# INTERGENERATIONAL CORESIDENCE AND THE COVID-19 PANDEMIC IN THE UNITED STATES

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# Intergenerational Coresidence and the Covid-19 Pandemic in the United States*

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**Abstract**

This paper investigates the relation between intergenerational coresidence and mortality from Covid-19 in 2020. Using a cross-section of U.S. counties, we show that this association is positive, significant, and robust to the inclusion of several demographic and socio-economic controls. Furthermore, using historical evidence from pre-pandemic years (1980-2019) and the Spanish influenza (1918), we argue that this positive association is specific to the Covid-19 pandemic only.

**Keywords**: family economics; Spanish influenza; mortality; disease; health economics
**JEL Classification**: I10, J10, J14

## 1 Introduction

This research enquires into the impact of intergenerational coresidence on the mortality from Covid-19.

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A specific aspect of Covid-19, which is common across countries worldwide, is the fact that it is particularly deadly for older persons (Verity et al. (2020)). For instance, as of February 10th 2021, persons aged 65 or more accounted for 81% of the overall number of deaths from Covid-19 in the United States (Centers for Disease Control and Prevention (2021c)).

Contagion and mortality, however, are diffused unevenly across and within countries. This geographical variability may hinge on several factors like the health care system and policies, the age structure of the population and its density, culture, institutions and the like. A key institutional element that might differ significantly across countries - but also within countries that are heterogenous like the United States - is the family structure. In this article, we argue that one aspect of the family structure, namely intergenerational coresidence – defined as one elderly living with at least one adult son/daughter – is relevant for the diffusion of Covid-19.

The rationale behind our claim lies in the hypothesis that when coresiding with their adult children, the elderly are more exposed to unprotected social contacts. This happens for two reasons. First, it is reasonable to assume that young adults in the working force typically have more social contacts outside the family than the elderly (Harris (2020), Malmgren et al. (2020)). This implies that coresiding elderly might have more indirect social contacts - i.e. social contacts through their family members - than the non-coresiding ones. Second, since preventive measures like masks and social distance are typically not implemented in the household (Lei et al. (2020) and Li et al. (2020)), those indirect social contacts will be unprotected.[1] All this suggests that intergenerational coresidence might foster contagion for the elderly. Since the fatality rate of Covid-19 is disproportionately huge for the elderly, we expect intergenerational coresidence to be associated with higher mortality.[2]

Using a sample of 411 U.S. metropolitan counties that represent 65% of the total American population in 2019, we show that intergenerational coresidence positively correlates with mortality from Covid-19. Quantitatively, a one percentage point increase in intergenerational coresidence is associated with more than 5 additional deaths from Covid-19 per 100,000

[1]Intergenerational coresidence represents only one of the possible interactions between the elderly and their adult children. A specific feature of intergenerational coresidence is that living in the same household makes the consistent use of preventive measures unrealistic.

[2]Notice that our reasoning abstracts from another type of intergenerational coresidence, that between parents and small or school-age children. The transmission of Covid-19 from children to adults is still an unsettled issue (see Forbes et al. (2021), Wood et al. (2021)).

persons.

This association is robust to controlling for several confounders, like the demographic structure of the population, its wealth and human capital, the number of hospital beds and residents in nursing homes. Interestingly, intergenerational coresidence is instead negatively associated with overall mortality in 2020, suggesting that there is something specific to Covid-19.

In order to show that the positive correlation with intergenerational coresidence is indeed specific to mortality from the Covid-19 pandemic, we perform several other exercises. To start with, we show that intergenerational coresidence does not have any positive, significant impact on the mortality rate in previous, non-pandemic years. We do so in two settings. First, in a balanced-panel of yearly data for 317 metropolitan U.S. counties from 2005 to 2019 that represents 56% of the American population in 2019. Second, in a balanced-panel of decennial data for 235 metropolitan U.S. counties for the period 1980-2010 that represents 48% of the American population in 2010.

Next, we turn to cause-specific mortality rates. Using the same panel of counties for the period 2005-2019, we show that there is no significant association between intergenerational coresidence and mortality from cardiovascular diseases, largely the first cause of mortality in the United States,[3] which moreover is not directly linked to an infectious disease. This points to the singularity of the Covid-19 positive mortality-intergenerational coresidence association. Interestingly, we find instead evidence of a positive, if small, relationship between intergenerational coresidence and mortality rates due to pneumonia and influenza, two diseases that are similar to Covid-19 in terms of transmission and epidemiology.

Finally, we investigate the relationship between intergenerational coresidence and mortality in the case of the 1918 Spanish influenza. This was an episode of widespread pandemic due to a virus that transmitted via aerosols and salivary droplets like Covid-19, but which, contrary to Covid-19, was particularly deadly for prime-age persons, not the elderly (Beach et al. (2020), Garrett (2008), Taubenberger and Morens (2006)). Accordingly, we surmise that in this case intergenerational coresidence is of lesser relevance to the morbidity of the virus, and hence its mortality, since most social contacts of prime-age adults typically happen outside the family circle. To verify our surmise, we use a sample of 423 U.S. cities that represent two-thirds of American urban population in 1910 from Clay et al. (2019) and find that intergenerational coresidence was not associated with the excess mortality due to the Spanish influenza in 1918.

[3]See Centers for Disease Control and Prevention (2021b).

Our paper is closely related to the brand new literature on Covid-19 and family ties. Bayer and Kuhn (2020) were the first to explore the possibility that intergenerational coresidence could be positively related to deaths from Covid-19. They use a sample of 24 countries (Australia plus some European and Asian countries) and show that intergenerational coresidence - defined as a situation in which individuals aged 30-49 live with their parents - helps to explain cross-country differences in the case fatality rate of Covid-19. Fenoll and Grossbard (2020) expand on their study by using a larger sample represented by 79 geographical units (E.U. countries and U.S. states). They show that there is a positive association between the fraction of young adults (18-34 years old) living with their parents and the cumulative number of deaths from Covid-19. In their analysis, this association is arguably stronger and more significant when the E.U. countries are excluded from the sample and the analysis restricted to the U.S. states only. That intergenerational coresidence does not seem to be an important determinant of fatalities from Covid-19 in the European Union is maintained also by Arpino et al. (2020). On the contrary, in a mostly descriptive study, Mogi and Spijker (2021) analyse cross-country variation in the E.U. cumulative deaths between March and April 2020 and find that it is positively associated with social and/or cultural ties, including intergenerational coresidence, the average household size and the proportion of people having frequent social contacts.

Cross-country comparisons suffer from several known problems, going from how mortality and contagion are measured, to idiosyncratic differences like policy, culture, institutions and the like, to the trivial but significant complication represented by the reduced size of the sample. A first contribution of our paper is to overcome these problems by focusing on a more disaggregated geographical unit, the county, belonging to a single country, the United States. This way we reduce the heterogeneity of confounding factors that may pollute cross country analysis, and avoid the small sample bias that makes results from a cross-state analysis in the United States less compelling.[4]

A second contribution of this paper is to devise an empirical strategy based on historical comparisons to show that the positive correlation between mortality and intergenerational coresidence is actually specific to

[4]Desmet and Wacziarg (2021) study the determinants of spatial variation in Covid-19 across U.S. counties. They find that contagion and mortality from Covid-19 correlates with several variables, including, in particular, measures of what they call 'effective' population density. Our work complements their analysis, for we focus on the intergenerational dimension of the household, and, as explained here below, we provide some element for an identification, based on historical comparisons.

Covid-19. Although we do not fully venture into causal inference, we interpret this as a kind of placebo test suggesting that the positive correlation we find is not a statistical artefact.

The outburst of Covid-19 has determined a renewal of interest for the economics of pandemics. As stressed by Hauck (2018), the transmission of infectious diseases crucially depends on social interactions, which in turn depend on human behaviour. The economists' take on pandemics is that contrary to what is typically done in epidemiological models, human behaviour cannot be assumed as a given, for it is actually influenced by the presence and evolution of the infectious disease itself. Hence the need for an integration of epidemiological models (which explain the evolution of the contagion given human behaviour) and economic models (which show how the contagion and the different policies aimed at its mitigation influence social interactions). Examples of such integrated models include Adda (2016), Brotherhood et al. (2020), Eichenbaum et al. (2020), Favero et al. (2020), among others.[5]

The outburst of the Covid-19 pandemic has also renewed the interest for the Spanish influenza, on which there already exists a copious historical literature (see Crosby (2003) and the references therein). Beach et al. (2020) provide a detailed review of differences and similarities between Covid-19 and the Spanish influenza, while Barro et al. (2020) analyse the long-term macroeconomic consequences of the Spanish influenza in terms of GDP and consumption decline. Several studies analyse the determinants of within-country and cross-country variation of mortality rates during this pandemic episode. In particular, cross-sectional studies have shown that poverty, illiteracy and pollution contributed to the severity of the pandemic (Clay et al. (2019), Clay et al. (2018) Grantz et al. (2016), Chowell et al. (2014) among others). Markel et al. (2007) and Bootsma and Ferguson (2007) find that preventive measures such as quarantine and lockdown had a (small) negative impact on mortality. Our study complements this literature, showing the differential impact that intergenerational coresidence has on the mortality from Covid-19 and the Spanish influenza.

The paper is organized as follows. In Section 2, we provide a theoretical discussion of the link between intergenerational coresidence and mortality, explaining the specificity of Covid-19. In Section 3, we present our main empirical analysis. In Section 4, we extend the time window of our analysis back to the past, discussing the relationship between intergenerational coresidence and mortality since 1980. In this Section, we also investigate

[5]See also Boucekkine et al. (2021) and the special 2021 issue on the economics of epidemics in the *Journal of Mathematical Economics*.

cause-specific mortality rates. Finally, in Section 5, we explore the relationship between intergenerational coresidence and the excess mortality due to the Spanish influenza in 1918. Section 6 concludes.

## 2 A simple model of contagion

In this Section, we rationalise in a reduced-form model the impact of intergenerational coresidence on mortality from a viral disease that transmits through aerosols and saliva droplets.[6]

The probability of contagion is denoted as $\pi^i$ for $i = y, o$, where $y$ stands for young, and $o$ for old. $\pi^i$ is a function of the contacts outside home, $c$, and of the intergenerational coresidence status, $\kappa$, where $\kappa = h$ (for 'household') when there is coresidence, and $\kappa = a$ (for 'alone') when the young and the old live apart:

$$\pi^{i,\kappa} = \begin{cases} f(c^i) & \text{for } \kappa = a \\ f(c^i, c^{-i}) & \text{for } \kappa = h \end{cases} \tag{1}$$

The idea is that through coresidence, external contacts are indirectly shared among members of the household. [7] It is reasonable to assume that $c^y > c^o$, i.e. the number of external contacts of the young is superior with respect to the number of external contacts of the old, due to a more intense social life (working, leisurely activities . . . ). Hence, for the young (old) the number of indirect contacts brought by coresidence with the old (young) represents a marginal (important) increase with respect to their overall number of external contacts. Accordingly, we shall have

$$\pi^{o,h} > \pi^{o,a}, \tag{2}$$

$$\pi^{y,h} \cong \pi^{y,a}. \tag{3}$$

Thus, coresidence increases the probability of contagion for the old, but not for the young.

[6]Building a full-fledged epidemiological model like that standard SIR models in the epidemiological literature (Avery et al. (2020), Hethcote (2000)) falls beyond the scope of our analysis. Our specification only serves the purpose of illustrating the mechanism we expect to find at work behind our empirical results.

[7]Since the model is only used to illustrate the possible link between intergenerational coresidence and mortality from Covid-19, it is admittedly overly simplified. In particular, we are assuming that coresidence only implies one old living with one young adult son/daughter.

There are $N^i$ individuals of type $i$ in the economy, $N^{i,h}$ of whom are coresiding with their offspring/parent. Accordingly, the share of sick individuals, $S^i$, will be

$$S^i = \frac{N^{i,h}}{N^i}\pi^{i,h} + \frac{N^i - N^{i,h}}{N^i}\pi^{i,a}. \tag{4}$$

Assuming that the lethality rate from the disease is $\alpha^i$, the overall death rate, $D$, associated with the disease for the adult population reads

$$D = \sum_i \alpha^i S^i. \tag{5}$$

In this model, higher coresidence has an asymmetric impact by age, for it implies a higher contagion among the coresiding old, but not among the coresiding young. This higher contagion among the coresiding old translates in a sizeable increase of the death rate, provided that $\alpha^o$ is high enough. For a pandemic that is particularly deadly for the old, like Covid-19, we shall typically have a high $\alpha^o$. Hence, we expect that coresidence will have a positive effect on mortality. On the contrary, when the pandemic is particularly lethal for the young but not for the old, like the Spanish influenza, we shall have a low $\alpha^o$, and we expect intergenerational coresidence to have little effect on the overall mortality rate.

# 3 Mortality in 2020: the Covid-19 pandemic

In this Section, we investigate the link between intergenerational coresidence and mortality from Covid-19. Using the latest available (2019) U.S. Census data (Ruggles et al. (2021)), we build county-level intergenerational coresidence rates, defined as the percentage of households in which there is an elderly parent (65+) living with at least one adult child (18+).[8] We build a mortality rate due to Covid-19 for 2020 using county-level data on the number of deaths due to Covid-19 from Centers for Disease Control and Prevention (2021d), and population from Centers for Disease Control and Prevention (2021a).[9] We restrict the sample to 411 metropolitan counties as defined by the National Center of Health Statistics (NCHS) (Ingram and Franco (2014)).[10]

[8]The data are described more in details in Appendix A.

[9]Deaths are recorded by place of death. Concerns about cross-state migration due to health reasons are mitigated by the inclusion of hospital beds per 100,000 persons at the state level as control.

[10]We limit to metropolitan areas to exclude potential idiosyncrasies of rural areas. Notice that this excludes from the sample only 15 micropolitan counties, representing

In Figure 1, we show the distribution of the intergenerational coresidence rate at the county level in 2019. It ranges from 1.2% to 12.5%, with a median (mean) value of 5.3% (5.4%).

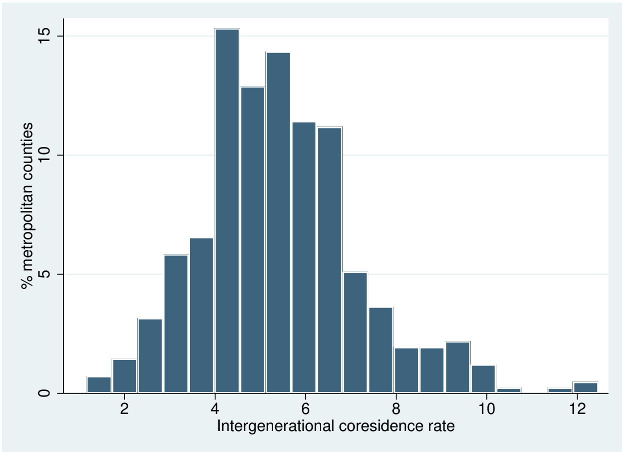


Figure 1: Intergenerational coresidence rate. 411 metropolitan U.S. counties, 2019.

In Figure 2, we show the mortality rate from Covid-19 in 2020. We observe that there is wide variation across counties, with mortality from Covid-19 ranging from 7.8 to 314.1 deaths per 100,000 persons. The distribution is skewed to the right, with only 6% of the counties (25) having more than 200 deaths per 100,000 persons. The median (mean) mortality rate is 86 (96) deaths per 100,000 persons.

Our regression takes the following general form:

$$D_{i,2020} = \beta_0 + \beta_1 h_{i,2019} + \beta_2 \mathbf{X}_{i,2019} + \beta_3 z_{j,2019} + \epsilon_i. \tag{6}$$

In Equation (6), $D$ is the mortality rate, $h$ is the intergenerational coresidence rate, and $\mathbf{X}$ and $z$ are controls. Subscripts $i$ and $j$ stand for county and state, respectively. The controls in the vector $\mathbf{X}$ include several potential confounders: i) the demographic structure, represented by share of old persons (65 years old or more) in the population; ii) the high-school drop out rate, a measure of the percentage of population with low human capital;[11] iii) the percentage of households who are proprietor of their own

less than 6% of the population. Including them in our analysis does not change the results. Furthermore, the use of metropolitan areas also facilitates the comparison with our analysis of the Spanish influenza, for which we only have data at the city level.

[11] The use of high-school drop out rates facilitates the comparison with our analysis of

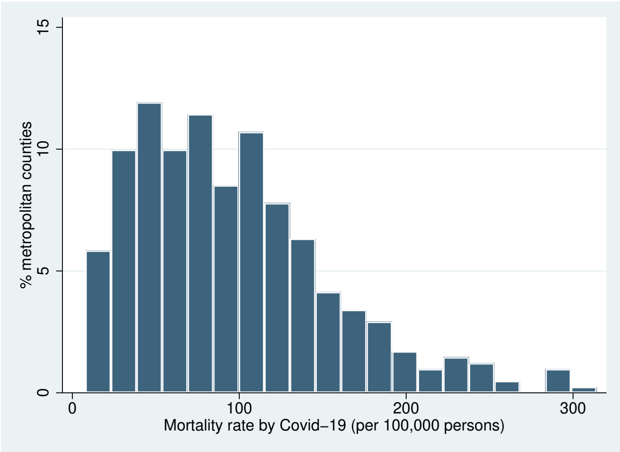


Figure 2: Incidence of mortality from Covid-19 (deaths per 100,000 persons). 411 metropolitan U.S. counties, 2020.

house, a proxy for wealth; iv) the number of nursing home residents per 100,000 persons. The variable $z$ stands for the number of hospital beds per 100,000 persons.[12]

The demographic structure of the population is included because a higher incidence of elderly in the population is obviously associated with higher mortality. The level of human capital might affect the comprehension of diseases and the intake of preventive measures to contrast them. Wealth should obviously improve living conditions and the access to medical services. The latter also depends on the number of hospital beds, a stand-in for the availability of health-care facilities in the state. Finally, we include the number of nursing home residents, for the number of deaths in nursing homes have been an important share of the overall death toll from Covid-19 (Cronin and Evans (2020)).

Column (1) in Table 1 reports results from regressing the mortality rate due to Covid-19 on intergenerational coresidence. They show that intergenerational coresidence is positively associated with mortality from Covid-19, after controlling for several potential confounders. Specifically,

the Spanish influenza, for which we only have data on illiteracy. As explained below, results are robust to using years of schooling in its stead as indicator for human capital.

[12] We have also performed the same regression with dummies for the Census regions to correct for possible spatial correlation. Furthermore, we have checked the robustness of the regression by including several other controls in the **X** vector: average household income, average years of schooling for individuals aged more than 25, population density, percentage of health workers, percentage of black. Results do not change appreciably and are available upon request.

|  | (1) Covid-19 | (2) Overall |
|---|---|---|
| Intergenerational coresidence rate | 5.424*** | -25.99*** |
|  | (1.997) | (6.518) |
| % elderly | -0.402 | 28.32*** |
|  | (0.502) | (2.924) |
| % high school dropouts | 3.112*** | 10.02** |
|  | (1.174) | (3.996) |
| % dwelling owners | -1.215*** | -7.687*** |
|  | (0.316) | (1.549) |
| $n°$ hospital beds | 0.282*** | 1.197*** |
|  | (0.0539) | (0.266) |
| Nursing home residents | 0.144*** | 0.683*** |
|  | (0.0190) | (0.0880) |
| Observations | 411 | 411 |
| Adjusted $R^2$ | 0.321 | 0.461 |

Robust standard errors in parentheses
$^{*}$ $p < 0.10$, $^{**}$ $p < 0.05$, $^{***}$ $p < 0.01$

Table 1: Regression results. Dependent variable: death rate from Covid-19, column (1); overall death rate, column (2). United States metropolitan counties, 2020.

an increase in the intergenerational coresidence rate of 1 percentage point is associated with 5.4 more deaths from Covid-19 per 100,000 persons, or an increase of 5.6% with respect to the mean mortality rate. All the controlling variables have the expected sign with the exception of the demographic structure, which is however not statistically significant.[13]

To verify that our findings are specific to mortality from Covid-19, as opposed to mortality in general, we run the same regression using overall mortality, i.e. mortality from all causes, as dependent variable. Results are shown in Column (2). The sign of the coefficient is now negative: an increase in intergenerational coresidence rate of 1 percentage point is associated with 26 fewer deaths per 100,000 persons.[14]

Hence, we have shown that mortality from Covid-19 is positively associated with intergenerational coresidence, while overall mortality is not.

[13]The sign of the demographic structure depends on the inclusion of the number of nursing home residents in the regression, which is a particularly strong predictor of mortality from Covid-19. Notice also that the positive coefficient associated with the number of hospital beds, which may look surprising, is actually consistent with several studies on Covid-19, for instance Khan et al. (2020).

[14]Results do not change if we use non-Covid deaths – i.e. the difference between total deaths and Covid-19 deaths – as dependent variable.

To further investigate whether this positive association is specific to the Covid-19 pandemic, we are now going to expand our analysis to previous non-pandemic years.

# 4 Mortality in other years: no pandemics

In this Section, we investigate the association between intergenerational coresidence and mortality in the recent non-pandemic past. The idea is to verify whether the positive correlation we found between Covid-19 mortality and intergenerational coresidence is somewhat specific to the Covid-19 pandemic. In other words, we are using past, non-pandemic years as a sort of placebo test.

## 4.1 Mortality and intergenerational coresidence since 1980

As a first exercise, we enlarge the time window of the analysis to the interval 2005-2019. Using county-level mortality rates from Centers for Disease Control and Prevention (2021a) and Census data from Ruggles et al. (2021) we build a balanced panel of 317 metropolitan counties, for a total of 4755 observations.[15] To control for time-invariant, county-specific characteristics that may affect mortality rates, we employ a Fixed Effect Model. We run, both with and without year fixed effects, the following regression

$$D_{i,t} = \beta_0 + \beta_1 h_{i,t} + \beta_2 \mathbf{X}_{i,t} + \beta_3 z_{j,t} + \epsilon_{i,t}, \tag{7}$$

in which variables have the same meaning as in Equation (6). Results are reported in Table 2, column (1) and (2), respectively. In column (1), intergenerational coresidence has a weakly negative association with mortality – a one percentage point increase in coresidence is associated with 1.6 fewer deaths per 100,000 persons in the period 2005-2019. The coefficient becomes non significant when adding year fixed effects.

As a second exercise, we further extend this panel analysis to the period 1980-2010. Using decennial Census data, we construct a balanced panel of 236 metropolitan counties, for a total of 944 observations.[16] Results

[15] Annual Census data exist from the year 2000. However, it is not possible to retrieve observations by county for the years 2001-2004. "Metropolitan" refers to the NHCS 2013 definition (Ingram and Franco (2014)). Notice that deaths are recorded by place of residence in the database from 1980 to 2019, while they are recorded by place of death in the databases for both the Covid-19 and the Spanish flu pandemics.

[16] Data for hospital beds and nursing home residents are not included in the regression since they are not available for the years 1980-2000.

| | (1) | (2) |
|---|---|---|
| Intergenerational coresidence rate | -1.630* | -1.107 |
| | (0.943) | (0.889) |
| % elderly | 20.93*** | 21.69*** |
| | (0.961) | (1.813) |
| % high school dropouts | -0.635 | -2.594*** |
| | (0.939) | (0.835) |
| % dwelling owners | 0.977** | -0.498 |
| | (0.382) | (0.368) |
| $n°$ hospital beds | 0.00744 | 0.000369 |
| | (0.0187) | (0.0196) |
| Nursing home residents | 0.0302 | 0.0298 |
| | (0.0291) | (0.0322) |
| County FE | Yes | Yes |
| Year FE | No | Yes |
| Observations | 4755 | 4755 |
| Counties | 317 | 317 |
| Adjusted $R^2$ | 0.511 | 0.557 |

Robust standard errors in parentheses
$^{*}$ $p < 0.10$, $^{**}$ $p < 0.05$, $^{***}$ $p < 0.01$

Table 2: Regression results. Fixed effect panel. Dependent variable: overall death rate. United States metropolitan counties, 2005-2019.

are presented in Table 3. Column (1) shows that a one percentage point increase in intergenerational coresidence is associated with 14 fewer deaths per 100,000 persons between 1980 and 2010. The coefficient becomes non significant when adding year fixed effects.[17]

In a nutshell, the positive association between intergenerational coresidence and mortality from Covid-19 in 2020 seems to be specific to the Covid-19 pandemic only. The association with overall mortality is instead negative or non significant for all the years for which we have data, i.e. from 1980 to 2020.

## 4.2 Mortality and intergenerational coresidence by type of disease

To further investigate the matter, we are now going to disentangle the correlation between intergenerational coresidence and mortality by type of disease in the 2005-2019 panel. In particular, we select two major causes of

[17] In both regressions, all the controls have the expected sign but for high school dropouts, which become negative once year fixed effects are taken into account. This negative sign disappears when limiting high school dropouts to individuals aged less than 55 in the 2005-2019 panel.

| | (1) | (2) |
|---|---|---|
| Intergenerational coresidence rate | -13.91*** | -0.950 |
| | (4.430) | (4.790) |
| % elderly | 42.18*** | 49.06*** |
| | (3.418) | (3.294) |
| % high school dropouts | 3.009*** | -2.209* |
| | (0.466) | (1.236) |
| % dwelling owners | 0.612 | -4.440*** |
| | (1.783) | (1.511) |
| County FE | Yes | Yes |
| Year FE | No | Yes |
| Observations | 944 | 944 |
| Counties | 236 | 236 |
| Adjusted $R^2$ | 0.444 | 0.611 |

Robust standard errors in parentheses
* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table 3: Regression results. Fixed effect panel. Dependent variable: overall death rate. United States metropolitan counties, 1980-2010.

mortality: 1) mortality from circulatory diseases, and 2) mortality from influenza and pneumonia. The rationale behind this comparison is that only influenza and pneumonia are transmitted via aerobic contagion, thereby making them more directly comparable to Covid-19.

Table 4 displays results from regression (6) with mortality from circulatory diseases as dependent variable. As in Table 2, we report results including only county fixed effects in column (1), and both time and county fixed effects in column (2). No association between intergenerational coresidence and mortality from circulatory diseases emerges. Next, we repeat the same exercise using mortality from influenza and pneumonia as dependent variable. Results are shown in Table 5. In this case, intergenerational coresidence has a slight positive effect on mortality from influenza and pneumonia, once year fixed effects are taken into account (column 2). Quantitatively, one percentage point increase in the intergenerational coresidence rate is associated with 0.28 more deaths from influenza and pneumonia per 100,000 persons.

Coupled with the results on overall mortality between 1980 and 2020, this analysis suggests that intergenerational coresidence is positively associated with mortality from Covid-19 and (slightly) with mortality from influenza and pneumonia – diseases whose transmission is similar to Covid-19 – while the association with overall mortality is negative or not significant.

| | (1) | (2) |
|---|---|---|
| Intergenerational coresidence rate | -0.584 | 0.0119 |
| | (0.515) | (0.473) |
| % elderly | 3.799*** | 5.906*** |
| | (0.458) | (0.810) |
| % high school dropouts | 2.601*** | 0.103 |
| | (0.487) | (0.425) |
| % dwelling owners | 1.471*** | -0.338* |
| | (0.195) | (0.189) |
| $n°$ hospital beds | 0.0312*** | 0.0140 |
| | (0.00869) | (0.00930) |
| Nursing home residents | 0.0272* | 0.0311* |
| | (0.0161) | (0.0183) |
| County FE | Yes | Yes |
| Year FE | No | Yes |
| Observations | 4755 | 4755 |
| Counties | 317 | 317 |
| Adjusted $R^2$ | 0.072 | 0.293 |

Robust standard errors in parentheses
* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table 4: Regression results. Fixed effect panel. Dependent variable: Mortality rate from circulatory diseases. United States counties, 2005-2019.

| | (1) | (2) |
|---|---|---|
| Intergenerational coresidence rate | -0.0567 | 0.276* |
| | (0.183) | (0.151) |
| % elderly | 0.179 | 0.821** |
| | (0.165) | (0.368) |
| % high school dropouts | 0.394*** | -0.133 |
| | (0.152) | (0.126) |
| % dwelling owners | 0.132*** | -0.0916 |
| | (0.0486) | (0.0710) |
| $n°$ hospital beds | -0.00268 | -0.00295 |
| | (0.00285) | (0.00253) |
| Nursing home residents | 0.0114*** | 0.00167 |
| | (0.00381) | (0.00490) |
| County FE | Yes | Yes |
| Year FE | No | Yes |
| Observations | 3195 | 3195 |
| Counties | 213 | 213 |
| Adjusted $R^2$ | 0.034 | 0.146 |

Robust standard errors in parentheses
* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table 5: Regression results. Fixed effect panel. Dependent variable: Mortality rate from influenza and pneumonia diseases. United States counties, 2005-2019.

# 5 Mortality in 1918: the Spanish influenza pandemic

In this Section, we are going to compare the Covid-19 experience with the 1918 Spanish influenza, which is a pandemic episode with transmission features similar to Covid-19, but a different epidemiological impact by demographic cluster (Beach et al. (2020)). Indeed, it witnessed an unusual age-specific incidence of mortality, with a peak for individuals aged 18-40 (Taubenberger and Morens (2006)).

In order to investigate the role of intergenerational coresidence during the Spanish Influenza pandemic, we build a cross-section of 423 American cities, using city-level mortality data from Clay et al. (2019) and U.S. 1910 Census data from Ruggles et al. (2021). We have two indicators of mortality from Clay et al. (2019), the mortality rate in 1918 and the (computed) excess mortality rate allegedly due to the Spanish influenza.[18] We estimated city-level intergenerational coresidence rates from the Census.

Figure 3 shows the relative frequency of the intergenerational coresidence rate in 1910. The distribution is slightly skewed to the right. It ranges from 0% to 29%; the median (mean) is 8.9 (9.5). A glance at Figures 1 and 3 suggests that, as expected, intergenerational coresidence was more widely diffused and more volatile in 1910 than in 2019.

Figure 4 plots the relative frequency of the excess mortality rate in 1918. It shows considerable variation across cities. Excess mortality ranges from -144.7 to 1788, with median (mean) 541.1 (567.5).[19]

Given the data at our disposal, Equation (6) becomes

$$D_\iota = \beta_0 + \beta_1 h_\iota + \beta_2 \mathbf{X}_\iota + \epsilon_\iota. \tag{8}$$

In Equation (8), $D$ is the (excess) mortality rate, $h$ is the intergenerational coresidence rate, $\mathbf{X}$ is a vector of controls and "$\iota$" stands for city. In this regression, the controls in the vector $\mathbf{X}$ include: i) the demographic structure, represented by share of old persons (65 years old or more) in the population; ii) the illiteracy rate; iii) the percentage of households who are proprietor of their own house, a proxy for wealth.[20] Due to the lack of

[18] Both variables are expressed in per 100,000 persons terms.

[19] For comparison, total mortality rate (not reported) ranges from 574.2 to 4723.1, with median (mean) 1867.6 (1954.2).

[20] For robustness, we have also performed the same regressions with several other controls in the $\mathbf{X}$ vector: population density, percentage of health workers, percentage of black, percentage of foreign born, percentage of employment in agriculture. Results do not change appreciably and are available upon request.

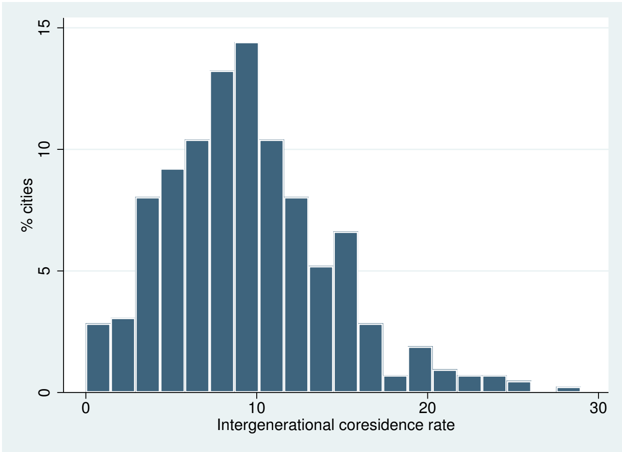


Figure 3: Intergenerational coresidence rate. 423 American cities, 1910.

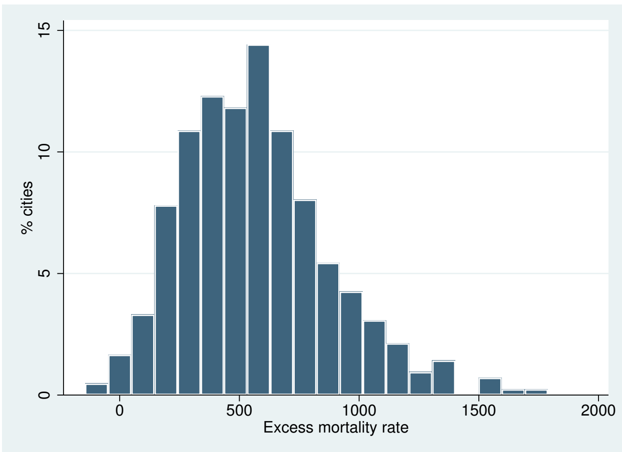


Figure 4: Excess mortality rate (per 100,000 persons). 423 American cities, 1918.

data, we could not include the number of hospital beds and the number of nursing home residents among the controls.

Results for the excess mortality rate and the mortality rate are presented in Table 6, column (1) and (2), respectively. Both columns show that intergenerational coresidence rate is not significantly associated with either the excess or the overall mortality rate. The lack of association between intergenerational coresidence and the excess mortality during the Spanish influenza may be interpreted as a consequence of its peculiar epidemiological pattern, in which, contrary to what experienced during the Covid-19 pandemic, adults aged between 18 and 40 were disproportionately hit.

The comparison of these results with those obtained in the analysis of the Covid-19 pandemic suggests that intergenerational coresidence might be a mechanism fostering the transmission of this type of viral diseases from the young (adults) to the elderly. This translates into higher observed mortality only when the disease is particularly deadly for the elderly.

| | (1) Excess | (2) Overall |
|---|---|---|
| Intergenerational coresidence rate | 6.572 | 6.727 |
| | (5.236) | (9.148) |
| % elderly | -5.808 | 37.56** |
| | (10.48) | (15.98) |
| % illiterates | 17.21*** | 50.94*** |
| | (4.764) | (9.098) |
| % dwelling owners | -5.736*** | -5.577** |
| | (1.224) | (2.234) |
| Observations | 423 | 423 |
| Adjusted $R^2$ | 0.116 | 0.138 |

Standard errors in parentheses
* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table 6: Spanish influenza, regression results. Dependent variable: excess mortality, column (1), overall mortality, column (2). United States cities, 1918. Source: Ruggles et al. (2021) and Clay et al. (2019)

# 6 Conclusions

In this paper, we investigate whether intergenerational coresidence may have been a mechanism fostering the transmission of Covid-19 to the elderly strata of the population. We present evidence that intergenerational coresidence is positively associated with mortality from Covid-19 in a sample of 411 metropolitan American counties in 2020. The effect is statistically significant, and quantitatively non negligible. A one percentage point increase in the intergenerational coresidence rate is associated with 5 more deaths per 100,000 persons due to Covid-19. Results are robust to the inclusion of several socio-economic confounders.

The value added of our research is twofold. First, we are able to establish the existence of a robust, positive correlation between intergenerational coresidence and mortality from Covid-19 in a larger, more homogeneous sample relative to what is currently done in the literature.

Second, we use history as a loose form of identification. In particular, we rely on historical comparisons – both with pre-pandemic years and with the Spanish influenza pandemic episode – as a sort of placebo test, for our theoretical mechanism does not suggest any obvious positive correlation between intergenerational coresidence and mortality in non-pandemic years and during the 1918 Spanish influenza. We show that the positive association between intergenerational coresidence and mortality is indeed specific to the Covid-19 pandemic only. In the same vain, we show that the intergenerational coresidence rate is not positively associated with overall mortality rate in 2020, nor with the mortality from circulatory diseases in pre-pandemic years. Interestingly, a (slight) positive association emerges with mortality from influenza and pneumonia, diseases whose transmission mechanism and age-specific mortality are similar to the Covid-19's.

The general effect of intergenerational coresidence on mortality is likely to operate through various channels. We have provided evidence in favour of one channel, namely the transmission to the elderly of respiratory diseases that are particularly deadly for them. Other mechanisms may be relevant under different circumstances. For instance, intergenerational coresidence may provide the elderly with psychological and physical support when it comes to cancer or degenerative diseases. Further research is necessary to detect such possible mechanisms and assess their empirical relevance.

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# A Appendix: Data

## A.1 Mortality variables

Mortality data come from several sources.

Provisional data on cumulative COVID-19 and all-causes deaths for the period 6/1/2020- 2/1/2021 were obtained from the American Center for Disease and Control Prevention (CDC) and downloaded on 6/01/2021 Centers for Disease Control and Prevention (2021c). To make the data comparable across counties, we construct Covid-19 and all-cause mortality rates per 100000 persons using 2019 county-level population available in the Compressed Mortality dataset (Centers for Disease Control and Prevention (2021a)).

Mortality rates for the panel analysis were also obtained from Centers for Disease Control and Prevention (2021a).

## A.2 Explanatory variables

Person and household-level data on family structure, demographic and socio-economic variables were taken from 1% sample of the 2005-2019 American Community Survey available from the Minnesota Population Center Ruggles et al. (2021). Data from the 2019 sample were used in the Covid-19 analysis. 5% 1980 sample, 1% 1990 sample, 5% 2000 sample were selected for the 1980-2010 panel analysis.

Data were aggregated at the county level by constructing a 5-digit identifier using the Federal Information Processing Standard (FIPS) county code classification. Group quarters and fragments were excluded from the analysis. Households are identified using the 1970, 1990 and 2000 definition Ruggles et al. (2021).

Intergenerational coresidence rate is defined as the percentage of households in which an elderly parent (i.e. aged more than 64 years old) living with their eldest child aged between 18 and 64 years old.

County-level controls include: i) dwelling-owning rate, i.e. the percentage of households who own or bought by loan their housing unit; ii) high-school dropouts rate, defined as the percentage of people aged more than 25 who did not complete high school; iv) percentage of elderly (i.e. aged more than 64 years old).

The number of hospital beds per 100,000 persons is measured at the state level and was obtained from the American Hospital Association.[21]

[21] `http://ghdx.healthdata.org/record/united-states-hospital-beds-1000-population-state`.

For the COVID-19 analysis, data from 2019 were used.

The number of occupied nursing home beds per 100,000 persons comes from the the Brown University Center for Gerontology and Healthcare Research and the National Institute on Ageing available at `www.ltcfocus.org`.

The analysis was restricted to counties defined as Metropolitan Statistical Areas (MSAs) by the 2013 NHCS Urban-Rural Classification Scheme for Counties Ingram and Franco (2014). This include: large central, large fringe, medium and small metro counties.

## A.3 Spanish Flu

The analysis of the Spanish Influenza pandemic was carried out using mortality rates from Clay et al. (2019). Data were merged with 1% sample from the 1910 American Census available on IPUMS (Ruggles et al. (2021). Group quarters and fragments were excluded from the sample. Data were aggregated at the city level.

Excess mortality rates were calculated as in Clay et al. (2019). Excess mortality is defined as the difference between observed mortality and predicted mortality. Predicted mortality was calculated based on a city-specific linear trend for the period 1915-1925 and excluding 1918 (the pandemic year).

The same definition of the variables as in the COVID-19 section applies. In addition, we computed i) illiteracy rate, i.e. the percentage of people who cannot read or write.

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