

Understanding Mortality Data: A Step-by-Step Guide to CDC WONDER, Joinpoint Analysis, and Forecasting Models

Received: 17 January 2026

Accepted: 13 April 2026

Published online: 08 May 2026

Cite this article as: Shubietah A., Ruzieh M., Hamed B.M. *et al.*

Understanding Mortality Data: A Step-by-Step Guide to CDC WONDER, Joinpoint Analysis, and Forecasting Models. *J Epidemiol Glob Health* (2026). <https://doi.org/10.1007/s44197-026-00561-8>

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REVIEW ARTICLE

Title.

**Understanding Mortality Data: A Step-by-Step Guide to CDC
WONDER, Joinpoint Analysis, and Forecasting Models**

Running Title: *CDC WONDER Guide*

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Abstract

Background: The use of mortality data in public health research has surged with the rise of open-access databases such as CDC WONDER. However, caution is needed when defining the relationship between ICD codes and when transitioning from older to newer versions of the data. This review provides a practical, step-by-step guide to using the CDC WONDER mortality database.

Methods: We outline key functionalities of the CDC WONDER interface, explain mortality rate calculations, and describe best practices for configuring queries using underlying and multiple causes of death. The review further introduces Joinpoint regression to identify temporal trend changes and compares forecasting approaches using traditional ARIMA models and modern deep learning architectures.

Results: Using illustrative examples and visual guides, we demonstrate how data interpretations can vary significantly depending on query configuration, Boolean logic (AND vs. OR), and coding practices. We highlight the strengths and limitations of different analytical strategies and show how

misinterpretation can arise from common errors, such as misunderstanding age adjustment or combining ICD codes without appropriate logic.

Conclusion: CDC WONDER is a powerful tool for mortality analysis, but its effective use requires a clear understanding of its data structure, coding logic, and statistical tools. Joinpoint regression and forecasting models complement WONDER data by enabling trend segmentation and future projections. This guide empowers researchers to use these tools accurately, improving the rigor and reproducibility of public health research.

Keywords: CDC WONDER guide, Joinpoint analysis, ARIMA forecasting, deep learning forecasting.

1. Introduction

We write this paper to provide a practical guide for researchers, public health professionals, epidemiologists, clinicians, and medical students to understand what the CDC WONDER is, what mortality data (both age-adjusted and crude) represent, and how to interpret them accurately. We also discuss Joinpoint analysis, which involves dividing mortality trends over the years into segments rather than just one piece to evaluate each group or segment of years together, as well as forecasting analysis, a fancy way of saying we need to see the future mortality trends of our sample based on existing data (what the future looks like given the available data).

With the rising popularity of databases such as CDC WONDER, NHANES, GBD, TriNetX, and MAUDE, among others, journals have become

increasingly receptive to publishing research based on these databases. CDC WONDER, in particular, is one of the oldest and reflects data from the US population exclusively. Since its inception, the number of publications using this database has increased significantly. From the PubMed search alone, from 1993 (the database's inception) to 2010, there were 58 publications, followed by 119 from 2010 to 2020. In recent years, this growth has accelerated even further, as illustrated in **Figure 1**.

□ **Insert Figure 1 here.**

2. Overview of the CDC WONDER Database

What is this database, and how is it used?

Essentially, CDC WONDER is a publicly available database published by the Centers for Disease Control and Prevention (CDC) that provides annual data on causes of death in the United States, among other data. An individual may die from a single primary condition that initiated the sequence of events leading to death—referred to as the *underlying cause of death*—but other conditions that contributed to the death may also be recorded. These are known as *multiple* or *contributing* causes of death. Both types of death causes are documented on the death certificate, which is typically completed by the treating physician or a member of the care team. The certificate reflects the physician's clinical judgment about the primary cause of death and any

contributing conditions—essentially, what directly caused the death and what other factors played a supporting role (1,2).

The database offers valuable insights into mortality data—both crude and age-adjusted rates—dating back to 1968. Updated annually, it also provides early, incomplete estimates of deaths (counts and often rates) based on death certificates received and coded as of a cutoff date, before the complete set of records is processed. These preliminary figures, referred to as *provisional deaths*, reflect deaths occurring through January 5, 2025, as of January 12, 2026, update (i.e., one week before this inquiry).

3. Mortality Rates: Crude vs. Age-Adjusted

In CDC WONDER, the age-adjusted mortality rate (AAMR) is a method for comparing death rates as if every population group had the same age distribution as a standard chosen population. It does this by calculating death rates within 11 age groups and then combining them using a fixed “standard” age distribution (by default, the year 2000 US standard population). Therefore, the differences you observe are less likely to be driven solely by one group being older than another. The 11 age groups used for standard age-adjustment in WONDER are: <1, 1-4, 5-14, 15-24, 25-34, 35-44, 45-54, 55-64, 65-74, 75-84, and ≥ 85 years.

By contrast, the crude mortality rate is the simple “raw” death rate in the population without adjusting for age. Because older people die at higher rates, a population with more older adults will often have a higher crude rate

than its age-adjusted rate—but this isn't guaranteed (it depends on how old the population is compared with the standard population). Both rates are typically reported per 100,000 people in WONDER.

When we say age-adjusted mortality is calculated “as if every group had the same age makeup,” we mean this:

- You first compute age-specific death rates (a rate within each age band).
- Then you re-weight those age-specific rates using the same fixed age distribution (the “standard population”) for everyone you're comparing—so differences aren't just because one population is older.

A simple example: Imagine two towns, each with 100,000 people:

Town A (older):

- 80% under 65
- 20% age 65+

Town B (younger):

- 95% under 65
- 5% age 65+

Now, assume both towns have the same age-specific death rates:

- Under 65: 100 deaths per 100,000

- 65+: 2,000 deaths per 100,000

Crude rate (raw rate):

- Town A: $0.80 \times 100 + 0.20 \times 2000 = 80 + 400 = \mathbf{480 \text{ per } 100,000}$
- Town B: $0.95 \times 100 + 0.05 \times 2000 = 95 + 100 = \mathbf{195 \text{ per } 100,000}$

So Town A *looks* much worse—but only because it has more older people.

Age-adjusted rate (“as if both towns had the same age makeup”):

Pick a single “standard” age mix (for illustration): 90% under 65, 10% age 65+

Apply those same weights to *both* towns:

- $0.90 \times 100 + 0.10 \times 2000 = 90 + 200 = 290 \text{ per } 100,000$ (for both towns)

The two towns in the above example may represent two states (e.g., Florida vs. Utah), two racial groups (e.g., non-Hispanic White vs. Hispanic), or even two time points (e.g., 1999 vs. 2017).

This is exactly the logic used in CDC WONDER: it applies a fixed (standardized) age distribution to ensure fair comparisons of mortality across populations or time periods. **Figure 2** illustrates this age adjustment process.

- **Insert Figure 2 here.**

The platform can be accessed at <https://wonder.cdc.gov>. Upon entering the site, users are prompted to select the dataset type they wish to explore. The most frequently used datasets are Underlying Cause of Death (UCD), Multiple

Cause of Death (MCD), and Compressed Mortality, which will be the focus of our talk here.

The UCD dataset provides data on the underlying cause of death only, starting in 1999, while the MCD dataset includes data on both underlying and multiple causes of death beginning in 1999. The Compressed Mortality dataset contains older mortality data dating back to 1968, along with some more recent data.

4. ICD Coding Systems and Time Transitions

Still, it is essential to recognize that the International Classification of Diseases (ICD) coding system used in CDC WONDER has evolved over time. ICD-8 was used from 1968 to 1978; ICD-9 from 1979 to 1998; and ICD-10 has been used for US mortality (death certificate) cause-of-death coding, starting with deaths in 1999 and continuing through 2016 and beyond. This can be confusing because the “2015 ICD-10 adoption” refers to a separate transition in clinical billing/claims (ICD-9-CM → ICD-10-CM/PCS) that took effect on October 1, 2015 (3), not the mortality system used in WONDER. When analyzing trends across multiple decades, it is essential to account for these coding transitions to ensure comparability and accurate interpretation.

5. Step-by-Step Guide to Using the CDC WONDER Interface

After selecting the desired dataset, the user accesses a configuration interface to define the parameters of their query. One of the initial steps involves selecting the year or range of years of interest—for example, 1999

to 2020. The user then proceeds to Step 1 in **Figure 3**, where they choose how to group the data. Grouping can be based on demographic or geographic variables such as sex, race, year, census region, or state. It is essential to note that if the underlying or multiple causes of death and demographic categories, such as age groups, selected in Step 3 remain unchanged, the data output will be the same, with differences only in how the results are displayed—for instance, in the Excel file structure. Also, in Step 1, users should check boxes to include age-adjusted mortality rates (AAMR), confidence intervals (CI), standard error (SE), and percentage of total deaths—if desired. It is also important to note that if users choose to group the data by age groups in Step 1, the AAMR will not be available, as it cannot be calculated for the same age groups used in the age adjustment process. In such cases, the AAMR checkbox can be omitted; if it is selected, it will not yield results.

In Step 2, users can narrow the data by location, filtering by state or urbanization level, though these fields are often left at their default settings. Step 3 enables users to define demographic filters such as sex, race, and age group. For analyses focused on adults, the "25 years and over" age group is commonly selected, particularly because data for younger age bands, such as 18-24 years, are often unavailable. WONDER has predefined age strata for the AAMR calculation, which is why the 18-24 age group is unavailable; it's not used in the AAMR calculation.

Further refinements are available in Step 5, where users can filter by the weekday of death, autopsy status, and place of death. However, these filters are typically not altered unless the research question requires them. The most crucial part of the process is in Steps 6 and 7, where the causes of death are defined using ICD codes. In Step 6, which addresses the underlying cause of death, users can input one or more ICD codes, interpreted as an “OR” condition—meaning any of the selected codes can qualify as the underlying cause. In Step 7, which allows multiple causes of death, users can enter up to 20 ICD codes. These can all be entered in a single box (also interpreted as “OR”), or split between two boxes that use “AND” logic.

For example, one might define ischemic heart disease (IHD) as the underlying cause of death and then add diabetes mellitus type 2 (DM-2), hypertension (HTN), or chronic kidney disease (CKD) in one “OR” box, with stroke listed in the “AND” box. This setup would return data on deaths where IHD was the primary cause, and any of the listed conditions—DM-2, HTN, or CKD—were present, along with stroke as a contributing cause. To do this, you must select the appropriate ICD coding system for ischemic heart disease. Under ICD-8, the codes are 410–413; under ICD-9, the codes are 410–414; and under ICD-10, the codes are I20–I25. Once selected, you can download datasets that include both age-adjusted and crude mortality rates.

Finally, in Step 8, users can configure export settings and specify how the data should be displayed or downloaded. It is recommended to set the number of decimal places to at least 3 or 4, as selecting only 1 decimal place

will cause any death rate below that threshold to be displayed as zero. In this case, we selected the maximum value of 9 decimal places to ensure the most precise representation of the data. Generally, Steps 1, 3, 6, and 7—covering data grouping, demographic filters, and cause-of-death coding—are the most essential and frequently used components in most analyses conducted through this interface.

□ **Insert Figure 3 here.**

A simplified version of the CDC WONDER query process is illustrated in **Figure 4.**

It is important to note that some data may not be available when certain variables are selected in Step 1, but may become available after filtering in subsequent steps. What does this mean in practice? For example, if you choose to group the data by Weekday in Step 1, the output will include only the number of deaths, without any associated crude death rate or age-adjusted mortality rate (AAMR). This is illustrated in the example for ICD-10 codes C00-D48 (Neoplasms).

However, if you instead go to Step 5 and use Ctrl or Shift to select Monday through Friday, the data output will include both AAMR and crude rates. This is because the system does not provide rate-based data for each day individually, likely due to insufficient sample size. However, when multiple weekdays are combined, the resulting larger sample size enables the calculation of these rates.

It is also important to note that if you use this second method (filtering for weekdays in Step 5) and download the data, the results will represent all selected weekdays combined—without a corresponding comparison group (e.g., weekends). As such, this combined weekday group should not be directly compared to weekend data. Not only is the result age-adjusted only (and not adjusted for other demographic or contextual factors), but it is also not volume-adjusted. In other words, more deaths naturally occur on weekdays than on weekends, so any comparison between the two must be interpreted with caution to avoid misleading conclusions. See **Figure 5** for illustrations.

□ **Insert Figure 5 here.**

In addition to mortality data, the CDC WONDER database provides information on environmental changes, cancer incidence and mortality, infant deaths and natality, and the distribution of tuberculosis cases. Refer to **Figure 6** for a detailed overview of the datasets available on the platform. Among these, the datasets on underlying and multiple causes of death are the most widely used for research, which we discussed above.

□ **Insert Figure 6 here.**

6. Case Study: CAD and COPD Mortality Queries

Consider the following research topic you want to write up. What is the mortality rate of stable coronary artery disease (CAD) among patients with chronic obstructive pulmonary disease (COPD)?

This title carries four possible interpretations:

First possibility: You designate stable CAD as the *underlying* cause of death and COPD as the *multiple* cause. This means these are patients who died primarily *from stable CAD* and had *COPD recorded as a contributing factor*. In this case, you are not capturing the entire population of people with COPD. Some patients had COPD, but for various reasons, the physician who filled out the death certificate did not judge that COPD contributed to the death, even though the patient had it. This process is very subjective and doesn't reflect the full sample.

Second possibility: The data was extracted with both stable CAD and COPD listed as *multiple causes*, and the relationship between them was set to *OR (in the same box)*. This includes all patients who had either COPD or stable CAD mentioned anywhere on the death certificate, whether as an underlying or contributing cause. Why? Because if the *underlying cause* field is left blank (by blank, we mean it holds the possibility of any disease to be listed), the main cause of death could be anything. "Anything" could include stable CAD or COPD, but it might also be something else entirely—like stroke, for example. This means the person died and had either COPD or stable CAD or even both listed on their death certificate, without specifying whether it was

the primary or a contributing cause. This can make the interpretation very vague.

Third possibility: You selected both stable CAD and COPD as multiple causes, with the relationship set to 'AND' rather than 'OR' (each in a separate box). This means you're capturing only those death certificates where *both conditions* appear—whether one is listed as underlying and the other as contributing, or both as contributing. This approach is generally more precise than the previous one.

Fourth possibility: The user selected stable CAD and COPD, both as *underlying causes*. In this case, the CDC WONDER system will always treat the relationship as *OR*, because a person can only have one underlying cause of death. This means the individual died *either from stable CAD or from COPD*—but not both. This approach lacks precision. For this, we are against calling it “among patients with COPD” because there are people with COPD who died from stable CAD. Still, the physician did not acknowledge COPD as a contributing factor to death, so it's better to be revised as “What is the mortality rate of stable CAD when COPD is present as a contributing condition?” See **Table 1 and Figure 7** for details.

□ **Insert Table 1 here.**

□ **Insert Figure 7 here.**

From our standpoint, WONDER is an effective tool for understanding underlying causes of mortality, such as stroke, atrial fibrillation (AF), or acute

coronary syndrome (ACS), over time. Combining earlier data from before 1999 with later data from after 1999 provides a more comprehensive historical perspective. While earlier datasets lack the detailed subgroupings and categories found in more recent datasets (e.g., ethnicity and races beyond Black or White), they still provide valuable insights when analyzing large mortality datasets. This historical view helps illustrate how mortality rates have evolved and raises important questions about the contributing factors. For instance, have public health policies played a role in reducing mortality? Or has the absence of such policies contributed to an increase or plateau in deaths?

Recently, Lippi et al. examined the data from a different angle by focusing on within-year monthly seasonality rather than long-term secular trends, showing that U.S. acute myocardial infarction mortality from 2018 to 2022 consistently peaked in December and January and was lowest during the summer months (4), which provides another useful perspective for examining these data.

Sometimes, an observed rise in mortality may be due to improved detection rather than an actual increase in death rates, as seen in the study examining mortality from amyloidosis over the years, where the increase is likely due to better identification rather than a true rise in cases per se (5). If users choose to use the multiple causes of death in analyses, caution is necessary. The interpretation can vary depending on how Boolean logic is applied in the literature, which may influence the conclusions drawn.

Accordingly, the methodological choices employed when querying CDC WONDER have significant implications for public health. In our CAD and COPD case study, employing a comprehensive 'OR' logic includes a significantly diverse population, in which the actual cause of death may be unrelated to either condition. If researchers depend on this vague question, they could be overestimating how many people die because of the connection between CAD and COPD, which might lead to wrong public health priorities, and could mean that resources for disease prevention are not used as well as they could be (6). On the other hand, using the more exact "AND" logic only looks at the group of people who died with both criteria at the same time. This level of accuracy enables policymakers and doctors to accurately assess the true comorbidity burden, develop integrated care pathways, and develop evidence-based solutions that meet the community's health needs (7).

7. Joinpoint Analysis: Understanding Trend Changes

We now transition to **Joinpoint analysis**.

What is Joinpoint analysis?

In simple terms, Joinpoint analysis is a statistical tool that breaks down a single, long-term trend into smaller, specific time segments. Instead of drawing a single straight line across decades of data, it connects multiple lines to pinpoint exactly when mortality rates changed course, such as the year when a steady decline suddenly turned into an increase.

Consider the following hypothetical example:

The age-adjusted mortality rate (AAMR) for acute myocardial infarction was 0.3 in 1999 and 0.9 in 2020. If you draw a straight line between these two points, you could say that the AAMR increased by 0.6 over 21 years, resulting in an average annual increase of 0.02857 (0.6/21).

While this provides a broad view of the data, it misses important details.

For instance, suppose that between 1999 and 2005, the AAMR actually decreased from 0.3 to 0.1; then from 2005 to 2012, it increased sharply to 1.6; and finally, from 2012 to 2020, it declined again to 0.9. This segmentation provides a much deeper understanding of how the AAMR evolved over the 21 years.

Some of these segmental trends may be statistically significant—for example, a p-value < 0.05 from 1999 to 2005—while others may not (e.g., p-value > 0.05 in subsequent periods).

Joinpoint analysis (or Joinpoint regression) is a method used to examine how mortality trends change over time. Joinpoint models fit multiple connected line segments and identify the years in which the slope changes significantly or non-significantly—these are known as joinpoints. The main objective is to detect the timing of these trend changes and to analyze rate patterns before and after each joinpoint. This approach is well-suited for CDC WONDER data, which often exhibits non-uniform mortality trends.

Joinpoint analysis is commonly conducted using the National Cancer Institute (NCI) Joinpoint Regression Program (8,9), a widely used tool for surveillance

analysis of rates. The software allows users to set a minimum and maximum number of joinpoints and then tests whether adding joinpoints significantly improves model fit. The output reports the identified joinpoint years and the slope of each segment, expressed as Annual Percent Change (APC). It also provides an Average Annual Percent Change (AAPC) to summarize overall trends.

For CDC WONDER data, Joinpoint is typically applied to age-adjusted mortality rates (AAMR), which help enable fair comparisons across years despite changes in the population's age structure. Still, it can also be applied to crude rates, death count, or percentage. The NCI Joinpoint Regression Program includes several models and option settings that are particularly important for analyzing CDC-type mortality data.

The model needs to decide how many "joinpoints" (change-points) to include. One method, the Permutation Test (10), adds joinpoints only when there's strong evidence that the change is real, based on many simulated datasets (e.g., 4499 permutations). This is like running a detailed test to see if adding a joinpoint significantly improves the model. The other method, Weighted BIC (WBIC) (11), skips formal testing and instead picks the number of joinpoints by balancing how well the model fits the data versus how simple it is. WBIC might allow more joinpoints if they slightly improve the model, even without strong statistical proof.

Another difference is in how confidence intervals (CIs) are calculated. These intervals show how certain we are about trend estimates, such as Annual Percent Change (APC). The older Parametric Method assumes that the data follow a specific distribution and tends to yield wider, more cautious intervals. The newer Empirical Quantile (12,13) Method uses resampling (e.g., 5001 model repeats) to directly estimate variability, often resulting in narrower, more accurate intervals. These differences may not matter much in large, smooth datasets. Still, in smaller or noisier subgroups (like by age or race), they can lead to different joinpoint years, different APC values, or even change whether a trend is considered statistically significant. Running both methods can help confirm the robustness of your findings.

Both the Permutation Test and Weighted BIC methods use the same setting for the maximum number of joinpoints—for example, 7—because this is a general rule that limits how complex the model is allowed to get, no matter which selection method you're using. It works like a cap: the software looks at all models from the minimum (usually 0 joinpoints) to the maximum (e.g., 7), and then the chosen method (Permutation or WBIC) picks the “best” one from that range.

However, the number 7 isn't always the default setting. Joinpoint software usually recommends a maximum number of joinpoints based on the amount of data you have. For example, if your data has 27 or more time points (e.g., 27 years), it might suggest a maximum of 5 join points. But you're allowed to

set a higher maximum manually (up to 9) if you're using a more detailed search, called a grid search, though this can take longer to run.

It is important to note that the software accepts a grouping variable (such as ethnicity, race, or gender) alongside the year as the independent variable, and requires the count or rate to be analyzed—such as age-adjusted mortality rate (AAMR), crude rate, or death count—along with its standard error (SE). Confidence intervals (CIs) are not required. We advise using the Empirical Quantile method for confidence intervals and the Weighted BIC for model selection, as shown in **Figure 8**.

For a simple explanation of Joinpoint analysis, please see **Figure 9**.

□ **Insert Figure 8 here.**

8. Forecasting Mortality Trends

Forecasting uses historical data to predict future mortality trends, assuming no major changes in clinical care or public health policies occur. This section includes two main approaches: traditional statistical models (such as ARIMA), which are excellent for straightforward, historical patterns, and modern machine learning models (such as deep learning), which are better suited for massive, complex datasets with multiple variables.

Two commonly used approaches are ARIMA (AutoRegressive Integrated Moving Average) and deep learning (DL) models, both of which fall under the

broader umbrella of machine learning. However, ARIMA is often considered a traditional statistical method, while deep learning reflects modern computational advances.

These models generally assume that underlying mortality trends remain stable, meaning that there are no significant changes in treatment practices, diagnostic criteria, or external interventions over time. In other words, they attempt to answer the question:

“If we make no changes to clinical care or public health interventions, what will mortality look like in 5, 10, or 20 years?”

ARIMA models are most effective for small to moderately sized datasets—typically when working with monthly or annual data spanning 10–30 years and involving relatively few variables (14). These models are highly interpretable and well-suited to data with consistent seasonal or linear patterns. They rely on previous observations and errors to capture time dependence and are widely used because of their simplicity and ease of interpretation (15,16). In practice, ARIMA models are commonly implemented using R packages such as “forecast”, or Python packages such as “pmdarima” and “statsmodels”.

On the other hand, deep learning models, such as LSTM, GRU, or Transformer-based architectures, are more powerful for handling larger and more complex datasets, including high-frequency data (e.g., daily or hourly), longer time spans, or multivariate time series with many features (e.g.,

clinical, demographic, or policy variables). While these models require more data and computational power, they can capture non-linear trends and complex dependencies that ARIMA models cannot (17). They are typically implemented in R using Keras, or in Python using TensorFlow/Keras or PyTorch, and perform best when applied to large or complex datasets.

For a simple explanation of forecasting models, please see **Figure 9**.

□ **Insert Figure 9 here.**

9. Examples from the Literature Where CDC WONDER's Interpretation Matters.

It's important to understand that studies based on CDC WONDER are cross-sectional in nature, involving population-level death-certificate data of deaths from a given condition or conditions in the United States. There is no comparative arm, and therefore, these studies cannot be classified as retrospective cohort studies. However, they can appropriately be described as retrospective cross-sectional studies.

In the study by Billion et al.(18), the authors examined trends and disparities in lung cancer mortality, but incorrectly described their work as a retrospective cohort study. The same issue applies to the study by Maniya et al. (19), which analyzed atherosclerotic cardiovascular disease-related mortality among older adults, but also misclassified the study design as a

retrospective cohort study. In another study by Nabi et al. (20), the authors used “AND” logic to link both obesity and hypertension. ICD codes for one condition were entered into the first box of the MCD section, while codes for the other condition were entered into the second box. The UCD was left at the default setting of “All Causes of Death,” meaning the primary cause could be obesity, hypertension, or another condition entirely. The authors appropriately defined and applied their logic.

Additionally, in Dort et al. (21), the authors titled their work *“Trends in pulmonary embolism mortality in cancer patients,”* suggesting that the study included all cancer patients whose primary cause of death was pulmonary embolism (PE). However, the authors used AND logic, similar to Nabi et al., meaning that both PE and cancer were listed somewhere on the death certificate—either as an MCD or UCD—but not necessarily that PE was the direct cause of death in cancer patients. In this configuration, the actual UCD could be PE, cancer, or another unrelated condition. A more accurate and transparent title for their study would be: *“Mortality trends related to PE and cancer patients.”* In another study by the same lead author (Nabi et al.) (22), they used acute myocardial infarction (AMI) as the underlying cause and chronic kidney disease (CKD) as a contributing cause of death, titling the study *“Mortality Trends from Acute MI with Underlying CKD.”* While it is true that if CKD is listed as an MCD, the patient had it at the time of death, the approach does not capture all AMI cases in which CKD was recorded as an MCD, as this is entirely dependent on how the death certificate was

completed. Instead, it identifies only a subset of patients in whom AMI was the UCD and CKD was explicitly documented as a contributing cause.

10. Adaptation of Analytical Methods to Global Mortality

Databases

While the CDC WONDER database provides comprehensive mortality data for the US only, the analytical principles and statistical techniques discussed in this guide can be translated to global health research. Researchers investigating international mortality trends can apply similar workflows, such as differentiating between underlying and multiple causes of death, adjusting for age to allow cross-population comparisons, and accounting for ICD coding transitions when using global repositories.

Prominent global resources include the World Health Organization (WHO) Mortality Database, which provides cause-of-death statistics based on ICD classifications (23) (24), and the Global Burden of Disease (GBD) studies, which provide comprehensive demographic and epidemiological estimates across 204 countries and territories (25) (26). When applying tools like Joinpoint regression and forecasting models to these international datasets, investigators must remain vigilant about database-specific limitations. For example, the quality, completeness, and reporting of death certificates vary significantly between low- and high-income countries (27) (28). Also, global databases often aggregate data using different standard populations for age-adjustment (29). However, by adapting the rigorous query configurations and

statistical modeling approaches outlined in this guide, researchers can effectively leverage global databases to track disease burden, evaluate international public health interventions, and forecast future epidemiological challenges on a global scale.

11. Limitations of CDC WONDER and Cautions in Interpretation

The CDC WONDER mortality databases have several key limitations. First, they are based on death certificates rather than clinical registries and therefore offer limited clinical detail and sparse demographic data. They do not include laboratory results, imaging, medications, procedures, or adjudicated diagnoses. Instead, a single designated certifier makes the medical judgment, and the underlying cause is determined afterward through standardized coding rules rather than through a multiperson adjudication process. Prior literature has shown that certifiers may record terminal mechanisms such as “cardiopulmonary arrest” or “cardiac arrest” instead of the actual disease process causing death, even though these terms reflect mechanisms of dying rather than valid underlying causes of death. As a result, mortality data may be influenced not only by disease burden and survival, but also by certification practices and coding behavior. Additionally, WONDER cannot distinguish whether mortality trends reflect changes in disease occurrence, survival, treatment, or coding practices; thus, causal interpretation requires caution. Suppression rules also present a practical challenge: counts under 10 are suppressed and cannot be published, which

distorts analyses of rare outcomes or small populations. In addition, low-count rates (for example, <20) may be flagged as unreliable. Finally, changes in coding systems, such as transitions from ICD-8 to ICD-9 and ICD-10, can introduce discontinuities in trends, necessitating the use of comparability ratios (30-32).

Misclassification of race/ethnicity—particularly among American Indian/Alaska Native and Hispanic groups—can bias disparity analyses, while inaccuracies in recording education and occupation (reported after 2020) can distort trends and analyses related to socioeconomic and occupational factors. Provisional mortality files are affected by reporting delays, increased suppression, and flagged unreliability, making them more suitable for surveillance than for detailed subgroup analysis. Finally, analytic decisions about whether to use only underlying causes or include multiple causes can substantially affect results, as multiple-cause data may reflect comorbidity rather than true causation.

12. Strategies for Overcoming Data Limitations.

While the inherent limitations of CDC WONDER cannot be avoided, researchers can employ specific methodological strategies to mitigate their impact.

Regarding suppressed data: To protect confidentiality, CDC WONDER suppresses death counts of fewer than 10, which disproportionately affects rural areas and rare causes of death. The most straightforward strategy to

overcome this is temporal or spatial aggregation, such as pooling 3- to 5-year periods into rolling averages or grouping individual counties into larger geographic regions to surpass the reporting threshold. For more advanced geospatial analyses, researchers can apply Bayesian spatial smoothing or multiple imputation techniques that weight population data and regional averages to estimate suppressed values without discarding incomplete datasets (33,34).

Additionally, to correct for misclassification, researchers evaluating demographic disparities should apply the misclassification correction ratios routinely published by the National Center for Health Statistics (NCHS) to adjust their age-adjusted mortality rates (35). Alternatively, if detailed demographic specifics are not a primary aim of the study, researchers may limit comparative analyses to non-Hispanic White and non-Hispanic Black cohorts. These groups have historically exhibited superior validity and minimal misclassification in vital statistics records (36).

13. Conclusion

CDC WONDER is a valuable tool for analyzing US mortality trends. Still, its effective use depends on a clear understanding of its data structure, including the distinction between crude and age-adjusted mortality rates, ICD coding transitions, and the logic applied when selecting underlying and multiple causes of death. This review provides practical guidance on navigating the platform, configuring accurate queries, and applying advanced analytical

methods such as Joinpoint regression and forecasting models. When used thoughtfully, CDC WONDER, paired with robust statistical tools, can offer powerful insights into temporal mortality patterns and inform evidence-based public health decisions.

Statements

Data Availability Statement

All data supporting the findings of this study are included in the manuscript or its supplementary materials.

Author Contributions

Abdalkhalek Shubietah was responsible for conceptualization, project leadership, and writing the initial manuscript draft. Mohammed Ruzieh supervised the project and provided critical insights and revisions to the initial draft. Belal Mohamed Hamed contributed to the writing of the sections on Joinpoint analysis and forecasting models. Sarah Saife designed the figures and wrote their interpretations. Mohamed Abuelazm, Mohamed S. Elgendy, Ahmed Emara, Ahmed Ibrahim, Ameer Awashra, Ibrahim Gowaily, Elsayed Balbaa, Mohamed Saad Rakab, and Mohammed AbuBaha contributed to the writing of the second version of the manuscript and the literature review. Ghada Shbeitah contributed critical language editing and revised the final manuscript for clarity, coherence, and academic style. Mohammed Mhanna supervised the project and provided critical insights throughout the research process.

Funding

No funding was received for conducting this study.

Conflict of Interest

The authors declare no competing interests relevant to the content of this article.

Ethics Approval

Not applicable.

Declaration of AI use

Figure 9 was created using the AI tool Image Generator, while all other figures were created using BioRender.

Consent to Publish

Not applicable.

Consent to Participate

Not applicable.

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Tables

Table 1. Interpretation of CDC WONDER Query Combinations for Stable CAD and COPD in Mortality Data.

Scenario	WONDER Configuration	Logic Applied	What This Query Captures	Implication for Research
1. Primary & Contributory	Underlying Cause: CAD Multiple Cause: COPD	AND	Patients whose primary cause of death was CAD, and who had COPD recorded specifically as a contributing factor.	Too Restrictive: Misses COPD patients where the physician failed to list it as a contributor (subjective error).
2. Broad Inclusion (OR)	Multiple Cause (Box 1): CAD, COPD	OR	Patients who had either CAD or COPD were mentioned anywhere on the certificate. The actual cause of death could be unrelated (e.g., Stroke).	Too Vague: Captures an overly broad population; difficult to attribute mortality specifically to the interaction of these diseases.
3. Co-Occurrence (AND)	Multiple Cause (Box 1): CAD Multiple Cause (Box 2): COPD	AND	Patients where both conditions appear on the death certificate, regardless of which was primary or contributory.	Recommended: The most precise method for analyzing the mortality burden of co-occurring conditions.
4. Underlying Exclusive	Underlying Cause: CAD, COPD	OR	Patients who died either primarily from CAD or primarily from COPD. A person cannot have two underlying causes.	Misleading: This creates two separate cohorts (one dying of CAD, one of COPD) rather than a cohort with both conditions.

*By CAD, we refer to stable CAD.

Figures Legend

Figure 1. Rising use of the CDC WONDER database in published research over time.

Figure 2. Calculation and interpretation of crude versus age-adjusted mortality rates.

Figure 3. Step-by-step configuration interface for querying mortality data in CDC WONDER (Multiple Cause of Death, 1999–2020).

Figure 4. Simplified overview of the CDC WONDER query workflow.

Figure 5. Comparison of weekday filtering in Step 5 (right) versus grouping by weekday in Step 1 (left) using the CDC WONDER Multiple Cause of Death database (1999–2020). Filtering weekdays (e.g., Monday to Friday) in Step 5 yields full output including deaths, crude death rates, age-adjusted mortality rates (AAMR), and their respective confidence intervals and standard errors. In contrast, grouping by weekday in Step 1 provides only death counts, with all rate-based measures labeled “Not Applicable.” This visual comparison highlights how the choice of step affects data availability and interpretability.

Figure 6. CDC WONDER system interface displaying the range of available public health data sources.

Figure 7. Common methodological pitfalls in CDC WONDER-based mortality analyses.

Figure 8. Joinpoint Regression Program setup for trend analysis of age-adjusted mortality rates.

Top Panel (Step 1 - Variable Selection):

Loads the dataset containing age-adjusted mortality rates (AAMR), year, subgroup (e.g., race), and standard error. The year is set as the independent variable, and AAMR is selected as the dependent variable. Log transformation is applied to linearize exponential trends.

Middle Panel (Step 2 - Joinpoint Configuration):

The model defaults to the number of joinpoints based on the loaded data. Confidence intervals are calculated using the Empirical Quantile Method with 5,001 resamples for increased precision, and model selection is based on the Weighted Bayesian Information Criterion (WBIC).

Bottom Panel (Step 3 - Model Selection & Execution):

The model switches from BIC-based methods to the Permutation Test, which uses 4,499 permutations to determine whether each joinpoint significantly improves model fit. Trends are summarized over the full time range (1968–2023) using the Average Annual Percent Change (AAPC), with confidence intervals calculated using parametric methods.

Figure 9. Overview of the analytical framework for mortality trend research, showing a two-stage workflow: joinpoint regression to identify changes in temporal trends and estimate APC/AAPC, followed by forecasting models such as ARIMA and deep learning to project future mortality patterns.

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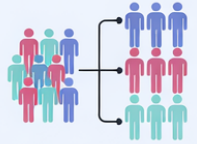
CDC WONDER Query Workflow

1 Dataset selection



UCD | MCD | Compressed

2 Grouping variables



Year, sex, race, state
⚠ Grouping by age → no AAMR

3 Location filters



States, Census Regions

4 Demographics



Age, sex, race

5 Additional filters



weekday of death, autopsy
status, and place of death

6 Underlying cause



Underlying cause of death

7 Multiple causes



Multiple causes
AND vs OR logic

8 Export & decimals



Decimal precision
Crude rate
AAMR

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File Session View Help Sample Sessions

Input File

Method And Parameters

Advanced Analysis Tools

Input Data File

Column Headers

Displaying 20 Lines

By-Variable	Independent Variable		Age-Adjusted Rate Variable			Standard Error Variable
Race	Year	Deaths	Age Adjusted Rate	Age Adjusted Rate Lower 95%	Age Adjusted Rate Upper 95%	Age Adjusted Rate Standard
Black or African ...	1968	357	3.895347	3.468202	4.322492	0.217931
Black or African ...	1969	347	3.673576	3.267378	4.079775	0.207244
Black or African ...	1970	331	3.467622	3.079662	3.855583	0.197939

Delimiters: Tab Semi-colon Comma Space

Missing Characters: Space NA Period

Thousands Separator: Period Comma

Decimal Separator: Period Comma

Dependent Variable: [What type of data do I have?](#)

Type of Variable:

Age-Adjusted Rate:

Independent Variable:

Interval Type:

Shift data points by:

To Exclude Data Points use the 'Define' button

By Variables:

Exclude... All cohorts to be executed.

Log Transformation: No { y = xb } Yes { ln(y) = xb }

Heteroscedastic/Correlated Errors Option: [What are the options?](#)

Standard Error (Provided):

Standard Error:

Choose an errors model to fit:

Uncorrelated

First Order Autocorrelation estimated from the data

First Order Autocorrelation with correlation =

File Session View Help Sample Sessions

Input File

Method And Parameters

Advanced Analysis Tools

Method: Grid Search Hudson's [Why is Hudson's Method disabled?](#)

Minimum number of observations before the first joinpoint and after the last joinpoint:

Minimum number of observations between two joinpoints:

Number of points to place between adjacent observed x values in the grid search:

Min. percentage points difference (PPD) between consecutive APC segments ([MADWD](#)) Min. PPD:

Number of Joinpoints: Minimum: Maximum:

[How are the Maximum Joinpoints determined?](#)

APC/AAPC/Tau Confidence Intervals

Empirical Quantile [Learn More](#)

Final Selected Model Only (Parametric used for other models)

of Resamples:

Parametric Method

AAPC Segment Ranges

Entire Range

Last

Last

Custom Ranges:

Model Selection Method: [Which method should I choose?](#)

Data Driven BIC Methods

Weighted BIC

Data Dependent Selection

Traditional BIC Methods

Bayesian Information Criterion (BIC)

BIC3

Modified BIC

Permutation Test

Overall significance level:

Max number of permutations:

File Session View Help Sample Sessions

Input File

Method And Parameters

Advanced Analysis Tools

Method: Grid Search Hudson's [Why is Hudson's Method disabled?](#)

Minimum number of observations before the first joinpoint and after the last joinpoint:

Minimum number of observations between two joinpoints:

Number of points to place between adjacent observed x values in the grid search:

Min. percentage points difference (PPD) between consecutive APC segments ([MADWD](#)) Min. PPD:

Number of Joinpoints: Minimum: Maximum:

[How are the Maximum Joinpoints determined?](#)

APC/AAPC/Tau Confidence Intervals

Empirical Quantile [Learn More](#)

Final Selected Model Only (Parametric used for other models)

of Resamples:

Parametric Method

AAPC Segment Ranges

Entire Range

Last

Last

Custom Ranges:

Model Selection Method: [Which method should I choose?](#)

Data Driven BIC Methods

Weighted BIC

Data Dependent Selection

Traditional BIC Methods

Bayesian Information Criterion (BIC)

BIC3

Modified BIC

Permutation Test

Overall significance level:

Number of permutations:

CDC WONDER

Hispanic Origin
Race
Year and Month
Year
Month
Weekday, Autopsy, Place of Death
Weekday
Autopsy
Place of Death
Underlying Cause of Death
UCD - 15 Leading Causes of Death (infants)
UCD - ICD Chapter
UCD - ICD Sub-Chapter
Underlying Cause of death
ICD-10-CM-10.113.Cause1 list

Request Form | [Rate](#)
[Multiple Cause of Death](#)

1. Organize Tab:
Group Results By
And By
And By
And By

Measures (Default measures always checked and included. Check box to include any others.)
Deaths Population Crude Rate Standard Error
For crude rates: 95% Confidence Interval Standard Error
 Age Adjusted Rate 95% Confidence Interval Standard Error

Multiple Cause of Death, 1999-2020 Results
Deaths occurring through 2020

WONDER Search
Cause of Death, 1999-2020 Request
Deaths occurring through 2020
Data Use Restrictions | [How to Use WONDER](#)
Options and then click any **Send** button one time to send your request.

Notes:
• Group Results By "15 Leading Causes" to see the top 15 rankable cause
Cause List: None Information

Request Form | Results | Map | Chart | About
[Multiple Cause of Death Data](#) | [Data and Documentation](#) | [Other Data Access](#) | [Help for Results](#) | [Printing Tips](#) | [Help with Exports](#)

Quick Options | More Options | API Options | [Top](#) | [Notes](#) | [Citation](#) | [Query Criteria](#)

Weekday	Deaths	Population	Crude Rate Per 100,000 (95% Confidence Interval)	Crude Rate Standard Error	Age Adjusted Rate Per 100,000 (95% Confidence Interval)	Age Adjusted Rate Standard Error
Sunday	1,834,918	not applicable	not applicable	not applicable	not applicable	not applicable
Monday	1,833,909	not applicable	not applicable	not applicable	not applicable	not applicable
Tuesday	1,835,720	not applicable	not applicable	not applicable	not applicable	not applicable
Wednesday	1,833,845	not applicable	not applicable	not applicable	not applicable	not applicable
Thursday	1,863,962	not applicable	not applicable	not applicable	not applicable	not applicable
Friday	1,885,225	not applicable	not applicable	not applicable	not applicable	not applicable
Saturday	1,880,093	not applicable	not applicable	not applicable	not applicable	not applicable
Unknown	48	not applicable	not applicable	not applicable	not applicable	not applicable
Total	12,968,664	not applicable	not applicable	not applicable	not applicable	not applicable

5. Select weekday, autopsy and place of death: Send Help

Hint: Use Ctrl + Click for multiple selections, or Shift + Click for a range.

Weekday
All Weekdays
Sunday
Monday
Tuesday
Wednesday
Thursday
Friday
Saturday
Unknown

Autopsy
All Values
No
Yes
Unknown

Place of Death
All Places
Medical Facility - Inpatient
Medical Facility - Outpatient or ER
Medical Facility - Dead on Arrival
Medical Facility - Status unknown
Decedent's home
Hospice facility
Nursing home/long term care
Other

Multiple Cause of Death, 1999-2020 Results
Deaths occurring through 2020

Request Form | Results | Map | Chart | About
[Multiple Cause of Death Data](#) | [Data and Documentation](#) | [Other Data Access](#) | [Help for Results](#) | [Printing Tips](#) | [Help with Exports](#)

Quick Options | More Options | API Options | [Top](#) | [Notes](#) | [Citation](#) | [Query Criteria](#)

Year	Deaths	Population	Crude Rate Per 100,000 (95% Confidence Interval)	Crude Rate Standard Error	Age Adjusted Rate Per 100,000 (95% Confidence Interval)	Age Adjusted Rate Standard Error
1999	401,675	279,040,168	143.948809549 (143.503638669 - 144.393980429)	0.227128000	146.667196909 (146.213663505 - 147.120830313)	0.231445614
2000	401,985	281,421,906	142.840692721 (142.399119127 - 143.282266316)	0.225292650	145.082503831 (144.633977814 - 145.531029847)	0.228839804
2001	404,871	284,968,955	142.075476257 (141.637836411 - 142.513116103)	0.223285636	143.050247957 (143.207694759 - 144.092801155)	0.225792448
2002	407,307	287,625,193	141.610332225 (141.175434547 - 142.045235904)	0.221888101	142.074488392 (141.637916179 - 142.511060605)	0.222740925

Step 1. Organize table layout

Multiple Cause of Death, 1999-2020 Request
Deaths occurring through 2020

Request Form | Results | Map | Chart | About

Multiple Cause of Death Data | Dataset Documentation | Other Data Access | Data Use Restrictions | How to Use WONDER

Save | Reset

Make all desired selections and then click any **Send** button one time to send your request.

1. Organize Table Layout: Send | Help

Group Results By: Census Region

And By: None

And By: None

And By: None

And By: None

Measures: (Default measures always checked and included. Check box to include any others.)

Deaths Population Crude Rate

For crude rates: 95% Confidence Interval Standard Error

Age Adjusted Rate 95% Confidence Interval Standard Error

Percent of Total Deaths

Title: _____

+ Additional Rate Options Click "+" for non-standard age adjusted rates and other options. Help

Step 2. Select location

2. Select location: Send | Help

States Census Regions HHS Regions

Click a button to choose locations by State, Census Region or HHS Region.

Browse or search to find items in the States Finder Tool, then **highlight** the items to use for this request. (The Currently selected box displays all current request items.)

Finder Tool Help | Advanced Finder Options

Browse | Search | Details

States

All* (The United States)

01 (Alabama)

02 (Alaska)

04 (Arizona)

05 (Arkansas)

06 (California)

08 (Colorado)

09 (Connecticut)

10 (Delaware)

11 (District of Columbia)

Currently selected: All* (The United States)

Open | Close | Close All

Browse the list by opening and closing items. Use Ctrl+Click to multiple select, Shift+Click for a range.

Pick between: 2013 Urbanization 2013 Urbanization 2006 Urbanization

All Categories

Large Central Metro

Large Fringe Metro

Medium Metro

Small Metro

Metropolitan (Nonmetro)

NonCore (Nonmetro)

Step 3. Select demographics

3. Select demographics: Send | Help

Hint: Use Ctrl + Click for multiple selections, or Shift + Click for a range.

Pick between: Ten-Year Age Groups Five-Year Age Groups Single Year Ages Infant Age Groups

Ten-Year Age Groups: < 1 year, 1-4 years, 5-14 years, 15-24 years, 25-34 years, 35-44 years, 45-54 years, 55-64 years, 65-74 years, 75-84 years, 85+ years

Sex: All Ages Female Male

Race: All Races American Indian or Alaska Native Asian or Pacific Islander Black or African American White

Hispanic Origin: All Origins Hispanic or Latino Not Hispanic or Latino Not Stated

Default rates per 100,000

Step 4. Select year and month

4. Select year and month: Send | Help

Browse or search to find items in the Year/Month Finder Tool, then **highlight** the items to use for this request. (The Currently selected box displays all current request items.)

Finder Tool Help | Advanced Finder Options

Browse | Search | Details

Year/Month

All* (All Dates)

1999 (1999)

2000 (2000)

2001 (2001)

2002 (2002)

2003 (2003)

2004 (2004)

2005 (2005)

2006 (2006)

2007 (2007)

Currently selected: All* (All Dates)

Open | Close | Close All

Browse the list by opening and closing items. Use Ctrl+Click to multiple select, Shift+Click for a range.

Step 5. Weekday, autopsy, and place of death

5. Select weekday, autopsy and place of death: Send | Help

Hint: Use Ctrl + Click for multiple selections, or Shift + Click for a range.

Weekday: All Weekdays Sunday Monday Tuesday Wednesday Thursday Friday Saturday Unknown

Autopsy: All Autopsies No Yes Unknown

Place of Death: All Places Medical Facility - Inpatient Medical Facility - Outpatient or ER Medical Facility - Dead on Arrival Medical Facility - Status unknown Decedent's home Hospice facility Nursing home/long term care Other

Step 6. Select underlying cause of death

6. Select underlying cause of death: Send | Help

Click a button to select ICD codes by Chapters or by Groups.

ICD - ICD-10 Codes ICD - ICD-10 130 Cause List (Infants) ICD - Drug/Alcohol Induced Causes ICD - ICD-10 113 Cause List ICD - Injury Intent and Mechanism

Browse or search to find items in the ICD - ICD-10 Codes Finder Tool, then **highlight** the items to use for this request. (The Currently selected box displays all current request items.)

Finder Tool Help | Advanced Finder Options

Browse | Search | Details

ICD - ICD-10 Codes

All* (All Causes of Death)

A00-B99 (Certain infectious and parasitic diseases)

C00-D48 (Neoplasms)

D50-D89 (Diseases of the blood and blood-forming organs and certain disorders involving the immune mechanism)

E00-E89 (Endocrine, nutritional and metabolic diseases)

F01-F99 (Mental and behavioural disorders)

G00-G98 (Diseases of the nervous system)

H00-H59 (Diseases of the eye and adnexa)

H60-H95 (Diseases of the ear and mastoid process)

I00-I99 (Diseases of the circulatory system)

Currently selected: All* (All Causes of Death)

Open | Open Fully | Close | Close All

Browse the list by opening and closing items. Use Ctrl+Click to multiple select, Shift+Click for a range.

Step 7. Select multiple cause of death

7. Select multiple cause of death: Send | Help

Click a button to select ICD codes by Chapters or by Groups.

MCD - ICD-10 Codes MCD - ICD-10 130 Cause List (Infants) MCD - Drug/Alcohol Induced Causes MCD - ICD-10 113 Cause List

Items in the Select Records box will be used for your request. Enter codes by hand, one per line, or find items in the Finder Tool and Move (highlighted) items Over.

Finder Tool Help

Select Records with any of these items: _____

AND any of these items: _____

Move Items Over <<< | Clear

Move Items Over <<< | Clear

Browse | Search | Details

MCD - ICD-10 Codes

All* (All Causes of Death)

A00-B99 (Certain infectious and parasitic diseases)

C00-D48 (Neoplasms)

D50-D89 (Diseases of the blood and blood-forming organs and certain disorders involving the immune mechanism)

E00-E89 (Endocrine, nutritional and metabolic diseases)

F01-F99 (Mental and behavioural disorders)

G00-G98 (Diseases of the nervous system)

H00-H59 (Diseases of the eye and adnexa)

H60-H95 (Diseases of the ear and mastoid process)

I00-I99 (Diseases of the circulatory system)

J00-J98 (Diseases of the respiratory system)

K00-K92 (Diseases of the digestive system)

L00-L98 (Diseases of the skin and subcutaneous tissue)

Open | Open Fully | Close | Close All

Browse the list by opening and closing items. Use Ctrl+Click to multiple select, Shift+Click for a range.

Note: Use both selection boxes to select results that contain items from both the first AND second box. See the [feature description](#) for more information.

Note: Javascript must be enabled for the "Move" and "Clear" buttons to work. Enter or clear codes by hand if the buttons don't work.

Step 8. Other options / export settings

8. Other options: Send | Help

Export Results: (Check box to download results to a file)

Export Type: (Select an export format) XLS (Export as Excel compatible)

Show Totals:

Show Zero Values:

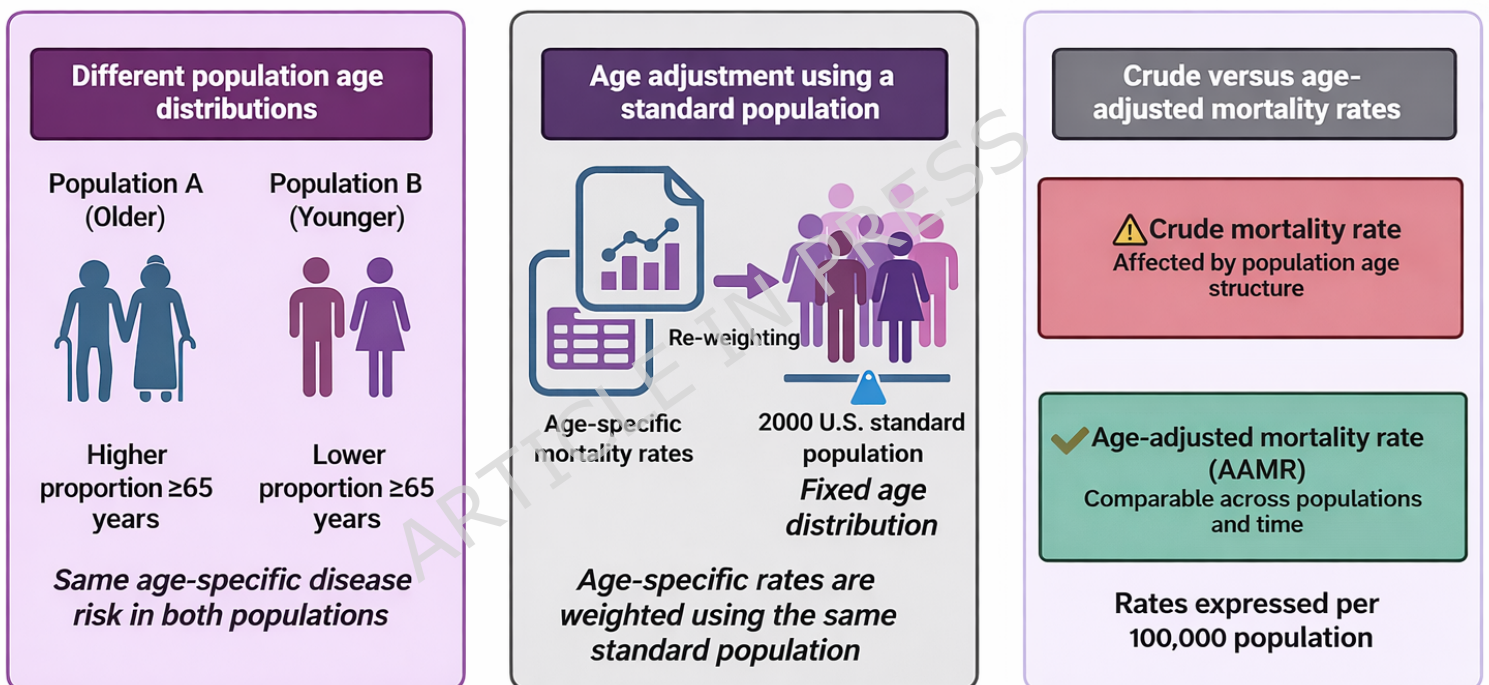
Show Suppressed Values:

Precision: 9 decimal places

Data Access Timeout: 15 minutes

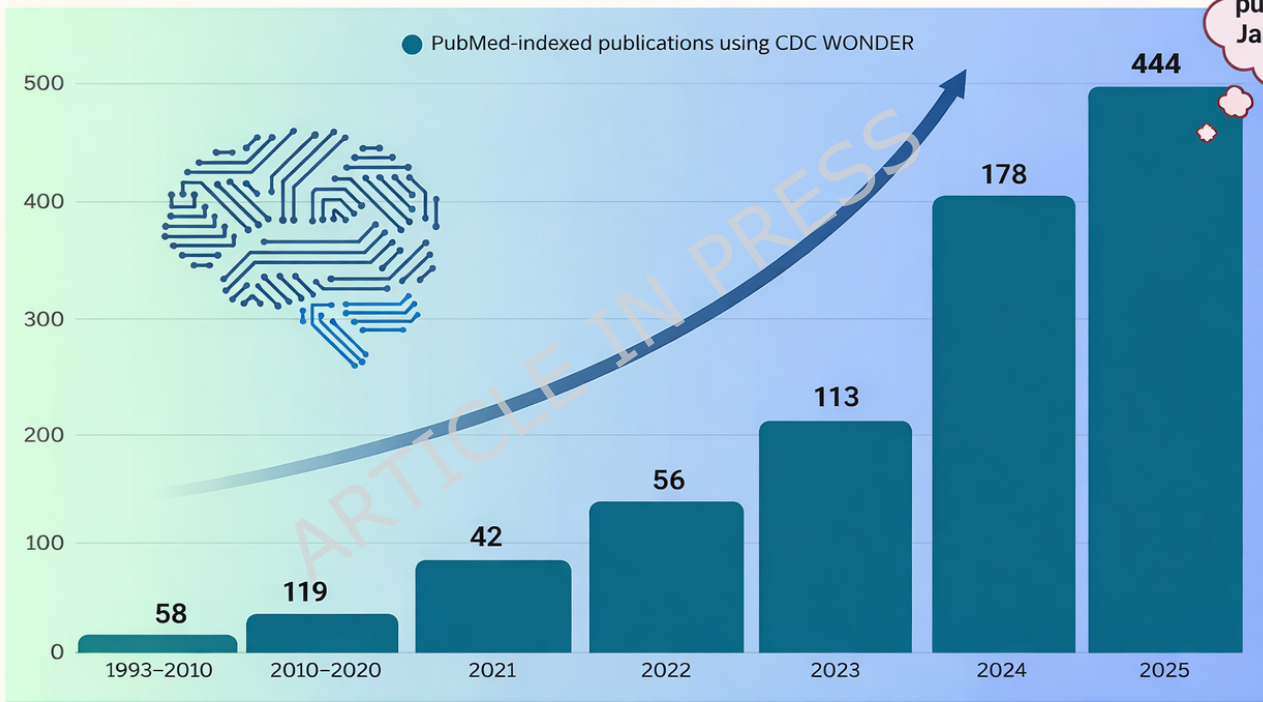
Send | Reset

Calculation and interpretation of crude and age-adjusted mortality rates





CDC WONDER reflects U.S. population-based data and is among the oldest continuously utilized databases



23 publications
January 12,
2026



ARTICLE IN PRESS



Common Methodological Pitfalls in CDC WONDER–Based Mortality Analyses

Grouping versus filtering the same variable



Grouping by weekday (Step 1)

- Death
- AAMR

Filtering weekdays (Step 5)

- Death
- Mortality rate
- AAMR
- CI/SE

The same variable yields different outputs depending on where it is applied in the query workflow.

⚠ Important note: Combined weekdays represent aggregated data and should not be directly compared with weekends

Defining disease relationships using ICD coding



Includes deaths with either condition, regardless of primary cause



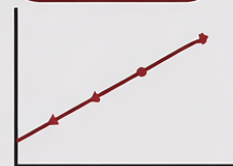
Includes only deaths where both conditions are recorded

ICD logic determines which population is actually being studied.

Underlying cause and contributing causes are subject to physician judgment on death certificates

Trend analysis choices

Single linear trend



Masks important changes over time

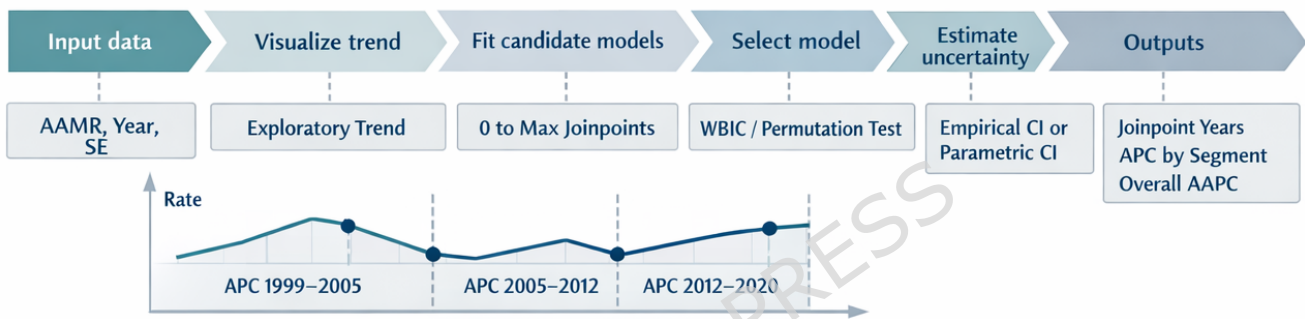
Joinpoint regression with forecasting



- Joinpoint analysis
- Segment-specific trends
- Forecasting based on existing data

Segmented models better capture temporal changes in mortality trends.

Joinpoint Analysis Process



Forecasting Models for Mortality Trends

