

# DEMOGRAPHIC RESEARCH

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*Data Description*

**KINMATRIX: A new data resource for studies  
of families and kinship**

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## **KINMATRIX: A new data resource for studies of families and kinship**

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### **Abstract**

#### **BACKGROUND**

How cohesive are families and how do they respond to their members' needs? How do families transmit advantages and disadvantages within and across generations? Current data confine our answers to these questions to solidarity and transmission in the immediate family, overlooking other relatives who play a significant role in socialization, social integration, social support, and the reproduction of social status and inequality.

#### **OBJECTIVE**

This article presents the KINMATRIX project, a novel comparative survey that collected extensive data on a wide array of family members, moving beyond the traditional focus on the immediate family.

#### **METHODS**

The KINMATRIX data map out families as ego-centric networks of younger adults aged 25 to 35, including their parents, grandparents, siblings, aunts, uncles, cousins, and step- or half-relatives. The data prepared for scientific use include  $N = 12,438$  egos (anchor-respondents) and  $N = 252,278$  alters (anchor-kin dyads) in 10 countries (Denmark, Finland, Germany, Italy, Netherlands, Norway, Poland, Sweden, United Kingdom, United States).

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## **CONTRIBUTION**

KINMATRIX contributes to research infrastructure by offering detailed relational and attribute data collected on family networks, covering a wide range of relatives and diverse family forms. These data reflect the complexity of contemporary families and add to our understanding of key family processes, such as solidarity and transmission. The broad scope supports comparative analyses across European societies and beyond.

## **1. Introduction**

The family is not only a critical source of individual well-being and social support, but also a prime arena for status transmission and the reproduction of inequality. Given this central role, the quantitative social sciences have produced a vast literature on the family. Yet, much of contemporary theory, data, and empirical research focuses on only a narrow segment of the family – often stripped down to a unit containing only parents and children. This emphasis on the nuclear form, disconnected from the larger network surrounding it, excludes family members and family ties that may influence outcomes in the domains of socialization, social integration, social support and safety, demographic and health behaviors, educational attainment, and economic well-being (Bengtson 2001; Gerstel 2011; Johnson 2000; Mare 2011, 2015).

The need for an expanded coverage of family members and family ties is reinforced by demographic shifts that have changed the face of families. Demographic aging has transformed generational structures, while rising rates of divorce, separation, non-marital cohabitation, and multi-partner fertility have increased the complexity of kinship ties (Raley and Sweeney 2020; Sobotka 2008). A view of the family reduced to parent–child relationships is increasingly out of step with the demographic reality of families, many of which are replete with relations that extend beyond traditional boundaries.

The KINMATRIX survey addresses the need for family data that extends beyond the nuclear family. Its design is informed by several comparative surveys that include comprehensive modules on family relations, such as the Generations and Gender Programme (GGP; Gauthier, Cabaço, and Emery 2018), the International Social Survey Programme (ISSP; ISSP Research Group 2022), and the Survey of Health, Ageing and Retirement in Europe (SHARE; Börsch-Supan et al. 2013). It also draws on national surveys focusing on families, including the German Family Demography Panel Study (FReDA; Schneider et al. 2021), the German Family Panel (pairfam; Huinink et al. 2011), the Longitudinal Study of Generations (LSOG; Silverstein and Bengtson 2019), the Netherlands Kinship Panel Study (NKPS; Dykstra et al. 2012), and the survey Parents and Children in the Netherlands (OKiN; Kalmijn et al. 2018). Key elements of the

KINMATRIX questionnaire, particularly questions about relations to and attributes of kin, were adapted from these surveys.

The KINMATRIX data represent families as ego-centric networks of younger adults (ages 25 to 35) and capture an array of family members that is unprecedented in scope and detail: biological parents; all grandparents; all full siblings; all paternal and maternal half-siblings; all aunts, uncles, and first-degree cousins; and half- and step-relatives resulting from separation, re-partnering, and multi-partner fertility. Samples come from 10 countries in 5 areas: Northern Europe (Sweden, Norway, Finland, Denmark), Central-Western Europe (the Netherlands, Germany, the United Kingdom), Central-Eastern Europe (Poland), Southern Europe (Italy), and the United States. The cleaned data prepared for scientific use include a total of  $N = 12,438$  egos (anchor-respondents) and  $N = 252,278$  alters (anchor-kin dyads).

Data were collected within the remit of a European Research Council (ERC) project focusing on two family processes: solidarity and transmission.<sup>5</sup> Research on both processes shares a pronounced focus on the parent–child relationship, and in both fields of study the limitations of this focus are recognized. The study of family solidarity has long emphasized that a narrow view restricted to nuclear ties misses resources residing in relationships with extended kin, who may constitute confidants, role models, friends, advisors, financial contributors, and a part of the ‘latent kin matrix’ activated in times of need (Coall and Hertwig 2010; Gerstel 2011; Milardo 2010; Riley 1983). Similarly, the study of family transmission has emphasized that a narrow view restricted to nuclear ties misses resources that may matter in processes of status attainment, especially the potential influence of extended kin and complex kin on educational and occupational outcomes (Anderson, Sheppard, and Monden 2018; Clark 2014; Erola et al. 2018; Jæger 2012; Sheppard and Monden 2018; de Leeuw, Kalmijn, and van Gaalen 2018).

The lack of quantitative data on the presence and characteristics of, as well as social ties to, extended kin has been identified as a major reason for persisting knowledge gaps in research on solidarity and transmission (Gerstel 2011; Mare 2011). The KINMATRIX data add to the infrastructure required to close these gaps, situating both processes within a multigenerational structure of vertical and collateral ties to nuclear, extended, and complex kin. With the release of these data, the KINMATRIX project aims to enable new studies that advance our understanding of the scope of and mechanisms behind solidarity and transmission.

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<sup>5</sup> ERC Starting Grant 2019 (Grant agreement No. 848861): Uncovering the Kinship Matrix: A New Study of Solidarity and Transmission in European Families (KINMATRIX).

## 2. Methods

KINMATRIX is a web-based survey conducted in two rounds. The first round, fielded between December 2022 and March 2023 in all 10 countries, collected data on  $N = 10,065$  anchor respondents aged 25 to 35 and  $N = 199,243$  anchor–kin dyads (after cleaning). The second round, fielded in the US one year later (December 2023 – January 2024), repeated the survey, with slight modifications, on a new US sample ( $N = 2,373$  anchor respondents and  $N = 53,035$  anchor–kin dyads) to obtain a pooled single-country sample of sufficient size for detailed analyses of demographic subgroups. All samples were recruited from Dynata’s access panels using soft sampling quotas for anchor sex, anchor age (within the range of 25 to 35), education level (low, medium, high), and region. Sampling quotas were calculated from official statistics (OECD) for the age range of 25 to 35 in the year 2022 (see the [online supplement](#)). Post-stratification weights are available to adjust the data to match the marginal population distribution of the quota variables.

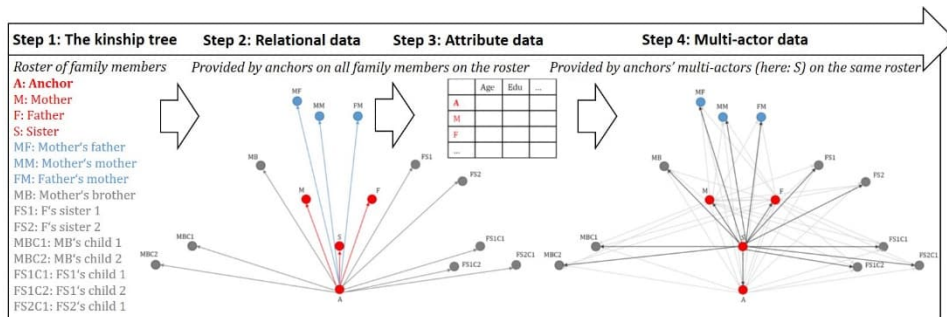
*Selection of egos and alters:* The narrow age bounds used for the recruitment of anchor respondents (‘egos’) were aimed at selecting one family generation – the youngest to have reached adulthood – within a life stage in which the outcomes of intergenerational transmission have already surfaced, while career and family demands are near their peak, rendering family solidarity particularly relevant. The selection of family members (‘alters’) was aimed at broadening the nuclear focus by adding extended and complex kin, with an emphasis on genealogical kinship. The set of alters included both biological parents, all full siblings, all four grandparents, and all aunts, uncles, and first-degree cousins. In addition, ‘complex kin’ from separation, re-partnering, and multi-partner fertility were included, consisting of all paternal and maternal half-siblings and step-kin defined as the partners of each biological parent and the children of these partners for all parent–partner unions lasting two or more years (see Kalmijn et al. 2018).

This nominalist definition of alters contrasts with the realist approach, affording respondents freedom in defining their ‘own’ family network based on personal perceptions and including, for example, fictive kin, friends, or neighbors. The nominalist approach of KINMATRIX provided benefits in terms of aggregation facilitated by consistent definitions of genealogical and complex kinship, coverage of not only close and intact ties but also loose and broken ties, and integration with other datasets using similar definitions of kinship.

*Web-survey instrument.* The instrument was developed between 2020 and 2022 in the English language and translated into 8 other languages (Danish, Dutch, Finnish, German, Italian, Norwegian, Polish, Swedish). Its main sections are illustrated in Figure 1. The [online supplement](#) includes a full documentation of questionnaires,

programming, web design, respondent look-and-feel, sampling, and translation procedures.

**Figure 1: Data collection for an example family with 14 biological family members**



After an initial section of personal questions, anchor respondents build their family trees, which grew with every completed subsection (parents, siblings, grandparents, etc.). Each family tree subsection concluded with a visual display of the updated tree and gave respondents the option to correct potential errors. For each kinship category of unknown size, the instrument first determined the size (e.g., the mother's number of sisters) to define the matrix for subsequent entries. For each family member (alter), data about name, vital status, and where applicable sex and family structure were collected (e.g., occurrence and timing of parental and grandparental separation, duration of co-residence). The family tree section produced a list of names (freely chosen by anchor respondents, usually real first names) to which the corresponding kinship relations to the anchor respondent were added in parentheses. This list was exported into subsequent modules (Steps 2, 3, and 4 in Figure 1). These modules used different response formats that supported a rapid collection of relational and attribute data while minimizing nonresponse and response bias (e.g., name carousels: see survey screenshots in the [online supplement](#)). The survey questions about relation to and attributes of family members captured important constructs for the study of solidarity and transmission, respectively.

At the end of the survey, respondents could invite selected family members (parents and full siblings) to participate as multi-actors. For multi-actors who participated in the survey ( $N = 1,887$  multi-actors sourced from  $N = 1,396$  anchor respondents), the family tree created by anchor respondents was imported and adapted to fit each multi-actor's perspective. Subsequently, multi-actors completed Step 2 and Step 3 of the survey (Figure 1). The collection of multi-actor data was limited to round 1 and discontinued in

round 2. Anchor respondents were incentivized by the access panel provider Dynata for their own participation and for each multi-actor who completed the survey.

### **3. Overview of KINMATRIX samples and variables**

#### **3.1 Samples**

Summary statistics on anchor respondents' demographic characteristics and their family networks are shown in Tables 1, 2, and 3. The data in Table 1 and 2 are broadly consistent with known country differences in union formation, fertility, divorce and separation, and the prevalence of family complexity and multi-partner fertility (Andersson, Thomson, and Duntava 2017; Thomson, Gray, and Carlson 2020). For example, the US and the Northern European countries show the expected elevated levels of parental separation and higher numbers of complex kin. Moreover, within-country differences (not shown) on important family indicators are in line with known patterns (e.g., differences between US racial/ethnic groups in marital and cohabitation status, in the risk of parental separation, and in socioeconomic gradients in kin mortality). For Sweden, the KINMATRIX estimates of numbers of different kin types align well with those reported in a recent study drawing on Swedish register data (Kolk et al. 2023). However, it is important to note that the distributions across education categories (Table 1) show a substantial underrepresentation of lower-educated people in all countries and no accurate representation of country differences across intermediate and higher education levels.

A unique aspect of KINMATRIX is that the data represent extended and complex kin by their strength in numbers. In anchor respondents' family networks, extended kin vastly outnumber nuclear kin (Table 2) and hence account for the large majority of anchor-kin dyads (Table 3). In other large-scale family data, these kin are typically lumped into residual categories as 'other relatives,' and their absolute number is ignored. KINMATRIX, by contrast, covers more than 50,000 dyads between anchors and their aunts and uncles, more than 85,000 dyads between anchors and their first cousins, around 50,000 anchor-grandparent dyads, and more than 17,000 dyads between anchors and complex kin.



**Table 1: Demographic characteristics of anchor respondents**

Country	Age	Sex: Woman	Educational level			Lives with partner	Has child(ren)	Parents separated
			low	medium	high			
Denmark (N = 154)	29.63	0.57	0.04	0.37	0.59	0.53	0.31	0.38
Finland (N = 241)	29.67	0.48	0.05	0.20	0.76	0.54	0.30	0.31
Germany (N = 1,208)	30.23	0.56	0.04	0.49	0.47	0.58	0.36	0.29
Italy (N = 1,909)	30.26	0.55	0.03	0.42	0.55	0.48	0.24	0.16
Netherlands (N = 394)	29.80	0.62	0.04	0.28	0.68	0.64	0.43	0.26
Norway (N = 127)	29.83	0.55	0.02	0.28	0.70	0.55	0.30	0.37
Poland (N = 1,732)	30.09	0.59	0.08	0.29	0.63	0.68	0.51	0.19
Sweden (N = 355)	30.17	0.48	0.03	0.44	0.52	0.51	0.28	0.38
UK (N = 1,313)	30.17	0.58	0.01	0.26	0.73	0.57	0.37	0.30
USA (N = 5,005)	30.29	0.60	0.02	0.16	0.82	0.52	0.41	0.39
Total (N = 12,438)	30.20	0.58	0.03	0.28	0.69	0.55	0.38	0.30

**Table 2: Number of nuclear, extended, and complex kin (anchor-kin dyads)**

Country	Nuclear kin			Extended kin			Complex kin			All kin			Histogram <sup>1</sup>				
	Min	Max	Mean	p50	Min	Max	Mean	p50	Min	Max	Mean	p50					
Denmark (N = 154)	2	11	3.54	3	4	81	14.19	12	0	13	1.79	0	6	87	19.52	18	
Finland (N = 241)	2	13	3.52	3	4	90	14.39	12	0	16	1.56	0	6	103	19.48	17	
Germany (N = 1,208)	2	12	3.20	3	4	88	11.89	10	0	20	1.24	0	6	111	16.33	14	
Italy (N = 1,909)	2	12	3.13	3	4	69	14.90	13	0	25	0.49	0	6	73	18.53	16	
Netherlands (N = 394)	2	11	3.42	3	4	59	15.25	13	0	22	1.10	0	6	64	19.78	18	
Norway (N = 127)	2	9	3.56	3	4	47	15.20	14	0	12	1.55	0	6	62	20.31	19	
Poland (N = 1,732)	2	13	3.46	3	4	59	14.96	13	0	18	0.59	0	6	66	19.01	17	
Sweden (N = 355)	2	13	3.58	3	4	73	13.68	12	0	22	2.03	0	6	91	19.29	18	
UK (N = 1,313)	2	11	3.41	3	4	71	14.91	12	0	30	1.21	0	6	76	19.53	17	
USA (N = 5,005)	2	14	3.59	3	4	113	17.00	15	0	33	2.13	0	6	117	22.72	20	

Note: <sup>1</sup>Histograms are cut at a maximum of 50 relatives. This threshold was exceeded by 245 of 12 438 respondents. All anchor respondents have a minimum of six biological kin by definition (biological parents and grandparents). Nuclear kin are biological parents and full siblings. Extended kin are grandparents, aunts, uncles, and first cousins. Complex kin are anchors' half-siblings, their parents' partners, and their parents' partners' children. See text for details.

**Table 3: Number of living kin by kinship type**

Kin category	Denmark	Finland	Germany	Italy	Netherlands	Norway	Poland	Sweden	UK	USA	Total
<b>Nuclear</b>											
Father	138	219	1,075	1,743	356	111	1,426	320	1,166	4,292	10,846
Mother	143	229	1,136	1,830	372	125	1,646	341	1,251	4,625	11,698
Brother	136	189	743	1,082	253	108	1,224	277	938	3,836	8,786
Sister	92	171	672	1,045	281	82	1,225	265	873	3,873	8,579
<b>Extended</b>											
Grandfather	43	59	303	298	101	28	289	65	296	1,092	2,574
Maternal	50	75	377	376	112	35	343	131	362	1,338	3,199
Grandmother	62	89	457	609	136	46	604	129	469	1,845	4,446
Maternal	74	105	557	740	168	52	772	171	550	2,067	5,256
Uncle	112	205	920	1,870	454	128	1,428	302	1,262	5,407	12,088
Maternal	134	195	795	1,724	346	110	1,366	245	1,098	4,663	10,676
Paternal	131	224	914	1,871	411	114	1,570	287	1,207	5,411	12,140
Aunt	106	191	833	1,731	334	102	1,533	275	1,044	5,047	11,196
Maternal	491	746	2,706	6,386	1,330	451	5,678	1,033	4,420	19,774	43,015
Cousin	432	745	2,469	5,768	1,127	438	5,408	993	3,873	18,453	39,706
Maternal	57	75	303	215	106	45	174	126	325	1,993	3,419
Complex											
Parent's new partner	46	55	242	163	66	25	172	112	229	1,509	2,619
Maternal	50	76	219	148	88	44	194	111	300	1,922	3,152
Half sibling	20	43	118	63	37	16	97	97	153	1,234	1,878
Maternal	43	26	144	101	49	27	73	89	173	1,090	1,815
Stepsibling	41	41	122	110	40	24	104	66	150	1,018	1,716
Maternal											
<b>Total</b>	2,401	3,758	15,105	27,873	6,167	2,111	25,326	5,435	20,139	90,489	196,804

Note: Table shows counts of living family members. In addition, the KINMATRIX data include information on 46,270 dead relatives, as well as 7,204 relatives whose living status has been reported as unknown.

### 3.2 Variables

The KINMATRIX data include four main sets of variables.

- *Anchor variables*: In addition to socioeconomic and demographic characteristics, the data include detailed information about anchor respondents' family structure and family biography (e.g., parental and grandparental separation), family-related norms and attitudes, and personal characteristics such as sexual orientation, subjective social status, life satisfaction, and self-rated health.
- *Anchor-kin relational variables*: Data about current relationships with living alters cover key dimensions of the solidarity model. These include emotional closeness, frequency of contact, distance (measured as travel time), conflict, and different types of support received from family members (money, advice, comfort, childcare). In addition, retrospective data are available about the importance of each alter (alive or deceased) and prospective data about alters as a safety net in future times of need.
- *Kin attribute variables*: In addition to demographic information on age and sex, data about attributes of living and deceased alters cover key dimensions of transmission (e.g., education, employment status, subjective social status, health). For complex kin, detailed data about family structure (e.g., time and duration of coresidence) are available.
- *Survey and data quality variables*: These indicators include standard information (e.g., weights, interview date and duration) as well as data about self-assessed response quality and several flag variables pertaining to observed response quality (e.g., number and fraction of 'don't knows,' invalid names, straightlining, implausible kin attribute data, etc.).

The full questionnaires and complete information on question and answer formats (survey screenshots) are available in the [online supplement](#).

### 4. KINMATRIX data for scientific use: Potential and limitations

Research in survey methodology has highlighted concerns about data from non-probability samples in general and data quality issues specifically arising from recruitment from crowdsourcing marketplaces and access panels (Arndt et al. 2022; Chmielewski and Kucker 2020; Moss et al. 2023; Peer et al. 2022). Although doubts about non-probability samples remain prevalent in demography and quantitative

sociology, collection and analysis of such data are on the rise. This trend is reinforced not only by increasing quality concerns about the high cost of probability sampling, but also by advances in non-probability survey methodology showing a reasonable extent of ‘natural’ randomization, especially in broadly recruited quota samples, the effectiveness of quality controls, cleaning, and adjustment steps during and after data collection, and the robustness of many results – especially bivariate and multivariate estimates – to sampling technique (Vehovar, Toepoel, and Steinmetz 2016; Rohr, Silber, and Felderer 2023).

Selection bias by uncontrolled inclusion probabilities was inevitable but mitigated by the focus on a young target group of anchor respondents well-suited to the web-based design of the KINMATRIX survey (Dillman and Smyth 2007; Kaplowitz, Hadlock, and Levine 2004; Shih and Fan 2008). Despite this benefit, quality issues remained in the raw data, notably response problems related to task difficulty (large numbers of alters and kinship types, recollection issues), confidentiality and sensitive topics (real names, intimate relations, death), and strong satisficing (survey speeding, straightlining, and excessive ‘don’t knows’). These issues were addressed by several quality checks that removed invalid data either during the survey or in the course of cleaning the raw data. Cleaning procedures were based on validity checks focusing especially on reported knowledge about alters’ numbers, names, and dead/alive status (see the [online supplement](#) for details).

The scientific use file obtained after cleaning was validated by comparisons with various benchmarks calculated from several probability-based surveys (ESS, EVS, ISSP, SOEP, FReDA-pairfam, GSS). Selected benchmarking results are presented in the [online supplement](#). In several of the countries studied, the KINMATRIX samples closely matched external benchmark data for the number of siblings, living parents and grandparents, the probability of grandparental separation, and relational characteristics such as contact frequency and emotional closeness to nuclear kin.

#### **4.1 Limitations**

Users of the KINMATRIX data should be aware of several data limitations. First, even the comprehensive coverage of extended kin remains partial. Specifically, the KINMATRIX data tend to underestimate the true number of extended kin (see the [online supplement](#)). This underestimate partly reflects kin that were unknown to anchors and partly kin that anchors knew but did not report. For studies on solidarity and transmission, their omission may be less consequential if those kin were peripheral or irrelevant to anchor respondents’ lives. Second, the maternal line was more strongly affected by the incomplete coverage of extended kin. As visible in Table 3, paternal extended kin were

more numerous than their maternal counterpart, a bias most likely caused by the questionnaire ordering whereby paternal kin were surveyed before maternal kin. For analyses of solidarity and transmission in paternal and maternal lines, this bias – although moderate in magnitude – should be considered.

Third, the sample is biased towards higher education levels among anchor respondents (Table 1), and this bias extends also to their parental background. Consideration of this selectivity (common also in probability samples) is particularly relevant to studies of family transmission. It also limits the case numbers available for the analysis of lower-educated anchor respondents and for comparisons across fine-grained educational categories. Fourth, a general limitation affecting transmission studies is the restricted coverage of relevant constructs (e.g., data on alters' wealth and earnings are not available) and the reliability of data on alters' attributes, such as their education, social status, employment status, age, demographic behavior, and even vital status. The latter point concerns in particular extended and complex kin about whom anchor respondents' knowledge may be vague or absent.

Moreover, while KINMATRIX covers biologically related kin, we recognize the limitation of not including fictive kin such as close friends or neighbors, who can be crucial, especially for single parents or childless individuals (Brumbaugh 2017). In some cases, these non-biological relationships may provide more support than distant biological relatives (Voorpostel 2013). As a result, KINMATRIX is selective in capturing the full range of significant social ties, particularly for those in specific family situations.

Finally, case numbers for the multi-actor data are limited. The causes were anchor respondents' limited willingness to invite multi-actors to the survey, multi-actors' low response rates, and technical and legal constraints undermining the effectiveness and yield of the approach. The data ( $N = 1,887$  multi-actors clustered in  $N = 1,396$  families) still carry potential for validation and in-depth analysis, especially in the Italian sample in which multi-actor response rates were relatively high. Moreover, complete network data are available for families in which all nuclear family members (parents and full siblings) participated.

## 4.2 Potentials

Despite these limitations, the KINMATRIX data offer unique research potential, allowing analysts of solidarity and transmission to ask new questions and to give new answers to pertinent questions in these fields (see Leopold et al. 2024 for a summary of initial results). The following list highlights selected potentials:

- An expanded view of solidarity and transmission: In contrast to narrow representations of the family in extant data, KINMATRIX allows extending the study of both processes to a much larger set of relevant family members. The data support new assessments of, for example, the size of the family safety net, how intimacy and support potential vary by the degree and line of kinship, and the influence of the wider family on status attainment.
- An integrative view of solidarity and transmission: Theories of reproduction are predicated on social relations as conduits of status transmission, but analyses are commonly reduced to attribute correlations. KINMATRIX data on both the attributes of and social relations to a large array of family members allow linking transmission to solidarity by combining relational data on the quality of ties with attribute data on status and behaviors. This integration carries a potential for building stronger explanatory models of the family.
- A comparative view of solidarity and transmission: KINMATRIX data allow obtaining new insights from European diversity in terms of kinship structures, the quality of family ties, and contextual factors that may promote or undermine solidarity and transmission in the immediate and the extended family.
- Relative and absolute perspectives on solidarity and transmission: Even if the ties to extended kin are weaker on average, their larger absolute number offers a wide opportunity structure for both processes. In KINMATRIX data, the comprehensive coverage of extended kin adequately weights extended kin by their strength in numbers to assess both the relative and absolute importance of nuclear and extended kin for solidarity and transmission outcomes.
- A closer fit between the empirics and realities of family life: KINMATRIX data provide a more inclusive (although still partial) coverage of family members who matter to individuals, a benefit that is especially relevant in ethnic minorities and lower-status families in which extended kin are recognized as vital not only as a safety net but also as facilitators – or inhibitors – of upward social mobility (Bott 1957; Stack 1974; Hansen 2005; Lareau 2003; Sarkisian and Gerstel 2004).
- A new view of family erosion and decline: KINMATRIX data allow examining contemporary families not only as prime sources of solidarity and transmission but also as dispersed and voluntarist arrangements, which may or may not provide support and exert social influence. The nominalist boundaries of ego-centric networks surveyed in KINMATRIX offer name generators that are not predicated on close relations or important roles in respondents' lives. Inclusion of absent, disrupted, and strained relationships renders the data suitable not only for the analysis of family cohesion but for empirical tests of competing models

highlighting relationships that are increasingly diverse, uncertain, and competing for legitimacy and resources (Popenoe 1993; Stacey 1997).

- Unique data suitable for import into various related research fields beyond solidarity and transmission: These potentials include combining novel demographic estimates on the presence and number of kin (Caswell 2019; Alburez-Gutierrez, Williams, and Caswell 2023) with KINMATRIX data on the substantive content of relationships with these kin; exploring the role of ‘forgotten kin’ by leveraging the exceptionally large numbers of dyads available in KINMATRIX on relationships with aunts, uncles, and cousins; assessing the consequences of parental divorce, separation, and death for cohesion, erosion, and compensation within the wider family network; providing new assessments of gendered family roles (e.g., kinkeeping) and contrasting maternal vs. paternal lines in Western kinship systems; assessing transnational family networks of first- and second-generation immigrants; and evaluating the benefits and limitations of access panels and large-scale online web surveys for research on family relations and social networks.

## 5. Conclusion

KINMATRIX contributes to the research infrastructure by offering comprehensive relational and attribute data collected for entire kinship networks, a wide range of relatives, and diverse family forms. These data align with the complex demographic and social reality of contemporary families and can add to our understanding of key family processes such as solidarity and transmission. Despite its limitations, such as incomplete kin coverage and potential bias due to non-probability sampling, KINMATRIX offers a unique data resource for examining family ties and their influence on individual and collective outcomes. Its broad scope supports comparative analyses across European societies and beyond. Researchers interested in KINMATRIX can apply for early access at [OSF](#). The full public release is scheduled for the end of 2024 and will be announced on the project’s website [www.kinmatrix.eu](http://www.kinmatrix.eu).

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