The Role of Households in the Spread of COVID-19. Example of Switzerland in 2020 and 2021

Introduction: aims

The private household, as a group of people living in the same dwelling, was one of the most critical targets of the health policies implemented in Western countries during the COVID-19 pandemic. The containment policies that were put in place, as well as the social distance policies, made a significant contribution to reinforcing enclosure between people not living in the same household and isolating households from each other while at the same time strengthening social ties within a household (Widmer et al., 2020). However, this focus on households during the pandemic comes in a social context in which household structure has become much more diversified in recent decades (Trotter, 2021). Single-person households involving young and older adults have increased, as have non-family households of people living in shared accommodation, but to a lesser extent.

Our general research question examines the consequences of this heterogeneity in household composition on the spread of COVID-19. This propagation can be seen to take place through two possible channels. The first is the virus transmission from a sick person outside the household to someone in the household. The second channel is the transmission of the virus from one member of the household to another. Our starting hypotheses are: 1) external transmission depends on the degree of isolation of households; 2) internal transmission depends on the degree and type of social relations between people within the same household.

The case of Switzerland

These hypotheses are tested in the case of Switzerland, where health policies were halfway between a strict containment policy and a policy of social distance. The so-called semi-confinement policy implemented in spring 2020 resulted in the closure of schools, universities, government departments, most service companies, and social venues (bars, restaurants, libraries, cinemas, theatres, etc.). On the other hand, people had not been strongly restricted in their movements, with meetings either outside or inside a home being limited to a maximum of five people. After the spring of 2020, while schools and universities remained open (except those in the canton of Geneva during the autumn of 2020), services and social venues reopened temporarily, closing as soon as a new wave arrived. Similarly, measures to limit the number of people in five-person meetings were re-implemented as quickly as there was an ascending phase of infection. Social distancing policies discouraged contact between generations (particularly between grandparents and grandchildren) and made it compulsory from June 2020 to wear masks in transport, schools, administrations, and workplaces.

Data and methodology

Our investigations are based on Swiss Household Panel (SHP) data. This longitudinal survey has been in existence since 1999 (Tillmann et al., 2022). At the end of each year, it questions all the people aged 14 and over in a representative sample of Swiss households on various topics relating to health, work, income, etc. In 2020 and 2021, the interviewers asked each respondent whether they had been ill with covid. This information enables us to investigate how the COVID-19 virus infects households. It should be noted, however, that this database does not allow us to examine family households with children under 14, as they were not interviewed.

Our investigations are based on the estimation of Longini-Koopman models (Longini & Koopman, 1982), which aims to analyze the transmission of an epidemic within social groups such as households. These models are based on the estimation of two probabilities. The first, B, corresponds to the likelihood of not being contaminated by a person from outside the group. The analysis of this probability is based on the idea that all the people in a group are likely to be contaminated by an external route, even if there is already at least one person in the group who has contracted the virus. The second probability, Q, corresponds to the likelihood of becoming ill when at least one person in the group has contracted the virus. Since we do not have the dates of occurrence of the events, and therefore the order of the people falling ill within a household, estimating the model is pretty complex, involving a sort of combinatorics of the different possibilities. The effects of household and individual characteristics on each of the two probabilities can be estimated by adopting a logit relationship. The models are calculated using a Bayesian approach, using stan software (Stan Development Team, 2024).

As we have two years in which respondents were interviewed, we have adopted a data structure similar to that adopted in discrete-time event history analysis models (Allison, 1984). In 2020, the households in which each member responded were considered. In addition to attrition, households in which at least one person was ill the previous year are excluded for 2021. Therefore, 5141 and 4256 households are considered for 2020 and 2021, respectively.

Preliminary results

A preliminary model that did not consider any characteristics indicated a probability B of not being externally contaminated of 96% (credibility interval—CI—of 95-96%), while the probability of not being internally contaminated was 80% (CI 79-82%). The risk of contracting the disease externally was low. However, the risk of becoming ill rose sharply once a person in the group had already contracted COVID-19.

The first model analyses differences according to year, linguistic region, and household type (table 1). The probability of not being externally infected is lower in 2021 than in 2020, consistent with the greater contagiousness of COVID-19 over time. Internal contagion is also increasing (Q is lower in 2021 than 2020). This increase confirms the idea of greater contagiousness during the second year. It may also indicate that the precautions taken within households to avoid contagion have become weaker, for example, due to vaccination, which a high proportion of people adopted from spring 2021 onwards, or because of the lesser severity of COVID-19.

Probability B is lower in French- and Italian-speaking Switzerland than in German-speaking Switzerland, corresponding to the differences in incidence observed in the Ligurian regions. Contagiousness within households is also higher in French- and Italian-speaking Switzerland (Q decreases).

The B probability increases in the case of couples without children households, compared with family households (with children aged 14 and over). On the other hand, B decreases in the case of single-parent households. In both cases, however, the probability Q is lower than for family households, indicating higher proximity between the members of these households.

Single-person households do not differ from family households in terms of external contagiousness. Similarly, there is no difference in external contagiousness between family households and 'other' households (including three-generation households, relative households, and shared households). The latter has a lower probability Q.

Table 1: Models with contextual and household characteristics – log(odds)

	External contagiousness		Internal contagiousness	
	Estimate	Credibility interval	Estimate	Credibility interval
Intercept	3,98	3,81 - 4,16	2,13	1,85 - 2,43
2020	Ref.		Ref.	
2021	-1,25	-1,40 - -1,11	-0,49	-0,77 - -0,22
German speaking area	Ref.		Ref.	
French and Italian speaking	-0,50	-0,63 - -0,37	-0,24	-0,43 - -0,05
Family household	Ref.		Ref.	
Couples Household	0,21	0,04 - 0,37	-1,10	-1,35 - -1,86
Mono-Parental households	-0,39	-0,64 - -0,34	-0,49	-0,80 - -0,19
One-person household	-0,09	-0,27 - 0,08		
Other type household	-0,23	-0,60 - 0,19	-0,42	-0,86 - 0,03

The results of this model are somewhat transformed when the gender and age composition of the household are taken into account (table 2). While the differences according to year and linguistic region are maintained, there are virtually no differences according to family type regarding external contagiousness. Only single people appear to have a lower B probability. On the other hand, only the difference between family and couple households remains in terms of the likelihood of not being sick internally. This confirms the idea of more excellent proximity between partners in a couple's household.

There were no gender differences, either in terms of external or internal contagiousness. B increases with age, while Q decreases, reflecting the higher social isolation of the elderly compared with younger people and the greater contagiousness of COVID-19 when the disease is present in their household.

Table 2: Models with contextual, household and individual characteristics – log(odds)

	Estimate	Credibility interval	Estimate	Credibility interval
Intercept	4,23	4,03 - 4,44	1,67	1,23 - 2,12
2020	Ref.		Ref.	
2021	-1,40	-1,54 - -1,26	0,34	-0,01 - 0,69
German speaking area	Ref.		Ref.	
French and Italian speaking	-0,54	-0,67 - -0,41	-0,14	-0,46 - 0,19
Family household	Ref.		Ref.	
Couples Household	-0,03	-0,22 - 0,15	-0,79	-1,16 - -0,42
Mono-Parental households	-0,26	-0,52 - 0,01	-0,22	-0,79 - 0,39
One-person household	-0,26	-0,46 - -0,08		
Other type household	-0,26	-0,65 - 0,14	1,03	-0,25 - 2,81
Men	Ref.		Ref.	
Women	-0,05	-0,21 - 0,10	-0,21	-0,69 - 0,28
Age	0.02	0,02 - 0,03	-0,02	-0,03 - -0,01

In our further investigations, we will continue to examine the role of social ties in the spread of the COVID-19 epidemic by introducing characteristics linked to the role or status of individuals within a household, for example, their family role (father, mother, child, etc.).

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