation**

The model utilizes information from both the queried and unqueried observations.

The method was not yet derived or implemented in existing software.

Outcome Model Options

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Putting Together the MLE Roadmap

We have four cases of data quality.

- 1. *No misclassification or missingness* (X_r = X^{*}_r always)
- 2. *Misclassification without missingness* (always have Xr and X* r)
- 3. *Misclassification and total missingness* (never have Xr but always X* r)
- 4. Misclassification and partial missingness (sometimes have X_r but always X^{*}r)

$P_{\beta,\eta}(Y,X,Z) = P_{\beta}(Y | X,Z)P_{\eta}(X | Z)P(Z)$

$P_{\beta,\eta}(Y,X,Z) = P_{\beta}(Y | X,Z)P_{\eta}(X | Z)P(Z)$ outcome model

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$P_{\beta,\eta}(Y,X^*,Z) =$ 1 ∑ *x*=0 *P*_{*β*}(*Y* | *X* = *x*, *Z*)*P*_{*n*}(*X* = *x* | *Z*)*P*(*X*^{*}, *Z*)

$P_{\beta,\eta}(Y,X^*,Z) =$ 1 ∑ *x*=0 outcome model *P*_{*β*}(*Y* | *X* = *x*, *Z*)*P*_{*n*}(*X* = *x* | *Z*)*P*(*X*^{*}, *Z*)

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$\mathscr{L}_N(\beta,\eta) =$ *N* ∏ $i=1$ ${P(X_i, X_i^*, Y_i, Z_i)}$)[}] Q_i </sup>{ $P(X_i^*, Y_i, Z_i)$)}1−*Qi*

$\mathscr{L}_N(\beta,\eta) =$ *N* ∏ $i=1$ $\{P(X_i, X_i^*, Y_i, Z_i)$)^{**} Q_i </sup> $\{P(X_i^*, Y_i, Z_i)$)}1−*Qi* from case 2

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from case 3

$\mathscr{L}_N(\beta,\eta) =$ *N* ∏ $i=1$ ${P(X_i, X_i^*, Y_i, Z_i)}$)[}] Q_i </sup>{ $P(X_i^*, Y_i, Z_i)$)}1−*Qi*

$\mathscr{L}_N(\beta,\eta) =$ *N* ∏ $i=1$ ${P(X_i, X_i^*, Y_i, Z_i)}$

)^{*Q*_{*i*}(*P*(*X*^{*}, *Y*_{*i*}, *Z*_{*i*}})}1−*Qi*

query indicators

$$
\mathscr{L}_N(\beta,\eta) = \prod_{i=1}^N \{P(X_i, X_i^*)
$$

, X_i^*, Y_i^*, Z_i^*)[}] Q_i </sup>{ $P(X_i^*, Y_i, Z_i)$)}1−*Qi*

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product over all (independent) neighborhoods

$\mathscr{L}_N(\beta,\eta) =$ *N* ∏ $i=1$ ${P(X_i, X_i^*, Y_i, Z_i)}$)[}] Q_i </sup>{ $P(X_i^*, Y_i, Z_i)$)}1−*Qi*

Maximizing the Likelihood

- We do not have an analytical form for the MLE, so we use **numerical methods**.
- We use the optim() function in R with the BFGS routine (Bonnans et al., 2006).
- We find the **minimum** of the **negative** log likelihood, which is **convex**.
- We **initialize** with the **complete case** estimates (Little and Rubin, 2002).
- We invert the numerical estimate of the **Hessian** matrix as the **standard error estimator**.

As N goes to infinity, the MLE $(\hat{\boldsymbol{\theta}}_{N})$ is:

1. Consistent

 achieves the Cramer-Rao lower bound $\mathscr{I}^{-1}(\boldsymbol{\theta})$

$\bm{\theta}_N$

2. Asymptotically Normal

3. Asymptotically Efficient

$$
\sqrt{N}\left(\hat{\theta}_N-\theta\right) \sim \text{Normal}(0, \mathcal{I}^{-1})
$$

(*θ*))

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POSSUM

#devtools::install_github(repo = "sarahlotspeich/possum")

Example

library(possum) #for the MLE library(dplyr) #for data wrangling set.seed(1031) #for reproducibility

#generate data

beta <- $c(-2.2, 0.15)$ #governs Poisson outcome eta <- $c(-2.2, 4.4)$ #governs logistic error model $xstar = rbinom(n = 500, size = 1, prob = 0.5)$ #error-prone exposure $x =$ rbinom(n = 500, size = 1, #error-free exposure X/X^* $prob = 1 / (1 + exp(-(eta[1] + eta[2] * xstar))))$ $lambda = exp(beta[1] + beta[2] * x)$ #mean of Y/X $y = \text{rpois}(n = 500, \text{lambda} = \text{lambda})$ #Poisson outcome with mean lambda $q =$ rbinom(n = 500, size = 1, prob = 0.75) #queried indicator df <- data.frame(xstar, x, y, q) #construct complete dataset df <- df \vert > mutate(x = ifelse(q == 1, x, NA)) #redact X for unqueried rows

#call MLE function

mle_output <- mlePossum(error_formula = $x \sim x$ star, analysis_formula = $y \sim x$, $data = df$

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> mle_output

\$coefficients

Est (Intercept) -2.07087196 0.1595924 0.01085821 0.2378044 $\boldsymbol{\mathsf{X}}$

\$convergence $[1] 0$

Simulations

*X** ∼ Bernoulli(0.496)

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X | *X** ~ Bernoulli(*π*), where $\pi = \expit(\eta_0 + \eta_1 X^*)$

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$$
\eta_0 = -\log\left(\frac{1 - FPR}{FPR}\right)
$$

$$
\frac{-FPR}{FPR}\bigg\}\qquad \eta_1 = -\log\left(\frac{1 - TPR}{TPR}\right) - \eta_0
$$

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Y ∼ Poisson(λ), where $\lambda = \exp(\beta_0 + \beta_1 X)$

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$$

Q ∼ Bernoulli(*q*)

- •Sample size N
- •Queried proportion q
- •Error mechanism (FPR, TPR)
- •Prevalence ratio exp(*β*1)
- •Prevalence exp(β_0)

We **observe** the effect of interest β_1 and the relative efficiency. ̂ 1 and the relative emotion by.
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We **vary**:

Simulation Studies Roadmap

We **compare**:

- Gold standard
- Complete case
- Naive model
- MLE

Takeaways Simulation Studies

• As we vary the size of the queried sample, the MLE recovers up to 91% of the **efficiency** of the gold standard model and beats the complete case model in

- Across all four query settings, the MLE remains **fairly unbiased**.
- every case.
- As we introduce more error into the input data, the MLE remains **fairly unbiased**.
- of the gold standard model.

• As we vary the error, the MLE recovers between 70 and 83% of the **efficiency**

Case Study: Diabetes in the Piedmont Triad

N = 387 Census Tracts The Piedmont Triad

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Our "Neighborhoods" What We Have

- **Population center** of the neighborhood
- **Haversine distance** from the nearest healthy food retailer to the center
- **Route-based distance** from the nearest healthy food retailer to the center
- **Population size** of the tract
- Count of **diabetes cases** in the tract

- Neighborhood population centers ($N = 387$) are from the Census Bureau (census tracts, 2010 release).
- (historical SNAP retailer locator dataset, 2022 release).
- Diabetes prevalences are from the Centers for Disease Control and Prevention (PLACES dataset, 2022 release).
- The data were adapted from Lotspeich et al., 2023+.

• Healthy food retailers (M = 701) are from the US Department of Agriculture

Where They Came From Our "Neighborhoods"

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- Discretized both distance measurements to **create Xr and X*r**
- Used **radii** of 0.5, 1, 5, and 10 miles
- Chose 25% of the tracts randomly to **throw out** X_r (i.e., let $q = 0.75$)

What We Did Our "Neighborhoods"

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- Statewide prevalence in 2021 was **12.4%** (American Diabetes Association)
- Most tracts have **8-12%** prevalence
- Prevalence **varies** across the **Triad**
- Lower prevalences coincide with smaller, urban tracts

Diabetes Landscape

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Diabetes Landscape

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- As radius **increases**, more tracts **flip** from blue to gold or black
- 22% of tracts have **over a mile difference** between their distance measures to the nearest retailer

Food Access Landscape

1 Mile Radius

5 Mile Radius

10 Mile Radius

Error Rates

Route-Based Route-Based

0.5 Mile Radius Straight-Line

No Access Access

1 Mile Radius Straight-Line

No Access Access No Access ACCESS No ACC Access

5 Mile Radius Straight-Line

No Access Access No Access Access Access Access Access Access

Route-Based Route-Based

10 Mile Radius Straight-Line

No Access Access No Access COPSS NO ACC Access

Error Rates

$log{E_{\beta}(Diabetes\ Cases \mid Access)} = \beta_0 + \beta_1 Access + log(Population))$

log{E_β(Diabetes Cases | Access)} = $\beta_0 + \beta_1$ Access + log(Population) log(outcome prevalence)

$log{E_{\beta}(Diabetes\ Cases \mid Access)} = \beta_0 + \beta_1 Access + log(Population))$

log{E_β(Diabetes Cases | Access)} = $\beta_0 + \beta_1$ Access + log(Population) log(prevalence ratio of exposure)

$log{E_{\beta}(Diabetes\ Cases \mid Access)} = \beta_0 + \beta_1 Access + log(Population))$

$log{E_\beta(Diabetes\ Cases \mid Access)} = \beta_0 + \beta_1 Access + log(Population))$

offset

$log{E_{\beta}(Diabetes\ Cases \mid Access)} = \beta_0 + \beta_1 Access + log(Population))$

Model Results

- In the **worst case**, we need a confounder-outcome effect of **9.5%** to tip the prevalence ratio to the null.
- In the **best case**, we need a confounder-outcome effect of **54.9%** to tip the prevalence ratio.

What if we missed a confounder? Hypothetical $β_2$

• Can we use a function of distance to healthy food retailers to

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- and missingness?

• Can we estimate the relationship between **food access** and **diabetes prevalence** in the presence of misclassifications

Guiding Questions

• Can we use a function of distance to healthy food retailers to

quantify food access in the Piedmont Triad, even if this function is **subject to misclassification**?

• Can we estimate the relationship between **food access** and **diabetes prevalence** in the presence of misclassifications

and missingness?

Guiding Questions

• Can we use a function of distance to healthy food retailers to

quantify food access in the Piedmont Triad, even if this function is **subject to misclassification**?

• Can we estimate the relationship between **food access** and **diabetes prevalence** in the presence of misclassifications and missingness?

Guiding Questions

Strengths and Limitations

WUses all available data

EXOnly two parametric assumptions

ExLower bias than naive analysis

Ex Recovers efficiency lost by the complete case analysis

W Finicky numerical behavior, especially in the standard error estimators

Poisson assumptions in the case study

Recommendations

• Use the **MLE** if you have high error rates and missingness, as it **avoids the bias** of the naive analysis and **recovers more efficiency** than the complete

- Use the **gold standard** in a setting where there is no missingness or misclassification.
- case analysis.
- **case analysis.**

• If you have very **little missingness**, you can get away with the **complete**

Future Directions

- adjacent tracts
- Vary the outcome model of interest
- Extend past the binary exposure case
- Improve the query design

• Incorporate a spatial model to explore relationships among

Ashley's Future Directions

Ashley's Future Directions

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- The SESH Lab