Intergenerational transfers of infant mortality in historical contexts: a comparative study of five European populations

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Abstract

Earlier research has shown that the burden of infant mortality is not shared equally by all families, but clusters in high risk families, a phenomenon known as death clustering. The phenomenon is not limited to one generation, but is transmitted from grandmothers to mothers. This paper investigates whether intergenerational transmission of infant mortality from maternal grandmother to mother can be found in five historical populations, controlling for demographic characteristics of the families. Data originates from family reconstitution and population register datasets from populations in Northern and Southern Sweden, Norway, The Netherlands and Belgium. Datasets are converted to the Intermediate Data Structure, and samples are drawn and variables constructed in an identical fashion. Results show that in all regions the risk of infant mortality increases if the maternal grandmother experienced infant deaths, and that the increase in the hazard is similar between regions, notwithstanding large contextual differences.

Introduction

Previous research has shown that mortality in early life clusters in a subset of high-risk families (Curtis, Diamond, & McDonald, 1993; Das Gupta, 1990; Edvinsson et al., 2005; Janssens, Messelink, & Need, 2010; Lynch & Greenhouse, 1994; Vandezande, 2012). Studies conducted in historical populations as well as in developing countries have found evidence that a large proportion of families do not experience any infant death, while a more limited number of families experience multiple infant deaths. These types of studies have identified the importance of considering the family, instead of a single child, as the unit of analysis (Edvinsson et al., 2005). Possible causes of clustering in infant mortality are genetic inheritance, social and cultural factors related to education, socioeconomic status, biological characteristics, and shared disease environment (Janssens et al., 2010). Other factors shown to be related to a high risk of early deaths in certain

families include family size (Zaba & David, 1996), maternal ability (Das Gupta, 1990; 1997), maternal death (Pavard et al., 2005), remarriage of the mother (Edvinsson et al., 2005), earlier stillbirths (Edvinsson et al., 2005) and Rh disease (Häggström Lundevaller & Edvinsson, 2012).

The consequences of mortality clustering appear not to be limited to only one generation, but instead seem to have an influence extending beyond the family of origin, as earlier research conducted with data for Northern Sweden and Antwerp, Belgium, has shown that infant mortality is transmitted from mother to daughter (Lindkvist & Broström, 2006; Vandezande, 2012). It is unclear to which extent this phenomenon can be found in other regions with different mortality regimes, besides those considered in such studies, and to which extent it can be explained by other demographic characteristics of the family.

The aim of this article is to study intergenerational transfers of infant mortality along the maternal line across five different historical populations in Europe. More specifically, this work analyzes whether the likelihood that a woman's children will die in infancy is affected by whether her mother lost infants in their first year of life. The work is conducted using intergenerational longitudinal micro-level data from five family reconstitution or population register data sets from Scania in Southern Sweden, Skellefteå in Northern Sweden, the province of Troms in Northern Norway, the province of Zeeland in The Netherlands and the district of Antwerp in Belgium.

The five databases used in this study have been formatted into the Intermediate Data Structure (IDS). The IDS was developed to simplify the collection, storing and sharing of longitudinal micro level historical demographic data (Alter & Mandemakers, 2014). The structure provides a common platform to store data from different databases, regardless of their original form, and reduces the complexity of using this type of data. It also allows for standardized solutions for storing constructed variables, making data extractions and preparing datasets for analysis (Quaranta, 2015). In the current project, identical scripts are used to create the dataset for analysis from each region and to analyze the data (Quaranta, 2016a; Quaranta, 2016b). This work therefore does not only aim to contribute to the literature focusing on the role of the family in early-life mortality, but it is also the first attempt of its kind to use the IDS in an international cooperative project to conduct research on several data sets using a single approach, making the study fully comparative and reproducible. One common problem of most research studies is the lack of ability to identify whether the results obtained are specific to the context analyzed, or whether they can be generalized across different populations. This work will show whether the IDS can help to overcome such limitations, in this way identifying some of the advantages of adopting the IDS for research using longitudinal historical demographic databases.

Study areas and data sources

The current study considers five different populations located in Southern and Northern Sweden, Northern Norway, Belgium and The Netherlands. The databases for each of these areas were constructed using family reconstitution and/or population register data. All datasets were formatted to follow the IDS.

For Northern Sweden we study Skellefteå, a very large rural parish located in the province of Västerbotten. The data was obtained from POPLINK (Westberg, Edvinsson, & Engberg, 2016); a database on 392,000 individuals constructed from linked parish registers of births, deaths, migration and catechetical examinations from the 17th century until the 1950s. In the catechetical registers the clergy kept continuous records of all demographic events for all individuals residing in a parish, therefore also providing information on migration. These detailed records make it possible to follow individuals over time and to identify their kin over time and throughout the life course. The present IDS version of POPLINK includes data only until 1900, which is the end date for observing births and deaths. The sample selected for this study comprises mothers born between January 1, 1826 and December 31, 1855. The children born to these mothers are born between 1844 and 1901.

In Southern Sweden we study five rural parishes located in the western part of Scania, the southernmost province of Sweden. The data used comes from the Scanian Economic Demographic Database (SEDD – (Bengtsson et al., 2016), which contains family reconstitutions for about 100,000 individuals conducted from parish records of births, deaths and marriages occurring between the years 1630-1968. After 1813 catechetical examination registers are also available. In addition, the SEDD also stores data obtained from annual poll-tax records and land registers. The quality and representativeness of such registers improved starting from 1766 when a much greater proportion of landless families were included. For the period before the start of the catechetical examination registers, poll-tax registers can also be considered to define which individuals were under exposure, by using a mixture of family and farm reconstitutions for such period. The sample selected for the study include children whose mothers were born on or after 1700. The children born to these mothers are born between 1720 and 1968.

For Northern Norway we study the province of Troms, the second northernmost province in the country. The data used for the analysis is based on the Norwegian Historical Population Register (HPR), which aim towards a national population register covering individual life courses from 1801, when Norway had its first nominative census, until 1964, when the modern register was established. The construction of the register is done by automatic and semi-automatic record linkage from church books and census enumerations, along with manual linkage provided by volunteers (Thorvaldsen, Andersen, & Sommerseth, 2015). Troms province acts as a pilot database in the HPR project, and contains data on 310,000 individuals whose life courses have been constructed by extracting vital events from baptism, marriage, and burial protocols along with individual and contextualized census characteristics. The sample selected for this study comprises children whose mothers were born on or after 1803. The children born to these mothers are born between 1846 and 1923.

For Belgium we use data from the Antwerp district for the period 1846-1920. The data is drawn from the COR*- database (Matthijs & Moreels, 2010), a family reconstitution database based on a letter sample from population registers and birth, marriage, and death certificates. The database covers life course information –e.g. birth, marriage, death, migration, and occupational changes– on more than 30,000 individuals and spans up to three generations. All persons who lived at some time in their life in the Antwerp district between 1846 and 1920 and whose family name started with the letters 'C-O-R' were selected, and their life courses were 'reconstructed' from the primary source material. The study sample consists of children born between 1839 and 1915.

For The Netherlands, we consider the province of Zeeland, located in the southwestern coastal region of the country. The data comes from the LINKS database (Mandemakers & Laan, 2016), which contains family reconstitution data on the whole population of the province of Zeeland and is based on the indexes of the certificates of birth, marriage and death as provided by the Zeeuws Archief (see www.wiewaswie.nl). Vital event registration was introduced in The Netherlands in 1812, and records have been digitized for the period 1812-1912 for births, 1812-1937 for marriages, and 1812-1962 for deaths. Certificates have been linked using names of individuals and parents, resulting in a multi-generational data set containing vital events of almost 2 million individuals in seven generations, spanning from the period from the early 19th century until the mid-20th century. For this study, we selected grandmothers and mothers with an observed marriage after 1812, so that their full fertility may be observed. The study sample consists of children born between 1833 and 1912.

Each of the five contexts included in this study differed in many aspects, as can be seen in the summary information presented in Table 1. The size of the populations vary greatly, the smallest being the sample for Antwerp, which includes 1,906 children, and the largest being the sample for Zeeland, which includes 117,848 children. The time periods considered in the areas also varied, with the first cohort of children ranging from 1720 to 1845 and the last cohort of children ranging from 1899 to 1968. The types of refinements made to the data selection with regard to observed calendar years, cohorts to consider and whether a marriage must have been observed or not varied across the different databases. Such refinements were based on the expertise of each research group on the specific characteristics of their data. The sensitivity analysis includes models that consider specific censoring criteria for children and grandmothers, allowing to exclude the possibility that such differences in definition affect the comparability of the results.

Substantial differences are also observed in terms of the rates of infant mortality (Table 1), and probably also the underlying causes of such deaths. In the samples that were created for analysis, IMRs in fact ranged between 80 per thousand for Troms and 189 per thousand for Zeeland. The change over time in infant mortality rates in each area, also calculated for the analysis samples, is shown in Figure 1. Differences in the IMR between the populations also become evident in this figure. There are large fluctuations during the initial years of the study period for Antwerp and Scania, probably due to small numbers. In Figure 2 the IMR for the years 1845-1899 are shown for all populations. Given the vast diversity of the underlying

characteristics of these territories, this project allows us to identify (1) whether intergenerational transfer of infant mortality was significantly present in all areas, irrespectively of their diversity, and (2) similarities and differences across the five regions.

Methods

The IDS consists of five main tables: INDIVIDUAL which is used to store information relating to individuals; INDIV_INDIV which defines relationships between individuals; CONTEXT which defines geographical contexts and contains information about them; CONTEXT_CONTEXT which defines contexts that are nested in other higher level contexts; and INDIV_CONTEXT which defines spells of times during which individuals are present in a specific context. The structure also contains a METADATA table which is used to describe the variables included in the five main tables and their values. A detailed description of how to store data into IDS is given in (Alter & Mandemakers, 2014).

The current work was developed using one common program to extract the data and create the variables for analysis, one common program to convert such data extraction to a rectangular episodes file for analysis, and one common program to run the statistical models. The programs were developed in STATA and are discussed in detail in (Quaranta, 2016a; Quaranta, 2016b). These programs were used across all five databases, making the results of this work not only fully comparable but also reproducible for other contexts where the databases have been formatted into the IDS structure. The programs use as input the INDIVIDUAL and INDIV_INDIV tables, and produce output of graphs and Excel sheets with descriptive statistics and model results. As stated earlier, further refinements with regard to the data selection have been made by research groups familiar with the structure of the database, including requirements with regard to observed calendar years, generations, and observations of vital events, including marriage and census observation. We follow children from birth until age one or death/outmigration in cases where a date of death or outmigration before age one is recorded. A more restrictive censoring criterion is also considered in the sensitivity analysis.

The sample selected for analysis consists of women for whom information is available about their births and survival of their offspring and about the births and survival of these women's siblings. In other words, we consider women for whom the reproductive behavior of the prior generation – the grandmothers – is known. Analyses are based on grandmothers who gave birth to at least two children, of which one was a daughter who survived to adulthood and became a mother herself. Mothers without siblings were not at risk of losing siblings and therefore of intergenerational transmission of losing children in infancy, and such women are excluded from the analysis. Moreover, we only study the risk of dying in infancy for singleton births. The selected study samples can include cases where a woman may appear more than once, with different roles (grandmother, mother, infant). This issues and its possible implications on the results will be addressed in future versions of this work.

We estimate the intergenerational transmission of mortality by estimating Cox proportional hazards survival models (Cox & Oakes, 1984), which are based on the survival of the infant between birth and the first birthday. Cox models are selected in order to account for censoring. The main explanatory variable included in the models is the number of observed infant deaths of the maternal grandmother, which is categorized as zero deaths, one death, or two or more infant deaths. The models also control for the number of observed births of the maternal grandmother (categorized as 2, 3, 4-6 and 7+), the mother's age at the birth of the child (categorized as 15-24, 25-34 and 35-50), the sex of the child, the birth order of the child (categorized as 2, 3, 4-6 and 7+) and the birth date of the child. To account for unmeasured shared characteristics of the mother in the likelihood of survival of all her infants the models consider clustered standard errors on mother ID number. In a future version of this work, instead of estimating Cox models with clustered standard errors we will estimate mixed effects survival models with groupings, respectively, on mother ID number and grandmother ID number.

As a sensitivity analysis, five additional survival models are estimated considering different restrictions to the data. The first selects only the period for which children were under observation. In this model, children are censored one day after their date of birth if no other observations are available for themselves or their mothers after their date of birth. The types of information considered to identify dates of observation include the child's own death, marriage, birth of his/her children and out-migration, and the mother's death, birth of other children and out-migration. Adopting censoring criteria is of particular importance for family reconstitution data. Additional models included in the sensitivity analysis aim to only consider grandmothers for whom we have greater certainty that the number of observed infant deaths is equal to the true number of infant deaths experienced. Such models consider the following restrictions to the datasets: having observed the grandmother for her entire reproductive period (i.e. at least from age 20-50 or from age 20 until age 50 or death); having observed the grandmother for her entire reproductive period and the husband of the grandmother at least until her 50th birthday; having observed the grandmother for her entire reproductive period and no unknown birthdates for her children.

The analysis is divided into two parts. Part one consists on estimating separate models for each of the five populations considered and pooling the results of these estimations. Descriptive statistics for the five areas are shown in Table 2. We first interpret the results of the Cox regressions estimated for each area separately, thus testing the null hypothesis that no intergenerational transmission of infant mortality existed within each specific population. We next interpret the results of the five areas jointly, thus testing the null hypothesis that no intergenerational transmission of infant mortality exists in historical populations. One important aspect to account for when making the latter interpretation is the multiple comparisons problem (Bonferroni, 1936). To deal with this issue we apply the Bonferroni correction, by dividing the nominal significance level by ten when defining statistical significance[1]. In other words, we consider each of these results to be statistically significant if the *p*-value is below 0.5% (0.005).

[1] We divide by ten since the main interpretations made relate to two *p*-values (maternal grandmother experienced one infant death; maternal grandmother experienced two or more infant deaths) for five different populations.

Part two of the analysis consists of estimating a model for a pooled dataset containing the data of the five populations. To increase comparability the estimation is restricted to children born between 1845 and 1899, which are the cohorts that are available in all databases. Two models are estimated. The first is a simple model containing the same control variables as in the country-specific models, and additionally controlling for study area. The second model includes an interaction between the intergenerational transmission variable and the study area. To assess the overall statistical significance of the interaction test we estimate likelihood ratio tests comparing the models without and with interactions. Descriptive statistics for the pooled dataset are shown in Table 3. As can be seen in this table, Zeeland is the largest population among those studied and accounts for 80% of the observations in the pooled dataset.

Results

When estimating Cox proportional hazards models for each population separately, the results show that in all of the five areas intergenerational transmission of infant mortality risk existed along the maternal line (Table 4). The risk of dying in the first year of life was between 12 and 42 percent higher for children whose maternal grandmother had experienced two or more infant deaths. When making separate interpretations for the results of each population, statistical significance is observed, and thus the null hypothesis can be rejected, for all populations except for Antwerp. The low statistical power of the estimates for Antwerp is probably due to small numbers. In Zeeland and Troms significantly higher risks of death were also observed even if the grandmother had experienced only one infant death. When making a joint interpretation of the results in Table 4 and accounting for the multiple comparisons problem, no statistical significance can be identified for Antwerp and Scania.

The magnitude and direction of the hazard ratio as well as the statistical significance of control variables varies between each population. The only variable for which the direction of the results remains consistent across all areas is the number of infant deaths of the grandmother, for children whose maternal grandmothers experienced two or more infant deaths. The results of the intergenerational transmission variable remained consistent when conducting sensitivity analyses for different data selections (Table 5). For Antwerp the results become statistically significant for children whose grandmothers experienced two or more infant deaths if the study sample is restricted to cases where the grandmother is observed for her entire reproductive period. The statistical power for such variable also increases in Scania when adopting the same restriction. However, for Skellefteå the statistical power in such model is reduced.

Table 6 shows the results of pooled regressions for children born between 1845 and 1899 in the five study areas. In model 1, relative to children whose maternal grandmother had not experienced any infant deaths, the risk of dying in infancy were 12% and 34% higher, respectively, for children whose maternal grandmother had experienced one or two or more infant deaths. In the same model children living in Antwerp, Zeeland and in Troms show statistically significantly higher risks of dying than children living in Skellefteå. The likelihood ratio test conducted to compare model 1 with model 2 shows that the interaction between the

population and the intergenerational transmission variable is not statistically significant. This indicates that regardless of the differences in the underlying rates of infant mortality across the different populations, the risk of children dying in infancy increased in similar ways for infants whose maternal grandmother experienced a high number of infant deaths.

Figure 3 presents a summary of the results obtained both in the individual models and in the pooled regression. In particular, it shows the relative risk of death in infancy by number of infant deaths experienced by the maternal grandmother and the 95% confidence intervals. A consistent pattern is evident for children whose maternal grandmother had experienced two or more infant deaths in the pooled regression and each individual area. An exception is Antwerp, which shows higher relative risks but very wide confidence intervals, a pattern that, as pointed out earlier, is due to small numbers.

Discussion

This work had the aim of studying intergenerational transmissions in infant mortality along the maternal line in five European populations: Scania in Southern Sweden, Skellefteå in Northern Sweden, the province of Troms in Northern Norway, the province of Zeeland in The Netherlands and the district of Antwerp in Belgium. The study samples varied largely in terms of contextual characteristics and time periods, which started between 1720 and 1845 and ended between 1899 and 1968. Large variations were also observed in the underlying infant mortality rates of the selected samples between the territories, ranging from 80 per thousand for Troms and 189 per thousand for Zeeland.

The analysis was divided into two parts, one containing individual models for each study area and the second containing a pooled regression from all regions for a common time period – infants born between 1845 and 1899. The results of this work have shown that in the past infant mortality was not randomly distributed, but rather that certain families had a higher mortality burden and that this increased risk was transmitted through the maternal line. Results from the individual Cox models showed that children whose maternal grandmothers had experienced two or more infant deaths had a risk of dying in infancy that was between 12% and 34% higher than children whose maternal grandmothers had not experienced any infant deaths. The observed effect was strong and consistent across the five populations considered, even if such areas differed substantially with respect to their contextual characteristics, time period and underlying infant mortality rates. The results were statistically significant in all areas except for Antwerp, something probably due to small numbers. In the pooled regression, significantly higher risks of death in infancy for children whose maternal grandmother had experienced two or more infant deaths were also observed. Even if there were base differences in the risk of dying across the five populations, no statistically significant differences were found across such areas for children whose maternal grandmothers experienced a high number of infant deaths.

Identifying the causal mechanisms that explain why the risk of dying in infancy is transmitted across generations is complex. Such patterns can, in fact, be related to a combination of cultural, social and

biological factors. One explanation for these effects could be the parental transmission of fecundity, fertility intentions and parental behavior (e.g. Bras, Van Bavel, & Mandemakers, 2013; Kotte & Volker, 2011; Reher, Ortega, & Sanz-Gimeno, 2008). Characteristics such as family size and age of the mother at birth can affect the likelihood of experiencing early offspring mortality. However, in this paper we have shown that mortality patterns among the grandmothers' offspring exercised a significant influence over survival chances of the mothers' own offspring, even after taking demographic characteristics of the family into account.

Other possible explanations for intergenerational continuities of survival chances in infancy include the transfer of socioeconomic status and parental resources and of parental care. In future versions of this work we will estimate additional models controlling for socioeconomic status. Other factors could be related to genetic transfers of health across generations, which affect fetal selection during pregnancy as well as the chances of survival of an infant. An example is Rh disease, which may lead to stillbirths of Rh positive fetuses from a Rh negative mother. In the next generation, similar patterns may occur if a surviving rhesus-negative daughter conceives rhesus-positive children. Earlier research has suggested that clustering of perinatal deaths may have been caused by Rh disease (Häggström Lundevaller & Edvinsson, 2012). Furthermore, a mother and her sibling may have shared the same adverse early life exposures, which may have caused early death for one or more of her siblings and, at the same time, may have scarred her health for life, reducing her ability to carry pregnancies to term and also increasing the mortality risk of her children (Quaranta, 2013). Further research focusing on the same five populations will be conducted in order to try to distinguish between these possible causal pathways. When trying to identify such pathways, we will also estimate models measuring the possible transmission in infant mortality along the paternal line.

Besides expanding our knowledge of intergenerational transmissions of infant mortality, this paper had the additional aim of using for the first time the IDS in an international cooperative project to conduct research on several data sets. Thanks to the IDS it was possible to adopt the same approach in all areas, using the same programs to create the datasets for analysis and to run the statistical models. Variables were created in an identical fashion and selections were made in the same exact way. This approach has made the calculation of key statistics and the results of the statistical models fully comparable across the five areas. We are in fact able to state that any differences in the results are not related to problems or differences in the modelling and data generating process, but are rather the result of underlying differences in the (selected sample or) database. Moreover, this approach is also fully reproducible for other populations outside our study.

In terms of limitations of an IDS-based approach, using exactly the same statistical models reduces the flexibility that may be adopted in each study population, and models do not necessarily fit as well in one population as in the next. In addition, the data selections made may differ as a result of differences in the structure of the database if both populations based on family reconstitution and on population/parish register data are considered, and it is difficult to see how this influences the selected sample and possibly also the results. Moreover, starting years of full observations differ between datasets, which is a selection requirement that varies by definition between the datasets. Regardless of these limitations, this work has shown that there

are great advantages in adopting the IDS for research that is based on longitudinal historical demographic databases. Within this project the IDS has in fact allowed us to determine that the observed patterns of intergenerational transmissions in infant mortality were not specific to a single context, but instead are context-independent and widely spread among different historical populations.

The findings of this work emphasize that when trying to identify the determinants of the health and mortality of children it is not only important to take into consideration the characteristics of the child, but also those of the mother and even the grandmother. We have, in fact, shown that regardless of underlying contextual characteristics, there are some families which are more frail than others and that such frailty is transferred across generations. The widespread nature of the results obtained in this study provide important incentives for the development of future research aimed at identifying possible causal determinants of intergenerational transfers of infant mortality, and our findings also provide information that is useful for the establishment of policy interventions in developed, as well as developing countries. For example, the results of our study show that infants born to women who lost any of her siblings in infancy may require additional and/or special screening and care. Such interventions can have important implications in the reduction of infant mortality and overall improvement of early life health.

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Tables and Figures

Table 1: Summary information of the populations

	Antwerp, Belgium	Zeeland, The Netherlands	Scania, Southern Sweden	Skellefteå, Northern Sweden	Troms, Northern Norway
Cohorts of children considered	1839-1915	1833-1912	1720-1968	1844-1901	1846-1923
IMR in study sample (x 1000)	170	189	134	83	80
Number of children in sample	1,906	117,848	8,816	13,049	25,466
Number of mothers in sample	381	21,072	2,453	2,685	5,477
Number of grandmothers in sample	255	14,253	1,875	1,633	3,506
Number of infant deaths in sample	246	22,283	1,184	1,083	2,045

Table 2: Descriptive statistics for the five populations

	Antwerp	Zeeland	Scania	Skellefteå	Troms
Sex of the child					
Female	49.0%	48.2%	48.4%	48.4%	48.6%
Male	51.0%	51.8%	51.6%	51.6%	51.4%
N. of infant deaths of the grandmother					
0 infant death	66.2%	30.8%	51.7%	60.7%	56.7%
1 infant death	13.7%	27.4%	26.9%	26.0%	27.8%
2+ infant death	20.1%	41.8%	21.4%	13.3%	15.4%
N. of births of the grandmother					
2 births	7.8%	3.6%	8.0%	2.6%	4.3%
3 births	15.9%	5.2%	8.8%	4.8%	6.1%
4-6 births	42.1%	24.0%	37.7%	29.4%	31.9%
7+ births	34.2%	67.1%	45.5%	63.3%	57.7%
Birth order					
1	21.5%	17.9%	24.6%	20.3%	21.0%
2	18.3%	15.5%	19.3%	17.5%	17.3%
3	14.7%	13.4%	14.8%	14.7%	14.7%
4-6	27.7%	28.9%	28.7%	31.7%	30.5%
7+	17.8%	24.2%	12.6%	15.8%	16.5%
Child birth year (average)	1887.5	1878.0	1850.6	1872.8	1893.4
N of children	1,445	140,607	8,816	13,049	25,466
N of infant deaths	246	25,470	1,184	1,083	2,045

Table 3: Descriptive statistics for the pooled regression, children born between 1845 and 1899

	Percent / average
Sex of the child	
Female	48.2%
Male	51.8%
N. of infant deaths of the grandmother	
0 infant death	36.4%
1 infant death	27.1%
2+ infant death	36.5%
N. of births of the grandmother	
2 births	3.8%
3 births	5.6%
4-6 births	25.8%
7+ births	64.8%
Birth order	
1	18.4%
2	16.0%
3	13.8%
4-6	29.7%
7+	22.0%
Mother age at birth	
15-24	17.6%
25-34	55.5%
35-50	26.9%
Population	
Antwerp	0.8%
Skellefteå	9.1%
Zeeland	80.2%
Scania	1.7%
Troms	8.2%
Child birth year (average)	1874.7

Table 4: Cox proportional hazards models estimating the risk of death in infancy – individual models for the five populations

	Antwerp		Zeeland		Scania		Skellefteå		Troms	
	HR	p-value	HR	p-value	HR	p-value	HR	p-value	HR	p-value
N. of infant deaths of the grandmother, (ref: 0)	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.
1 infant death	0.955	0.879	1.132	0.000	1.041	0.625	1.142	0.103	1.190	0.003
2+ infant death	1.192	0.486	1.349	0.000	1.217	0.027	1.423	0.000	1.274	0.002
N. of births of the grandmother (ref:2)	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.
3 births	0.926	0.806	0.904	0.050	1.172	0.299	1.303	0.319	0.947	0.711
4-6 births	1.008	0.975	0.872	0.001	1.099	0.450	1.352	0.167	0.942	0.633
7+ births	0.866	0.672	0.813	0.000	1.156	0.248	1.076	0.733	0.902	0.406
Sex of the child (ref: female)	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.
Male	0.846	0.270	1.233	0.000	1.145	0.018	1.245	0.000	1.043	0.344
Birth order (ref:1)	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.
2	1.104	0.624	1.060	0.010	0.809	0.020	0.932	0.486	0.757	0.000
3	1.360	0.166	1.097	0.000	0.849	0.110	0.957	0.694	0.841	0.030
4-6	1.774	0.006	1.219	0.000	0.863	0.123	0.916	0.394	0.856	0.036
7+	2.812	0.000	1.569	0.000	1.112	0.361	1.035	0.804	0.945	0.573
Child birth date centered	0.994	0.311	0.986	0.000	0.990	0.000	1.022	0.000	0.987	0.000
Mother age 15-24	1.705	0.001	1.047	0.023	1.047	0.632	1.364	0.002	1.168	0.022
25-34 (ref.)	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.	1.000	ref.
35-50	0.626	0.019	0.980	0.258	1.010	0.901	1.176	0.064	1.033	0.616
N of children	1,445		140,607		8,816		13,049		25,466	
N of infant deaths	246		25,470		1,184		1,083		2,045	

Table 5: Sensitivity analysis - Cox proportional hazards models estimating the risk of death in infancy in the five populations considering different data selections

	Model 1	Model 2	Model 3	Model 4	Model 5
			Antwerp		
1 infant death	1.006	1.461	1.301	1.400	1.414
2+ infant death	1.208	1.921**	2.010**	1.890**	1.984*
			Zeeland		
1 infant death	1.131***	1.130***	1.128***	1.146***	1.140***
2+ infant death	1.345***	1.353***	1.337***	1.375***	1.357***
			Scania		
1 infant death	1.041	1.09	1.02	1.074	0.981
2+ infant death	1.214**	1.362***	1.312***	1.370**	1.246*
			Skellefteå		
1 infant death	1.119	1.238*	1.214**	1.245*	1.222*
2+ infant death	1.380***	1.284*	1.276**	1.231	1.340**
			Troms		
1 infant death	1.187***	1.165	1.227**	1.184	1.168
2+ infant death	1.251***	1.413**	1.398***	1.393**	1.428***

Note: Model 1 – child under observation; Model 2 – grandmother observed at least from age 20 to 50; Model 3 – grandmother observed at least from age 20 to age 50 or death; Model 4 – grandmother observed at least from age 20 to 50 and first husband of the grandmother observed at least until the grandmother's 50th birthday; Model 5 – grandmother observed at least from age 20 to 50 and no children with unknown birthdates for the grandmother.

Table 6: Cox proportional hazards models estimating the risk of death in infancy – pooled model for the five populations. Children born between 1845 and 1899

	Model 1		Model 2	
	HR	p-value	HR	p-value
N. of infant deaths of the grandmother (ref: 0)	1.000	ref.	1.000	ref.
1 infant death	1.118	0.000	1.079	0.356
2+ infant death	1.339	0.000	1.314	0.005
Population, (ref: Skellefteå)	1.000	ref.	1.000	ref.
Antwerp	2.041	0.000	2.126	0.000
Zeeland	1.752	0.000	1.722	0.000
Scania	0.916	0.213	0.964	0.708
Troms	1.123	0.013	1.113	0.085
N. of infant deaths of the grandmother * Population				
1 infant death * Antwerp			0.940	0.868
1 infant death * Zeeland			1.042	0.628
1 infant death * Scania			0.956	0.783
1 infant death * Troms			1.050	0.649
2+ infant death * Antwerp			0.835	0.455
2+ infant death * Zeeland			1.026	0.791
2+ infant death * Scania			0.836	0.343
2+ infant death * Troms			0.981	0.878
N. of births of the grandmother (ref:2)	1.000	ref.	1.000	ref.
3 births	0.940	0.222	0.939	0.215
4-6 births	0.906	0.017	0.905	0.017
7+ births	0.840	0.000	0.840	0.000
Sex of the child (ref: female)	1.000	ref.	1.000	ref.
Male	1.201	0.000	1.201	0.000
Birth order (ref:1)	1.000	ref.	1.000	ref.
2	1.009	0.680	1.009	0.678
3	1.045	0.067	1.045	0.067
4-6	1.135	0.000	1.135	0.000
7+	1.460	0.000	1.461	0.000
Child birth date centered	0.988	0.000	0.988	0.000
Mother's age 15-24	1.072	0.001	1.072	0.001
25-34 (ref.)	1.000	ref.	1.000	ref.
35-50	1.001	0.951	1.001	0.947
N of children	146,534			
N of infant deaths	24,851			
Likelihood ratio test *p*-value	0.873			

Figure 1: Infant mortality rate in the selected study samples for the five populations over the years considered in each sample

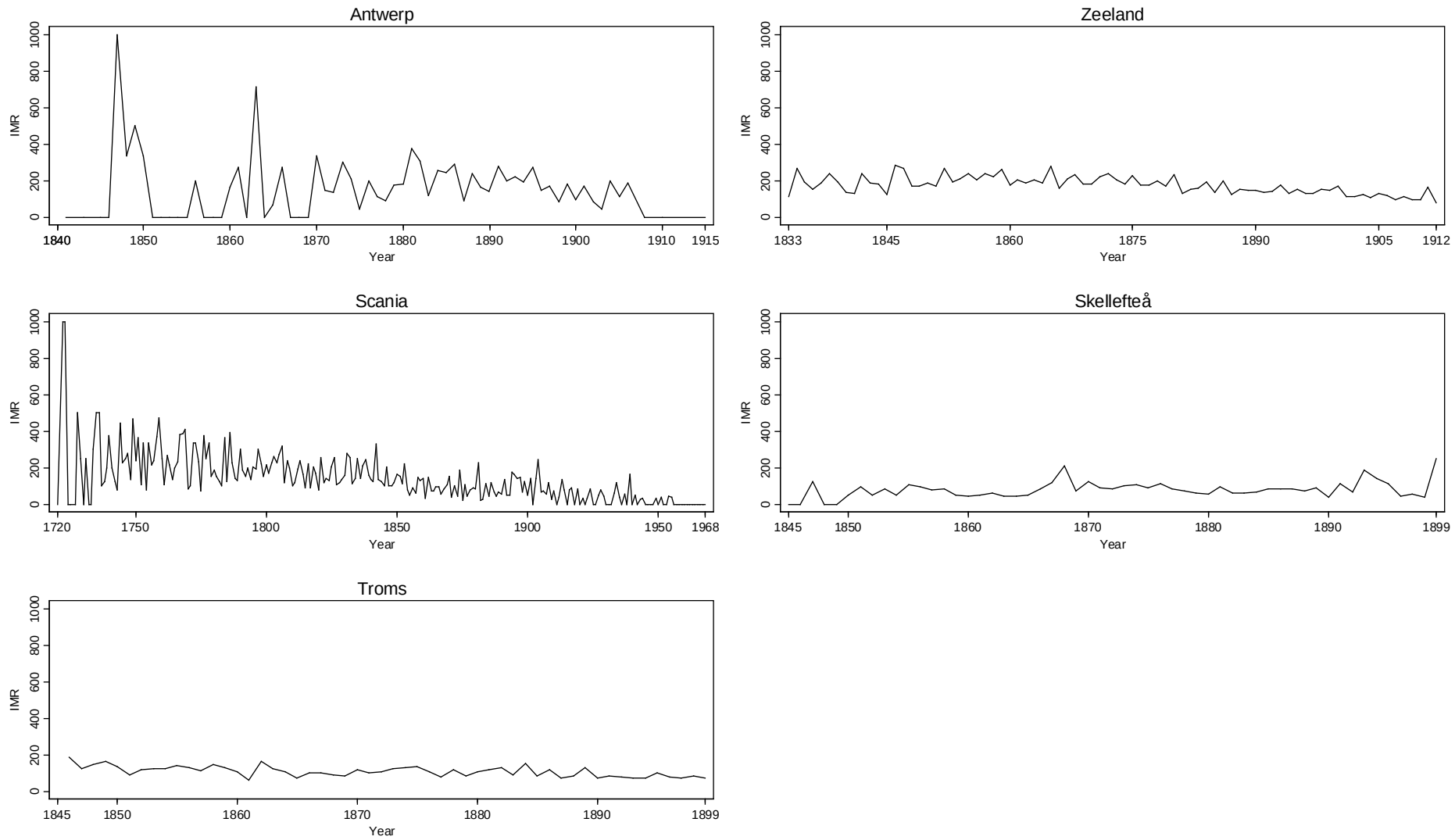


Figure 2: Infant mortality rate in the selected study samples for the five populations over the years 1845-1899

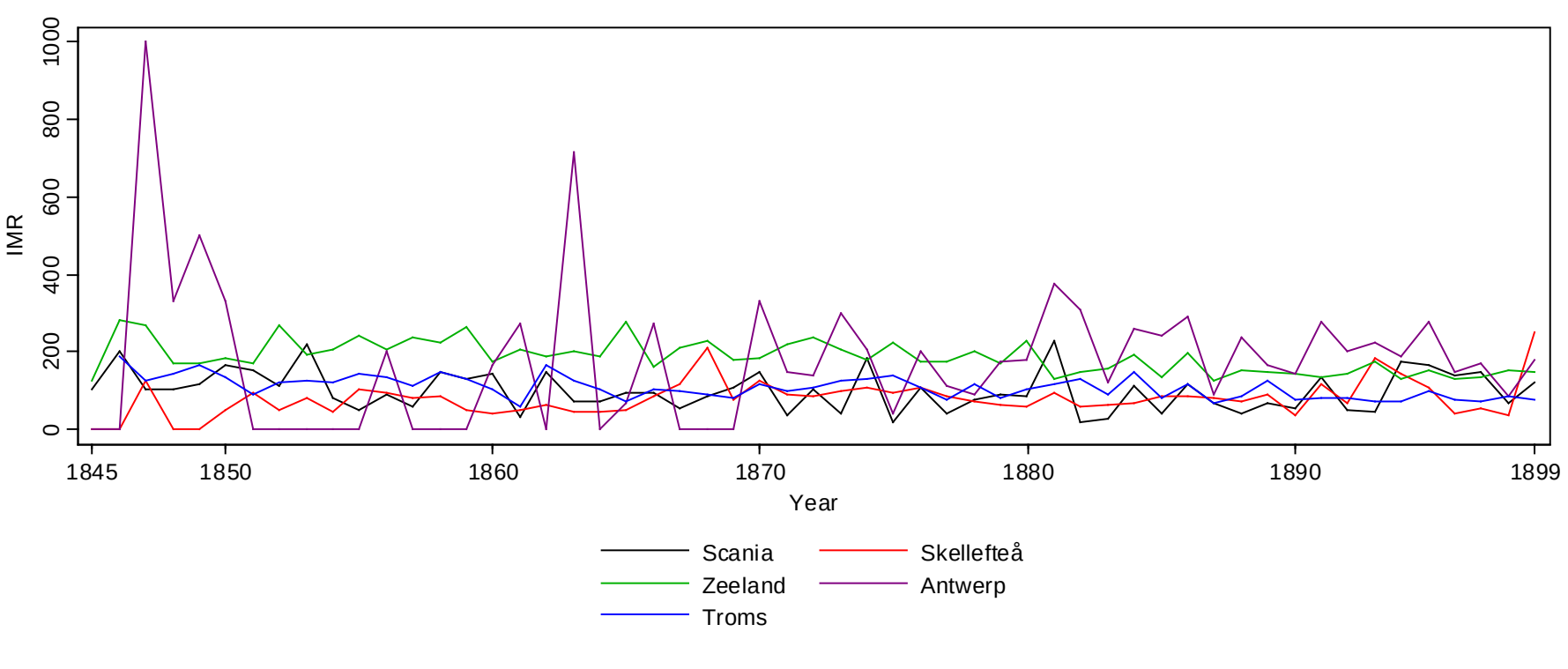
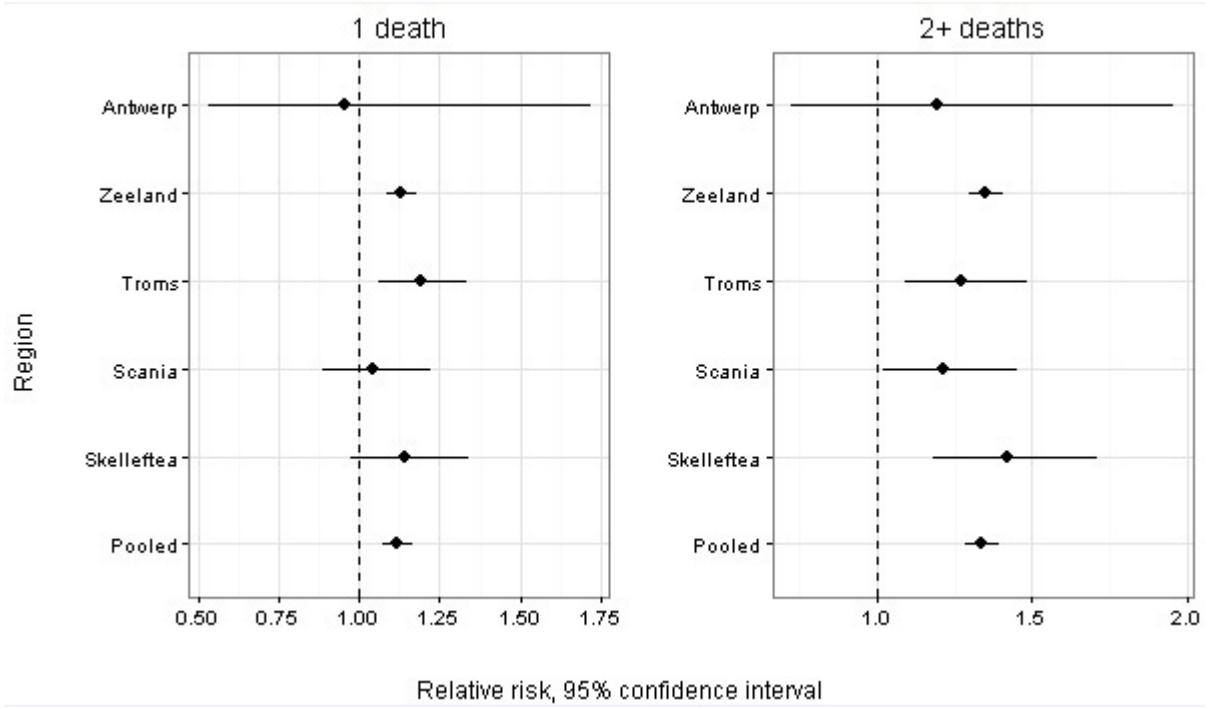


Figure 3: Relative risks of death in infancy by number of infant deaths experienced by the maternal grandmother



Note: Results obtained by estimating separate Cox proportional hazards models for each population. Each model controls for number of births of the grandmother, age of the mother at birth of the child, and child's sex, birth order and centered date of birth.

Infant mortality is the death of young children under the age of 1. This death toll is measured by the infant mortality rate (IMR), which is the probability of deaths of children under one year of age per 1000 live births. The under-five mortality rate, which is referred to as the child mortality rate, is also an important statistic, considering the infant mortality rate focuses only on children under one year of age. International comparative studies show that infant mortality rates vary gradually from one country to another. 4,[9][10][11][12][13] Other studies have focused on showing important variations in infant mortality rates within a country or a region and in different geographical contexts, particularly in Austria, 14 Brazil, 15 South Africa, 2,16 West Africa, 17,18 Michigan (US), 19 and Alexandria in Egypt. 20 Racial and ethnic disparities in infant mortality have been largely documented, especially in the US. ...Â The population density predictor is only significantly and positively associated with clusters obtained for the non-MÄori population.Â We aimed to examine the changes and trends of infant mortality in the European Union (EU) and its 28 member states in the 1994-2015 period. Infant mortality (the death of an infant within the first year of life) is a widely-reported indicator of population health. This chart collection highlights key infant mortality trends and demographic variation within the United States and also explores infant mortality rates in the U.S. compared to countries that are similarly wealthy and sizable (based on GDP and GDP per capita). Overall, the U.S. and comparable countries have seen a decrease in infant mortality rates in recent years, but the U.S. has been slower to improve its consistently higher average rate of infant deaths, and signific European countries should invest more on mortality surveillance systems to improve the publicly available data.Â Beyond this qualitative analysis, we found four studies of excess mortality during COVID-19. Switzer-land has a mortality surveillance system in place with data from the Federal Statistical Of-ce [8] that estimates 892 excess deaths for those above-65 up to April 12th.Â a comparative evolution of weekly mortality in each country. Deviation from the expected value from homologue periods (DEV) Mortal-ity is relatively stable across the years for all analyzed datasets.Â Men over 65 are the most affected population group, with around twice the increase in deaths compared to that of women over 65. This may reect a higher.