

Family Trajectories across Time and Space:
Increasing Complexity in Family Life Courses in Europe?

Abstract:

Family life courses are thought to have become more complex in Europe. This study uses SHARELIFE data from 14 different European countries to analyze the family life courses of individuals born 1924-1956 from age 15-50. A new methodological approach, combining complexity metrics developed in sequence analysis with cross-classified multilevel modeling, is utilized to simultaneously quantify the proportions of variance that are attributable to birth cohort and country differences. This allows the direct comparison of changing levels of family trajectory differentiation across birth cohorts to cross-national variation, which provides a benchmark against which temporal change may be evaluated. The results demonstrate that family trajectories have indeed become more differentiated, but also show that change over time is minor compared to substantial cross-national variation. Further, cross-national differences in family trajectory differentiation correspond with differences in dominant family life course patterns. With regard to debates surrounding the second demographic transition thesis and the comparative life course literature, the results indicate that the degree of change over time tends to be overstated relative to large cross-national differences.

Keywords: *Family, Sequence Analysis, Multilevel Modeling, Comparative, Life Course*

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1. Introduction

Many scholars claim that patterns of family formation and living arrangements have undergone great changes in European societies during the 20th century (see Buchmann and Kriesi 2011 for a review). Young adults leave the parental home, marry and enter parenthood at later ages (Gauthier 2007; Settersten Jr. 2007) and the odds of returning to the parental home as well as never entering marriage or parenthood have increased (Goldscheider 1997; Rowland 2007). Additionally, cohabitation (e.g. Heuveline and Timberlake 2004), divorce (e.g. Schoen and Canudas-Romo 2006), remarriage (e.g. Coleman, Ganong, and Fine 2000) and single parenthood (e.g. Heuveline, Timberlake, and Furstenberg 2003) have become more common. Billari and Liefbroer (2010) speak of a shift from an early, contracted, and simple to a late, protracted, and complex transition to adulthood. Thomson (2014) emphasizes that more complex families are produced through lone childbirth, union dissolution, re-partnering and stepfamily childbearing well after the transition to adulthood is complete.

A shift towards more complex family life courses is consistent with the concept of the second demographic transition (SDT). The SDT (Lesthaeghe and Van de Kaa 1986; Van De Kaa 1987) is used by family demographers to account for changes in family behavior through a universal value shift towards post-materialism within and across societies. However, recent research has displayed stable or growing cross-national differences rather than convergence as suggested by the SDT thesis (Corijn and Klijzing 2001; Billari and Wilson 2001; Blossfeld et al. 2005; Sobotka and Toulemon 2008; Elzinga and Liefbroer 2007; Fokkema and Liefbroer 2008). Life course sociologists emphasize institutional variations to account for these cross-national differences, arguing that welfare states shape individual family life courses both directly (Mayer and Müller 1986; Mayer and Schoepflin 1989) and indirectly (Mayer 2004). While these two perspectives may not be mutually exclusive accounts of family life course variation, they do emphasize very different dimensions of variation: change across time versus differences across countries.

The aim of this paper is not only to investigate 1) how family life courses vary across historical time, i.e. birth cohorts and 2) how family life courses vary across countries, but especially 3) whether family life courses vary more across birth cohorts or across countries.

Despite the wide discussion around cross-temporal and cross-national variation in family formation, the comparative literature has either compared family trajectories across birth cohorts within a single country (Robette 2010; Chaloupková 2010; Baizan, Michielin, and Billari 2002; Bras, Liefbroer, and Elzinga 2010) or between a small set of countries (Potârca,

Mills, and Lesnard 2013; see Elzinga and Liefbroer 2007 for a notable exception). However, no research has attempted to directly compare change in family formation over historical time with cross-national differences (for notable exceptions in other fields see Günther and Harttgen 2016 on realized fertility intentions; Fowler, Lee, and Matthews 2016 on ethnoracial diversity; Van Winkle and Fasang 2017 on employment trajectories). Research that puts change over time in direct perspective with differences between countries is important, because it can provide a benchmark against which change over time can be evaluated. Further, research that directly compares temporal and cross-national variation simultaneously informs two of the most prominent research traditions in comparative family demography and sociology: the ideational account of the SDT and the institutional arguments of comparative life course sociology.

I contribute to the existing comparative literature by introducing a new methodological approach that enables researchers to directly compare change across birth cohorts with cross-national differences in longitudinal life courses. Specifically, I simultaneously quantify family life course variation across birth cohorts and variation across countries by incorporating a sequence based metric in cross-classified multilevel regressions. This methodological approach enables me to put changing levels of family trajectory complexity across birth cohorts in perspective with cross-national variation. Further, I demonstrate how other researchers can expand upon this methodological approach by estimating conditional cross-classified models. This allows me to investigate relationships between individual characteristics and family formation complexity as well as the extent that individual characteristics account for variation across birth cohorts and countries.

I use sequence analysis to conceptualize family formation holistically, as a long life “process outcome” (Abbott 2005). Abbott conceptualizes process outcomes as global results of multiple individual events, such as careers, opposed to “point-in-time” outcomes, which are the results of a process, such as lifetime income. While many have used sequence analysis to study family processes (e.g. Elzinga and Liefbroer 2007; Raab et al. 2014; Fasang and Raab 2014), the majority of the literature concentrates on events in the early life course as a part of the transition to adulthood. However, changes in family life courses need to be studied as a lifelong process, because changes associated with the SDT impact the timing of multiple life course events, their sequencing as well as the occurrence of “new” events in later life, such as divorce and remarriage. Using retrospective data from the Survey of Health, Ageing and Retirement in Europe (Borsch-Supan et al. 2013; Schröder 2011) I am able to observe family formation until age 50 for men and women born from 1924 to 1956 in 14 European countries.

In the remainder of this article, I first discuss the conceptual and theoretical background for studying changing family life courses across time and across Europe. Then, I introduce the data, methods and my analytical strategy. After I present the results of the cross-classified regressions, I use cluster analysis to substantiate the regression results with a typology of family formation patterns that vary in prevalence across time and across countries. I conclude with a discussion of the results in light of the ideational research tradition of the SDT and the institutional research tradition of comparative life course sociology.

2. Theoretical Background

Conceptualizing Complexity in Family Trajectories

How should increasing complexity in family life courses be conceptualized? Concepts surrounding increasing family life course complexity are used ambiguously in the literature (see Brückner and Mayer 2005). While differentiation (Mayer 1991) generally refers to variation within individual life courses, institutionalization (Kohli 1997; Mayer and Müller 1986) and standardization (Modell and Furstenberg 1976) refer to variation between life courses. Other concepts such as individualization (Beck and Beck-Gernsheim 1994) and pluralization (Brüderl 2004) have been used less systematically. It is essential to develop clearly defined concepts prior to their operationalization to ensure valid measurement of family trajectory complexity.

I conceptualize increasing complexity in family formation as differentiation. Brückner & Mayer (2005) developed a comprehensive categorization of life course variation that either occurs within individual life courses over the life time or between individual life courses within a population. They define differentiation as a process where life courses are characterized by an increasing number of distinct life course states. Differentiation further implies increasing unpredictability and uncertainty in individual life courses. An example of family formation differentiation is when unmarried cohabitation precedes marriage or a first union is followed by divorce and further unions. Contrary to differentiation, de-differentiation refers to a process where the number of distinct life course stages decreases. Family life courses become de-differentiated if high parity families are replaced by single child families.

Family Trajectories across Time

The SDT thesis is the most prominent account of family life course differentiation. Van de Kaa (1987, 11) postulates the establishment of a new demographic regime following four shifts: from marriage to cohabitation, from child-centric to pair-centric relationships, from precautionary contraception to conception for self-fulfillment, and from uniform to pluralistic families. The change in demographic behavior associated with the SDT, such as cohabitation and childlessness, is accounted for by a shift from materialism to post-materialism (Van de Kaa, 2001). The higher educated and socio-economically advantaged act as forerunners of this value shift towards self-actualization and non-conformism as well as the forerunners of more complex family demographic behavior associated with it (Lesthaeghe 1995; Lesthaeghe and Surkyn 1988; Sobotka 2008).

Cohorts born in the mid to late 1920s just entered courtship age as the Second World War began. Those cohorts that experienced the Second World War or its aftermath in Europe held primarily materialist values associated with securing economic and social standing. The family formation patterns of these early-industrialist and industrialist cohorts are considered to have been relatively simple, consisting mostly of leaving the parental home early and entering directly into marriage followed by parenthood (Mayer 2004). Cohorts born in the early and mid-1950s entered courtship age during the 1970s. Stable economic growth and the expansion of welfare state and educational systems facilitated a value shift towards post-materialism among the early members of this post-industrialist and contraceptive revolution cohort. According to the SDT thesis, this shift towards self-actualization lead to postponed marriage and parenthood as well as an increase in cohabitation, childlessness, and divorce. Therefore, I expect that *family trajectories have become more differentiated across birth cohorts (H1)*.

Family Trajectories across Countries

Proponents of the SDT have utilized institutional arguments to account for cross-national variation in family demographic behavior. For example, Lesthaeghe (2010, 244–45) argues that the foundations of traditional family formation patterns will weaken first in egalitarian liberal market democracies that respect individual choice despite normative ideals. Comparative life course sociologists focus on institutions and their impact on family formation (see Mayer 2009). At the core lies the proposition that welfare regimes, labor market institutions and educational systems shape societal life course patterns. Institutions may influence life courses directly by means of age-gradation (Mayer and Schoepflin 1989)

or indirectly by incentivizing the adherence to dominant life course patterns or enabling individuals to tread new paths (Buchmann 1989; Breen and Buchmann 2002).

Esping-Andersen's (1990) worlds of welfare capitalism typology has been widely used as a heuristic to classify and compare European countries (see Arts and Gelissen 2002; Emmenegger et al. 2015). The extended typology developed by Esping-Andersen (1999) clusters countries based on levels of decommodification, i.e. protection from labor market risks, and defamilization, i.e. public assumption of family care tasks. While the *social democratic regime* is characterized by universal and generous social protection as well as public child and elderly care, the *liberal regime* provides only limited welfare benefits and child care is privately arranged. Unfortunately, common representatives of the liberal welfare state regime type, e.g. the UK and Ireland, did not participate in the survey used in this study, SHARELIFE, or the data was not available at the time the analyses were performed. Social protection is targeted towards specific groups and is less generous in the *conservative regime* and in the *Mediterranean regime*, but families are especially responsible to compensate residual welfare coverage in the latter. Eastern European countries were considered to constitute an authoritarian welfare state during state socialism. Following their transition to liberal market democracy, scholars have debated whether these countries still comprise a single welfare regime or have shifted to existing models (Aidukaite 2009).

Scandinavian social democratic welfare states were forerunners in the implementation of defamilizing and individualizing family policies, which reduced gender and intergenerational dependencies and allowed greater freedom in family formation (Lohmann and Zigel 2016). In Sweden, paid and job protected maternity leave¹ was introduced in 1955 and supplemented by paternal leave² in 1974 (Ifo-Institute 2015). In Denmark, publicly funded childcare for children within one year after birth was introduced as early as 1964 (Garrouste 2010). Further, generous old-age benefits following retirement and unconditional old-age pensions were introduced in Sweden in 1953 and 1913, respectively.³ These policies allowed cohorts born in the early 1930s to maintain a high labor market attachment after entry into parenthood and when elderly family members were in need of care. High female labor force participation rates coupled with high levels of decommodification safeguards individuals, especially

¹ Maternity leave is defined as a minimum of 14 weeks paid and job protected leave of absence according to the ILO convention on maternity leave.

² Paternal leave is defined as a minimum of 1 week paid and job protected leave of absence following childbirth or maternity leave.

³ See ILO Ratifications of Social Security Convention, 1952 (No. 102): http://www.ilo.org/dyn/normlex/en/f?p=NORMLEXPUB:11300:0::NO::P11300_INSTRUMENT_ID:312247 and the Country Fact Files of HelpAge International: <http://www.pension-watch.net/country-fact-file/>

women, from economic downturns (DiPrete et al. 1997) as well as life course risks, such as divorce and lone childbirth (DiPrete 2002). Therefore, the social democratic welfare regime reduces the costs and risks of family demographic behavior associated with more complex family life courses, such as cohabitation, non-marital childbirth and divorce.

Contrary to welfare systems in Scandinavian countries, the social protection systems and family policies in conservative Continental European countries incentivize a male-breadwinner female-homemaker division of labor. Many western and central European countries implemented family and child allowances before maternity leave and well before any paternal leave policies (Gauthier and Monna 2004; Ifo-Institute 2015). For example, Austria introduced family allowances in 1967, paid and job protected maternity leave in 1974, and paternal leave in 1990. Further, publicly funded childcare in most Continental countries is available only for children starting at age 3 (Garrouste 2010). The concentration of family policy on family allowances and maternity leave rather than childcare and paternal leave incentives traditional family formation by making women primary care providers and limiting female labor market participation (Morel 2007; Gottschall and Bird 2003). Gendered decommodification and highly familistic policies make family behavior associated with complex family formation, such as divorce and lone parenthood, highly costly, especially for women.

In Southern Europe, authoritarian regimes, e.g. Mussolini in Italy and Franco in Spain, coupled with the moral teachings of the Greek Orthodox and Roman Catholic churches, contributed to the production of a welfare model with the family at its center (Flaquer 2000). For example, maternity leave was introduced in 1976 in Spain and 1984 in Greece (Ifo-Institute 2015). Without widespread early childcare and paternal leave policies, child care has to be arranged by the family, usually women. A late introduction of unconditional old-age benefits additionally burdened families when elderly family members need care. These welfare states are additionally characterized by highly gendered labor market segmentation and very low female labor market participation rates as well as a context where families must compensate for low levels of benefits following unemployment or income loss (Ferrera 1996). Consequently, processes that produce family complexity are very risky in the context of Mediterranean welfare states and reliance on families to secure individual welfare often leads to a dramatic delay in leaving the parental home.

Generally, levels of decommodification and defamilialization were high in Eastern European countries, comparable to social democratic countries, during the era of state socialism. For

example, East Germany introduced maternity leave in 1950, early childcare in 1965 and paternal leave in 1972 (Maul et al. 2009; Garrouste 2010). However, many societies encouraged early marriage and implemented pro-natalist policies (Fodor et al. 2002; Kreyenfeld 2004), thus incentivizing traditional family formation processes. While the family trajectories of very young cohorts may be differentiated to a greater extent following the turbulent transition to liberal market democracy, this is not likely the case for cohorts born before the 1970s.

In sum, defamilizing and decommodifying institutions characteristic of social democratic welfare states reduce the risks of complex family formation patterns involving cohabitation, lone parenthood, and divorce. Gendered decommodification in conservative welfare states enables men to pursue more complex family patterns similar to social democratic welfare states, but incentivizes less complex patterns of early marriage and parenthood for women. Familism in Southern Europe and natalism during state socialism in Eastern Europe promotes less complex family patterns consisting of early marriage and parenthood. Therefore, I expect that *family trajectories are most differentiated in social democratic countries, i.e. Sweden and Denmark, followed by conservative countries, i.e. Austria, West Germany, the Netherlands, France, Switzerland and Belgium, and least differentiated in Southern European countries, i.e. Spain, Italy and Greece, as well as in Eastern European countries, i.e. the Czech Republic, Poland and East Germany (H2).*

Comparing Family Trajectories across Time and Space

Across all countries, family formation differentiation resulting from a shift towards post-materialism can be conceived as the result of cohort replacement (Ryder 1965). Inglehart (1990) predicts levels of post-materialism to increase as young cohorts raised in socio-economically secure contexts gradually replace older cohorts. Similarly, levels of differentiation within countries will gradually rise as younger cohorts with more complex family trajectories replace older cohorts with relatively simple trajectories. In a world devoid of institutional arrangements that influence family formation differently across countries, levels of family formation differentiation could be expected to increase at similar rates across countries.

However, changes in institutional arrangements that influence family formation have lagged the shift towards post-materialism in most European countries. Studies have demonstrated that for cohorts born as early as 1946, post-materialists became increasingly common across

Continental European countries (Inglehart 2008; Abramson and Inglehart 1986). In certain countries such as West Germany and the Netherlands, post-materialism had become predominant among the entire population by the late 1970s and early 1980s. Nevertheless, paternal leave was not implemented until 1986 in West Germany and 2009 in the Netherlands, and neither country has yet to introduce universal early childcare. While social democratic institutions in Scandinavian countries enabled post-materialists to follow alternative family pathways, institutions in Continental Europe inhibited complex family formation even as post-materialism became ever more common. Therefore, I expect that *family trajectory variation across birth cohorts is country specific (H3)*, rather than a contemporaneous process across countries.

Social change through cohort replacement is generally a slow process, but will be especially slow when institutions impede behavior that would correspond with ideational change. Pronounced increases in family formation differentiation not only require post-materialist socialization at a relatively early age, but also institutional arrangements that correspond to new family formation patterns involving cohabitation, lone parenthood and divorce. In light of the large cross-national differences in family trajectories (Corijn and Klijzing 2001; Billari and Wilson 2001; Blossfeld et al. 2005; Sobotka and Toulemon 2008; Elzinga and Liefbroer 2007; Billari 2004), it is unlikely that variation across birth cohorts will be larger than variation across countries before defamilizing institutions are integrated across European welfare states. I therefore expect that *family trajectory differentiation varies more across countries than across birth cohorts (H4)*.

3 Data & Methods

Study Sample and Sequence Definition

I use the third wave of SHARE⁴, SHARELIFE, which consists of retrospectively collected life history data on multiple life domains, such as partnership, family demographics, living

⁴ This paper uses data from SHARE Waves 1, 2, and 3 (SHARELIFE). (DOIs: [10.6103/SHARE.w1.500](https://doi.org/10.6103/SHARE.w1.500), [10.6103/SHARE.w2.500](https://doi.org/10.6103/SHARE.w2.500), [10.6103/SHARE.w3.500](https://doi.org/10.6103/SHARE.w3.500)), see Börsch-Supan et al. (2013) for methodological details. The SHARE data collection has been primarily funded by the European Commission through FP5 (QLK6-CT-2001-00360), FP6 (SHARE-I3: RII-CT-2006-062193, COMPARE: CIT5-CT-2005-028857, SHARELIFE: CIT4-CT-2006-028812) and FP7 (SHARE-PREP: N°211909, SHARE-LEAP: N°227822, SHARE M4: N°261982). Additional funding from the German Ministry of Education and Research, the Max Planck Society for the Advancement of Science, the U.S. National Institute on Aging (U01_AG09740-13S2, P01_AG005842, P01_AG08291, P30_AG12815, R21_AG025169, Y1-AG-4553-01, IAG_BSR06-11, OGHA_04-064, HHSN271201300071C) and from various national funding sources is gratefully acknowledged (see www.share-project.org). This paper uses data from the generated Job Episodes Panel (DOI: [10.6103/SHARE.jep.500](https://doi.org/10.6103/SHARE.jep.500)), see Brugiavini et al. (2013) and Antonova et al. (2014) for methodological details. The Job

arrangements and employment, for a number of birth cohorts and countries (Borsch-Supan et al. 2013; Schröder 2011). The SHARELIFE population consists of individuals born before 1957 and their partners, and contains data on 26,768 individuals born between 1908 and 1984. Family life course trajectories are operationalized as sequences using the SHARELIFE accommodation, retrospective children and partner modules. My sample consists of individuals born between 1924 and 1956 in 14 European countries. I exclude individuals born before 1924 due to insufficient sample sizes. All individuals born after 1956 are partners of SHARELIFE respondents that must be excluded from the analysis. Their inclusion leads to grossly underestimated complexity values for cohorts born after 1956, because individuals that never married, or divorced and never re-partnered, would not be included in the sample.

Four variables were generated containing annual information on four dimensions of family life: 1) whether respondents were living in the parental home, 2) were cohabiting, 3) were married, and 4) the timing of childbirths and adoptions. Family sequences are constructed from age 15 to 50, and thereby not only capture early family formation, i.e. first marriage and childbirth, but later family formation events, such as divorce and remarriage. An age range of 35 years is also much longer than in recent research with family trajectories (e.g. Elzinga and Liefbroer 2007; Raab et al. 2014; Fasang and Raab 2014).

Sequences are composed of 35 consecutive, annual states. The results displayed in this study use a simplified state definition.⁵ Each sequence state is either: 1) in the parental home, 2) single, 3) cohabiting or 4) married. Further, each state element can be extended by the presence of at least one child, e.g. married with at least one child (see Table A1 in manuscript appendix for a comprehensive overview). Note that single indicates that the respondent was neither in the parental home nor cohabitating, and does not specify the relationship status of the respondent. Full information is available for 22,272 individuals (see Table A2 in manuscript appendix for case sizes by birth cohort and country). I present results using birth cohorts in 3-year groups from 1924-1926 to 1954-1956.

Measuring Differentiation as Sequence Complexity

This study aims to describe family life course differentiation across birth cohorts and countries. I utilize a composite measure developed in sequence analysis that corresponds with

Episodes Panel release 5.0.0 is based on SHARE Waves 1, 2 and 3 (SHARELIFE) (DOIs: [10.6103/SHARE.w1.500](https://doi.org/10.6103/SHARE.w1.500), [10.6103/SHARE.w2.500](https://doi.org/10.6103/SHARE.w2.500), [10.6103/SHARE.w3.500](https://doi.org/10.6103/SHARE.w3.500)).

⁵ The analyses were performed with different sequence state definitions to ensure that the results are not dependent on the alphabet. The results are robust to more differentiated sequence state definitions.

the life course concept of differentiation: the sequence complexity index. This index measures variability within sequences as the geometric mean of normalized sequence transitions and normalized longitudinal sequence entropy (Gabadinho et al. 2010; 2011). Formally, the complexity, C , of a sequence, x , is defined as:

$$C(x) = 100 * \sqrt{\frac{q(x)}{q_{max}} * \frac{h(x)}{h_{max}}}, \quad (1)$$

where the number of transitions within a sequence, $q(x)$, is divided by the theoretical maximum number of transitions possible, q_{max} , and the longitudinal entropy of a sequence, $h(x)$, is divided by the theoretical maximum, h_{max} .

Formally, longitudinal sequence entropy is:

$$h(x) = -\sum_i^s \pi_i \log \pi_i, \quad (1.1)$$

where π is the proportion of occurrences in a given state, i , of the sequence alphabet, s . Entropy within sequences is maximal when each state occurs an equal number of times, which reflects that the unpredictability of a given state is maximal. Complexity is minimal in sequences composed of a single state and maximal in sequences that contain each state element with equal durations and have the maximum number of transitions. The complexity index provides a more nuanced indicator of life course differentiation compared to just the number of transitions or distinct states, because the degree of uncertainty within life courses is incorporated through sequence entropy.

Fig. 1: Artificial Example of Family Trajectories and Sequence Complexity

As an example, consider the three artificial family trajectories in Figure 1 (see manuscript appendix for the calculation of sequence complexity in Figure 1). The first sequence, composed of two parental home states (P), two single states (S), two married states (M) followed by four married with children states (MC), has a lower complexity value than sequences two and three. Sequences two and three have an additional transition into (or out of) cohabitation, which makes them more complex than sequence one. Sequence two and three differ in regard to the durations spent in distinct states, thus the degree of predictability displayed by the sequences. While the second sequence is characterized by frequent transitions, the third sequence shows high stability within the state married with children.

Therefore, the complexity of sequence three is lower than that of sequence two, because the longitudinal entropy, i.e. the degree of unpredictability, of the third sequence is lower.

Covariates

I introduce individual level characteristics in the cross-classified models discussed below that were theorized to be related with family formation complexity: educational attainment, socio-economic status, and gender. Educational attainment is operationalized using the ISCED 1997 scale recoded as 1) no formal education, 2) pre-primary, 3) primary, 4) secondary and 5) post-secondary education. I use two socio-economic status indicators that either precede or occur early in individuals' active family formation phase. First, I use the occupation of the main breadwinner at age 10 using the reduced ISCO88 scale as a proxy for childhood socio-economic status. Even though occupation is not equivalent to socio-economic condition or social class, it is an approximation. Second, whether the respondent's first employment was in the public or private sector serves as proxy for the stability of employment and amount of benefits available during the early phase of family formation.

Modeling Sequence Complexity

I use a cross-classified random effects approach to analyze how family trajectories vary across countries and across birth cohorts, and whether they vary more across countries or cohorts. This not only enables me to investigate levels of family trajectory complexity across countries and cohorts, but also to decompose the proportion of family trajectory complexity variance attributable to countries and to cohorts. These models represent a special case of multilevel modeling, in which the higher level units cannot be hierarchically ordered (Rabe-Hesketh & Skrondal, 2012 p. 433f.; Snijders, 2011, p. 155f.). Individuals are cross-classified by birth cohort membership and country of residence. Formally, sequence complexity is modelled as:

$$y_{ijk} = \beta_0 + \zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}, \quad (2)$$

where the sequence complexity, y_{ijk} , is composed of the constant β_0 , i.e. the grand mean, the group specific error terms, ζ_j , ζ_k , ζ_{jk} , and the individual error term, ε_{ijk} .⁶ The variance attributable to countries and birth cohorts is identified through country and birth cohort specific deviations from the grand mean, ζ_j and ζ_k respectively. The group specific deviations

⁶ The models are estimated using restricted maximum likelihood estimates (REML) and identity covariance matrices.

from the constant are also referred to as random intercepts or effects. Change caused by universal trends that affect cohorts identically across all countries will be captured in the cohort specific deviations, whereas country specific differences across all cohorts will be captured by the country specific deviations. To capture country specific change across birth cohorts, the additive cross-classified model is extended through an interacted random effect, ζ_{jk} .⁷ The relative proportion of complexity variance that is accountable to country or birth cohort specific differences are calculated as intraclass correlation coefficients (ICC), ρ :

$$Var(y_{ijk}) = Var(\zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}) = \psi_j + \psi_k + \psi_{jk} + \sigma, \quad (2.1)$$

$$\rho_{Country} = \frac{\psi_j}{\psi_j + \psi_k + \psi_{jk} + \sigma} \text{ and alternatively} \quad (2.2)$$

$$\rho_{Cohort} = \frac{\psi_k}{\psi_j + \psi_k + \psi_{jk} + \sigma}, \quad (2.3)$$

where σ is the constant variance of the level-1 residuals and ψ_j , ψ_k , and ψ_{jk} are the variances of the country-specific, cohort-specific, and interacted random intercepts, respectively, of the parameters in equation 2. Equation 2.2 calculates the correlation of observations from the same country but different cohorts by dividing the country-specific variance by the total variance. Likewise, equation 2.3 calculates the correlation of observations from the same cohort but different countries.

Cross-classified random effects regressions can also be estimated with covariates. In this case, sequence complexity is modeled as:

$$y_{ijk} = \beta_0 + \mathbf{X}_{ij}\boldsymbol{\beta} + \zeta_j + \zeta_k + \zeta_{jk} + \varepsilon_{ijk}, \quad (3)$$

where $\mathbf{X}_{ij}\boldsymbol{\beta}$ contains the covariates and their coefficients. Similar to linear multilevel models with hierarchically nested random effects, the reduction of country-specific and cohort-specific variation by the covariates can be calculated as a pseudo- R^2 :

$$R^2_{Country} = \frac{\psi_j - \psi_{j,C}}{\psi_j + \psi_k + \psi_{jk} + \sigma} \text{ and alternatively} \quad (3.1)$$

$$R^2_{Cohort} = \frac{\psi_k - \psi_{k,C}}{\psi_j + \psi_k + \psi_{jk} + \sigma} \quad (3.2)$$

where the variance component of the conditional model is denoted with the subscript C. The standard assumptions for random effects multilevel modeling apply and are clearly stated and

⁷ Shi, Leite & Algina (2010) recommend that researchers include random interaction effects, as their simulations and empirical tests show that higher level random effects estimates are biased if significant interacted crossed factors are omitted.

examined in the online supplement (see section 6). I conclude that the model parameters are generally consistently and efficiently estimated.

Overview of the Analytical Strategy

My analytical strategy entails four steps.⁸ First, I address my first two research questions: how do family trajectories vary across birth cohorts and how do they vary across countries. To do this, I estimate unconditional cross-classified random effects regressions on sequence complexity and investigate the country and birth cohort averages using empirical Bayes predictions of the random effects, ζ_j and ζ_k , and their standard errors (Rabe-Hesketh and Skrondal 2012, 109f.). Comparing empirical Bayes predictions of the country and cohort specific complexity intercepts is better than comparing OLS estimates, because information is weighted by its reliability.⁹ Examining the empirical Bayes estimates allows me to test whether levels of family trajectory complexity have increased across birth cohorts (H1) and whether they are highest in Scandinavian countries, followed by Continental European countries, and lowest in Southern and Eastern Europe (H2). I additionally analyze the empirical Bayes predictions of the interacted random intercepts, which indicate the average deviations of countries from the birth cohort random intercepts. If there are significant deviations, then I can conclude that family trajectory variation across time is country specific (H3).

Second, I address my third and core research question: whether family trajectories vary more across countries or across birth cohorts. I calculate the country and birth cohort intraclass correlation coefficients for both the unconditional and conditional cross-classified models, which enables me to enumerate the proportions of complexity variance attributable to countries and to cohorts. If the intraclass correlation coefficients are higher for countries than cohorts, then my expectation that cross-national variation is larger than cross-temporal variation (H4) is validated. As a third step, I then estimate conditional cross-classified models by introducing educational attainment, socio-economic status, and gender as covariates.

⁸ I use the TraMineR (Gabadinho et al. 2011) package to calculate sequence complexities and the WeightedCluster (Studer 2013) package to perform cluster analyses on the sequence based distance matrixes in R, version 3.2.0. The cross-classified regressions are calculated using the `mixed` command in STATA, version 14.

⁹ Country, cohort and country-cohort balanced panels were generated and analyzed to test the robustness of the empirical Bayes predictions, i.e. predictions without reliability coefficients. The results do not change substantially and lead to the same substantive conclusions.

Finally, I use results from cluster analysis to illuminate the qualitative differences between family life courses within countries and birth cohorts that underlie the regression results. In addition, I show that sequence complexity is a valid construct for life course differentiation. Specifically, I analyze complexity distributions within family trajectory clusters and describe how these differ across Europe and across birth cohorts as well as across gender, educational attainment and socio-economic status. Combining sequence and cluster analysis is a common method to inductively establish common trajectory patterns or groups (see Aisenbrey and Fasang 2010). I calculate a pairwise sequence distances matrix using Optimal Matching. This distance matrix is then subjected to a Ward cluster analysis, a hierarchical clustering method that minimizes the residual variance to establish groups with low within group distance and high between group distance.

I rely on the Average Silhouette Width (ASW) to determine the optimal number of clusters. The ASW is calculated by computing the silhouette of each observation, i.e. how close an observation is to the observations within its own cluster compared to how close it is to the observations in other clusters, then averaging the silhouettes within each cluster, and finally averaging the cluster specific silhouette values. Kaufman and Rousseeuw (1990, 88) propose an interpretation of ASW values, where 0.25-0.50 denote weak structure, 0.51-0.75 a reasonable structure, and 0.76-1.0 a strong structure indicating a clear-cut clusters in the data. Cluster solution quality measures displayed in Figure A1 (see manuscript appendix) indicate that family trajectories are reasonably well structured into family patterns involving marriage as well as parenthood and those following different pathways. The two cluster solution (ASW=0.61) shows that there is variation in family trajectories across countries and across birth cohorts, but mask important differences as diverse family trajectories are “dumped” together into one cluster. Therefore, I discuss the second best solution with six clusters (ASW=0.29) in the results section below.

5 Results

Family Trajectory Differentiation

The unconditional cross-classified random effects regression results for family trajectory complexity are presented in columns one and two of Table 1. The first model, column one, excludes the interacted random effect. The results of the conditional model on sequence complexity are displayed in column three of Table 1. I will first describe how family

trajectories vary across birth cohorts and countries using empirical Bayes predictions of random intercepts from model 2 (see Table 1, column 2) shown in Figure 2.

Table 1: Cross-Classified Random Effects Regression on Sequence Complexity

There is a clear trend towards increasing trajectory complexity across birth cohorts, however it is much less pronounced than expected. As seen in Figure 2, the estimated sequence complexity for the birth cohorts 1951-1953 and 1954-1956 are, on average, significantly higher than the cohorts 1939-1941 and older. As expected, the family trajectories of birth cohorts born in the early 1950s are more complex than older birth cohorts (H1).

Family trajectories are least complex in Spain, Poland and Italy, and are most complex in Denmark and Sweden. Family trajectories in East Germany, Belgium, and the Netherlands have average values. With the exception of East Germany and Austria, the empirical Bayes estimates support my expectation that family trajectories are most complex in Scandinavian social democratic countries, followed by the corporatist Continental European countries, with family life courses being the least complex in Southern and Eastern Europe (H2).

Fig. 2: *Empirical Bayes Estimates of Mean Sequence Complexity by Cohort and Country*

The significant interacted random effect parameter of column two (Table 1) indicates that sequence complexity variation across birth cohorts is not identical in all countries (H3). The country specific deviations from the birth cohort estimates displayed in Figure 2 are depicted in Figure 3. The only statistically significant deviations are found in Switzerland and Sweden for the 1951-1953 cohorts, which have estimated ca. 1.5 higher average complexity than the general trend. This indicates that levels of family life course complexity began to increase earlier in Sweden and Switzerland, most likely associated with an early shift towards prolonged family formation involving periods of cohabitation or independent living before marriage in these two countries. All other countries display no significant deviations from the estimated general trend. Although there are some country specific time trends, the results demonstrate an unexpected level of persistent cross-national differences with common trends of increasing complexity.

Fig. 3: Empirical Bayes Estimates of Country-Specific Deviations from Mean Birth Cohort Complexity

I now turn to partitioning the sequence complexity variance between countries and birth cohorts using cross-classified random effects modeling. As expected, the results demonstrate that the complexity of family trajectories varies more across countries than across birth cohorts (H4). The unconditional average of family trajectory complexity is 15, as indicated by the constant in columns one and two (see Table 1). The country specific variation from the average is 2.56, and is thus substantially larger than the birth cohort specific variation estimate of 0.58, displayed under the random effects of Table 1. An estimated 8% of the family trajectory variance is attributable to country differences, opposed to a marginal 1.8% accounted for by birth cohort differences, as shown by the intraclass correlations in column two.

The associations between educational attainment, socio-economic status, gender and sequence complexity are displayed in column three of Table 1. As can be seen, the family sequences of women are an average of 0.57 points less complex than those of men. Higher educational attainment is significantly associated with more complex family trajectories. Further, family formation is more complex if the main breadwinner of the respondent's childhood household had an occupation requiring a higher skill level than agricultural labor. However, family formation trajectories are also more complex for respondents that had no main breadwinner in their childhood household.¹⁰ The sector of first employment is not significantly associated with sequence complexity. With the exception of the respondent's sector of first employment, these associations are in line with what would be anticipated based on the SDT thesis and institutional arguments of comparative life course sociology.

The conditional intraclass correlations, i.e. the proportion of complexity variance attributable to cohort and country differences conditioned on the covariates, also indicate that family trajectories vary considerably more across countries than across birth cohorts when conditioned on the covariates. More than 6.5% of complexity variation can be attributed to cross-national differences compared to 1% for differences across birth cohorts. Educational attainment, the occupation of the main breadwinner when the respondent was 10, and gender

¹⁰ This response could mean that there was no main breadwinner or that the main breadwinner had no occupation, e.g. was unemployed.

reduce the country-specific complexity variation by 23% and the cohort-specific variation by 43.6%. This indicates that compositional differences account for a considerable amount of complexity variation across countries and cohorts. For example, higher levels of educational attainment in younger cohorts partially account for increasing levels of family formation complexity. These three covariates reduce the total sequence complexity variation by 5.3%, which is considerable for composite sequence metrics (cf. Biemann, Fasang, and Grunow 2011; Van Winkle and Fasang 2017).

Family Trajectory Patterns – Results from Exploratory Cluster Analysis

Family life courses can be categorized as 1) early family formation, 2) parental home, single or cohabitation trajectories, 3) prolonged family formation, 4) union dissolution trajectories, 5) childless marriages, or 6) delayed family formation (see Figure 4). The family life courses of these clusters are displayed in Figure 4 as relative frequency sequence plots, which display 100 representative sequences from each cluster on the left and a box plot of the dissimilarities from the respective sequence on the right (Fasang and Liao 2014).¹¹

Fig. 4: Relative Frequency Sequence Plots of Family Trajectory Patterns

Early and delayed family formation trajectories are characterized by highly coupled transitions out of the parental home into marriage and parenthood by the early to late twenties. Prolonged family formation trajectories are characterized by decoupled transitions in the early life course. A majority live independently for a period after leaving the parental home before marriage, while some substantially delay entering parenthood after marriage. Other family trajectories include childless marriages or marriages that either dissolve due to death or divorce into independent households or into cohabitation with children. A final cluster includes trajectories that consist of independent living, of cohabitation or of living in the parental home.

¹¹ Relative frequency sequence plots are generated by 1) sorting the sequences, 2) dividing the sorted sample into subgroups, 3) choosing mediod sequences from the subgroups to represent them, 4) plotting the mediod sequences and 5) plotting dissimilarities from the mediod sequences as box-plots with R^2 and F statistics that evaluate the goodness of fit of the chosen mediod sequences. I sort the sequences using multidimensional scaling and divide the sample into 100 mediod sequences. The dissimilarities are calculated using OM distance. The plots were created with the `seqplot.rf` function developed by Matthias Studer, Anette Fasang and Tim Liao implemented in the `TraMineRextras` package using R, version 3.2.0.

The distribution of sequence complexity within the clusters as well as the cluster sizes are displayed in Table 2. The early and delayed family formation clusters are the largest, each incorporating ca. 30% of family trajectories. Delayed family trajectories are slightly more complex than early family trajectories, because there is less state stability within marriage with children due to a longer duration in the parental home. The highest complexity averages are found within the prolonged family formation and union dissolution clusters, because trajectories within these clusters include an additional transition into a single state out of the parental home or out of marriage.

Table 2: Distribution of Sequence Complexity by Family Trajectory Clusters

The prevalence of the different family formation patterns varies across countries in a manner consistent with the regression results. The distribution of family trajectory patterns within countries and cohorts is displayed in Table A3 (see manuscript appendix). Levels of differentiation are highest in Sweden and Denmark, because early and delayed family formation trajectories are underrepresented in these countries, while prolonged family formation and union dissolution trajectories are overrepresented. Low levels of differentiation in the Czech Republic and Poland are associated with the dominance of early family formation trajectories. Similarly, a dominance of delayed family formation trajectories in Spain, Italy and Greece account for low levels of differentiation in Southern Europe.

Consistent with the regression results, the prevalence of the distinct family trajectory patterns varies little between birth cohorts. While early family formation trajectories have become somewhat more common between 1924-1926 and 1954-1956, delayed family trajectories have become considerably less common. Prolonged family formation and childless marriage trajectories have remained at a relatively constant level, however the parental home, single or cohabitation as well as union dissolution patterns have become more prevalent. Levels of differentiation in the 1951-1953 and 1954-1956 cohorts are slightly higher, because delayed family formation patterns have decreased while patterns involving divorce have increased. The distribution of family formation patterns across countries and across birth cohorts is in line with the SDT and comparative life course sociology.

The distribution of gender, educational attainment, and socio-economic status across family trajectory clusters is also consistent with the regression results (see Table A4 in manuscript

appendix). While women are overrepresented in the early family formation cluster, men delay family formation, which corresponds to the finding that women's family life courses are somewhat less complex than men's. The educational gradient in family trajectory complexity is likely attributable to individuals with primary education following early and delayed patterns of family formation while individuals with post-secondary education commonly form independent households before marrying. This pattern can also be observed among individuals whose main breadwinner during childhood was in the professional occupational classes rather than in the agricultural sector.

Sensitivity Analyses

I conducted multiple sensitivity analyses to test the robustness of my results. The first set of robustness checks addresses the question whether complexity would vary more across cohorts relative to countries if I would observe younger cohorts born after 1956. Unfortunately, no other suitable data sets exist that would allow me to analyze the family formation trajectories of men and women age 15-50 for cohorts born after 1956.¹² I nonetheless replicated my analyses using the Harmonized Histories data from the Generations and Gender Programme (UN 2005; Perelli-Harris, Kreyenfeld, and Kubisch 2010) with trajectories of individuals age 15-35 for cohorts born between 1939-1971 from 13 European countries. I find that differences across cohort are still small compared to cross-national differences, and in some cases even smaller than the analysis presented above (see section 4 in the online supplement for more details). The results solidify my conclusion that the increase in family trajectory complexity is still minor even if the cohort range is extended beyond 1956. Further, the analyses demonstrating even smaller cross-temporal variation using shorter trajectories underline the importance of using long family life courses when analyzing change partially due to events in later life, e.g. divorce and remarriage.

The second set of sensitivity analyses pertain to the dependent variable, sequence complexity, and its influence on the results. First, I conducted separate analyses on entropy, the number of transitions as well as logarithmic complexity and its components. The results are substantively

¹² While the Generations and Gender Programme has extremely rich life history data on a number of countries, using them would only extend the cohort range past 1956 for Poland, Belgium and Sweden for long life trajectories. An alternative data source would be the 2006 European Social Survey used by Hofäcker and Chaloupková (2014) to analyze family formation trajectories across 23 European countries from age 18-35; however these data would not expand the cohort range of individuals observed until age 50. Moreover, the 2006 European Social Survey did not collect information on the timing of divorce, which is necessary when analyzing family life courses until age 50.

similar and lead to the same conclusions (see section 1 in the online supplement). Second, I performed robustness checks on complexity weighted by durations in specific sequence states. While the results are very much alike to the results presented above, cross-national differences are inflated when complexity is weighted to give more importance to durations of being single without children and gender differences become larger when weighted by durations spent in the parental home with children or single with children (see section 2 in the online supplement).

A final set of sensitivity analyses examined how model specifications influence the results. I estimated models with yearly, two-year, four-year, and five-year cohorts rather than three-year cohorts used in the analyses above. The results are highly robust to different cohort groupings (see section 3 in the online supplement). As another robustness test, I analyzed two-level models with country-cohort clusters, which indicate that the intraclass correlation coefficients from the cross-classified models are well estimated (see section 7 in the online supplement). Finally, I conducted sensitivity analyses omitting single countries and cohorts that demonstrate that my results are not driven by a single country or cohort (see section 5 in the online supplement).

6. Discussion & Conclusion

I set out to ascertain 1) how family trajectories vary over time, 2) across countries and 3) whether family trajectories vary more across time or across countries. These questions are motivated by two research traditions in the field of comparative family demography and sociology: the ideational account of the SDT (Lesthaeghe and Van de Kaa 1986) and institutional account of comparative life course sociology (Mayer 2009; 1997). Based on these theoretical perspectives, I hypothesized that family trajectories have become more differentiated across cohorts (H1) and that family trajectories within social democratic countries are most differentiated followed by corporatist countries, and lowest within Southern and Eastern European countries (H2). Finally, I argued that the speed and extent of change in family formation within countries results from an interaction between the dissemination of post-materialism and the implementation of defamilizing institutions. It follows that change over time is country specific (H3) and that cross-national variation is larger than cross-temporal variation (H4). All my hypotheses were supported by the empirical results, although I observed a higher level of contemporaneous change across countries than expected.

The analyses presented have various potential limitations. The SHARELIFE data were collected retrospectively from elderly respondents, posing the problem of recall error. Havari & Mazzonna (2015) compare information collected in the SHARELIFE childhood circumstances module with national registry data and conclude that recall error does not compromise the validity or usefulness of the data. Further, the life history calendar used in SHARELIFE collected data on an annual rather than monthly basis. Both recall error and the coarseness of annual life history data may cause an underestimation of family life course differentiation, especially in the early cohorts and in countries with high differentiation levels.

Another potential limitation lies within the birth cohorts analyzed as well as the clustering of cohorts and countries. I lack birth cohorts entering family formation at the dawn of the 20th century and after the 1980's, which could display considerably higher levels of family trajectory differentiation. Even with the relatively large number of birth cohorts and countries included in this study, the estimated variance components may be biased downwards due to small cluster sizes (Bryan and Jenkins 2016). All of these limitations, if anything, point to a potential underestimation of the true degree of differentiation in family life courses. Therefore, the analyses can be understood as lower bound estimates. The finding of a strong influence of institutional path dependency on family life courses suggests that cross-temporal variation will probably not outweigh cross-national differences for decades to come, although this is an empirical question.

One of my main contributions to the literature is the introduction of a novel methodological approach that simultaneously quantifies cross-national and cross-temporal variation in family life courses. This methodological approach is important for three reasons. First, it enables family demographers and sociologists to describe the extent of increasing family formation complexity by using cross-national differences as a point of reference. I have demonstrated that the extent of change in family formation is often overstated in light of much more substantial variation across European countries. Second, this approach addresses two theoretical accounts of family life course variation and enables family demographers and sociologists to investigate processes of family formation without neglecting either the temporal or spatial dimension. For example, I demonstrate that educational attainment is associated with family formation complexity, and that compositional differences in educational attainment account for both cross-national and cross-temporal variation. Third, my methodological approach is applicable to other areas of research on temporal and spatial variation of process outcomes, such as democratic consolidation or health histories.

The implications of my results both advance the SDT thesis and substantiate previous research. I bring a long generational perspective into the debate on increasing complexity in family formation by integrating the theoretical perspectives of the SDT and comparative life course sociology with a focus on temporal order. This is important to gain a deeper understanding of how family formation differentiation engendered by the dissemination of post-materialism over time can be inhibited by national institutional arrangements that lag this cultural change. For example, although studies have demonstrated that the dissemination of post-materialism developed similarly in Denmark and the Netherlands (e.g. Inglehart and Abramson 1994), defamilizing institutions, such as maternity and paternal leave as well as early childcare, that facilitate high female labor market participation were introduced much later or not at all in the Netherlands. While defamilization lowered the risks of complex family formation associated with post-materialism in Denmark, continued familization and gendered decommmodification in the Netherlands further incentivize early marriage and parenthood, especially for women. This process of institutional lag and the suppression of family formation differentiation is likely to continue in Continental Europe, but also in Southern and Eastern Europe.

More generally, my study underlines large and relatively stable cross-national differences in levels of family life course differentiation. This supports the notion that “societies change very gradually” (Mayer 2005, 17) and that path dependency in institutions may be the primary source of gradual change in family life courses. Many of the cross-national differences and changes across cohorts are consistent with the comparative life course literature as well as the SDT thesis. Future research should further investigate how ideational and institutional change jointly unfolds over time to shape family life courses and how these trends may be associated with social inequality.

Tables & Figures

Fig. 1: Artificial Example of Family Trajectories and Sequence Complexity

Family Trajectory 1: $C(x) = 46.213$

P	P	S	S	M	M	MC	MC	MC	MC
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Family Trajectory 2: $C(x) = 58.648$

P	P	S	S	C	C	M	M	MC	MC
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Family Trajectory 3: $C(x) = 51.215$

P	S	C	M	MC	MC	MC	MC	MC	MC
t_1	t_2	t_3	t_4	t_5	t_6	t_7	t_8	t_9	t_{10}

Fig. 2: Empirical Bayes Estimates of Mean Sequence Complexity by Cohort and Country

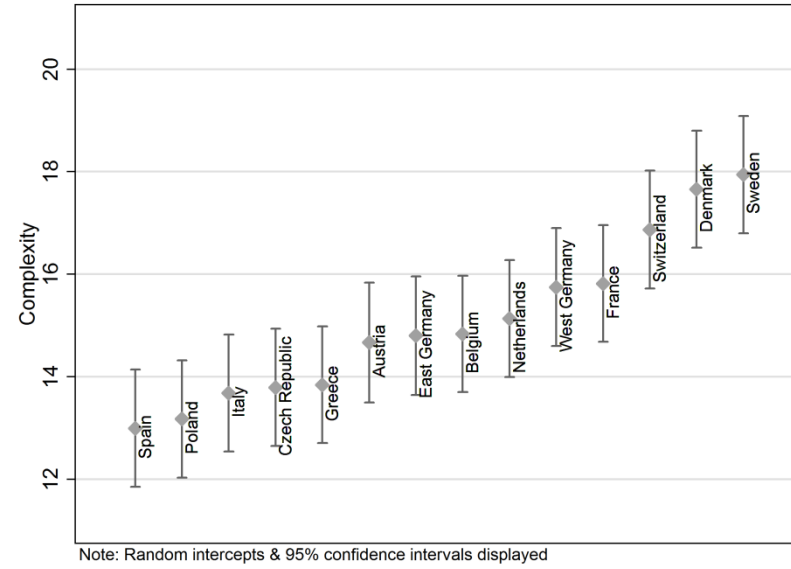
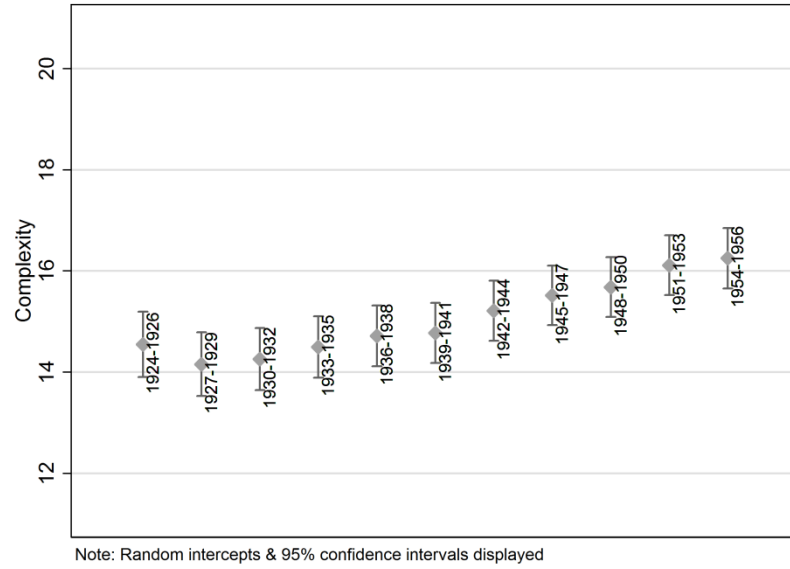
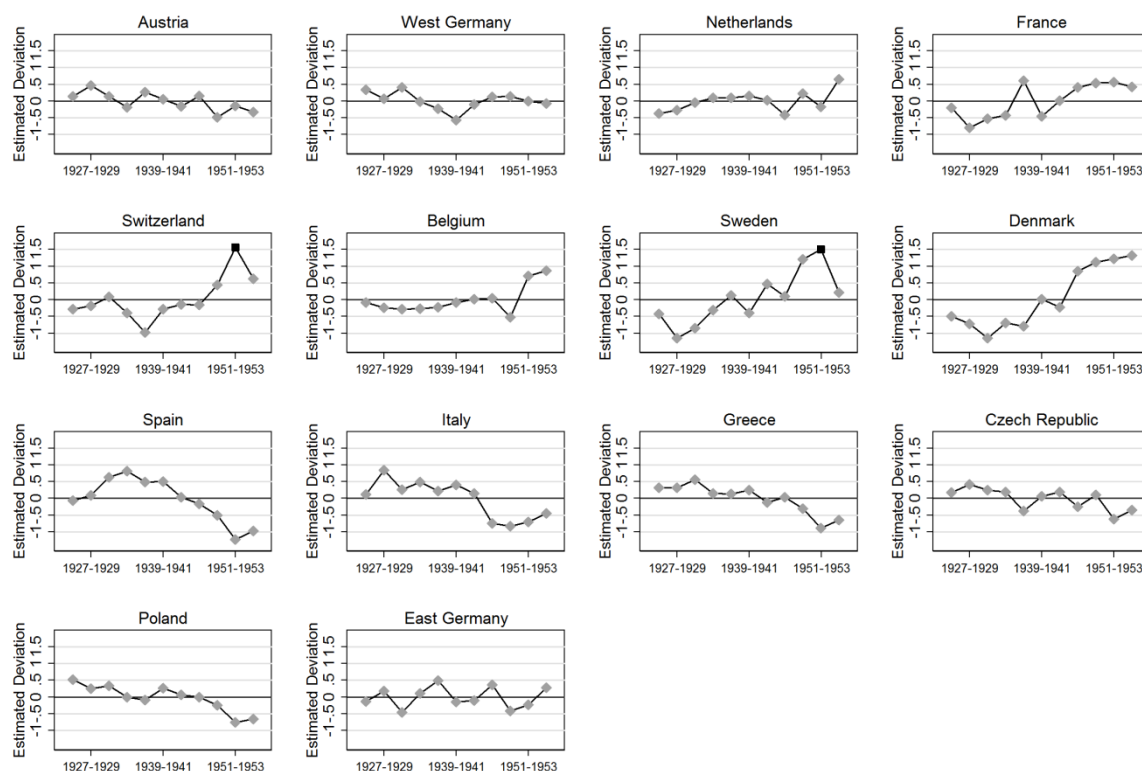


Fig. 3: Empirical Bayes Estimates of Country Specific Deviations from Mean Birth Cohort Complexity



Note: Random intercepts & 95% confidence intervals displayed
Black denotes significant deviations; $p < 0.05$

Fig. 4: Relative Frequency Sequence Plots of Family Trajectory Patterns

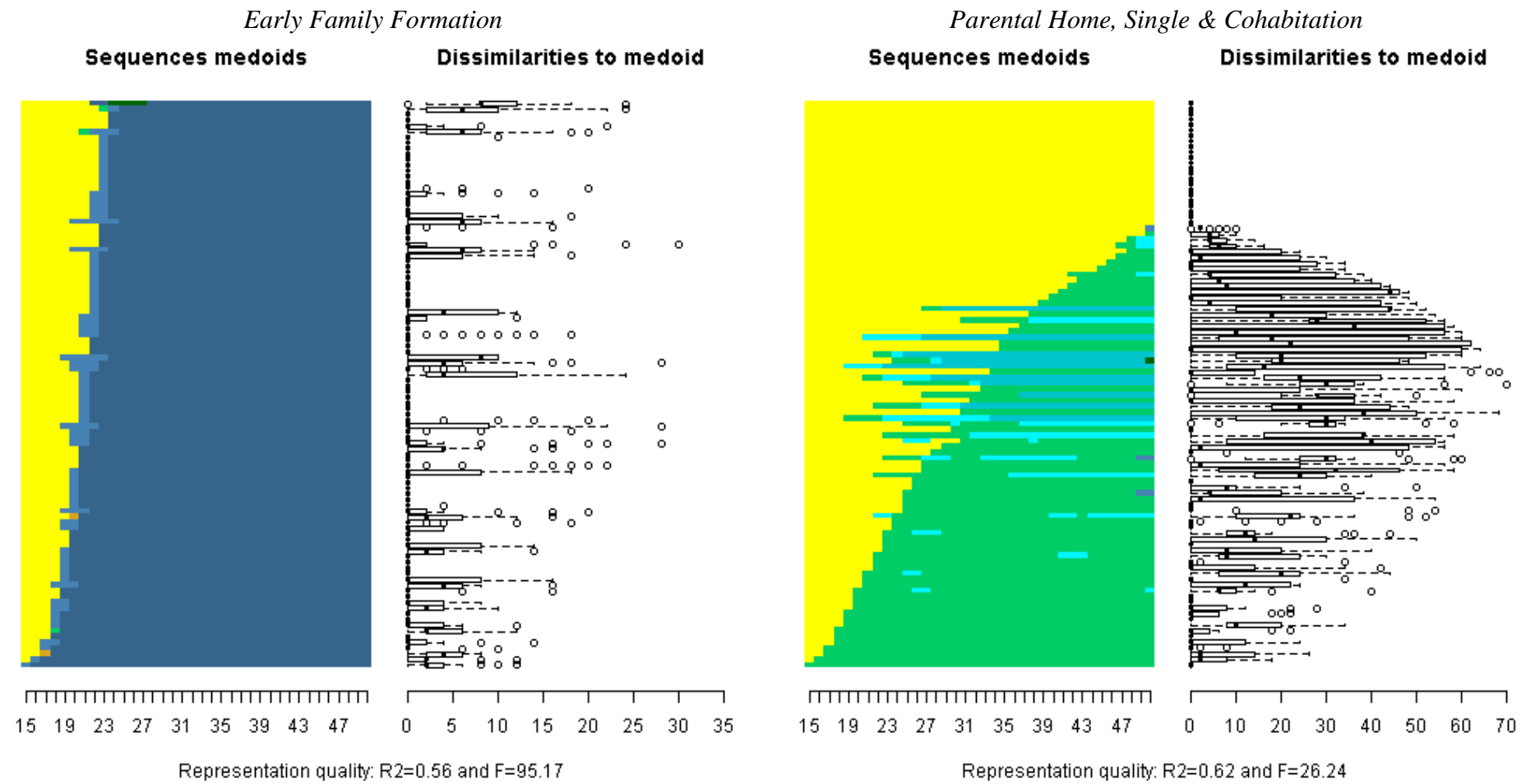


Fig. 4: continued

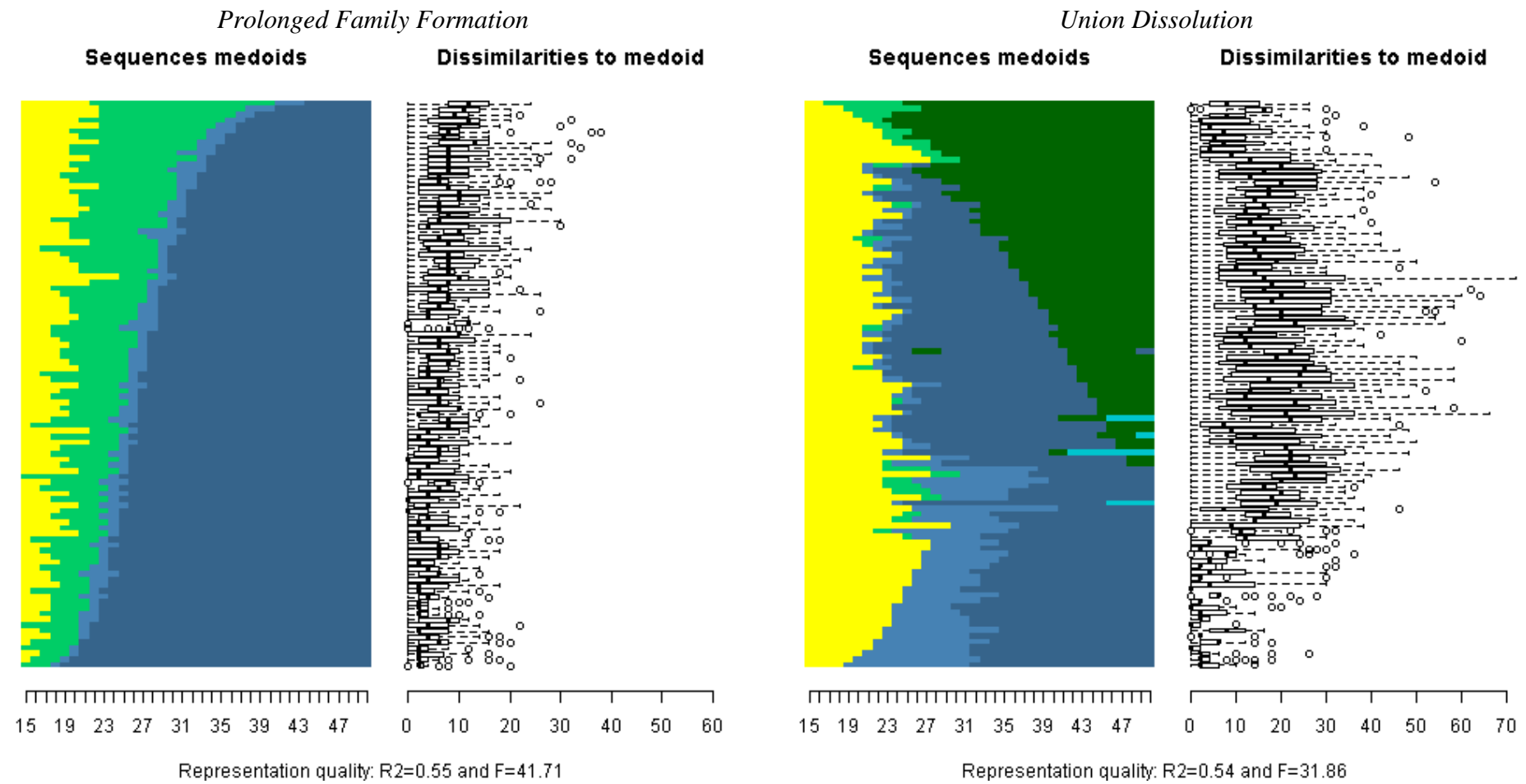


Fig. 4: continued

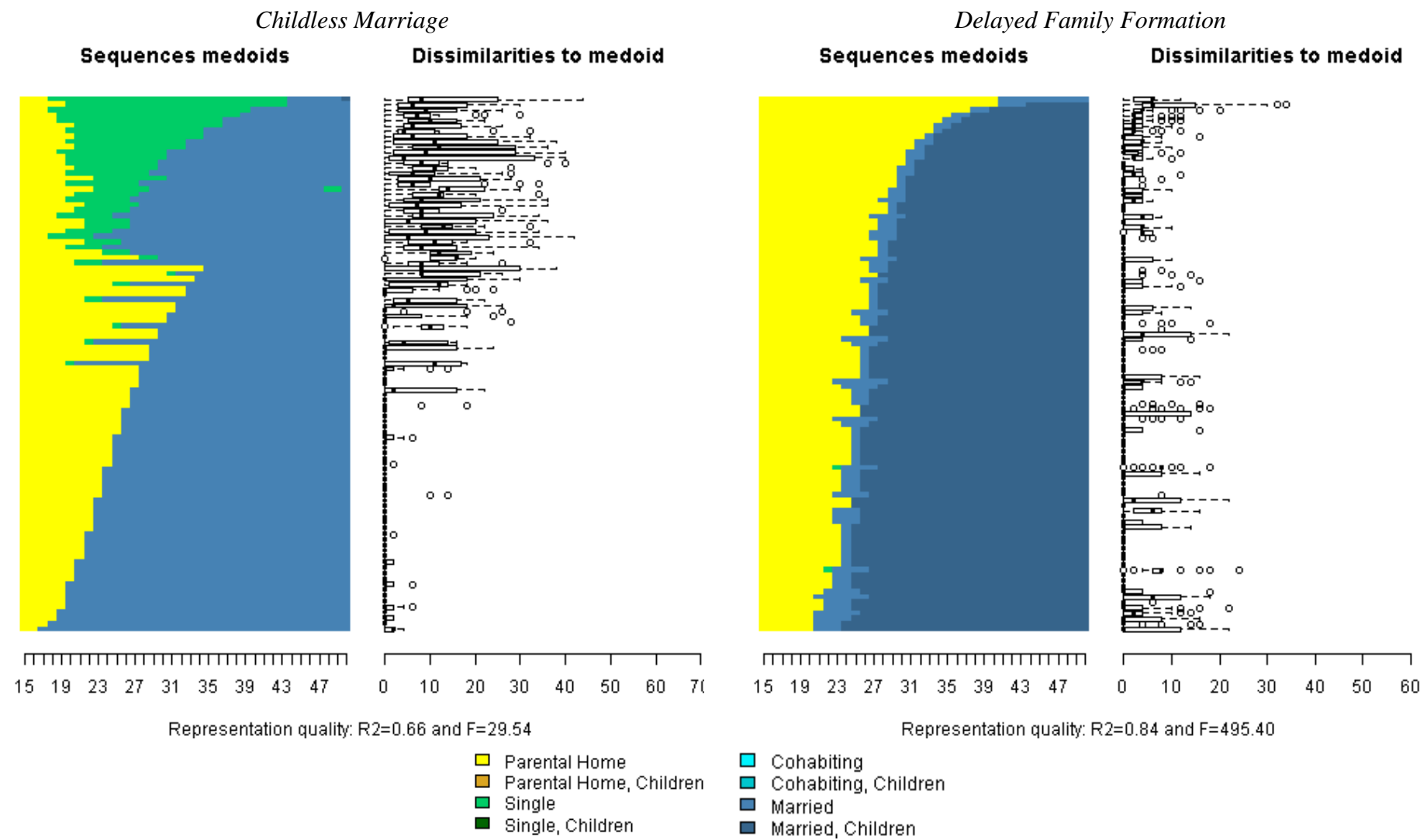


Table 1: Cross-Classified Random Effects Regression on Sequence Complexity

	1 Unconditional Additive	2 Unconditional Interacted	3 Conditional Interacted
Female			-0.570*** (0.071)
Education (Ref. Secondary)			
None			-0.802*** (0.212)
Pre-Primary			-0.899*** (0.106)
Primary			-0.523*** (0.109)
Post-Secondary			1.160*** (0.103)
Public Sector			0.156 (0.137)
Occupation of Breadwinner (Ref. Agriculture)			
Senior Prof.			1.301*** (0.185)
Prof.			1.115*** (0.199)
Technician			1.060*** (0.184)
Clerk			0.970*** (0.166)
Service			0.589*** (0.148)
Craftsman			0.296** (0.107)
Industry			0.358* (0.176)
Unskilled			0.147 (0.113)
Armed Services			0.592* (0.290)
None			0.945** (0.289)
Constant	15.063*** (0.521)	15.068*** (0.491)	15.089*** (0.429)

Table 1 continued

var(Cohort)	0.655*** (0.301)	0.584*** (0.284)	0.330*** (0.170)
var(Country)	2.942*** (1.161)	2.561*** (1.029)	1.971*** (0.798)
var(Interacted)		0.455*** (0.083)	0.456*** (0.082)
var(Residual)	28.764*** (0.273)	28.387*** (0.270)	27.512*** (0.262)
ρ_{Cohort}	2.02	1.82	1.08
ρ_{Country}	9.09	8.00	6.51
R^2_{Cohort}			43.60
R^2_{Country}			23.03
R^2_{Total}			5.37
N	22,272	22,272	22,272
R Log Lik.	-69,064	-68,989	-68,647

Note: Significance Levels: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; Unstandardized regression coefficients displayed; Standard errors in parentheses; Significance of random effect parameters determined by likelihood-ratio tests; Data not weighted

Table 2: Distribution of Sequence Complexity and Distance by Family Trajectory Clusters

	Early Family Formation	Parental Home, Single & Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation	Total
Complexity	12.51 (3.48)	12.29 (8.48)	19.87 (4.61)	22.40 (6.41)	12.76 (5.69)	14.72 (2.46)	15.51 (5.66)
N	6,034	1,473	3,161	2,524	1,381	7,699	22,272
(Percent)	(28.38)	(5.97)	(14.96)	(11.87)	(6.16)	(32.66)	(100.00)

Note: Means and standard deviations in parentheses displayed; Data weighted

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8. Appendix

Table A1. List of Sequence State Elements and Average Durations

State Abbreviation	State Definition	Average State Duration (Years)
P	In the parental home and without children	8.487
PC	In the parental home with at least one child	0.091
S	Outside the parental home, not cohabitating with an intimate partner, and without children	2.103
SC	Outside the parental home, not cohabitating with an intimate partner, and with at least one child	1.023
C	Cohabitating with an intimate partner without children	0.234
CC	Cohabitating with an intimate partner with at least one child	0.370
M	Married without children	3.337
MC	Married with at least one child	20.354

Table A2: Sample Frequencies Cross-Classified by Country and Birth Cohort

	1924 1926	1927 1929	1930 1932	1933 1935	1936 1938	1939 1941	1942 1944	1945 1947	1948 1950	1951 1953	1954 1956	Total
Austria	22	59	49	65	72	119	112	95	87	77	32	789
West	45	57	61	83	132	168	154	113	168	177	95	1253
Germany												
Sweden	77	84	106	138	159	197	218	239	193	167	69	1647
Netherlands	53	70	91	132	141	181	228	281	263	240	183	1863
Spain	63	100	131	168	126	146	138	157	153	162	152	1496
Italy	56	77	140	158	209	238	219	232	237	181	170	1917
France	73	119	135	151	150	174	192	233	276	250	231	1984
Denmark	75	91	118	122	132	155	207	234	222	217	289	1862
Greece	70	75	136	174	168	156	193	241	267	321	199	2000
Switzerland	43	59	77	82	97	93	133	135	124	122	132	1097
Belgium	102	119	168	183	189	194	237	264	308	294	248	2306
Czech	47	53	102	111	117	165	202	215	211	188	162	1573
Republic												
Poland	43	63	88	79	120	115	122	189	209	222	228	1478
East	29	38	47	73	95	108	120	126	132	136	103	1007
Germany												
Total	798	1064	1449	1719	1907	2209	2475	2754	2850	2754	2293	22272

Note: Data not weighted

Table A3: Descriptive Statistics on the Study Countries and Birth Cohorts by Cluster

Grouping

	Early Family Formation	Parental Home, Single & Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation
Countries						
Austria	33.84	6.97	15.21	15.08	7.35	21.55
West	27.11	3.87	19.50	9.70	7.15	32.67
Germany						
Sweden	22.37	7.29	32.33	13.90	5.34	18.77
Netherlands	21.27	5.24	13.22	13.32	8.95	38.00
Spain	22.38	7.65	3.13	4.98	5.78	56.08
Italy	23.99	4.22	6.42	5.83	4.92	54.62
France	27.65	8.01	17.71	15.06	5.82	25.75
Denmark	22.44	6.49	37.07	13.45	6.85	13.71
Greece	17.23	7.53	7.31	6.64	7.80	53.49
Switzerland	17.38	10.11	23.62	13.72	7.60	27.56
Belgium	30.51	5.79	3.72	14.03	6.07	39.89
Czech	48.60	2.63	1.42	10.87	3.96	32.52
Republic						
Poland	47.25	2.38	7.71	4.79	4.62	33.25
East	22.63	6.18	24.40	6.52	4.61	35.66
Germany						
Birth Cohorts						
1924-1926	21.99	5.61	16.53	7.81	9.39	38.68
1927-1929	23.33	6.18	14.23	8.15	7.72	40.39
1930-1932	28.99	4.56	13.21	5.57	6.21	41.46
1933-1935	24.65	5.11	13.04	9.23	6.23	41.73
1936-1938	26.30	5.22	16.07	9.41	7.41	35.60
1939-1941	30.15	4.41	17.27	10.70	5.26	32.21
1942-1944	28.84	6.31	15.86	12.30	5.86	30.82
1945-1947	29.15	5.51	14.47	13.03	5.12	32.72
1948-1950	30.94	6.34	14.36	15.27	5.00	28.08
1951-1953	29.12	7.43	15.04	14.21	7.33	26.88
1954-1956	29.63	7.61	14.40	14.86	5.83	27.67
Total	28.38	5.97	14.96	11.87	6.16	32.66

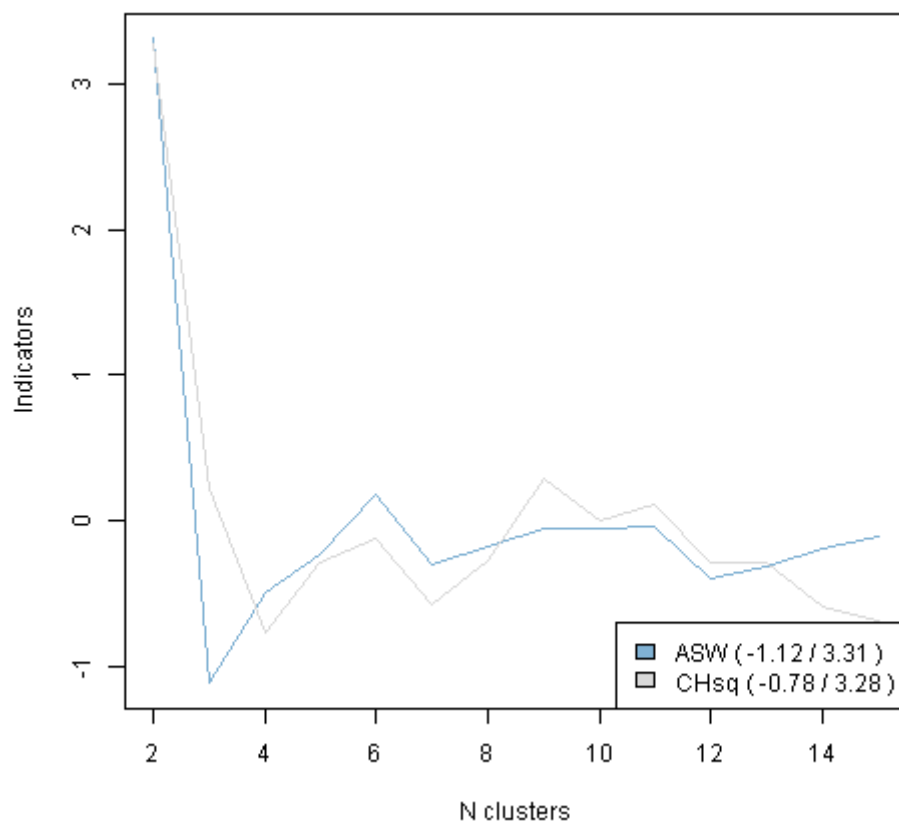
Note: Row percentages displayed; Data weighted

Table A4: Summary Statistics by Cluster Grouping

	Early Family Formation	Parental Home, Single & Cohabitation	Prolonged Family Formation	Union Dissolution	Childless Marriage	Delayed Family Formation
Gender						
Male	18.17	6.71	15.97	10.92	6.06	42.16
Female	37.90	5.27	14.01	12.75	6.25	23.81
Education						
None	32.30	6.05	5.36	7.16	5.42	43.72
Pre-Prim.	35.48	5.39	10.54	8.73	6.26	33.60
Primary	36.14	5.18	7.97	11.93	6.05	32.73
	27.48	5.75	16.11	12.93	6.20	31.52
Secondary						
Post-Sec.	14.87	7.60	25.35	13.75	6.19	32.25
Sector 1st Employment						
Private	29.26	5.85	14.71	11.82	6.10	32.27
Public	19.74	7.17	17.37	12.36	6.77	36.58
Occupation of Breadwinner						
Sen.	17.65	8.28	26.34	15.06	7.02	25.66
Prof.						
Prof.	16.03	8.91	24.82	13.80	7.70	28.73
Tech.	25.78	6.40	15.53	15.22	7.60	29.46
Clerk	23.01	6.64	12.66	14.88	6.06	36.76
Service	25.77	5.08	16.12	13.50	7.32	32.21
Agric.	26.45	6.05	18.69	7.97	5.31	35.53
Craft.	31.44	5.28	11.48	12.51	6.05	33.24
Industry	33.93	5.38	10.73	12.09	6.57	31.30
Unskilled	34.40	5.65	10.46	12.10	5.73	31.66
Armed F.	24.09	6.96	14.38	13.01	8.13	33.43
None	38.51	5.02	10.85	14.90	5.51	25.21
Total	28.38	5.97	14.96	11.87	6.16	32.66

Note: Row percentages displayed; Data weighted

Fig. A1: Average Silhouette Width and Chi-Squared Values for Diverse Ward Cluster Analysis Solutions on OM Distances



Calculation of Sequence Complexity for Figure 1

I. Maximum Longitudinal Entropy

Calculation for maximum entropy of a sequence with 10 consecutive states and 8 possible sequence elements. An equal occurrence of each state element implies that each element is observed 1.25 times.

$$h_{max} = - \left[10 * \left(\frac{1.25}{10} \log \frac{1.25}{10} \right) \right]$$
$$= 2.079$$

II. Family Trajectory 1: P/2 S/2 M/2 MC/4

$$h(x) = - \left[3 * \left(\frac{2}{10} \log \frac{2}{10} \right) + \left(\frac{4}{10} \log \frac{4}{10} \right) \right]$$
$$= 1.332$$

$$C(x) = 100 * \sqrt{\frac{3}{9} * \frac{1.332}{2.079}}$$
$$= 46.213$$

III. Family Trajectory 2: P/2 S/2 C/2 M/2 MC/2

$$h(x) = - \left[5 * \left(\frac{2}{10} \log \frac{2}{10} \right) \right]$$
$$= 1.609$$

$$C(x) = 100 * \sqrt{\frac{4}{9} * \frac{1.609}{2.079}}$$
$$= 58.648$$

IV. Family Trajectory 1: P/1 S/1 C/1 M/1 MC/6

$$h(x) = - \left[4 * \left(\frac{1}{10} \log \frac{1}{10} \right) + \left(\frac{6}{10} \log \frac{6}{10} \right) \right]$$
$$= 1.227$$

$$C(x) = 100 * \sqrt{\frac{4}{9} * \frac{1.227}{2.079}}$$
$$= 51.215$$