

Modeling future pandemic risk in R Shiny dashboard

Excess mortality modeling based on past pandemics and anticipation of future potential outbreaks

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Pandemic risk modeling is a recurring topic, particularly since the recent COVID-19 pandemic. Most often, classical epidemiological models are developed for this goal.

This article proposes a modeling solution that offers a compromise between simplicity and adjustment of multiple results according to the population at risk. The modeling solution framework has been implemented in an R Shiny application that can be used interactively for different use cases. In addition, this white paper offers insights into how to model potential future pandemics.

Past pandemics

Before discussing pandemics, it is important to clarify certain definitions. According to the World Health Organization, a **pandemic** is characterized by the global spread of a new disease.¹ An infection that is geographically restricted yet persists over time is referred to as an **endemic**.² In contrast, an infection that is geographically localized and occurs over a limited time period is defined as an **epidemic**.³

MAIN PAST PANDEMICS AND THEIR CHARACTERISTICS

Since the 20th century, the main global pandemics have been divided into several major categories according to their mode of transmission.

Respiratory pandemics

Respiratory diseases have been the most frequent and devastating, as demonstrated by influenza pandemics and COVID-19:

- The 1918 Spanish flu caused around 50 million deaths worldwide.⁴
- The Asian flu of 1957–1958 caused approximately 1 million deaths, specifically in India and Hong Kong.⁵
- The Hong Kong flu in 1968–1969 resulted in nearly 1 million deaths.⁶
- More recently, the H1N1 influenza pandemic of 2009 was responsible for an estimated 150,000 to 575,000 deaths.⁷
- Finally, the COVID-19 pandemic, which began in 2019, has officially caused over 7 million deaths globally, with a significant health and social impact.⁸

These diseases are primarily transmitted through respiratory droplets and quickly affect large populations, particularly the elderly, immunocompromised individuals, and, depending on the pandemic, sometimes young adults.

Nonrespiratory pandemics

In addition to airborne diseases, other types of pandemics also spread during the 20th century.

For example, the seventh cholera pandemic began in 1961 in Indonesia and subsequently spread across Asia, the Middle East, and Africa before reaching South America in the 1990s. This disease is still ongoing today, but considered endemic, with most cases now occurring in sub-Saharan Africa, South Asia, and Haiti.⁹ According to the World Health Organization, cholera causes about 100,000 deaths worldwide.¹⁰

Human immunodeficiency virus (HIV) weakens the immune system by attacking white blood cells, making it easier to contract infections and certain cancers. AIDS is the most advanced stage of HIV infection. The virus is transmitted through the body fluids of an infected person, such as blood, breast milk, semen, and vaginal fluids. First cases of AIDS were officially reported in 1981 in the United States, marking the start of global recognition of the disease, but HIV was isolated in 1983. Throughout the 1980s and 1990s, HIV spread rapidly across the world, with sub-Saharan Africa becoming the most-affected region. The introduction of antiretroviral therapy in the mid-1990s transformed HIV infection from a fatal disease to a manageable chronic condition for many.¹¹ Despite significant progress, HIV/AIDS remains a major global health issue, with more than 40 million people living with the virus, 65% of whom in Africa.¹²

Pandemic modeling approach

The model consists of two components: a baseline mortality model and an excess pandemic mortality model. Both models have been calibrated to both U.K. and U.S. databases for this white paper.

BASELINE MORTALITY MODEL

The baseline mortality model is a linear model that predicts the relative change in mortality for the following year based on the relative changes observed over the previous years. This model has been trained using data from the past 25 years—which can be adjusted as needed.

To construct the baseline mortality tables, data from the Human Mortality Database were used. For this project, death rates and exposures by year, gender, and five-year age intervals were considered.

EXCESS PANDEMIC MODEL

The excess pandemic model is used to simulate the occurrence of a pandemic. This model employs a frequency-severity approach: The frequency of pandemic occurrence is modeled as a binomial random variable, indicating whether a pandemic occurs in a given year.

Conditional on the occurrence of a pandemic, the severity of the pandemic is modeled. To model the severity, first the regime of the pandemic (mild or severe) is simulated. Both the regimes have a 50% chance of occurring. Secondly, the actual severity in terms of the percentage of excess mortality is modeled via a random variable S . The probability distribution of S is specified via its quantile function. The quantile function is calibrated for each of the pandemic regimes separately using historical excess mortality data from past pandemics, adjusted for the current population distribution.

To develop the excess mortality model, a literature review was first conducted to identify episodes of influenza or other diseases that could be classified as pandemics or epidemics, depending on whether or not they spread worldwide. In the developed tool, only airborne respiratory diseases are considered. Subsequently, mortality data related to these episodes were extracted from official sources, broken down by age and gender.

Implementation of the pandemic model into R Shiny dashboard and application to real population data

PANDEMIC MODEL AND PROPOSED EXTENSIONS

The R Shiny tool relies on the previously described pandemic model. In addition, it allows the user to adjust the impacts of the simulated pandemic scenarios according to several characteristics of the population. The tool comes with an

extensive user manual that together with this white paper can form a basis for internal documentation. Also, the R Shiny tool offers backtesting functionality that compares the observed and fitted mortality rates for pandemic years across age bands and by gender.

Combination of baseline and excess pandemic models

For a fixed number of scenarios, the model projects the observed baseline mortality. The occurrence of a pandemic is then simulated. If a pandemic is detected, its severity is simulated as well, being either mild or severe. A severity value between 0 and 1 is finally generated to apply the excess function considered. At the end, if a pandemic has occurred, the mortality rates from the initial model are adjusted, using the corresponding percentages of pandemic excess mortality.

Modeling granularity

The proposed modeling solution allows for differing impacts on a granular level, to refine the projections as accurately as possible for the target population:

- **Age:** The tool allows for consideration of different pandemic profiles and consequently enables the adjustment of excess mortality by age group. For example, while COVID-19 primarily affected older populations in the early years—resulting in a J-shaped mortality curve—other pandemics have had a greater impact on younger age groups. The 1918 Spanish flu, for instance, produced a V-shaped curve, whereas the 1957 and 1968 influenza pandemics were characterized by more of a U-shaped pattern.¹³
- **Gender:** In the United States, men have experienced slightly higher COVID-19 mortality than women. These differences reflect preexisting differences in overall mortality rates. The pandemic did not change the fundamental pattern; disparities may be due to longstanding demographic and social factors rather than a specific male vulnerability to COVID-19.¹⁴ Therefore, the tool takes existing gender differences in mortality into account, allowing for appropriate adjustments to excess mortality rates due to pandemics.
- **Consideration of comorbidities:** Comorbidities have an impact on pandemic mortality as the COVID-19 pandemic has shown.¹⁵ By using relative risk ratios for certain diseases, it is possible to estimate a specific mortality shock for individuals with these conditions.
- **Insurance status:** Furthermore, in countries with multiple health insurance schemes with variable health cover, it may be relevant to estimate a specific mortality shock for insured individuals. Indeed, the people under each scheme have different health and different rates of seeking healthcare, which both impact their overall mortality. This tool makes this possible by using risk ratios.

MODEL RESULTS

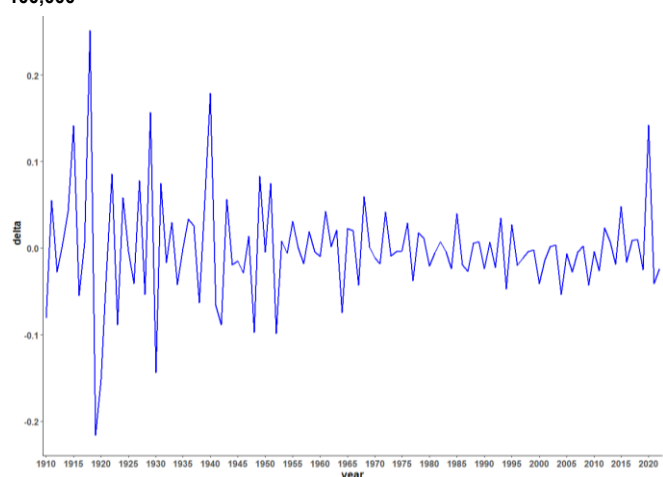
The baseline mortality model and excess pandemic model for both the U.S. and the U.K. are fitted on mortality data and pandemic data. This section is focusing on the calibration of the models on the U.K. data. A similar calibration, giving similar results, has been performed on the U.S. data.

Assessment of pandemic years

During the 20th and 21st centuries, a number of pandemics, like the Spanish flu (1918), Asian flu (1957–1958), Hong Kong flu (1968), Russian flu (1978), swine flu (2009), and COVID-19 (2020–2023), occurred and had a global impact. In the following paragraphs, it is investigated if these pandemics also affected the U.K. as well.

In Figure 1, the relative change in the number of deaths per 100,000 population is plotted for the civilian population of England and Wales, using data from the Human Mortality Database.

FIGURE 1: YEAR-ON-YEAR RELATIVE CHANGE IN U.K. DEATHS PER 100,000



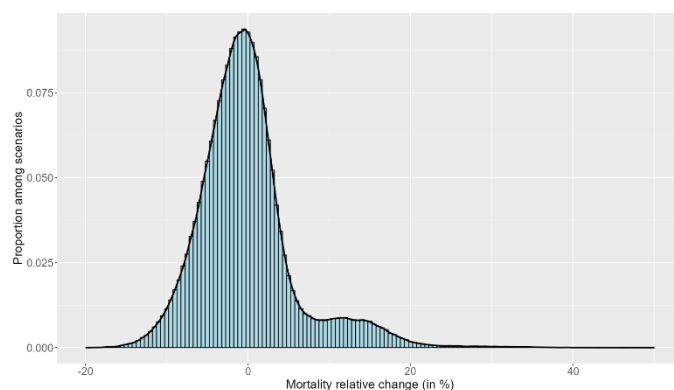
By combining the data from the Human Mortality Database with the civilian population mortality data from the Office for National Statistics, the causes of the spikes in Figure 1 can be found. It becomes clear that the spikes in 1918, 1968, and 2020 are indeed caused by the Spanish flu, the Hong Kong flu, and COVID-19, respectively. The Asian flu, Russian flu, and swine flu do not seem to have affected the U.K. mortality rates too much, whereas two flu epidemics in 1929 and 1951 seem to have had a significant impact on the U.K. mortality rates.

For the calibration of the excess mortality model, several pandemics or epidemics have to be selected for the mild and severe regimes. For the U.K., it was decided to calibrate the quantile function for the mild regime on the flu outbreak of 1951, the Hong Kong flu outbreak of 1968, and the swine flu outbreak of 2009 (although only having minimally affected the U.K., it is included as proxy as at least six events are required for the purpose of calibration). The quantile function for the severe regime is calibrated on the Spanish flu of 1918, the flu outbreak of 1929, and the COVID-19 pandemic of 2020.

Projected distributions of mortality

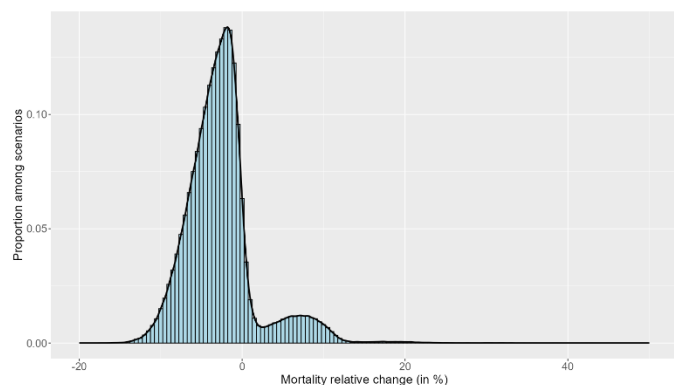
The distributions over the relative changes in mortality, resulting from running the model 100,000 times over a five-year horizon with 2019 as reference year, can be found in Figure 2 and Figure 3 for the U.K. and U.S., respectively. The shapes of the distributions are relatively similar, but the distribution for the U.S. is narrower and to the left of that for the U.K., meaning the U.S. distribution is smaller and less volatile than that from the U.K. In other words, the relative changes in the U.S. are smaller, while also the volatility (i.e., spread in the changes) is lower.

FIGURE 2: DISTRIBUTION OF RELATIVE CHANGES IN THE U.K. MORTALITY RATE OVER A 5-YEAR HORIZON FROM 2019 ONWARD



Furthermore, for the U.K. the mortality rate per 100,000 population in 2019 is 901.1, and the predicted 99.5 percentile rate is 1104.3 (a relative change of 22.5%), while for the U.S. the mortality rate per 100,000 population in 2019 is 872.9, and the predicted 99.5 percentile rate is 985 (a relative change of 12.8%).

FIGURE 3: DISTRIBUTION OF RELATIVE CHANGES IN THE U.S. MORTALITY RATE OVER A 5-YEAR HORIZON FROM 2019 ONWARD



The U.S. has a younger and larger population than the U.K. This, respectively, explains the lower mortality rate per 100,000 population and the lower volatility in the relative changes in U.S. in comparison to the U.K.

USE CASES

The previous sections describe the model behind the R Shiny dashboard and a sample of the output generated for the U.S. and U.K. populations. However, the tool can be employed for multiple practical use cases, such as:

- Deriving risk-based capital (RBC) levels for pandemic risk in regulatory frameworks such as RBC and Solvency II
- Pricing mortality catastrophe bonds
- Benchmarking of results for the above metrics

Emerging pandemic threats: The impact of climate change and zoonotic pathogens

The future landscape of pandemics is shaped by a convergence of ecological, climatic, and socioeconomic factors, all of which heighten the risk of emerging infectious diseases.

VECTOR-BORNE DISEASES

Vector-borne diseases, transmitted by arthropods such as mosquitoes, ticks, or flies, represent a growing threat to global health. Climate change, by increasing average temperatures and increasing frequency of extreme events, alters the geographic distribution and seasonality of vectors and facilitates expansion into nonendemic regions.^{16,17} Moreover, rapid urbanization, globalization of trade, and ecological degradation (including deforestation and land-use changes) foster closer contact between humans, animals, and vectors, thereby increasing the risk of emergence and spread of pathogens.^{18,19} In addition, the growing resistance of insects to insecticides, increased human mobility, and weak healthcare systems in certain regions increase vulnerability.²⁰

Several pathogens transmitted by vectors have been identified as posing a high pandemic risk in the coming decades:

- The Zika virus demonstrated its potential for rapid spread during the 2015–2016 epidemic in America and remains a threat due to the reproduction of nonendemic species in the U.S.²¹
- Incidence of the dengue virus is increasing dramatically, and the geographic expansion of the vector raises concerns about its spread to Europe and North America.^{22,23}
- Malaria could reappear in regions where it had been eradicated due to global warming.²⁴
- West Nile virus, chikungunya, and emerging diseases like Mayaro or Rift Valley fever are also monitored for their pandemic risk.^{25,26}

DEVELOPMENT OF ZOOONOTIC PATHOGENS

Another concern is the development and spread of zoonotic pathogens, diseases originating in wildlife and transmitted to humans. Notable examples from recent decades include HIV/AIDS, SARS, and H1N1 influenza.²⁷

The emergence of these diseases is part of a wider trend. Sixty percent of the infectious diseases that emerged between 1940 and 2004 are zoonotic, and their emergence has been increasing over time.²⁸ As mentioned in the previous section, ecological degradation increases contact between humans and animals, triggering the expansion of these pathogens and making new pandemics more likely.

Focus on bird flu

Bird flu (avian influenza) is a current pandemic threat due to its widespread outbreaks in birds and its ongoing genetic changes. Dairy cattle have been infected in the U.S. recently, with evidence of cattle-to-cattle and occasional animal-to-human transmission.^{29,30} While human cases have been mild so far, there is concern that future mutations could allow for easier spread among people and potentially cause a pandemic.^{31,32}

AGGRAVATION OF SEASONAL EPIDEMICS

Seasonal epidemics, such as influenza, have historically exhibited significant variation in both frequency and severity, influenced by environmental factors, viral evolution, and socioeconomic conditions. Climate variables have historically influenced the seasonality and transmission dynamics of influenza. Temperate regions experience peaks in winter,³³ while tropical regions may have less-pronounced seasonality but can experience multiple peaks linked to the rainy season.³⁴ Therefore, climate change could have several impacts on these epidemics:

- **Increased frequency and intensity:** Climate models predict warmer winters in temperate zones, potentially increasing humidity and therefore lengthening transmission periods and shifting peak timings of influenza.^{35,36}
- **Diversified geographical spread:** In addition to increases in incidence rate, climate-driven changes in humidity and rainfall could also affect the geographic spread of epidemics.³⁷
- **Emergence of new strains:** Climate-induced changes in animal migration and habitat, especially among wild birds, may increase the risk of novel, potentially pandemic strains.^{38,39}

SOCIOECONOMIC FACTORS AGGRAVATING PANDEMIC EFFECTS

Socioeconomic disparities can exacerbate the impact of influenza epidemics.⁴⁰ Urbanization and increased global connectivity facilitate rapid spread, while poverty and limited healthcare access increase vulnerability. In particular, in Europe, population over 65 years old represents 86% of the seasonal influenza deaths.⁴¹ Aging populations may indeed face greater risks due to higher baseline mortality, comorbidities, and poorer overall health and ability to fight pathogens.⁴² Additionally, vaccine hesitancy and inequitable distribution of antivirals/vaccines can undermine pandemic control.⁴³

Conclusion

This white paper describes a modeling solution where future pandemic mortality risk is assessed based on historical pandemic data. The solution is implemented in R Shiny and can easily be used for multiple practical use cases. Ongoing ecological disruption, climate change, increasing interconnectivity, and socioeconomic vulnerabilities are converging to create a world where the emergence and spread of pandemics are increasingly likely and potentially more severe, thereby underpinning the need for flexible modeling solutions such as the tool at hand.

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