



HUMAN EVOLUTIONARY DEMOGRAPHY

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26. Historical Family Reconstitution Databases in the Study of Kinship Influences on Demographic Outcomes

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Human life histories and demographic outcomes are impacted by kin behaviour in diverse ways, and human evolutionary theory is essential to understanding how environmental context and kin relationship moderate this behaviour in cooperative versus competitive directions. However, kin presence is simultaneously correlated with behavioural and non-behavioural factors such as risk of infection or familial wealth. As such, it can be hard to disentangle evolutionary effects from other factors correlated within a family. In this chapter we discuss how historical family reconstitution databases have assisted in the investigation of kin effects and their advantages in disentangling these behavioural kin effects from non-behavioural accompanying factors. A variety of family reconstitution studies exist across varying geographic and cultural contexts, and their application to kinship research has resulted in varying findings. This highlights how kin impacts differ depending on circumstance. We describe several family reconstitution studies and discuss the importance of evolutionary theory in understanding kin effects across different populations.

Introduction

Family matters for human life histories. Family is important in an active and operative sense, as social interactions between kin members can affect those members' outcomes. And family is important as a group identifier, marking groups where correlations in epidemiological conditions, socioeconomic status, genetic background, environmental and social conditions, and other factors may be common amongst their members. Kin, as the members of these groups, can affect outcomes both by their absence and their presence. For example, the absence of the biological father during early childhood may impact later reproductive behaviour and strategy (Shenk et al. 2013; Sheppard, Snopkowski, and Sear 2014), although this effect seems limited to Western, Educated, Industrialized, Rich, and Democratic (WEIRD) societies (Sear, Sheppard, and Coall, 2019). And the presence of additional siblings appears to have a direct effect on survival and fertility (e.g., Steelman et al. 2002; Fox et al. 2017). In addition, the presence of postmenopausal women tends to reduce the mortality of their reproductive daughters and those daughters' children (Sear and Mace 2008). For daughters-in-law, however, the impacts may rely on social strata differentials. Studies covering families at the lower end of the economic spectrum suggest

mothers-in-law increase stillbirth mortality (Voland and Beise 2005), whereas other studies indicate that in more affluent families they reduce the mortality of their sons' wife (Willführ, Johow, and Voland 2018). A study by Zang and Campbell (2018) suggests grandparental presence might also affect mortality later in life. They found that men in north-western China suffered from increased mortality if they resided as children with their father's parents. Depending on their relationship and other moderating factors, the impact of kin's presence or absence may constitute either a positive or a negative influence, and sometimes simultaneously both.

Darwinian or evolutionary theory helps to understand the variation in kin effects across kin types (e.g., paternal versus maternal grandmothers) and environments (e.g., resource constrained versus resource abundant). Evolutionary theory argues that evolved strategies and mechanisms interact with the contemporary environment and cause or determine the path of the individual phenotype over its life course. As we consider them, kinship effects constitute the impacts on individual outcomes arising from social interactions among kin. Social interactions are broadly defined to include any variety of active supportive or competitive behaviour.

Evolutionary theory provides a framework to understand when and why this supportive or competitive behaviour may arise. The supportive role of kin can be understood within the context of the cooperative-breeders model, where alloparental care is provided in support of the mother both to improve the outcomes of the offspring and allow for increased fertility from the mother. On the other hand, family resources per household member decline as the number of kin increase if these kin consume more family resources than they contribute. Resources are thus often scarcer in large families, with increased kin competition.

The role of grandmothers can also be understood using evolutionary theory. With supportive grandmothers, reproductive females exhibit increased fertility and lower offspring mortality, an effect attributable to grandmaternal support in childcare and knowledge transfer (Lahdenperä et al. 2004; Voland, Chasiotis, and Schiefenhövel 2005).

The kinship effects described above derive from social interaction and conscious or unconscious efforts to affect the outcomes of other family members. However, the presence of kin can also be associated with accompanying non-behavioural factors. This can create challenges in differentiating between the behavioural and non-behavioural impacts, and in identifying the role of evolutionary influences on kin interactions. The effects of sibling composition, for example, are often associated with both behavioural and non-behavioural influences. The impact of sibling composition on outcomes such as child mortality may result from behavioural factors such as sibling rivalry and competition, as well as from increased risk of cross infections associated with larger families or from improved family outcomes driven by the role of the familial unit in obtaining economic success (e.g., pioneer populations).

Separating behavioural from non-behavioural kinship influences on outcomes is possible if those non-behavioural accompanying factors are common to members within a family. This may not be true in all contexts but is a reasonable assumption for factors such as the risk of cross infections and socioeconomic status during childhood. When variation in unobserved factors occurs across but not within families, it is possible for researchers to exploit the role of family to identify kinship influences deriving from evolutionary factors. This requires information on

families observed over complete life courses, and, in some cases, across subsequent generations. Historical family reconstitution studies, with their provision of long-period information, are thus extremely valuable in the study of kinship from an evolutionary perspective. This chapter serves as both an introduction to historical family reconstitutions and their origins, as well as an argument of their importance in identifying the significance of evolutionarily driven behaviour in kinship interactions. We begin with an overview of the origins of historical family reconstitutions.

Origins of Family Reconstitution Studies

Although the pioneering work of family reconstitution studies is usually identified as that by Fleury and Henry in 1976, the history of family reconstitution studies starts with parochial studies of German population biologists from the pre-World-War-II period (e.g., Scheidt 1932). The context within which these scientists researched, and perceived connection to the racial ideas of the Nazis, has led to their works being ideologically tainted (Schlumbohm 2018). The procedure used by those early researchers, still used in contemporary studies, begins with the digitization of all marriages within one or more localities and recording the names of grooms and brides and their date of marriage in a database. Birth records that include the name of the parents along with the name and birthdate of the child are digitized in another database. The families are then reconstituted by linking the databases. The final step is to append parent and child dates of death from the available burial records. Fleury and Henry used these parish register data to reconstruct population levels and trends. These techniques were then further developed by E. A. Wrigley, R. S. Davies, Jim E. Oeppen, and Roger S. Schofield at the Cambridge Group for the History of Population and Social Structure (Wrigley and Schofield 1981; Wrigley et al. 1997).

From the beginning it was clear that using such family reconstitutions to estimate population levels and trends faced serious limitations. These included migration censoring (1), non-representativeness of the study parish/es (2), and record selection bias (3).

The problem of migration censoring is best illustrated with an example. Within Europe, many children left their parent's parish of residence as young adults, resulting in many unknown marriage and death dates. Since migrants tend to marry later, the observed mean age at marriage will be lower than the "true" mean age of marriage because later marriages among migrants are excluded (Kasakoff and Adams 1995). Although the impact of this may not be large, the problem persists in principle. Voland and Dunbar (Voland and Dunbar 1997) used a case study to show that the underestimation of age of marriage is small and is likely to be negligible for most research questions.

The non-representativeness of parishes or localities (2) and record bias (3) constitute source problems as demographic traits exhibit spatial dimensions. Some parishes are wealthier than others, some are under increased epidemiological stress due to high population density and/or trading traffic, and others suffer regularly from natural catastrophes like floods and droughts. The representativeness of the study parishes is therefore of enormous importance in establishing generality. Similar concerns exist regarding systematic bias in individual records within the parish registers. This bias is often present in historical parish registers, which prioritized socially important individuals and families. As such, historical family reconstitution studies must be carefully applied in estimating population

level statistics. However, they are of great value for studies focusing on the individual and family level, which can in turn help to understand trends at the population level (Dribe et al. 2016).

Like historical family reconstitutions, longitudinal studies of contemporary populations also provide long-period information. These include studies such as the 1958 National Child Development Study and British Cohort Study of 1970,¹ the Dutch Famine Birth Cohort Study,² The German SOEP dataset,³ and the U.S. National Longitudinal Surveys.⁴ These studies often combine demographic traits with anthropometric, medical, and socio-economic information. However, unless a subject expires between survey waves, they generally do not cover completed life histories. Completed life histories and those that link several subsequent generations are generally provided only by register-based family reconstitution studies. We survey five of these reconstitution studies below.

An Incomplete List of Family Reconstitution Studies in Use

In the following we briefly introduce five different datasets from Europe and North America. These datasets exhibit different advantages and are linkable to information from other sources. Our selection is to be understood as an introduction and makes no claims of completeness.

Many more datasets are carried together by the European Historical Population Sample Network (EHPS network) and are accessible online.⁵

Canada (Quebec, St Lawrence Valley)

The Programme de recherche en démographie historique (PRDH, Research Programme in Historical Demography) at the Université de Montréal reconstitutes the population of Quebec from the beginnings of French colonization in the seventeenth century. Data collection and processing is still underway; currently, data from the early beginning of the colony up to the year 1849 is available for statistical analysis. The dataset covers the complete population over the whole territory on which the colony was established at the time, mitigating selection bias and other problems of observation exits through emigration. The population was naturally fertile and experienced exponential population growth after the final migration wave in 1671 due to settler births (Charbonneau, Desjardins, and Légaré 2000). An updated report on the PRDH was published in 2018⁶ by Dillon and colleagues (Dillon et al. 2018). The database was established to investigate the population history of New France including epidemiological, genetic, and many other research questions. Various studies focusing explicitly on kin effects include those studying parental loss (Pavard et al. 2005; Willführ and Gagnon 2013; Légaré and Naud 2001), sibling effects on marriage (Caron et al. 2017; Dillon 2010), and sibling effects on mortality (Fox et al. 2017).

1 <http://www.cls.ioe.ac.uk/>

2 <http://www.dutchfamine.nl/index.htm>

3 <http://www.diw.de/de/soep>

4 <https://www.bls.gov/nls/>

5 <https://ehps-net.eu/databases>

6 <https://www.prdh-igd.com/en/updates>

Germany (Krummhörn), 1720–1874

This family reconstitution project originated to evaluate hypotheses on human reproductive behaviour guided by sociobiology and behavioural ecology using the population of East Frisian Krummhörn, the marsh region northwest of the city of Emden, from eighteenth- and nineteenth-century parish records and tax lists. This database contains vital and social statistics for 118,778 persons (34,708 families) from thirty-three neighbouring parishes. Originally supported by the German Research Foundation (DFG), the German-language database is archived at the GESIS-Institute (Cologne) with the label ZA8630.⁷ A comprehensive description of the database can be found at the study founder's website: <http://eckart-voland.de/pdf/KH-LIT.pdf>. Currently, there are sixty-seven scientific publications based on this database. A list of publications derived from this project can also be found at the study founder's website: <https://eckart-voland.de/pdf/KH-LIT.pdf>. Most of these publications are on kin effects, including studies on differential parental investment (Voland and Dunbar 1995), differentials in reproductive success (Voland 1990), the opposite effects of maternal and paternal grandmothers (Voland and Beise 2002), in-law kin effects (Voland and Beise 2005), the effects of having siblings (Fox et al. 2017; Beise and Voland 2008), the impact of paternal death on life strategies (Voland and Willführ 2017) and on the impacts of kin on the mortality of reproductive women (Willführ, Johow, and Voland 2018).

The Demographic Database (Sweden)

The Demographic Data Base (DDB) is a research unit at Umeå University, Sweden which provides comprehensive information about the Swedish population history for research, education, and archives.⁸ The DDB consists of several datasets which provide different levels of information on the Swedish demographic history. Data for the POPUM dataset derived from catechetical examination registers (*husförhörslängder*) which cover vital events and marriages as well as detailed information about the individual residence since parishioners had to inform the minister about their in- and out-migration. In nineteenth- and twentieth-century Sweden there was substantial spatial variation in living conditions and socio-economic standards. Regions such as the Sundsvall region were industrialized, whereas other regions remained rural and agricultural. Studies on kinship using the DDB include those estimating the impact of consanguine marriages on reproductive behaviour and early mortality (Egerbladh and Bittles 2008), on family effects on social mobility (Miller 1995), and on the consequence of paternal loss (Wall 2002).

United States (Utah Population Database) from Early-Nineteenth to Mid-Twentieth Centuries

The Utah Population Database (UPDB) at Huntsman Cancer Institute at the University of Utah links historical family demographic records with the biomedical data of the descendants living today. The dataset includes more than 1.6 million individuals and has been an important resource for researchers in both the medical and social science fields. In addition, it has the

7 <http://dx.doi.org/10.4232/1.12643>

8 <https://www.umu.se/en/centre-for-demographic-and-ageing-research/databases/>

unique distinction of containing information on a Western polygamous society, as this was allowed within the Mormon religion for a short period in the nineteenth century. This social system allows researchers to disentangle paternal and maternal effects which are more difficult to separate in (serial) monogamous societies.

More generally, this dataset has proved a vast resource to research studying the genetic component of cancer risk. Studies using the genealogical data to investigate familial links in the incidence of breast and prostate cancer (Hunt et. al 1980 and Cannon et. al 1982, respectively) were among the first academic articles to apply the Utah Population Database towards research questions outside of its specific historical context. Articles related to cancer research continue to comprise most of the published research using the UPDB. Articles related to social science questions have a relatively younger history using the UPDB, beginning with studies of longevity and ageing. The first of these looked at the transmission of longevity through families, finding that excess longevity aggregates in families and arguing the role of genetics in driving these effects (Kerber et. al 2001). Since then, researchers have used the UPDB to look at questions related to partner loss (Mineau G, Smith K and Bean L, 2002), offspring impacts on paternal mortality (Harrell CJ, Smith KR, and Mineau GP, 2008), Grandmother effects (Hawkes and Smith 2009), and parental loss (Smith KR, Hanson HA, Norton MC, Hollingshaus, Mineau GP, 2014; Hollingshaus M, Smith KR. 2016; and Hollingshaus, M. S., Coon, H., Crowell, S. E., Gray, D. D., Hanson, H. A., Pimentel, R., & Smith, K. R. 2016).

Rural Finland, Eighteenth to Twentieth Centuries

Like the Krummhörn database, this dataset derived from protestant parish registers and was initially compiled to study human reproductive behaviour from a biological perspective. The project is overseen by the Human Life-History Group, an academic research group based at the University of Turku, Finland.⁹

Currently, the data consists of eight separate Finnish populations which differ regarding co-residence and marriage systems. Demographic data are augmented by individual information on socio-economic status and occupation, as well as by structural information on climate, conflicts, epidemics, famines, and annual crop yields. The database has been used in several studies on kin effects, including the impact of having elder siblings (Nitsch, Faurie, and Lummaa 2013; Rickard, Lummaa, and Russell 2008) and grandparents (Chapman et al. 2021), costs of male offspring production (Helle and Lummaa 2013), and the trade-off between reproduction and survival (Nenko et al. 2018).

The Importance of Historical Family Reconstitution Studies in the Study of Kinship

The primary purpose of family reconstitution methods has been to estimate mortality, fertility, and marriage patterns in historical populations. Such classical historical approaches have provided information on historical living situations and standards, debunking common misconceptions. For example, the popular idea that members of historical European

⁹ <http://human-life-history.science/datasets>. Last accessed March 18th, 2021).

populations married young and produced many children has been relatively widespread. However, individuals in pre-industrialized Europe usually married in their late twenties with an average family size generally less than five (Western European marriage pattern (Hajnal 1965)).

Family reconstitution datasets have also proved immensely valuable to other social and natural scientists to researching questions related to kinship. Observing multiple generations of the same families through time allows for the study of intergenerational transmission and intergenerational accumulation or de-accumulation of effects such as the heritability of fertility and longevity (Pettay et al. 2005). Furthermore, in contrast to traditional individual-level survey datasets which tend to indicate only the number of siblings at the time of the survey, family reconstitution datasets provide information on outcomes for all or most members of the family surveyed. This information is vital if the status of the siblings or their own outcomes have a bearing on the dynamics of kinship effects. Dillon (2010), for example, finds the likelihood of marriage increased if the subject had married older siblings, and decreased with the presence of unmarried older and marriage younger siblings. For this population, the marital status of siblings seems to have been an important moderating effect in sibling interactions.

Historical family reconstitution studies can also complement information compiled at the individual, local, or regional level, and used to create a hierarchical dataset through time. Reconstitution studies have been combined with tax rolls and food prices (economic variables; e.g., Bengtsson 1993), climate and weather data (environmental variables; e.g., Willführ and Störmer 2015), medical records and reports on epidemics (epidemiological variables; e.g., Gagnon and Mazan 2009; Quaranta 2014; Tommy Bengtsson and Lindström 2003), periods of war and social change (political variables; e.g., Kemkes 2006), and geographic information (Pantazatou et al. 2016). For some family reconstitutions it is possible to estimate the individual social-economic-status (SES) through information on occupation (see HISCO Historical Classification of Occupations (van Leeuwen, Maas, and Miles 2002)) or landownership (Bengtsson and Dribe 2011). Furthermore, the fertility and mortality response to economic fluctuations of the different SES groups can be studied if information on food and crop prices is available (Bengtsson and Dribe 2006; Willführ and Störmer 2015; Amialchuk and Dimitrova 2012). For reconstitution studies in which place(s) of residence is available, it is possible to compare kinship effects and outcomes across space. This can be of significant value, as mortality, especially child mortality, differed substantially between urban and rural areas. Increased pathogen risk due to higher population density, unhygienic conditions, and pollution associated with the beginning of industrialization all contributed to an urban mortality penalty. Additionally, trading by surface and sea regularly introduced infectious disease from other parts of the world. We note that in the contemporary developing world, the situation is the opposite. Urban residence is associated with access to better medical care and higher SES.

Observed and Unobserved Heterogeneity in Moderating Kinship Effects

The presence of kin is often correlated with other factors that impact outcomes of researcher interest, the effects of which may be difficult to disentangle. These factors may be either observed or unobserved, and can play a moderating role, thereby improving estimates and understanding of kinship effects, as well as create challenges to their identification. Historical family reconstitutions, with their focus on complete families observed over long periods of time, present unique opportunities in the identification of kinship effects, as well as those factors which may moderate their expression.

Historical family reconstitutions often combine individual vital data, such as date of birth, death, and marriage, with anthropometric, medical, socio-economic, or other statistics, and so provide information on individual, group, and environmental factors potentially correlated with kinship-related outcomes. Consideration of these observed statistics can show patterns of kinship effects across groups and how individual, group, and environmental factors can moderate kinship impacts. These observed effects provide information on how kinship effects may vary across occupation, geography, demographics, or other factors. The consequences of parental loss and parental remarriage (Willführ and Gagnon, 2012; Willführ and Gagnon, 2013), for example, varies in different geographic and historical groups. Using information on place of residence, it is possible to identify context-specific patterns of kin effects. This can be important when families migrate. Migration and kinship, especially as it related to siblings, are often interrelated processes as families delay childbearing until arrival in the destination (Andersson 2004, Wilson 2013). If migration is systematically associated with better or worse outcomes, then efforts to identify kinship effects would be confounded. This is an issue when families migrate from urban to rural areas or vice versa, who are immediately confronted with a different mortality regime and systematic differences related to disease risk. In addition, migration during pregnancy could result in a phenotype-environment mismatch, resulting in negative effects for infants born in the new environment (Willführ and Myrskylä 2013; Kuzawa 2005). Intra-rural and intra-urban migration can also result in notable environmental differentials. In the St. Lawrence Valley for example, although both the Northern and Southern shore areas are considered rural, there exist substantial differences in climate and farming conditions. These differences were meaningful enough to cause substantial differences in maternal and intrauterine condition (Gagnon 2012).

In addition to the effects of geographic variation, information on families over time can also help identify how kin effects may vary across different genetic groups. Biometric measurements (including genetic characteristics) and health conditions of individuals living in contemporary societies can be linked to information on their ancestors' living conditions and experiences to identify potential founder effects (Gagnon and Heyer 2001) or epigenetic effects (Bygren, Kaati, and Edvinsson 2001; Bygren et al. 2014).

Family reconstitutions, as well as other longitudinal datasets, can be used to control for unobserved effects correlated with outcomes and patterns of kinship. Unobserved effects may be jointly associated with the presence or absence of kin and individual outcomes and complicate efforts to identify kin effects. Since longitudinal datasets observe individuals over multiple time periods, they can be used to control for individual-level unobserved

effects through a fixed-effects modelling framework. Fixed-effects models, as referred to here, are models that allow for different intercepts (or the analogous concept for non-linear models) across individuals. Such techniques control for all individual-level factors constant through time, so rely on variable changes to identify factors of interest. The effect of sibling composition, for example, is then identified off changes in sibling composition through births or deaths. Given that many moderating factors related to kinship effects and of researcher interest are time-invariant (i.e. gender, race, maternal or paternal age at birth), individual-level fixed effects models are often impractical. This has resulted in a wide variety of kinship studies applying random effects models, sometimes referred to as hierarchical models or mixed models. Random effects methods parameterize the individual-specific effects as originating from the same overall distribution, and so can allow for the inclusion of time-invariant variables such as parental age at birth. If these individual specific effects are not correlated with any observed variables related to kinship composition, then random effects methods offer a method of estimating time-invariant kinship effects.¹⁰ However, this is a critical assumption in non-experimental settings, and if not met, random effects methods produce biased estimates of kinship effects. We should mention that hybrid models utilizing fixed effects for those variables correlated with the unobserved effects and random effects for those which are not, are an alternative framework in which it is both possible to include time-invariant factors and obtain unbiased estimates of kinship effects (Laird and Ware 1982, Goldstein 1986, StataCorp 2013). These models require careful, and sometimes arbitrary, judgement regarding which variables are not correlated with the unobserved effects.

Family reconstitution datasets offer an additional advantage over the typical longitudinal datasets that track individuals. Many unobserved individual effects related to kinship occur at the family level, and so controlling for unobserved family effects facilitates identification of kinship composition on outcomes. Exposure to the disease environment, genetic effects, ecological fitness, parenting techniques, and socioeconomic status are all unobserved effects correlated with kinship and kinship-related outcomes, and plausibly common within families.

The same fixed and random effects methods applicable to individuals can be applied to families. Family-level random effects methods, often referred to as shared frailty methods, allow for correlation across individuals in the same family and so produce more efficient estimates of kin impacts. As such, tests of significance for estimates of kinship impacts have greater statistical power. Rickard et al. (Rickard, Lummaa, and Russell 2008), for example, include a random term for a common mother in their linear mixed effects models to show that older brothers tend to reduce the probability of reproduction for their younger siblings in preindustrial Finnish farming and fishing communities. Suanet and Bras (Suanet and Bras 2014) apply this method using Cox proportional hazard models to determine that sibling position became less important for marriage timing within Dutch provinces between 1840 and 1922.

¹⁰ Researchers deciding between the application of fixed or random effects methods should produce some statistical test of the consistency of the random effects estimates. The best known of these is the Hausman Test (Hausman 1978)

Non-linear shared frailty models, such as the Cox proportional hazard framework with family-level random effects, can often be computationally intensive for large populations. As such, researchers must balance the gains from statistical power with the computational intensity of these shared frailty methods.

As described in the discussion of individual unobserved effects, random effects methods such as shared frailty models parameterize the unobserved effects and, as such, require they are not correlated with the observed variables related to kinship. If this assumption is not credible, fixed effects methods are necessary to identify the effect of the kinship presence. Families should then be allowed their own intercept terms and kin effects are identified through comparison of kin within the same family (typically the same household or common parent). Families thus require at least two members, but the role of individual time-invariant factors such as gender and parental age-at-birth can be estimated.

Unobserved effects can obscure our ability to observe kin effects, but by controlling for the effect of the family and the unobserved effects associated with it, one is able to tease out a more precise role of kinship effects. This can help researchers both better identify the presence of kinship effects, as well as separate behavioural effects from those accompanying non-behavioural factors. As an example of the former, selection effects have tended to complicate the ability to identify the relationship between longevity and fertility. Theoretically, maternal depletion increases with the number of childbirths, however empirical estimates from proportional models suggest that many childbirths are associated with increased post-menopausal survival and longevity (Gagnon et al. 2009). The reason for this positive association, often described as phenotypic correlation, is that the less vulnerable and more robust females live long and produce many babies, even though they might live longer had they reproduced less. For instance, child mortality and morbidity tend to be elevated among families with many children in historical populations (Edvinsson and Janssens 2012).

Sibling rivalry and competition constitute social interactions which may contribute to elevated mortality in these larger families, while sibling cooperation may tend to reduce child mortality. Determining the relative strength of these two behavioural elements can be challenging, as family size is correlated with other risk factors. For example, the risk of cross infections increases with the number of siblings, especially older siblings. Illnesses lead to increased mortality during childhood, as well as elevated frailty through adulthood. As such, being part of a larger family may be associated with reduced fitness in adulthood due to increased risk of sickness rather than any active role of the different siblings (Barclay and Myrskylä 2014). Siblings must be present in the household to pose an infectious risk, but social interactions in the manner of competition and cooperation is not needed. Cox proportional models stratified at the family level control for family-level fixed effects through a likelihood function that includes separate terms for each of the different families in the dataset. As such, each family is allowed their own individual baseline hazard function and family-specific frailty is controlled for.

Evolutionary Versus the “Classical” Approach in Understanding Kinship Effects

Historical family reconstitutions are a powerful tool to apply in the study of kinship effects. By providing information on complete families over time, they can help clarify the role different observed factors have in moderating the impact of kinship, and they can help researchers control for a great deal of unobserved factors that may otherwise complicate identification efforts. However, researchers must remain cognizant of the context in which these kinship effects are estimated and how peculiarities in the population or environment may lead to differences in kin impacts. Different empirical strategies such as those outlined above and applied to the family reconstitution datasets can mitigate these peculiarities but are unlikely to eliminate them.

Historical family reconstitutions represent different slices of societies in different time periods, and kinship interactions can be sensitive to these different contexts. It is thus essential to weigh different models regarding kinship interactions and judge their relative importance within the different contexts. We find, however, too little of this process in empirical studies of kinship, and a reluctance to consider scientific approaches guided by Darwinian theory in favour of approaches more in line with the “classical” perspective on human behaviour. This despite that both approaches have relied on similar, and frequently the same, datasets and methods for their purposes. This issue is improving, but nevertheless remains. For example, recent papers that draw on from both approaches include Mattison, Moya et al. (2018) on age at last birth, Mattison, Seabright, et al. (2018) on mortality of adopted and biological daughters, and Macfarlan et al. (2020) on marriage dynamics.

One factor that may contribute to insufficient knowledge exchange is the different understanding of how individual life courses are shaped by the environment. Traditional approaches to family reconstitution studies investigate the socio-economic, political, and cultural contexts that shape demographic outcomes, and draw explanatory approaches from disciplines including economics, epidemiology, sociology, and political science. Although historical demography includes many concepts of different origins, a framework that connects these explanatory approaches in a theoretical manner is absent. Rather, the concepts that exist in the traditional approach tend to be solitary. While there may be multiple models which explain the same phenomena, since they often rely on different assumptions, it becomes difficult to evaluate which has the greater explanatory power. From a theoretical perspective it is impossible to tell whether one concept is superior or whether multiple concepts are simultaneously correct. For this reason, many alternative concepts in historical demography coexist.

Evolutionary theory, on the other hand, considers all concepts within the Evolutionary approach to share the same paradigm: humans stockpile behavioural strategies and environmental response mechanisms which have been shaped by their phylogenetic history. As such, scientific approaches within the evolutionary theory framework are more interested in the variability than in the generality of traits. The opposite is true for the “classical” perspective which views variability more as an issue of disturbance and does not require such an active creator role of the individual or its traits.

This is not to say that the “classical” perspective neglects the role of individual traits or that concepts of response mechanisms are absent. In fact, the impact of individual traits and

characteristics like gender, age, and social position on the life course have been traditionally important study topics, and there exist theories about the mechanisms for how individuals respond to their environment. The key difference to evolutionary theory approaches is that the “classical” perspective is agnostic towards the origin of these mechanisms apart from their social development. In contrast, all disciplines which are guided by Darwinian Theory are connected in the same framework. A unifying theoretical framework results in a wellspring of hypotheses because a hypothesis successfully tested in one discipline can be transferred to another (Mattison and Sear 2016).

We illustrate this with the concept of cooperative breeding. Cooperative breeding originally derived from animal studies but has been introduced successfully into family demography (Kramer 2010). The trade-off between current and future reproduction is an essential concept for life history theory (Fisher 1930) and further explains cooperative breeding behaviour. Like any other resource, breeding places and breeding opportunities are almost always limited in the wild and therefore highly competitive. Young adult individuals might have trouble to find promising breeding places, because these are often occupied by older (and stronger) individuals. Consequently, young adults across many species relinquish their own reproduction for a breeding season (or more)¹¹ and instead support their parents as helpers-at-nest in raising new offspring (Lukas and Clutton-Brock 2012). The postponement or sacrifice of reproduction by the helpers may benefit them through increased reproductive success in the future or increased inclusive fitness. Cooperation thus is a strategy to achieve success beyond the limits of solitary enterprise.

Conclusion

Human life histories and demographic outcomes are impacted by kin in many ways, and human evolutionary theory is essential to understanding why these impacts may be sensitive to the kin relationship or the context in which the kin interact. However, because kin impacts may also be correlated with non-behavioural accompanying factors, it can be hard to disentangle evolutionarily driven effects from other factors correlated within a family. Historical family reconstitutions, with their coverage of family member life histories and often over several generations, provide a possible solution. Through controlling for the effect of the family, it may be possible to control for confounding unobserved factors and successfully identify the impact of kin.

We emphasize, however, that controlling for family effects does not eliminate researcher responsibility to consider the context of their results and the theoretical framework into which they fit. Other unobserved factors affecting kinship interaction and outcomes may remain. For example, kinship influences may still be environmentally dependent and require a comparative approach. Environmental factors such as the level of extrinsic mortality may not only directly affect the size and structure of kin compositions but might

11 It should be mentioned here that biology distinguishes between facultative and obligate cooperative breeders. Eusocial insects and mammals (e.g. naked mole-rats, *Heterocephalus glaber*) are obligate cooperative breeders, because they produce sterile helpers. These helpers are hereditarily predisposed to be helpers and are therefore not exposed to the trade-off between current and future reproduction as facultative cooperative breeders are.

also moderate the relationship between individual kin and, further, the population-specific family concept.

Placing kinship effects within a Darwinian framework illustrates how kinship interactions may be context dependent. In general, human family compositions are more complex when compared to other mammals and exhibit substantial variation between populations. There exist biological causes (among others) for this complexity and variety. For one, human life history is characterized by a long period in which children are not completely dependent on the care of others. Within this pre-reproductive period children can contribute to the family's resource pool. For another, female menopause results in a substantial period of post-reproductive life. Within these pre- and post-reproductive periods, individuals are predisposed to be helpers, but can exist as both breeder and helper. In case of pre-reproductive individuals, the helper role can quickly and unexpectedly turn into a breeder role which might affect the flow of support among a helper-breeder-network. This rationalizes the parental tendency across cultures to intervene in their children's start of reproduction (e.g., request for a parental permission to marry) and why there is a substantial conflict potential between siblings, especially of the same gender, who compete for parental permission to breed first (Beise and Volland 2008). The integration of both biological and social science explanations is thus essential to fully appreciate the complexity and variety of kin effects across different populations.

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12 Note this chapter has been posted on the Open Science Framework website since 15/10/2019, after it was accepted for publication, so the references will reflect when the chapter was written and not the OBP publication date.

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