Data Observer

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An Introduction to the German Twin Family Panel (TwinLife)

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1 Overview

The German Twin Family Panel (TwinLife) was designed to narrow the gap between behavior genetic and social scientific studies of social inequalities. To this end, TwinLife enables the investigation of genetic and environmental influences on the development of social inequalities over the life course. While many other countries (e. g. the Netherlands; Boomsma et al. 2006) have twin registries, there is no such registry for Germany. Previous studies that collected twin data in Germany have either focused on particular regions or have not used probability-based sampling designs (Busjahn 2013; Hahn et al. 2013; Kandler et al. 2013). By contrast, TwinLife is the first twin (family) study in Germany realizing a population register-based sampling design (Mönkediek et al. 2019; Hahn et al. 2016).

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In the first wave of the panel, data on 4,097 families with reared-together monozygotic or same-sex dizygotic twin children was collected (Diewald et al. 2019). The panel is running since 2014. Every other year face-to-face interviews are conducted in the households of the families and telephone interviews are carried out in the years in between. Until the spring of 2020, three face-to-face and two telephone data collections have been realized. TwinLife's sampling design includes all parts of Germany, and covers the whole range of the educational, occupational, and income structure (Lang/Kottwitz 2017). Thus, TwinLife allows for reliable comparisons with twin data from other countries as well as with other population data within Germany. The full coverage of the distributions of core socioeconomic indicators is especially important, since the lower and upper bounds of these distributions are particularly relevant for analyses of differential genetic and environmental influences on traits.

2 Panel design

TwinLife's target population consists of four cohorts of twins born 2009/10 (cohort 1), 2003/04 (cohort 2), 1997/98 (cohort 3), and between 1990 and 1993 (cohort 4). At the time of the first survey (2014/2015), these twins were aged 5 (cohort 1), 11 (cohort 2), 17 (cohort 3), and 23 to 24 (cohort 4). Over the course of the panel, these cohorts go through the major developmental transition phases of childhood, adolescence, and young adulthood (Mönkediek et al. 2019; Hahn et al. 2016). The youngest twins (cohort 1) were shortly before school-entry when they were interviewed for the first time. Their educational transitions until the end of secondary schooling will be comprised by the panel. In contrast, the oldest twins (cohort 4) were interviewed for the first time prior to or shortly after leaving the parental home and pursuing tertiary education or establishing themselves in the labor market. For them, the panel covers the life phase in which typically a family is formed as well as the early employment career.

In the TwinLife study, this cohort-sequential design is combined with an extended twin family design (ETFD) that includes parents and siblings. In the ETFD of TwinLife, the sibling who is closest in age to the twins (and at least five years old) as well as the biological and, if present, the social parents (i. e. partners of mothers or fathers) are surveyed in addition to the twins. Moreover, if the adult twins have partners, these partners are part of the sample, too. Such an ETFD enables a better assessment of family influences on the children's development and less biased estimates of genetic transmission than the classical twin design (Keller et al. 2010). However, such a design also necessitates collecting data from multiple informants per family who sometimes live in more than one household.

The zygosity of the twins in TwinLife was determined based on physical similarity questionnaires (Goldsmith 1991; Oniszczenko et al. 1993). The resulting zygosity classification was validated based on molecular genetic data for a subpopulation of 328 randomly selected twin pairs. The validation results showed that more than 95 % of the twin pairs were correctly classified (for more information regarding the zygosity classification, see Lenau et al. 2017). Due to cost and efficiency considerations, only same-sex and no opposite-sex dizygotic twins were sampled for TwinLife. On the one hand, this reduced the target sample size and thus, the number of necessary sampling points (communities). On the other hand, it simplified the identification process of potential twin families (Brix et al. 2017). However, as a result, it is not possible to examine the effects of within-twin-pair gender differences on phenotypes with TwinLife. Further, since the surveys are conducted in German, the sample is restricted to families with good proficiency of the German language.

Every other year face-to-face interviews with the twins and their families are realized at their homes. To shorten the time interviewers spent in a household, these face-to-face interviews use a combination of different survey modes which can be filled in simultaneously with different respondents. The mix of instruments consists of computer-assisted personal interviews (CAPI), computer-assisted self-interviews (CASI), and paper and pencil interviews (PAPI) (Brix et al. 2017). In the years between the face-to-face surveys, the families are interviewed by telephone for cost and efficiency reasons.

3 Sampling and representativeness

For the first face-to-face survey of the TwinLife panel, the target sample size comprised 1,000 twin families in each cohort sampled from official registries of 500 communities with more than 5,000 inhabitants all over Germany. Twin families from smaller communities were not sampled due to prohibitively high survey expenditures. The chosen communities were sampled out of an official registry of communities, listing approximately 11,900 communities. To achieve the target sample size, a purposeful oversampling of larger communities with more than 50,000 residents was necessary. The registration offices in the sampled communities were contacted to identify potential twin families based on registration information about persons with the same sex and same or similar birthdates registered at the same address. To identify twin families in the oldest cohort (cohort 4), in which the twins had potentially already moved out of their parents homes, registries of residents dating several years back were used (for more details on the register-based sampling design, see Lang/Kottwitz 2017).

Concerning zygosity, about 45 % of the twin pairs in cohorts 1, 2 and 3, and 53 % of the twin pairs in cohort 4 are monozygotic. These zygosity distributions show that the probability-based sampling design counteracted an overrepresentation of monozygotic twin pairs typical for non-probability-based twin samples (Lykken et al. 1987). To assess the sample's representativeness with regard to the social stratification in Germany, Lang and Kottwitz (2017) compared the distributions of parental education, occupational status, household income and migration background in the first wave of TwinLife with a proxy-twin sample based on the German Microcensus – a representative household register sample (Destatis 2014). The analyses revealed an overrepresentation of tertiary-educated families and an underrepresentation of families with no German citizenship as well as a slightly higher median income and mean of parental occupational status in the TwinLife sample. While the lower share of families with no German citizenship is partly due to only sampling families with good proficiency of the German language (see above), the findings overall indicate that taking part in the survey was to some degree influenced by socioeconomic factors. Nevertheless, the results also show that the sample covers the full distributions of core socioeconomic indicators facilitating social stratified analyses using the TwinLife data.

4 Panel description

In Table 1, the sample sizes and participation rates in the first two face-to-face interviews and the first telephone interview of TwinLife are depicted by cohort, twins' zygosity, and gender. The reported sample sizes and participation rates are calculated based on at least one family member participating in the respective survey. For the first face-to-face interview, sample sizes and participation rates of complete twin pairs are identical to those reported in Table 1 since only families in which both twins did partake in the survey were included in the sample. After the first face-to-face survey, 98 % of the families agreed to further participate in the panel.

In the first telephone interview, participation rates were above 70 % in each cohort (see Table 1) and around 5 % of the families dropped out of the panel by permanently refusing to participate. While in the face-to-face surveys so far data on all respondents aged 5 and above were collected, only individuals aged 10 and above who participated in the first face-to-face interview and were living with one of the twins were surveyed in the first telephone interview. For the other cohorts, participation rates calculated based on complete twin pairs were about 60 % in cohorts 2 and 3, and around 40 % in cohort 4.

Table 1: Families in the first two face-to-face and the first telephone interviews of TwinLife.[a]

1st face-to-face interview	Cohort 1 (%)	Cohort 2 (%)	Cohort 3 (%)	Cohort 4 (%)	Total (%)
Monozygotic, male	210 (20.8)	191 (18.3)	218 (20.6)	213 (21.7)	832 (20.3)
Monozygotic, female	225 (22.3)	230 (22.1)	280 (26.4)	311 (31.6)	1,046 (25.5)
Dizygotic, male	280 (27.8)	309 (29.6)	235 (22.2)	198 (20.1)	1,022 (25.0)
Dizygotic, female	292 (28.9)	311 (29.8)	327 (30.8)	260 (26.5)	1,190 (29.1)
No zygosity information	3 (0.3)	2 (0.2)	1 (0.1)	1 (0.1)	7 (0.2)
Total	1,010 (100.0)	1,043 (100.0)	1,061 (100.0)	983 (100.0)	4,097 (100.0)
1st telephone interview					
Monozygotic, male	142 (19.9)	138 (18.5)	162 (20.3)	155 (21.6)	597 (20.1)
Monozygotic, female	162 (22.7)	159 (21.3)	213 (26.7)	224 (31.2)	758 (25.5)
Dizygotic, male	193 (27.1)	224 (30.0)	187 (23.5)	147 (20.5)	751 (25.2)
Dizygotic, female	216 (30.3)	225 (30.1)	235 (29.5)	192 (26.7)	868 (29.2)
No zygosity information	–	1 (0.1)	–	1 (0.1)	2 (0.1)
Total	713 (100.0)	747 (100.0)	797 (100.0)	719 (100.0)	2,976 (100.0)
2nd face-to-face interview					
Monozygotic, male	150 (20.0)	144 (19.1)	133 (20.2)	129 (21.8)	556 (20.2)
Monozygotic, female	166 (22.2)	169 (22.4)	180 (27.4)	179 (30.2)	694 (25.2)
Dizygotic, male	212 (28.3)	229 (30.3)	143 (21.7)	124 (20.9)	708 (25.7)
Dizygotic, female	220 (29.4)	212 (28.0)	202 (30.7)	160 (27.0)	794 (28.8)
No zygosity information	1 (0.1)	2 (0.3)	–	1 (0.2)	4 (0.2)
Total	749 (100.0)	756 (100.0)	658 (100.0)	593 (100.0)	2,756 (100.0)

Source: TwinLife (doi: 10.4232/1.13208), own calculations.

[a]Reported sample sizes and participation rates are defined by at least one family member participating in the respective survey.

Regarding the second face-to-face interview at home, participation rates calculated with reference to the first face-to-face survey were again above 70 % in cohort 1 and 2, and slightly above 60 % in cohort 3 and 4 (see Table 1). Looking at complete twin pairs instead, participation rates were around 70 % in cohorts 1 and 2, above 50 % in cohort 3 and above 40 % in cohort 4. These results show that there is longitudinal information on both twins in almost all participating families of the two younger cohorts in the panel. The lower participations rates in the two older cohorts are largely due to the older twins being more mobile and leaving the parental home. In consequence, it is more difficult to contact these adolescents and young adults and to schedule interviews with them (Groves/Couper 1998).

On the individual level, the TwinLife panel contains information on 16,954 individuals for the first face-to-face interview, 8,721 individuals for the first telephone interview and 10,956 individuals for the second face-to-face interview. Thus, on average around 4 persons per family were interviewed in the first and second face-to-face survey, and about 3 persons per family were interviewed in the first telephone survey. The lower number of persons per family surveyed in the telephone interview is mostly due to age selection criteria for twins and siblings of the twins implemented for this type of data collection (see above).

5 Overview of measurements

The TwinLife study comprehensively captures characteristics of children and their families and related social inequalities in six different domains (Figure 1): (I) skill formation and education, (II) career and labor market attainment, (III) political and social integration and participation, (IV) subjective perception of quality of life, (V) physical and psychological health, and (VI) deviant behavior and behavioral problems. All available constructs can be found in a detailed overview at the TwinLife page of the GESIS Data Catalogue (https://doi.org/10.4232/1.13208).

For constructs which have also been assessed in other representative family or household samples in Germany like the German Socio-Economic Panel (SOEP) or the German Family Panel (Pairfam), TwinLife often implements the same measurements. Such similar measurements facilitate comparisons of findings with these non-twin panel studies. The measurements for TwinLife also include assessments of participant's cognitive abilities as well as transcripts of photos of children's medical records and school report cards. Cognitive abilities are measured using the Culture Fair Test (CFT; Weiß/Osterland 2012; Weiß 2006) which assesses nonverbal (fluid) intelligence as a proxy for general cognitive ability (for

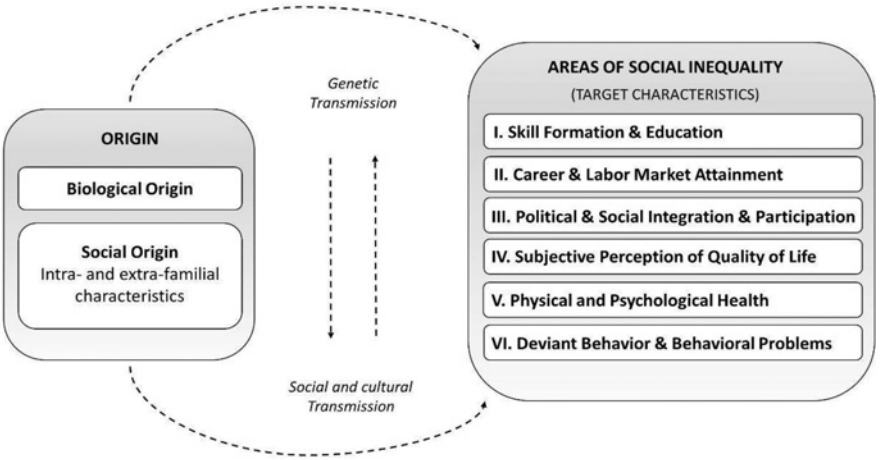

Figure 1: Basic concept and six domains of social inequality.

further details on the implementation of cognitive tests, see Gottschling 2017). Children's medical records were collected from booklets (called "U-Heft" in Germany) which document information on, for example, height, weight, head circumference and diseases. The transcripts of school report cards contain information about, for example, school type, class level and grades in specific subjects (for more information on the report card transcripts, see Mattheus et al. 2017).

6 Outlook: Molecular genetic extension

Traditionally, twin studies and registries are based on comparisons of monozygotic and dizygotic twins to measure the influence of genes and environments on traits. By examining an individual's deoxyribonucleic acid (DNA) sequence and comparing it to another individual's DNA sequence, genotyping offers further options to analyze genetic and environmental effects as well as their interplay – gene-environment correlations and interactions (Boomsma et al. 2002). Since measures based on such molecular genetic information can readily be used with standard social science models, a growing number of twin surveys and registries additionally genotype participants. For example, such extensions are implemented in the Twins Early Development Study (TEDS) (Haworth et al. 2013), the UK Adult Twin Registry (Spector/Williams 2006), or the Swedish Twin Registry (Magnusson et al. 2013).

For the TwinLife study, saliva samples of the twins, their biological parents, and their siblings are being collected between 2018 and 2020 as part of the third face-to-face survey in cooperation with the Universitätsklinikum Bonn. It is planned to integrate this molecular genetic information into the longitudinal survey data at a later point in time. Based on the molecular genetic data, it will be possible to construct polygenic scores (PGS) for a variety of phenotypes relevant to development, attainment and social mobility. Furthermore, computations of genome-wide association studies (GWAS) for specific traits can be used for comparisons with heritability estimates based on twin correlation or structural equation models as well as on single-nucleotide polymorphisms (SNPs).

7 Recent major findings

Important aspects of the TwinLife teams' research are educational outcomes and cognitive abilities. With regard to cognitive abilities, Gottschling et al. (2019) examined the Scarr-Rowe interaction-hypothesis, which suggests that the heritability of cognitive abilities is higher under more privileged socioeconomic conditions. Using a modified twin correlation model, they showed that the Scarr-Rowe hypothesis adequately describes the pattern of results in middle-childhood and – to some degree – in adolescence but not in adulthood in our German twin sample. Concerning the final educational degree attained, Baier and Lang (2019) found a pattern following the Scarr-Rowe hypothesis for the young adults in the oldest birth cohort of twins. Regarding the type of schooling track children attended, Schulz et al. (2017) showed influences of parental socioeconomic resources over and above children's as well as parent's cognitive abilities. With respect to achievement motivation as a prerequisite of educational success, Klassen et al. (2018) investigated its etiology and found that non-shared environmental factors as well as additive and non-additive genetic variance played major roles.

This section covers only a small selection of the publications based on TwinLife data. Research using the TwinLife panel also comprises other areas like social and political integration, health or personality development.

8 Data access

Data of the first home and telephone interviews of the TwinLife panel are available as a scientific use-file (SUF) at the data catalogue of the GESIS data archive (study identifier ZA6701). For the current release see: https://doi.org/10.4232/1.13208

The TwinLife SUF can be obtained free of charge. To access the SUF, researchers have to fill in and sign a data use agreement including a short description of their intended study and their institutional affiliation. The data use agreement can be downloaded at the GESIS data archive using the doi stated above. Detailed instructions how to fill in the data use agreement are available at the data catalogue webpage of GESIS which is also accessible using the doi stated above. The filled in and signed agreement has to be send by mail, post or fax to:

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All variables in the TwinLife SUF and the related instruments are documented at: https://paneldata.org/twinlife

Additional documentations of the TwinLife data (such as a codebook, a detailed description of missing codes or further information on the data structure) are available at: https://www.twin-life.de/de/twinlife-series

The TwinLife SUF can also be used for teaching. Therefore, the instructor and all participants of a course using the SUF have to fill in, sign, and send in the data use agreement described above.

For specific analyses, the TwinLife sample can be matched with a range of neighborhood-related variables (e. g. the type of housing of respondents). The variables were calculated based on data collected by the data research and marketing firm Microm. Prospectively, this additional neighborhood-related data will be accessible by special agreement.

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