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Knowing and understanding change: Methods insights using historical pandemic data

Taylor van Doren [1]

[1] University of Alaska Anchorage

Pandemic diseases, like COVID-19, have far-reaching effects that are difficult to identify or predict during the course of the pandemic itself. Case numbers and mortality due to pandemic diseases ebb and flow, but even after time has passed, it is useful to know (1) when the waves occurred, (2) if the pandemic disease had effects on the epidemiology of other chronic and/or infectious conditions, and (3) if we can learn more detail about inequalities in pandemic experience.

There are statistical modeling methods that allow researchers to study how rates of interest change at predetermined or statistically estimated points in a time series, namely piecewise, segmented, or spline regression. Another simple yet sparsely used modeling technique, Joinpoint regression can identify significant points of change in rates in a time series without requiring the researcher to input the location of potential points of change. One of the clearest applications today is the ability to identify changing rates in COVID-19 dynamics: How do we identify the beginning of a "wave" of COVID-19 morbidity or mortality? How are vaccination rates changing over time? How will we know when the COVID-19 pandemic is over?

It may be a while before all of these questions can be answered about the COVID-19 pandemic, but researchers can turn to historical pandemic events to better understand how they influence epidemiology of other diseases and demography. To learn more about historical mortality dynamics around the 1918 influenza pandemic, Taylor van Doren uses the joinpoint regression method to identify points of change in tuberculosis mortality during the early 20th century in Newfoundland, the progression of which is thought to be dependent on–or at least influenced by–the 1918 pandemic. The results show that tuberculosis mortality did not change after the 1918 flu pandemic in the study population, even though previous research by others has identified significant post-1918 flu declines in tuberculosis mortality in the U.S. Historical epidemiologists who study much older records (e.g., 17^{th}-19^{th} century) leverage the non-mutually exclusive nature of infectious diseases and focus on analyses of all-cause mortality. Joinpoint regression would be a useful tool for retroactively identifying moments of epidemic or pandemic activity, since the researcher need not know precisely where significant points of rate change occurred before those points are statistically estimated. This can ultimately help uncover missed waves or disease associations that could be useful to know in a modern context.

The Download

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Citation:

van Doren, T. (2024). Knowing and understanding change: Methods insights using historical pandemic data. https://doi.org/10.6069/HHRJ-QJ86

Published: 2024-04-17

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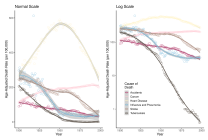

Estimating time points of significant change in cause-specific mortality: Joinpoint regression in R Those engaged in demographic research are often interested in how and why the vital demographic processes (fertility, mortality, and migration) change in response to certain ecological, cultural, or behavioral stimuli. Today, in the midst of a global pandemic event… read more

As we move towards a post-COVID-19 future, the joinpoint regression method would be useful to identify the different progression of the COVID waves through different populations, how burdens of other conditions (cardiovascular diseases, disability, chronic respiratory diseases) may increase in the future, and more.

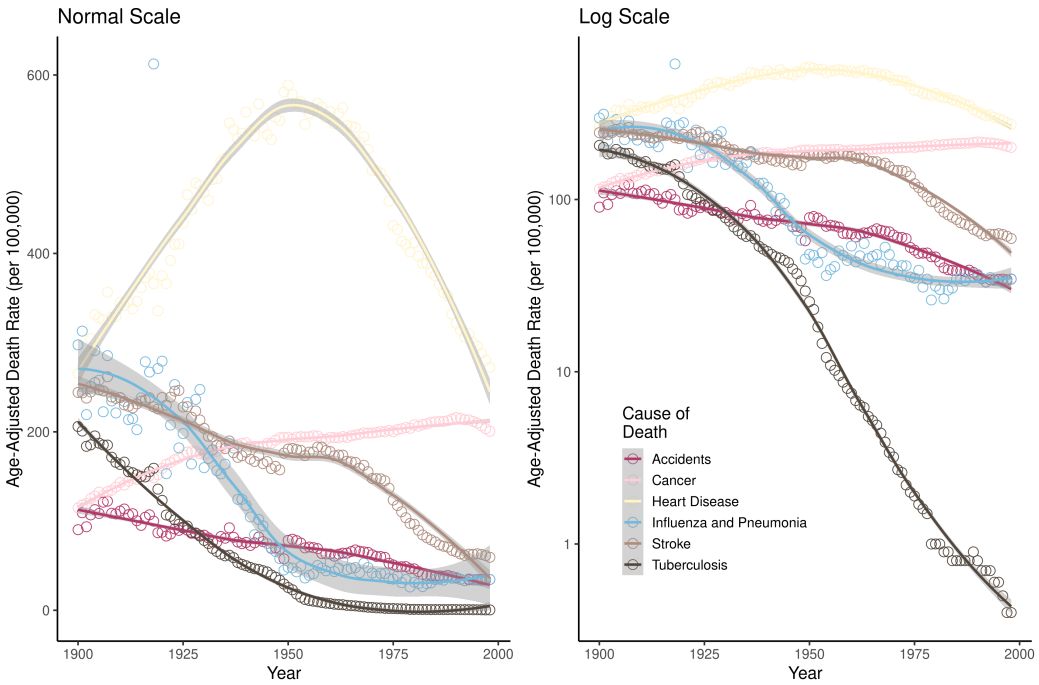

Figure 1: The age-adjusted mortality rates (left) and logarithmic transformation of age-adjusted mortality rates (right) for six major causes of death in the United States from 1900-1998. Source: CDC National Vital Statistics System.

Computation & Reproducibility

All code necessary to implement the methods and reproduce the figures and results in Knowing and understanding change: Methods insights using historical pandemic data has been archived as of publication on April 17, 2024 by the Population Dynamics Lab: https://github.com/Population-Dynamics-Lab/joinpoint-regression-tutorial.

The original repository maintained by Taylor van Doren can be found here: github.com/taylorvandoren/. Note: this repository is maintained by Taylor van Doren and may differ from that originally used to produce the results in this publication.