Temporal Trends in Heart Disease and Diabetes Mortality in Alberta: A Negative Binomial Regression Analysis of the Impact of Fast Food Consumption*

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First sentence. Second sentence. Third sentence. Fourth sentence.

1 Introduction

https://github.com/alexandersunliang/starter_folder-main-3 You can and should cross-reference sections and sub-sections. We use R Core Team (2023) and Wickham et al. (2019).

The remainder of this paper is structured as follows. Section 2….

In recent decades, the prevalence of heart disease and diabetes has surged globally, a trend paralleled by the increasing consumption of fast food. This paper focuses on Alberta, Canada, where these health challenges have become particularly pronounced. While numerous studies have linked fast food consumption to various health outcomes, few have directly examined its impact on mortality rates from heart disease and diabetes within this region. This gap in research motivates our study, which aims to analyze temporal trends in these mortality rates and discuss their potential association with the rise in fast food consumption, despite the absence of direct consumption data.

Using mortality data from the Alberta government, spanning two decades, we applied negative binomial regression models to analyze changes in heart disease and diabetes mortality rates. Our findings reveal significant temporal trends in these rates, with notable increases that correspond to periods of reported national and global rises in fast food consumption. While direct

*Code and data are available at: LINK.

causation cannot be established due to the lack of specific consumption data, the temporal correlations underscore the potential health impacts of dietary habits.

The importance of this research lies in its contribution to the ongoing dialogue about public health strategies aimed at combating heart disease and diabetes. By highlighting the temporal association between increased mortality rates and the era of rising fast food consumption, this study emphasizes the need for targeted public health interventions and policies.

This paper is organized as follows: Following the introduction, the second section reviews existing literature on the relationship between diet and chronic diseases, establishing the theoretical foundation for the study. The third section describes the data and methodology, including the rationale behind the choice of negative binomial regression. The fourth section presents our findings, detailing the correlation between fast food consumption and mortality rates. The fifth section discusses the implications of these findings for public health policy and suggests directions for future research. The final section concludes the paper, summarizing the key contributions and urging for proactive measures in dietary education and regulation. Through this structured exploration, the paper contributes valuable insights into the diet-disease nexus, advocating for informed dietary choices as a cornerstone of public health.****

2 Data

2.1 Data source

This analysis will be carried out in **R** (**R?**) using packages **tidyverse** (**tidyverse?**), **dplyr** (**dplyr?**), **ggplot2** (**ggplot2?**), **knitr** (**knitr?**). The data set used in this paper is called Leading causes of death and was collected from the Alberta Provincial Government. The data set consists of a ranking of the 30 most common causes of death each year in Alberta. The data covers the last two decades, but for our research purpose we will focus on the last five years.

2.2 Broader Context of the Dataset

The availability of detailed public health data, such as the mortality statistics from Alberta, is crucial for the formulation of informed public health policies and strategies. Within the broader Canadian context, Alberta's commitment to data transparency enables a deeper analysis of health trends and outcomes, serving as a model for other provinces and territories. The analysis of mortality data plays a pivotal role in identifying health trends, assessing the burden of diseases, and planning public health interventions. By focusing on specific causes of death, researchers and policymakers can tailor strategies to target the underlying factors contributing to these trends, ultimately aiming to improve health outcomes and reduce preventable deaths.

Table 1: Annual Deaths by Cause (2016-2021)

Year	Acute Myocardial Infarction	All Other Forms of Ischemic Heart Disease	Atherosclerotic Cardiovascular Disease	Diabetes Mellitus	Congestive Heart Failure
2016	1102	1626	885	502	352
2017	1028	1678	817	584	374
2018	1071	1788	630	577	347
2019	1061	1886	745	569	430
2020	1067	1897	678	743	387
2021	1075	1939	463	728	403

2.3 Variables

The dataset comprises several key variables, central to this study's focus on heart disease and diabetes mortality rates:

Causes of Death: Specifically, the dataset categorizes mortality into detailed causes, including:

- **All Other Forms of Ischemic Heart Disease**: This category encompasses various conditions related to reduced blood flow to the heart muscle, excluding acute myocardial infarction.
- **Acute Myocardial Infarction (Heart Attack)**: Fatalities resulting directly from heart attack incidents.
- **Atherosclerotic Cardiovascular Disease**: Deaths caused by atherosclerosis, a condition characterized by the hardening and narrowing of the arteries due to plaque buildup, leading to cardiovascular problems.
- **Diabetes Mellitus**: Mortality attributed to complications arising from diabetes, a chronic condition affecting blood sugar regulation.
- **Congestive Heart Failure**: Deaths resulting from the heart's inability to pump blood effectively, often a consequence of other heart conditions.

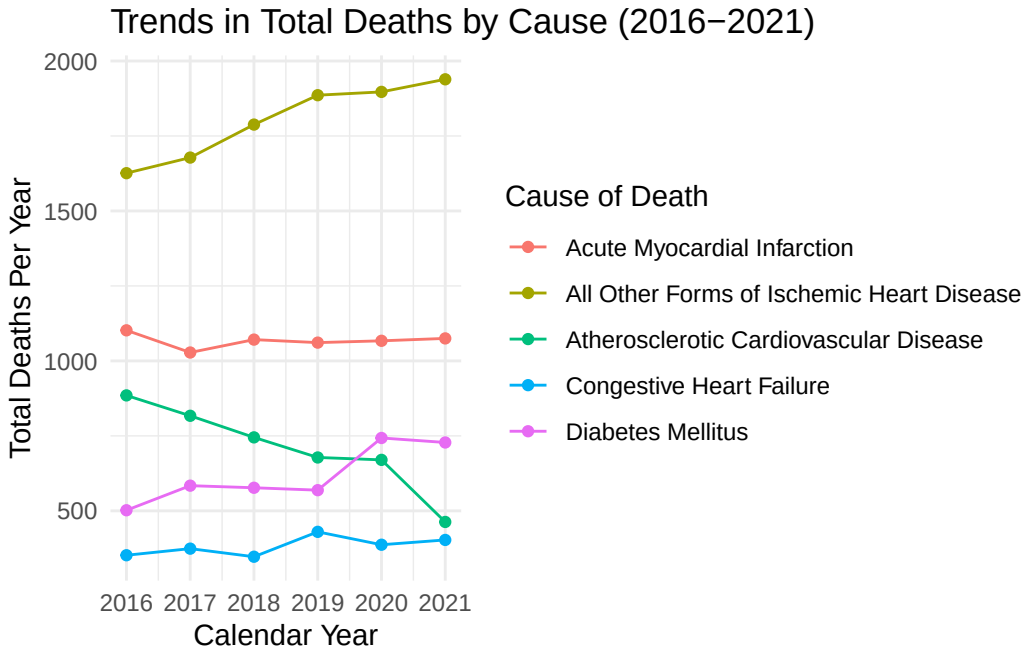
These five causes of death were chosen due to their correlation with unhealthy diets. We collected the recorded total deaths in Alberta from each of the above variables from 2016-2021 inclusive. This is shown in the table above.

2.4 Data Preparation and Cleaning

The dataset was filtered to isolate deaths attributed to our causes of interest: acute myocardial infarction, all other forms of ischemic heart disease, atherosclerotic cardiovascular disease, diabetes mellitus, and congestive heart failure. This selection was crucial to align our study with its objectives, ensuring a focused examination of these specific health outcomes. Subsequently, we removed all missing values from the dataset. The final data points were compiled for use in our analysis later in the paper.

2.5 Preliminary Observations and Exploration

Our initial analysis revealed several notable observations. First, the trend analysis suggested a correlation between the years and mortality rates for specific causes of death, hinting at the possible influence of external factors such as healthcare policies or changes in societal health behaviors. Since we are looking at a five-year span from 2016 to 2021, the onset of the COVID-19 pandemic introduced a plethora of health-related policies and regulations that may significantly impact our data. In the figure below, we plotted the total deaths from each of the causes to visualize if there were any spikes in the data.



From the graph depicted above, we see that although most causes kept their total death count per year roughly the same, Diabetes saw a noticeable spike form 2020 onwards and Atheroscleratic cardiovascular disease saw a significant decrease.

3 Model

In the realm of statistical modeling for count data, both the Poisson and Negative Binomial models are popular choices, each with its assumptions, benefits, and drawbacks. These models serve to elucidate the relationship between a set of predictors—in this case, the causes of death—and the count response variable, which is the total number of deaths.

The Poisson regression model is based on the assumption that the count of events follows a Poisson distribution, characterized by the property that its mean is equal to its variance

(equidispersion). This assumption is suitable for datasets where the occurrence of events is rare and independent over a fixed period or space, such as the number of deaths in a small population or rare diseases. The simplicity of the Poisson model lies in its single parameter, making it computationally efficient and easy to interpret. However, this simplicity also constitutes a limitation, particularly when it comes to overdispersion—a scenario often encountered in real-world data where the variance exceeds the mean due to heterogeneity in the data. When overdispersion is present, the Poisson model can underestimate the standard errors of the estimated coefficients, leading to an overstatement of the statistical significance of predictors.

In contrast, the Negative Binomial model adds an extra parameter to account for overdispersion, offering a more flexible fit for count data that exhibit greater variability. This model is especially apt when the data are counts of events that can occur more frequently than a rare event and when these counts have high variance. It can handle data from populations with heterogeneity that the Poisson model cannot accommodate. This flexibility comes with a trade-off in terms of increased model complexity and computational demand. The added dispersion parameter means that the Negative Binomial model has one more degree of freedom than the Poisson model, which can result in a better fit but also requires careful interpretation of the additional parameter.

For the current paper focusing on mortality rates due to diabetes and heart disease, it is imperative to choose a model that accurately reflects the underlying data distribution. If the mortality counts are subject to overdispersion, the Negative Binomial model would likely provide a more accurate representation of the data, enabling more reliable statistical inferences. For instance, if certain causes of death are more prevalent or exhibit more variability from year to year, the Negative Binomial model's capacity to incorporate this variability would make it a superior choice over the Poisson model.

Ultimately, the selection between the two models should be guided by diagnostic checks, such as the dispersion parameter and goodness-of-fit tests. For example, if the model comparison indicates a better fit for the Negative Binomial model and significant overdispersion in the Poisson model, it would justify the selection of the Negative Binomial model for the analysis. Additionally, both Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) can be instrumental in determining which model is more appropriate for the data at hand. These criteria consider both the likelihood of the data given the model and the complexity of the model, thus providing a balance between fit and parsimony.

3.1 Poisson Model

The Poisson regression model is characterized by its simplicity and efficiency in modeling the count data. It assumes that the event occurrence rate is constant across the observed period and that these events occur independently of each other. Despite its advantages, the Poisson

model may fall short in handling overdispersion, where the variance exceeds the mean in the count data.

$$y_i|\lambda_i \sim \text{Poisson}(\lambda_i)$$

$$\log(\lambda_i) = \alpha + \beta_1 \times \text{AMI}_i + \beta_2 \times \text{OtherIHD}_i + \beta_3 \times \text{ASCVD}_i + \beta_4 \times \text{Diabetes}_i + \beta_5 \times \text{CHF}_i$$

where:

- y_i is the count of deaths due to the i-th cause.
- λ_i is the expected count of deaths for the i-th cause.
- α, β_1, β_2, β_3, β_4, and β_5 are the model parameters to be estimated.
- AMI, OtherIHD, ASCVD, Diabetes, and CHF are abbreviations of our previously selected variables.

3.2 Negative Binomial Model

To address potential overdispersion in our data, we also applied the Negative Binomial regression model. This model extends the Poisson by introducing an extra parameter to account for the overdispersion, offering a more flexible approach to fit our data. The formulation of the Negative Binomial model is:

$$y_i|\mu_i, \phi \sim \text{NegBin}(\mu_i, \phi) \tag{1}$$

$$\mu_i = \exp(\alpha + \beta x_i) \tag{2}$$

$$\alpha \sim \text{Normal}(0, 2.5) \tag{3}$$

$$\beta \sim \text{Normal}(0, 2.5) \tag{4}$$

$$\phi \sim \text{Exponential}(1) \tag{5}$$

In this model, y_i denotes the total number of deaths per year, with μ_i being the expected count adjusted for overdispersion through the dispersion parameter θ. *β{0} represents the intercept and* β{i} represents the effects of a unique cause of death. The value and sign of β denote whether having that disease/sickness increase or decrease the death count of that year and by how much.

Given the observed overdispersion in our dataset, the Negative Binomial model is anticipated to offer a more accurate and reliable fit compared to the Poisson model. By incorporating the extra dispersion parameter, it allows us to better capture the variability in death counts across different causes, providing a nuanced understanding of how each cause contributes to overall mortality. In applying these models, we aim to discern the relative impact of specified causes of death on the total number of deaths, while also accounting for the distributional characteristics of our count data. Through this comparative analysis, we seek to identify the most suitable model for our dataset, thereby enhancing the reliability of our findings and conclusions.

We run the model in R (R Core Team 2023) using the `rstanarm` package of Goodrich et al. (2022). We use the default priors from `rstanarm`.

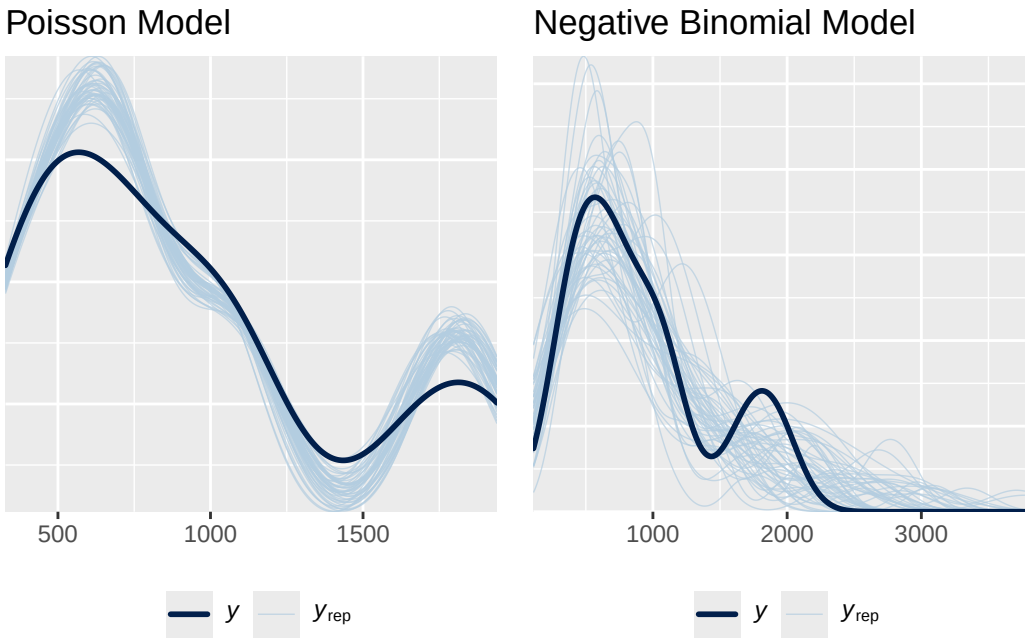
3.2.1 Model justification

Since we have two potential methods of modeling, we can directly compare the two to decide which regression to run. In the previous section, we hypothesized that the Poisson model will lead to more inaccurate results due to overdispersion of data. We can see if the assumption that variance is equal to the mean is true for our y_i value for total death count per year.

Table 2: Summary Statistics of the Number of Yearly Deaths by Cause

Minimum	Mean	Maximum	Standard Deviation	Variance	Count
347	915.7333	1939	511.7452	261883.1	30

From the table above, we see that the variance is significantly off of the mean. Therefore, the primary assumption for applying a Poisson model where the variance is equal to the mean does not hold. From this alone, we can reasonably conclude that a negative binomial model most likely fits our purpose of estimating the total death count per year better due to accounting for overdispersion with the μ_i variable. However, we can visualize this further by displaying the calculated y_i values versus the measured y_i values for both a Poisson and a negative binomial model side by side.



The graphs presented here illustrate the posterior predictive checks for the Poisson and Negative Binomial models applied to the mortality data concerning various causes of death. For both graphs, the x-axis represents the count of total deaths, and there are two sets of lines: one for the observed counts (denoted by y) and another for the predicted counts from the respective models (denoted by y_rep). The lines for predicted counts represent different simulated datasets generated by the model, reflecting its probabilistic predictions.

In the Poisson Model graph, the overlapping lines suggest that while the model captures the general trend of the observed data, it may not encapsulate the full variability, as indicated by the divergence between the observed and predicted counts particularly in regions of higher death counts. The model seems to generally underpredict the total death count per year when the data peaks which could be caused by the difference in variance and mean.

Conversely, in the Negative Binomial Model graph, the predicted counts lines appear to more closely follow the pattern of the observed data, including the peaks and valleys, which indicates a better fit. This model's ability to account for overdispersion with its μ_i term likely contributes to its more accurate representation of the variability in the data. The thicker lines indicating the observed counts y remain consistent across both models, serving as a benchmark for evaluating the predictive accuracy. The spread and concentration of the lighter lines (the predictive simulations y_rep) around these observed counts provide visual insight into the model's performance.

The Negative Binomial model appears to yield a better fit to the data, particularly for larger counts, which suggests it might be the more appropriate model for analyzing the impact of diabetes and heart disease on mortality rates within the studied population. This would be consistent with the expectation that mortality data, influenced by complex and varied factors, would exhibit overdispersion—an assumption better accommodated by the Negative Binomial model than by the Poisson model.

4 Results

Our results are summarized in Table 3.

5 Discussion

5.1 First discussion point

If my paper were 10 pages, then should be be at least 2.5 pages. The discussion is a chance to show off what you know and what you learnt from all this.

Table 3: Explanatory models of flight time based on wing width and wing length

	First model
(Intercept)	1.12
	(1.70)
length	0.01
	(0.01)
width	−0.01
	(0.02)
Num.Obs.	19
R2	0.320
R2 Adj.	0.019
Log.Lik.	−18.128
ELPD	−21.6
ELPD s.e.	2.1
LOOIC	43.2
LOOIC s.e.	4.3
WAIC	42.7
RMSE	0.60

5.2 Second discussion point

5.3 Third discussion point

5.4 Weaknesses and next steps

Weaknesses and next steps should also be included.

Appendix

A Additional data details

B Model details

B.1 Posterior predictive check

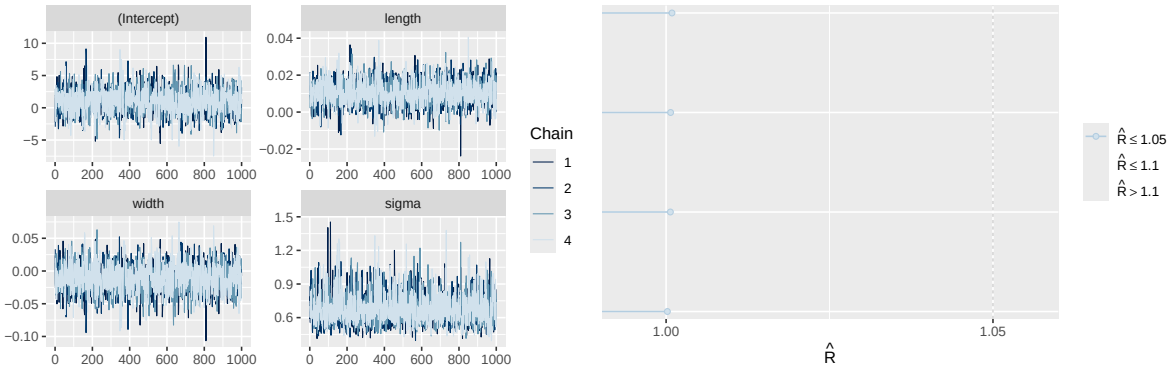
In **?@fig-ppcheckandposteriorvsprior-1** we implement a posterior predictive check. This shows...

In **?@fig-ppcheckandposteriorvsprior-2** we compare the posterior with the prior. This shows...

B.2 Diagnostics

Figure 1a is a trace plot. It shows... This suggests...

Figure 1b is a Rhat plot. It shows... This suggests...



(a) Trace plot

(b) Rhat plot

Figure 1: Checking the convergence of the MCMC algorithm

References

Goodrich, Ben, Jonah Gabry, Imad Ali, and Sam Brilleman. 2022. "Rstanarm: Bayesian Applied Regression Modeling via Stan." https://mc-stan.org/rstanarm/.

R Core Team. 2023. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. https://www.R-project.org/.

Wickham, Hadley, Mara Averick, Jennifer Bryan, Winston Chang, Lucy D'Agostino McGowan, Romain François, Garrett Grolemund, et al. 2019. "Welcome to the tidyverse." *Journal of Open Source Software* 4 (43): 1686. https://doi.org/10.21105/joss.01686.