**This is a guide to the Matlab and R Codes for the Atkeson-Kissler BPEA paper on the impact of behavior and vaccines on cumulative mortality from COVID-19 in the United States as well as the data sources used.**

**Data Sources:**

**Mortality Data for US** are from the following websites:

Weekly Deaths : <https://covid.cdc.gov/covid-data-tracker/#trends_weeklydeaths_select_00>

Cumulative Deaths: <https://covid.cdc.gov/covid-data-tracker/#trends_totaldeaths_select_00>

Our download of these data is in the spreadsheet

data/deaths/WeeklyDeaths.xlsx

In columns Q through S of this spreadsheet, we present these data starting with February 15, 2020 and ending February 17, 2024 with dates using Excel number format for the day. These data have been entered directly into the Matlab files where needed.

**Mortality Data for US States** are from

<https://data.cdc.gov/NCHS/Provisional-COVID-19-death-counts-rates-and-percen/mpx5-t7tu/about_data>

Our download of these data is in the spreadsheet

WeeklyDeaths3.xlsx with data through 1/11/2024

**CDC Data on COVID-19 Deaths by Vaccination Status** are from

<https://data.cdc.gov/Public-Health-Surveillance/Rates-of-COVID-19-Cases-or-Deaths-by-Age-Group-and/d6p8-wqjm/about_data>

Our download of these data is in the Excel Spreadsheet Deathsbyvaxstatus421on.xlsx

These data have been entered directly into the Matlab files where needed.

**The Blood Donor Survey Serology Data** are from

<https://data.cdc.gov/Laboratory-Surveillance/2020-2021-Nationwide-Blood-Donor-Seroprevalence-Su/mtc3-kq6r/about_data>

and

<https://data.cdc.gov/Laboratory-Surveillance/2022-2023-Nationwide-Blood-Donor-Seroprevalence-Su/ar8q-3jhn/about_data>

**The National Commercial Lab Survey Serology Data** are from

<https://data.cdc.gov/Laboratory-Surveillance/Nationwide-Commercial-Laboratory-Seroprevalence-Su/d2tw-32xv/about_data>

Our download of these seroprevalence data are in the csv files located in the folder

data/sero/

Our extract of the US data from these surveys used in the figures in the paper are in the spreadsheet data/sero/Seroprevalence.xlxs

These data have been entered directly into the Matlab files where needed.

**Matlab Programs:**

MainfileAK.m

The file MainfileAK.m runs eleven files that produce all of the figures in the paper and all of the figures in the Online Appendix except figures A3, A4, B6 and B8. Figures A3, A4, and B6 are taken from other papers as referenced in the Online Appendix. Figure B6 is produced with an R program as described below. This file also outputs model-implied cumulative deaths over the four-year simulation period in various scenarios in the command window. These numbers are reported in Table 1 in the main paper and Tables 1 and 2 in the online Appendix. Each of the 11 files called in this main file can be run independently.

Dataplotsmain.m

This file plots Figures 1 and 3 in the main paper as well as Figure A1 in the Online Appendix

OmicronvBPEAbaseline.m

This is our baseline file for solving the model baseline parameters with results reported in Table 1 and Figure 2 and 4 of the main paper. Parameters are set in this file and plots are made after the model is solved. The model is solved with two subroutines: omicronrunthemodelBPEAbaseline.m and omicronodefileBPEAbaseline.m. The first of these subroutines simply sets up the parameters in an input vector to go into the ode solver and then organizes the solution. The second of these files specifies the equations of the model to be solved using Matlab’s differential equation solver ode113. Note that we have set up different versions of these files for different parameter specifications of the model.

Note that this file also reports the cumulative death toll through September 15, 2021 reported in Online Appendix Table 1.

All of the model versions use the subroutines listed here except for the one with fast vaccines reported in the Online Appendix. That specification of the model is described below.

OmicronvBPEAnovaccines.m and OmicronvBPEAnobehavior.m run the alternative specifications of the model with baseline behavior and no vaccines and with vaccines but no behavior used in Table 1 and Figures 5, 6, and 7 of the main paper. Note that these files also reports the cumulative death toll through September 15, 2021 reported in Online Appendix Table 1.

OmicronvBPEAfastvaccines.m runs the specification of the model in which the pace of vaccines does not slow down. This alternative specification of the pace of vaccines is done in omicronodefileBPEAfastvaccines.m which is called by omicronrunthemodelBPEAfastvaccines.m

The output is reported in Table 1 and Figure A5 of the Online Appendix.

OmicronvBPEAweakbehavior.m, OmicronvBPEAstrongbehavior.m, OmicronvBPEAslowtransmission.m, and OmicronvBPEAfasttransmission.m produce the results reported in Table 2 and Figures B14 and B15 of the Online Appendix

plotcumdeathbystate.m produces Figures B7, B9, and B10 of the Online Appendix

Serology.m produces Figures A2, B11, B12, and B13.

**R Programs:**

The state level serology data plotted in Online Appendix Figure B8 was created using R. The R codes are in the folder code with the serology data in the folder data/sero