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Deaths Associated with Influenza Pandemic of 1918–19, Japan

Technical Appendix

Standard Population Growth Model

The model estimated in this paper is a standard population growth model with a breakpoint coinciding with the pandemic, adapted for panel data (i.e., multiple prefectures followed over multiple time periods) (*1,2*),

$$LPOP_{it} = \pi_{0i} + \pi_{1i}T_t + \pi_{2i}FLU_t + \pi_{3i}T_tFLU_t + \varepsilon_{it},$$

where $LPOP_{it}$ is the natural logarithm of population in prefecture i at time t; T_t is the linear time trend; FLU_t is the dummy variable representing the postpandemic years,

$$FLU_t = \begin{cases} 0, & t \leq 1918 \\ 1, & t > 1918 \end{cases}$$

ε_{it} is a random error term in the standard random coefficients model; and π_{0i}, π_{1i}, π_{2i}, and π_{3i} are random coefficients, each modeled as the sum of a fixed coefficient γ_{00}, γ_{10}, γ_{20}, or γ_{30} and a prefecture-specific random term with 0 mean. The random coefficients represent prefecture-specific estimates of the log of population in the initial year (1898 or 1903, depending on the model, π_{0i}), the rate of population growth before the pandemic (π_{1i}), the 1-time shift in the population trajectory due to the pandemic (π_{2i}), and the change in the rate of population growth after the pandemic (π_{3i}). SAS software was used to estimate the model (*3,4*). To compare various specifications of the model, we subjected them to 1) the Hausman test, used to determine whether a fixed effects specification is preferred to the random coefficients specification, and 2) the Breusch-Pagan test, which is used to determine whether the ordinary least squares specification is preferable to the random coefficients specification (Tables 1 and 2 in main article). Both tests favored the random coefficients specification.

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