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# The Socio-demographic Structure of the First Wave of the TwinLife Panel Study: A Comparison with the Microcensus

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## **Abstract**

The TwinLife panel is the first longitudinal study of twin families in Germany based on a national probability sample. TwinLife has been developed to facilitate genetic sensitive research on social inequalities. The aim of this paper is to assess the usability of the TwinLife sample for such research. Therefore, first, we analyze if the social background of twins living in Germany is adequately represented in the TwinLife sample; and second, we also investigate if there are socio-demographic differences between twin and other multiple-child households in Germany which would restrict the generalizability of findings based on the TwinLife study. Specifically, we compare the distributions of key socio-demographic indicators in TwinLife with the German Microcensus using a proxy-twin and a multiple-child household sample. Our analyses show that the TwinLife sample covers the full distributions of core social inequality indicators including the lower and upper bounds, enabling researchers to use TwinLife for detailed studies of the gene-environment interplay. Furthermore, we demonstrate that (proxy-)twin and other multiple-child households in Germany are similar regarding most socio-demographic indicators. However, our analyses also indicate that participation in the first wave of the TwinLife panel was slightly selective with respect to parental education and German citizenship, especially in the younger cohorts of the study. We suggest a weighting scheme to address this selectivity.

**Keywords:** Twin Families, Multiple-Child Families, Family Demography, Sampling Design, Extended Twin Family Design, Germany



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Studying twins reared together is a prominent research strategy to assess the influence of genetic endowment on human development (Polderman et al., 2015). By comparing monozygotic twins – who are genetically (almost) identical – with dizygotic twins – who share about half of the genes that vary between humans (like ordinary siblings), it is possible to estimate the share of variance in an outcome attributable to (additive) genetic influences (Plomin et al., 2016).<sup>1</sup> Nevertheless, such estimates of genetic influences are by no means a fixed quantity but strongly dependent on the development stage (i.e., the age) of the twins (Haworth et al., 2010; Turkheimer, 2000) as well as on the environmental conditions in which a genetic potential is actualized (Shanahan & Hofer, 2005; Bronfenbrenner & Ceci, 1994). A central facet of these environmental conditions is the social background (Guo & Stearns, 2002). In consequence, studying the different forms in which genetic influences depend on environments – so called gene-environment interactions and correlations – is a major focus of current behavior genetic research (Zavala et al. 2018; Tucker-Drob & Bates, 2016) as well as a topic of growing interest in the research on social inequalities (Selita & Kovas, 2019; Diewald et al., 2016; Nielsen, 2016).

However, twin samples covering a wide range of environmental conditions and development stages are needed to conduct studies on the influence of genes on social inequalities. The TwinLife panel – which is run in cooperation by research teams at Bielefeld University and Saarland University – was designed to facilitate such research and is the first longitudinal study of twin families in Germany based on a national probability sample (Mönkediek et al., 2019, Hahn et al., 2016). To assess the usability of the TwinLife sample for social stratified research on genetic influences, we address two research questions in this paper: first, is the social background of twins living in Germany captured by the TwinLife sample to facilitate genetic sensitive analyses differentiated by social background? And second, is the

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1 A basic estimate of additive genetic influences is given by two times the difference between monozygotic and dizygotic twins in the correlation within twin pairs of an outcome (so called Falconer's Formula, Falconer, 1960). For a discussion of the further assumptions involved in estimating genetic influences based on twins reared together, see Stenberg (2013).

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social background of twin households comparable to all multiple-child households in Germany in order to support the generalizability of social stratified analyses on genetic influences?

In contrast to many other countries (e.g., The Netherlands: Ligthart et al., 2019; Sweden: Zagai et al., 2019), no twin registry is available for Germany to answer these research questions. Alternatively, we compare the TwinLife sample with two selected samples based on the German Microcensus Survey conducted by the Federal Statistical Office (Destatis, 2014a, 2014b; Lengerer et al., 2007): a proxy-twin household sample and a multiple-child household sample. Specifically, we compare parental education, household income, parental citizenship status, the composition of the households, and the population sizes of the communities of residence. In addition, we investigate maternal age at childbirth as a potential reason for differences in the distributions of these social background indicators. Thus, if the TwinLife sample is representative for twin families in Germany, we expect to see no relevant differences in the distributions of these social background indicators between the TwinLife and the Microcensus proxy-twin samples (hypothesis 1).

Moreover, since the environmental conditions in which children are reared can systematically differ between twin and other types of multiple-child families, it can be questioned if results obtained by studying twins are generalizable to a whole population. In some cases – like the age gap between siblings – such differences are undeniable. Regarding the distributions of social background indicators, differences between twin and other multiple-child families cannot be precluded. If the social backgrounds of twin and other multiple-child families in Germany are similar, we should not find any relevant differences in the distributions of the analyzed indicators between the Microcensus proxy-twin and multiple-child samples (hypothesis 2).

The paper is structured as follows. The following section describes the TwinLife and Microcensus samples as well as the indicators and methods we apply to answer our two research questions. It also contains a deeper introduction into the study design and sampling strategy of the TwinLife panel to assist researchers in using the relatively new TwinLife data. Afterwards, the results of our comparisons are presented. The final part of the article provides a conclusion.

## Data and Methods

### The TwinLife Panel Study

#### *Study Design*

The TwinLife study collects longitudinal data on families with monozygotic or dizygotic twin children. To exclude effects of within-twin-pair gender differences, the study includes only same-sex dizygotic twins. The base population of TwinLife consists of four birth cohorts of twins: the youngest twins, in cohort 1, were born in 2009 or 2010, the twins in cohort 2 in 2003 or 2004, the twins in cohort 3 in 1997 or 1998, and the oldest twins, in cohort 4, between 1990 and 1993. At the time of the first survey, these twins were aged around 5, 11, 17, and 23 to 24. Over the planned panel period, TwinLife covers important life course transitions ranging from school entry to the labor market entry phase, and also important life stages for meeting a partner and starting a family. The TwinLife surveys are conducted annually and survey modes alternate between face-to-face interviews at home and telephone interviews.

In addition, the TwinLife study combines this cohort-sequential design with an extended twin family design (ETFD). As part of the ETFD, the biological and, if applicable, the social parents (i.e., partners of mothers and fathers), and the sibling that is closest in age to the twins are surveyed as well as the twins themselves. Moreover, the partners of adult twins are also included. All of these family members are included in the design irrespective of whether they live in the same household as the twins or not. A family in TwinLife can therefore consist of several households, i.e., the households are nested within the families. The minimum requirement for inclusion as a valid family case in the TwinLife panel was the participation of both twins and one of the biological or social parents in the first wave.<sup>2</sup> A further design requirement was that the twins were raised together, i.e., lived in the same household until age 16. The family perspective of the ETFD facilitates the study of different degrees of genetic similarity which is important for detailed analysis of the manifold influences of the family environment on the development of the twins.

#### *Sampling Strategy*

The target net sample size for wave 1 of the TwinLife panel was 1,000 twin families in each of the four birth cohorts with approximately half of the families having monozygotic and the other half having same-sex dizygotic twins. To obtain a sample with these design characteristics, a national probability-based sampling procedure was implemented in two steps (Brix et al., 2017): first, a sample of 500

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<sup>2</sup> Exceptions are orphan families where there is no parent to participate. There are four families of this type in the net sample of the panel.

out of approximately 11,900 communities was drawn to generate addresses where twin families matching the design requirements resided. Potential twin families in cohorts 1 to 3 were identified by locating persons of the same sex with the same or similar birthdates registered at the same address according to the current registry of residents for the respective communities. Families in cohort 4 were also selected based on previous registries of residents containing address data prior to reported house moves. Using these previous addresses, an inquiry for the current address of the persons identified as probable twins was carried out. Second, a gross sample of 13,359 addresses out of around 19,000 addresses provided by the local registry of residents was drawn; 2,736 for cohort 1, 2,697 for cohort 2, 2,823 for cohort 3, and 5,103 for cohort 4.

Given these gross sample sizes, it was a priori obvious that the sampling design could not be proportional. Thus, each of the cohorts 1 to 3 is composed of two years of birth and cohort 4 of four years of birth. Population statistics for twin families in Germany are not available, but it is known that there are approximately 7,000 same-sex twin births each year (about 0.01 percent of all annual births, Destatis, 2013). Consequently, a design using the gross sample sizes described above and based on a cohort composed of only one year of birth would have to cover around 40 percent of the population for cohorts 1 to 3 and 75 percent for cohort 4. Using multiple-year birth cohorts reduces these shares to approximately 20 percent.

A proportional implementation of this design would necessitate conducting face-to-face interviews in around 2,500 communities which is impracticable. Three subsamples of communities were therefore selected instead: first, a proportional sample of 180 communities with 10,000 or more inhabitants was drawn according to the political community size classification for Germany (GKPOL) (“base sample”). Second, a disproportionate sample (with higher sampling probabilities for larger communities) of 60 communities with 50,000 or more inhabitants was selected to obtain the necessary coverage of the target population (“urban sample”). Third, an additional proportional sample of 260 communities with between 5,000 and 19,999 inhabitants was drawn (“rural sample”).<sup>3</sup> The base sample consists of 5,575 addresses (41.7 percent of the gross sample), the urban sample of 6,558 addresses (49.1 percent of the gross sample), and the rural sample of 1,226 addresses (9.2 percent of the gross sample). This sampling, which is disproportional overall, leads to an overrepresentation of addresses located in urban communities in the TwinLife panel in comparison to all addresses registered in communities with 5,000 or more inhabitants (Brix et al., 2017).

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3 Communities with fewer than 5,000 inhabitants are excluded by the TwinLife design. This is because, on average, only one or two twin families over all birth cohorts studied are expected to reside in a community of this size, making conducting face-to-face twin family interviews in communities like this prohibitively expensive and at the same time particularly problematic with respect to a possible re-identification.

### *TwinLife Sample*

The gross sample of addresses described above was used for the face-to-face interviews of the TwinLife panel, wave 1. The data collection for twins born in 2009, 2003, 1997, and 1990 or 1991 was carried out between September 2014 and May 2015. For twins born in 2010, 2004, 1998, and 1992 or 1993, data collection started in September 2015 and was completed in April 2016.

Table 1 shows distributions of the gross and net samples differentiated by cohort. 10.5 percent of the addresses in the gross sample were invalid contact addresses and 4.2 percent did not comply with the requirements of the design, leaving an adjusted gross sample of 11,405 cases. In cohorts 1 to 3, around 10 percent of the cases in the adjusted gross sample were permanently absent or sick during

*Table 1* Gross and net samples of TwinLife

	Cohort 1 (%)	Cohort 2 (%)	Cohort 3 (%)	Cohort 4 (%)	Total (%)
Gross sample	2,736 (100.0)	2,697 (100.0)	2,823 (100.0)	5,103 (100.0)	13,359 (100.0)
▪ no contact address	338 (12.4)	261 (9.7)	220 (7.8)	580 (11.4)	1,399 (10.5)
▪ no match with design	127 (4.6)	93 (3.4)	89 (3.2)	246 (4.8)	555 (4.2)
Adjusted gross sample	2,271 (83.0)	2,343 (86.9)	2,514 (89.1)	4,277 (83.8)	11,405 (85.4)
Adjusted gross sample	2,271 (100.0)	2,343 (100.0)	2,514 (100.0)	4,277 (100.0)	11,405 (100.0)
▪ absent or sick	258 (11.4)	267 (11.4)	237 (9.4)	891 (20.8)	1,653 (14.5)
▪ refusal	870 (38.3)	906 (38.7)	1,060 (42.2)	2,190 (51.2)	5,026 (44.1)
▪ family not complete	31 (1.4)	25 (1.1)	28 (1.1)	45 (1.1)	129 (1.1)
▪ address not used	69 (3.0)	60 (2.6)	80 (3.2)	80 (1.9)	289 (2.5)
▪ other reason	33 (1.5)	42 (1.8)	48 (1.9)	88 (2.1)	211 (1.9)
Net sample	1,010 (44.5)	1,043 (44.5)	1,061 (42.2)	983 (23.0)	4,097 (35.9)
Male, monozygotic	209 (20.8)	191 (18.4)	218 (20.6)	212 (21.6)	830 (20.4)
Male, dizygotic	279 (27.8)	307 (29.6)	235 (22.2)	198 (20.2)	1,019 (25.0)
Female, monozygotic	225 (22.4)	229 (22.1)	280 (26.4)	311 (31.7)	1,045 (25.6)
Female, dizygotic	291 (29.0)	309 (29.8)	326 (30.8)	259 (26.4)	1,185 (29.1)
Total	1,004 (100.0)	1,036 (100.0)	1,059 (100.0)	980 (100.0)	4,079 (100.0)

*Note:* The number of families used in this study declines to 4,079 compared to the net sample since in 11 families the multiples are triplets and for seven twin pairs no information about their zygosity is available.

*Sources:* Brix et al. (2017) and TwinLife (doi: 10.4232/1.12665), own calculations

the field phase and 40 percent refused to participate. In cohort 4, the sickness rate was twice as high and half of the sample refused participation. In 1.1 percent of the cases, it was not possible to interview all the necessary family members according to the design requirements, 2.5 percent of the addresses were not used because the target sample size had already been obtained, and 1.9 percent of the cases did not participate for other reasons.

This results in a net sample for wave 1 of 1,010 families in cohort 1, 1,043 families in cohort 2, 1,060 families in cohort 3, and 984 families in cohort 4, which closely matches the target sample size. The participation rate based on the adjusted gross sample is therefore over 40 percent in cohorts 1 to 3 and 23.0 percent in cohort 4. A total of 39 percent of the families in the net sample are part of the base sample, 51 percent are part of the urban sample, and 10.1 percent are part of the rural sample. For more information on the field process see Brix et al. (2017).

The lower part of Table 1 displays distributions by sex and zygosity of the twin pairs over the four cohorts for the net sample of the TwinLife panel.<sup>4</sup> There are more dizygotic than monozygotic twin pairs in cohorts 1 to 3, and in cohort 4 the share of monozygotic twin pairs is 53.3 percent. These results indicate that the probability-based sampling design used for TwinLife successfully counteracted the overrepresentation of monozygotic twins typically characterizing twin samples based on self-recruitment (i.e., two-thirds monozygotic twin pairs, with overrepresentation particularly pronounced in adult samples, Lykken et al., 1987). The findings are also in line with research showing an increase in dizygotic twinning rates for OECD countries, including Germany, since the 1980s (Hoekstra et al., 2008). This is primarily because dizygotic twinning is more strongly influenced by environmental factors such as the increase in maternal age at childbirth over recent decades (Lambalk et al., 1998). Overall, the distributions demonstrate that the TwinLife sample enables genetic sensitive analyses differentiated by gender and age.

As described above, both twins, one sibling, their parents, and the partners of the adult twins are the target respondents for the interviews, irrespective of whether they live in the same household or not. Table 2 shows the composition of the families (upper part of Table 2) and the households (lower part of Table 2) interviewed in TwinLife, wave 1. Overall, the TwinLife net sample consists of 4,097 twin families living in 4,828 households. A total of 91.4 percent of these families are families with two parents.<sup>5</sup> However, the share of two-parent families decreases over the

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4 In 50 of these families, second twin pairs exist; in 38 cases these are full siblings of the other twins, in eight cases, they are half-siblings, and in three cases, step-siblings. Moreover, one of the families has full sibling triplets in addition to the twins.

5 In 99.1 percent of the families with a mother, the mothers are the biological mothers of the twins. The share of biological fathers is 96.6 percent. In 3.8 percent of the families there are more than two parents, i.e., partners of a father or mother in addition to the biological parents.



*Table 2* Family and household compositions in the net sample of TwinLife

	Cohort 1 (%)	Cohort 2 (%)	Cohort 3 (%)	Cohort 4 (%)	Total (%)
<i>Family composition</i>					
Mother and father, twins	431 (42.7)	337 (32.3)	350 (33.0)	290 (29.5)	1,408 (34.4)
Mother and father, twins, sibling	534 (52.9)	644 (61.7)	591 (55.7)	566 (57.6)	2,335 (57.0)
Mother or father, twins	25 (2.5)	23 (2.2)	46 (4.3)	45 (4.6)	139 (3.4)
Mother or father, twins, sibling	20 (2.0)	39 (3.7)	74 (7.0)	78 (7.9)	211 (5.2)
No parents, (sibling) <sup>a</sup>	0 (0)	0 (0)	0 (0)	4 (0.4)	4 (0.1)
Total	1,010 (100)	1,043 (100)	1,061 (100)	983 (100)	4,097 (100)
<i>Household composition</i>					
Parents, both twins, (sibling) <sup>b</sup>	917 (90.3)	883 (83.4)	815 (74.1)	428 (25.9)	3,043 (63.0)
Parent, both twins, (sibling) <sup>b</sup>	93 (9.2)	160 (15.1)	231 (21.0)	113 (6.8)	597 (12.4)
Parent(s), one twin, (sibling) <sup>b</sup>	0 (0)	0 (0)	22 (2.0)	184 (11.1)	206 (4.3)
Both twins, (sibling) <sup>b</sup>	0 (0)	0 (0)	0 (0)	84 (5.1)	84 (1.7)
One twin, (sibling) <sup>b</sup>	0 (0)	0 (0)	8 (0.7)	532 (32.2)	540 (11.2)
No twins	6 (0.6)	16 (1.5)	24 (2.2)	312 (18.9)	358 (7.4)
Total	1,016 (100)	1,059 (100)	1,100 (100)	1,653 (100)	4,828 (100)

<sup>a</sup> Orphan families; three with at least one sibling and one with no sibling.

<sup>b</sup> Living in a household either with or without at least one sibling.

Sources: TwinLife (doi: 10.4232/1.12665), own calculations

cohorts from 95.6 percent to 87.1 percent. In 62.2 percent of the families the twins have at least one sibling. Since parents of the earlier born twin cohorts had more time to have additional children, this share increases from 54.9 percent in cohort 1 to around 65 percent in cohorts 2 to 4. The mean number of siblings per family in families with at least one sibling is 1.6, and the maximum number of siblings is ten. Overall, the distributions indicate that TwinLife facilitates studies based on the ETFD.

The lower part of Table 2 illustrates the distribution of households in TwinLife across cohorts. As required by the study design, all of the twins in cohorts 1 and 2, and almost all of the twins in cohort 3 live together in one household. In more than 90 percent of the twin households in cohort 1, the twins live with two parents. This share drops to about 75 percent in cohort 3. For cohort 4, the share of twin

households with at least one parent is 54.1 percent. This corresponds to 43.9 percent of all households in cohort 4. A total of 76 percent of the twins from cohort 4 who had already moved out of the parental household are living without their co-twin. This represents 32.2 percent of all households in cohort 4. Further, the share of non-twin households increases from approximately 1 percent in cohorts 1 to 3 to 18.9 percent in cohort 4. These results illustrate that TwinLife captures the major shift in household structures resulting from the young adult twins starting to create their own families.<sup>6</sup>

The TwinLife sample for our comparisons comprises all twin households in which at least one twin resides together with at least one parent of the twins. This household definition is close to the household definition of the Microcensus (see section *The Microcensus Comparison Samples*) and retains most of the TwinLife families in the sample. This *parent-twin sample* consists of 3,640 (out of 4,828) households in TwinLife. For cohorts 1 to 3 almost all twin families and households are included in this sample. Within cohort 4, the sample covers 73.8 percent of all families and 54.1 percent of all households with twins.

## The Microcensus Comparison Samples

The comparison samples we use for this study are based on the German Microcensus 2013. The Microcensus is a household survey based on a nationally representative sample of one percent (Destatis, 2014a, 2014b; Lengerer et al., 2007).<sup>7</sup> While the sampling of TwinLife is focused on families defined by the ETFD, the sampling design of the Microcensus is based on households, specifically persons living together at the same address sampled from the population register (Lengerer et al. 2005).

As the Microcensus survey does not collect information on whether the children living in the household are twins or not, we need to construct a suitable comparison sample to match the cohort and person composition of the TwinLife parent-twin sample described above without this information. Therefore, we define two different household samples – the multiple-child and the proxy-twin sample – based on the Microcensus. First, the *multiple-child sample* consists of one-family households with one or two parents and at least two children under the age of 25 of which at least one child – the “anchor child” – belongs to the same birth cohorts as in TwinLife. Second, the *proxy-twin sample* contains one-family households in which

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6 43.4 percent of the twins in cohort 4 have a partner and 30.7 percent of these twins live in a household with their partners.

7 The 2013 Microcensus provides the most recent data currently available and thus most accurately reflects the population of 2015 – the year in which the majority of the families in the TwinLife panel was sampled.

two children of the same sex are born in the same year and live with at least one of their parents.

In view of the approximately 7,000 same-sex twin births each year (Destatis, 2013), we can expect to find around 70 proxy-twins in the 2013 Microcensus for each year of birth from circa 2000 and declining numbers for the years prior to 2000 based on the following assumptions: 1) a household sample of one percent from the population approximates a population sample of one percent; 2) there are only rare cases, other than twin births, of same-sex children in a household being born in the same year; 3) most twin children live together and with at least one parent.<sup>8</sup> To gain a proxy-twin sample of sufficient size for socio-demographic differentiated analyses, we use six-year birth cohorts: 2007-2012 (cohort 1), 2001-2006 (cohort 2), 1995-2000 (cohort 3), and 1989–1994 (cohort 4).

Moreover, to match the TwinLife sampling design, households in communities with fewer than 5,000 inhabitants are excluded. These represent about 16 percent of the households in the multiple-child and the proxy-twin Microcensus samples. This leaves us with 24,271 multiple-child and 1,039 proxy-twin households for our analysis.

## Indicators

With respect to the social structural indicators used for the analysis, we compare household structures, the size of the communities where the household is located, German citizenship status on the household level, highest education of parents in the household, and also monthly net equivalent household income in euros. To assess the potential use of the TwinLife study for multidimensional analysis of social structural (dis-)advantage, we also compare the bivariate distributions of highest education in the household by monthly net equivalent household income. Moreover, we contrast maternal age at birth of the twins or the anchor child as a potential reason for social structural differences between the samples since giving birth later in life could be correlated with higher educational degrees or higher earnings.

The size of the community where the household is located is categorized based on the German community size classification (GKPOL). German citizenship is used as a proxy for migration background since the alternative indicators for migration background available in TwinLife and the Microcensus are not comparable. We assign German citizenship status on the household level if both parents

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8 There are rarely any women who give birth to two children within the same calendar year. However, the Microcensus does not differentiate between biological and step-children. Thus, there might be a negligible number of cases which are spuriously considered as twin families. These might be foster or blended families with same-sex children born in the same year.

have German citizenship. The highest education within the household is based on the International Standard Classification of Education (ISCED) 1997 (Schneider, 2008). The individual-level information on parents' education is used to calculate the highest obtained degree on the household level. The ISCED is coded as an ordered categorical variable with "no educational degree" (1) as the lowest and "Ph.D. degree" (6) as the highest category. Information on monthly net income is surveyed on the household level. To make the household incomes comparable across different household structures, an equivalence weight according to the new OECD scheme (OECD 2011) and an adjustment for inflation dividing the nominal income by the Consumer Price Index for Germany using 2015 as base year are applied.

## Methods

To assess whether distributions of the social background indicators differ between the samples, we construct categorical variables based on these indicators and calculate the proportion of each category for the distributions of these categorical variables. In addition, we perform z-tests on equality of proportions between samples using the 95% confidence level and report their statistical significance for the substantial differences discussed in this paper. Cell-specific case numbers in the Microcensus proxy-twin sample are too small to show detailed distributions for highest ISCED in households and net equivalent monthly household income. Thus, we present ISCED levels 5a and 6 versus all lower levels and household's median income. For maternal age at childbirth, we compare the means.

To account for missing values in education, citizenship and monthly net household income in the TwinLife sample, we set up a multiple imputation model on the household level.<sup>9</sup> We impute 20 values for each missing observation using multiple imputation with chained equations (van Buuren et al., 2006), a method which iterates over a sequence of univariate imputation models for each variable. For the univariate imputation models, we use predictive mean matching with ten nearest neighbors in case of continuous variables and logistic or ordered logistic regressions in case of categorical variables.<sup>10</sup> The procedure assumes that the data is missing at random conditional on the predictors used. To preferably ensure that

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9 Information is missing on ISCED for 4.5 percent of the mothers and 22.9 percent of the fathers, on German citizenship status for 4 percent of the mothers and 22.6 percent of the fathers, and on monthly net household income for 12.2 percent of the households.

10 The values presented in the descriptions are calculated as the mean of imputations in case of continuous and as the mode of imputations in case of categorical variables.

this assumption is met, we use a comprehensive set of predictors.<sup>11</sup> We assess the influence of the imputation procedure on the distributions of the social structural indicators compared. Here, we find slight increases in the lower categories of the indicators (typically about 2 percent) and converse declines in the upper categories. However, there are only minor differences between imputed and non-imputed estimates. Thus, in the following results section, we refrain from presenting non-imputed in addition to imputed results for reasons of clarity and brevity.

## Results

### Comparisons of the Social Background Indicators

In this section, we present the results of the comparisons of the distributions of the social background indicators in the TwinLife parent-child, the Microcensus proxy-twin, and the Microcensus multiple-child sample.

#### *Household Structure*

Table 3 shows the household structures in the TwinLife parent-twin sample in contrast to the two Microcensus comparison samples. The number of children living in a household with both parents differs in the Microcensus multiple-child sample compared to the TwinLife parent-twin and the Microcensus proxy-twin samples.

While there are 58.9 percent of households with two children and both parents in the former sample, this share is approximately 40 percent in the latter two. This difference is plausible since potential parents often plan to have two children but if the second birth is a twin birth, they have three children (Ruckdeschel, 2007). The share of single-parent households is about 16 percent in all three samples. Overall, these results indicate that the main difference in the composition of twin and non-twin multiple-child households is the higher prevalence of households with two children in the latter group. In addition, the findings confirm that the probability-based sampling procedure used for TwinLife was appropriate in this regard since the household structures in the TwinLife parent-twin and the Microcensus proxy-twin samples are similar.

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11 We use all imputed variables as well as information on the years of birth, migration background, cognitive test scores, monthly gross income and weekly working hours of mothers and fathers, household structure, and community size as predictors.

**Table 3** Household structures in the TwinLife and Microcensus comparison samples

	Cohort 1 (%)	Cohort 2 (%)	Cohort 3 (%)	Cohort 4 (%)	Total (%)
<i>TwinLife parent-twin sample</i>					
Couples, twin(s)	428 (42.4)	355 (34.0)	401 (38.3)	259 (47.9)	1443 (39.6)
Couples, twin(s), sibling	489 (48.4)	528 (50.6)	414 (39.6)	169 (31.2)	1600 (44.0)
Single parent, twin(s)	50 (5.0)	80 (7.7)	149 (14.2)	76 (14)	355 (9.8)
Single parent, twin(s), sibling	43 (4.3)	80 (7.7)	82 (7.8)	37 (6.8)	242 (6.6)
Total	1,010 (100.0)	1,043 (100.0)	1,046 (100.0)	541 (100.0)	3,640 (100.0)
<i>Microcensus multiple-child sample</i>					
Couples, 2 children	3,680 (61.1)	3,523 (55.6)	3,531 (55.7)	3,558 (63.9)	14,292 (58.9)
Couples, 3 or more children	1,713 (28.5)	1,774 (28.0)	1,544 (24.3)	948 (17.0)	5,979 (24.6)
Single parent, 2 children	426 (7.1)	732 (11.5)	958 (15.1)	924 (16.6)	3,040 (12.5)
Single parent, 3+ children	199 (3.3)	310 (4.9)	309 (4.9)	142 (2.5)	960 (4.0)
Total	6,018 (100.0)	6,339 (100.0)	6,342 (100.0)	5,572 (100.0)	24,271 (100)
<i>Microcensus proxy-twin sample</i>					
Couples, 2 children	139 (46.8)	82 (28.3)	99 (33.2)	70 (45.5)	390 (37.5)
Couples, 3 or more children	122 (41.1)	149 (51.4)	139 (46.6)	48 (31.2)	458 (44.1)
Single parent, 2 children	20 (6.7)	34 (11.7)	30 (10.1)	27 (17.5)	111 (10.7)
Single parent, 3+ children	16 (5.4)	25 (8.6)	30 (10.1)	9 (5.8)	80 (7.7)
Total	297 (100.0)	290 (100.0)	298 (100.0)	154 (100.0)	1,039 (100.0)

Sources: TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

### Community Size

Table 4 reports shares of households by community size across the three samples. Around two-thirds of the TwinLife households are located in communities with 50,000 or more inhabitants while this share is around 40 percent in the Microcensus samples.

This difference is statistically significant and mainly attributable to the oversampling of urban communities in TwinLife which was implemented to obtain the necessary coverage of the twin family target population (see sub-section *Sampling*

*Strategy*). However, if we exclude the oversampled urban population, the distributions of the TwinLife and Microcensus samples are roughly comparable. The group of TwinLife households in communities with 500,000 or more inhabitants is around four percentage points larger than the Microcensus samples, and the share of households in communities with 100,000 to 499,999 inhabitants is approximately six percentage points smaller in the TwinLife sample than in the Microcensus samples. The latter of these two differences is statistically significant. Regarding the Microcensus proxy-twin and multi-child samples, there are no considerable differences in shares of households by community size between the samples.

*Table 4* Households by community size in percent

	Cohort 1	Cohort 2	Cohort 3	Cohort 4	Total
<i>TwinLife parent-twin sample</i>					
5,000–19,999 (in %)	18.4	18.9	19.2	21.8	19.3
20,000–49,999 (in %)	10.5	13.3	10.9	14.1	12.0
50,000–99,999 (in %)	18.0	16.1	15.2	16.1	16.4
100,000–499,999 (in %)	21.9	21.1	22.6	20.5	21.7
> 500,000 (in %)	31.2	30.6	32.1	27.5	30.7
<i>TwinLife, without urban sample</i>					
5,000–19,999 (in %)	38.4	37.4	39.0	37.0	38.1
20,000–49,999 (in %)	20.1	25.0	21.1	23.1	22.3
50,000–99,999 (in %)	10.1	9.3	8.8	10.5	9.5
100,000–499,999 (in %)	11.7	11.0	11.0	7.5	10.6
> 500,000 (in %)	19.7	17.3	20.1	22.0	19.5
<i>Microcensus multiple-child sample</i>					
5,000–19,999 (in %)	31.3	33.9	35.5	35.6	34.1
20,000–49,999 (in %)	22.1	23.8	23.5	24.1	23.4
50,000–99,999 (in %)	10.6	10.1	11.0	11.4	10.8
100,000–499,999 (in %)	17.4	16.2	15.9	15.6	16.3
> 500,000 (in %)	18.7	15.9	14.1	13.3	15.5
<i>Microcensus proxy-twin sample</i>					
5,000–19,999 (in %)	26.6	33.8	35.6	31.8	32.0
20,000–49,999 (in %)	22.9	22.1	20.1	23.4	21.9
50,000–99,999 (in %)	11.5	11.0	12.1	13.6	11.8
100,000–499,999 (in %)	18.2	17.9	15.1	18.8	17.3
> 500,000 (in %)	20.9	15.2	17.1	12.3	16.9

Sources: TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

*Parental Citizenship Status*

Table 5 contrasts the shares of households with German citizenship across the samples. Overall, this share is 84.7 percent in the TwinLife sample while the corresponding shares are around 80 percent in the Microcensus samples. The share is constant across cohorts in the TwinLife sample while it declines in the Microcensus samples from about 85 percent in the older cohorts to about 75 percent in the younger cohorts. Consequently, there are around five to ten percentage points more households with German citizenship in the TwinLife sample for cohorts 1 and 2 and these differences are statistically significant. The shares of households with German citizenship in the Microcensus proxy-twin and multiple-child samples are similar.

*Table 5* Households by German citizenship

	Cohort 1	Cohort 2	Cohort 3	Cohort 4	Total
<i>TwinLife parent-twin sample</i>					
German citizenship (in %)	85.5	85.0	84.1	83.7	84.7
No German citizenship (in %)	14.5	15.0	15.9	16.3	15.3
<i>Microcensus multiple-child sample</i>					
German citizenship (in %)	74.1	77.9	82.3	81.7	79.0
No German citizenship (in %)	25.9	22.1	17.7	18.3	21.1
<i>Microcensus proxy-twin sample</i>					
German citizenship (in %)	75.8	76.9	85.9	85.7	80.5
No German citizenship (in %)	24.2	23.1	14.1	14.3	19.5

Sources: TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

*Parental Education*

Table 6 describes the distributions of highest educational level in the households for the TwinLife parent-twin and the Microcensus multiple-child samples based on the ISCED. We observe that the TwinLife sample covers the full distribution of educational levels. The lower tail (ISCED 1 and 2) encompasses around 5 percent of the cases. The results indicate that there are more households with a university education (ISCED 5a and 6) and fewer with medium or low education (ISCED 1 to 3) in TwinLife than the Microcensus multiple-child sample, particularly in the younger cohorts.

To analyze potential reasons for these differences, the lower part of Table 6 shows the shares of university educated households compared to all other house-



**Table 6** Highest educational level (based on ISCED) in household

	Cohort 1	Cohort 2	Cohort 3	Cohort 4	Total
<i>TwinLife parent-twin sample</i>					
ISCED 1 (in %)	0.6	0.8	1.1	1.5	0.9
ISCED 2 (in %)	4.9	4.0	3.6	5.2	4.3
ISCED 3a, b, c (in %)	25.2	27.0	33.5	37.9	30.0
ISCED 4a, b (in %)	9.8	7.2	8.0	8.1	8.3
ISCED 5b (in %)	10.8	13.2	12.8	16.5	12.9
ISCED 5a (in %)	41.4	42.7	36.0	27.9	38.2
ISCED 6 (in %)	7.4	5.1	5.0	3.0	5.4
<i>Microcensus multiple-child sample</i>					
ISCED 1 (in %)	3.4	3.7	3.6	4.2	3.7
ISCED 2 (in %)	9.9	8.6	7.9	10.2	9.1
ISCED 3a, b, c (in %)	34.1	36.8	39.3	43.5	38.3
ISCED 4a, b (in %)	9.4	9.2	9.2	7.8	8.9
ISCED 5b (in %)	11.5	12.7	14.7	14.0	13.2
ISCED 5a (in %)	27.8	25.5	22.7	18.4	23.7
ISCED 6 (in %)	4.0	3.4	2.6	2.0	3.0
<i>TwinLife parent-twin sample</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	51.3	52.3	59.1	69.2	46.5
ISCED 5a or 6 (in %)	48.7	47.7	40.9	30.8	43.5
<i>Microcensus multiple-child sample</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	68.2	71.1	74.7	79.6	73.3
ISCED 5a or 6 (in %)	31.8	28.9	25.3	20.4	26.7
<i>Microcensus proxy-twin sample</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	43.6	74.4	76.4	77.8	72.4
ISCED 5a or 6 (in %)	36.4	25.6	23.6	22.2	27.6
<i>TwinLife, without urban sample</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	52.9	57.1	60.3	69.5	58.9
ISCED 5a or 6 (in %)	47.1	42.9	39.7	30.5	41.1
<i>TwinLife, only German citizenship</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	48.7	48.8	55.8	66.1	53.3
ISCED 5a or 6 (in %)	51.3	51.2	44.2	33.9	46.7
<i>Microcensus multiple-child sample, only German citizenship</i>					
ISCED 1, 2, 3, 4, or 5b (in %)	65.1	65.8	72.8	77.3	70.8
ISCED 5a or 6 (in %)	34.9	34.2	27.2	22.7	29.2

*Note:* Cell-specific case numbers in the Microcensus proxy-twin sample are too small to present detailed distributions for highest ISCED in households.

*Sources:* TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

holds. Overall, the share of university educated households is 43.5 percent in the TwinLife sample while it is around 27 percent in the Microcensus samples. In cohort 4 the difference is around ten percentage points between the samples while it is between 15 and 20 percentage points in cohorts 1 to 3. All of these differences are statistically significant. The differences in younger cohorts decline slightly if we restrict the samples to households with German citizenship to account for the higher shares of these households in TwinLife.<sup>12</sup> The shares of households with a university education in the Microcensus proxy-twin and multiple-child samples are approximately the same.

### *Household Income*

Table 7 reports the distributions of monthly net equivalent household incomes for the TwinLife and Microcensus samples. It can be shown that the TwinLife sample covers the full income distribution. Across all cohorts, around 20 percent of the households have an adjusted income of less than €1,000 per month, around 53 percent have between €1,000 and €2,000 per month, around 20 percent have between €2,000 and €3,000 per month, and approximately 7 percent have more than €3,000 per month.

These shares are roughly comparable to the Microcensus samples where the share of households with less than €1,000 per month is slightly higher and the share with between €2,000 and €3,000 per month is slightly lower. For these two income categories the differences between the TwinLife sample and the Microcensus samples are statistically significant. Overall, the median monthly net equivalent household income in the TwinLife sample is €1,528 while it is around €150 less in the Microcensus samples. Differentiated by cohort, these differences between monthly median incomes are approximately €100 in cohorts 3 and 4 and around €200 in cohorts 1 and 2. Restricting the TwinLife and Microcensus samples to households with German citizenship or excluding the TwinLife urban sample does not account for the differences observed. Conditional on parental education the household income medians are similar in the TwinLife and the Microcensus samples. This finding indicates that the differences in household income between the samples are mostly a consequence of the selective participation in TwinLife with respect to parental education (see sub-section *Parental Education*).

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12 Excluding the urban sample of TwinLife to address the oversampling of urban households in TwinLife (see sub-section *Parental Education*) does not change the differences observed in the shares of university educated households between TwinLife and the Microcensus samples to a relevant degree.

*Table 7* Monthly net equivalent household income

	Cohort 1	Cohort 2	Cohort 3	Cohort 4	Total
<i>TwinLife parent-twin sample</i>					
Household income in € (median)	1,618	1,574	1,403	1,610	1,528
Household income in € (in %):					
< €1,000	18.3	18.6	25.5	17.4	20.3
€1,000 to < €2,000	50.9	52.4	54.4	51.9	52.5
€2,000 to < €3,000	23.3	20.9	15.1	23.8	20.3
≥ €3,000	7.5	8.2	5.0	6.8	6.9
<i>Microcensus multiple child sample</i>					
Household income in € (median)	1,324	1,373	1,376	1,537	1,375
Household income in € (in %):					
< €1,000	26.6	23.9	25.8	19.8	24.1
€1,000 to < €2,000	50.8	50.1	55.0	56.6	53.0
€2,000 to < €3,000	16.2	18.3	14.2	18.7	16.8
≥ €3,000	6.4	7.7	4.9	5.0	6.0
<i>Microcensus proxy-twin sample</i>					
Household income in € (median)	1,433	1,285	1,303	1,537	1,373
<i>Median income in € in subsamples</i>					
TwinLife, without urban sample	1,574	1,549	1,405	1,612	1,520
TwinLife, only German citizenship	1,670	1,670	1,499	1,733	1,664
Microcensus multiple child sample, only German citizenship	1,469	1,478	1,433	1,601	1,495

*Note:* Cell-specific case numbers in the Microcensus proxy-twin sample are too small to present detailed distributions for net equivalent monthly household income.

*Sources:* TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

### *Parental Education and Household Income Combined*

In Table 8 the monthly net equivalent household income distributions are further differentiated by the highest educational status in the households based on ISCED in order to assess the TwinLife studies potential for multidimensional analysis of social structural (dis-)advantage. The parts of this two-dimensional social structural distribution covered in the Microcensus multiple-child sample are also represented in the TwinLife parent-twin sample indicating that the latter can be used for related multidimensional analysis. Further, the distributions are also roughly comparable; the shares of households with a university education (ISCED 5a or 6) and an adjusted income of between €1,000 and €3,000 are larger in the TwinLife parent-twin sample, while those with medium education (ISCED 3) and an income

of between €1,000 and €2,000 and also those with low education (ISCED 1 or 2) and an income of less than €1,000 are lower.

*Table 8* Highest educational level (ISCED) by net equivalent income in households

Monthly net equivalent household income	TwinLife parent-twin sample				Microcensus multiple child sample			
	Highest educational level (based on ISCED) in household in % (cell percentages)							
	1, 2	3a, b, c	4a, b, 5b	5a, 6	1, 2	3a, b, c	4a, b, 5b	5a, 6
<i>Cohort 1</i>								
< €1,000	3.8	7.8	2.2	4.6	10.0	11.6	2.8	2.2
€1,000 to < €2,000	1.7	16.0	14.1	19.1	3.1	20.9	13.8	13.0
€2,000 to < €3,000	0	1.1	4.0	18.2			3.4	11.2
≥ €3,000	0	0.2	0.4	6.9	0.1 <sup>a</sup>	1.8 <sup>a</sup>	0.6	5.4
<i>Cohort 2</i>								
< €1,000	2.6	8.6	3.3	4.1	8.3	10.7	3.1	1.7
€1,000 to < €2,000	2.2	16.4	13.7	20.0	4.1	23.1	13.4	9.6
€2,000 to < €3,000	0	1.7	2.8	16.4			4.2	11.6
≥ €3,000	0	0.3	0.7	7.2	0.2 <sup>a</sup>	2.9 <sup>a</sup>	1.1	6.0
<i>Cohort 3</i>								
< 1,000	3.7	12.5	3.7	5.5	7.9	12.7	3.2	2.0
€1,000 to < €2,000	1.0	18.9	14.4	20.1	3.4	24.2	16.2	11.2
€2,000 to < €3,000	0	1.7	2.3	11.1			3.4	8.5
≥ €3,000	0	0.3	0.4	4.3	0.2 <sup>a</sup>	2.5 <sup>a</sup>	0.9	3.6
<i>Cohort 4</i>								
< €1,000	2.8	7.4	3.0	4.3	7.3	8.9	2.3	1.2
€1,000 to < €2,000	3.1	21.8	15.0	12.0	6.8	28.0	13.1	8.8
€2,000 to < €3,000	0.7	7.2	6.3	9.6			4.9	7.2
≥ €3,000	0	1.5	0.4	5.0	0.5 <sup>a</sup>	6.8 <sup>a</sup>	1.1	3.2

<sup>a</sup> Due to small sample sizes, the shares of the categories €2,000 to < €3,000 and ≥ €3,000 are aggregated for ISCED 1, 2 and ISCED 3a, b, c.

Sources: TwinLife (doi: 10.4232/1.12665) and Microcensus 2013, own calculations

### *Maternal Age at Birth*

Finally, we compare the mean values of maternal age at the birth of the twins or the anchor child for the TwinLife and Microcensus samples. This value is approximately 31 years in all samples and the differences between samples are statistically not significant. It increases from around 30 years in cohort 4 to about 32 years in cohort 1 which is accompanied by an increase in the share of mothers aged 35 or older at childbirth (from around 15 to 30 percent). The changes are less pronounced in the Microcensus multiple-child sample. Overall, there are no indications of differences in maternal age at childbirth which could be responsible for the social structural differences observed.

## **Limitations**

With respect to the comparisons conducted in this study, the main limitation is the lack of a twin registry for Germany. Thus, we had to use a proxy-twin sample which is based on a one percent general population sample. As a result, the size of the proxy-twin sample is small. Moreover, we cannot conduct comparative analyses differentiating between monozygotic and dizygotic twins since there is no information on zygosity available for the proxy-twins. Nevertheless, our comparison samples are based on the Microcensus, a survey of high quality standards, particularly regarding representativity (Lengerer et al., 2007). Therefore, the Microcensus is the best dataset available for conducting a study on the generalizability of socio-structural differentiated analyses of twins in Germany.

The central limitation our study found with respect to using TwinLife for such analyses is the slight selectivity of the TwinLife sample with respect to parental education and German citizenship. Partly, the underrepresentation of families without German citizenship is due to conducting the study only in German and restricting the sampling to families with sufficient proficiency of the German language (Brix et al., 2017). The underrepresentation of respondents with migration background – often corresponding with having no German citizenship – can commonly be addressed using specialized sampling strategies (Brücker et al., 2014; Schupp & Wagner, 1995). However, TwinLife did not have funding for instruments in additional languages or an additional migration sample. A potential reason for the selectivity regarding parental education is the demanding questionnaire program for the first wave of TwinLife, particularly for the children aged around 5 at the time of the survey in cohort 1. To ensure panel stability, plans had already been made to shorten the survey for future TwinLife waves prior to the first wave and the program has been further reduced given the results of this study.<sup>13</sup>

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13 The expected workload on the family level for the second wave was reduced from around 180 minutes in the first wave to around 120 minutes.

## Selectivity Correction

To address the selective participation in TwinLife with regard to parental education and German citizenship (see sub-sections *Parental Citizenship Status* and *Parental Education*), we suggest conducting additional analyses using a cohort-specific weighting scheme based on the distribution of highest education in the households by German citizenship in the Microcensus multiple-child sample (see Appendix A). Since household income levels conditional on parental education are similar in both samples (see sub-section *Household Income*), we consider the differential incomes a consequence of the differences in education. In consequence, we did not include household income as additional indicator in our proposed weighting scheme. In principle, using such a weighting scheme for TwinLife is justified by the social structural similarity between (proxy-)twin and multiple-child households in Germany found in this study.

## Conclusion

In this paper, we addressed two research questions regarding the generalizability of research on the gene-environment interplay utilizing the TwinLife data: first, we assessed the usability of the TwinLife sample for social stratified analyses of genetic influences; and second, we analyzed whether the social background of twin households in Germany is comparable to the whole population of multiple-child households. Furthermore, we introduced the design and sampling strategy of TwinLife to assist researcher in using the TwinLife panel for their research.

## Social Stratified Genetic Sensitive Analyses using TwinLife

Addressing our first research question, our comparison shows larger shares of urban households in TwinLife due to the oversampling of populous communities that was necessary to achieve the target sample size. Furthermore, the share of households with migration background – indicated by no German citizenship – is approximately five to ten percentage points smaller in the younger cohorts of the TwinLife compared to the Microcensus samples. Moreover, we show that the probability-based sampling of the TwinLife study was successful in counteracting the overrepresentation of monozygotic twins typical of twin samples based on self-recruitment (Lykken et al., 1987).

Looking at the core socio-economic indicators – parental education and income – our results show that the TwinLife sample covers the full distributions including the lower and upper bounds. With regard to parental education, we found around 15 percentage points more university educated households in the Twin-

Life sample, particularly in the younger cohorts. The smaller share of households with no German citizenship in TwinLife can explain some of the differences in the shares of university educated households between the samples. For the monthly net equivalent household income, we found that median values were around €200 higher for the younger TwinLife cohorts and that the corresponding values were around €100 higher in the older cohorts. Additional analyses showed that the oversampling of urban communities in TwinLife cannot account for these differences.

In sum, our findings indicate that participation in TwinLife was, to some degree, selective with respect to parental education and German citizenship, specifically in the younger cohorts. We proposed a weighting scheme to address this selectivity. However, since the TwinLife sample covers the whole distributions of the social background indicators, this selectivity does not restrict the usability of the TwinLife sample for social stratified analyses of genetic influences. In principle, TwinLife can be used for multidimensional analyses of genetic influences on social inequalities based on an ETFD.

## **Social Background Differences between Twin and Multiple-child Households**

Regarding our second research question, our analyses show that (proxy-)twin and multiple-child households in Germany have comparable distributions for many socio-demographic indicators such as community size, parental citizenship status, parental education, household income, and maternal age at birth of the twins or anchor children. The only difference we found between twin and multiple-child households is the higher prevalence of households with two children in the latter group. This difference can be explained by parents often planning to have two children (Ruckdeschel, 2007).

The absence of relevant differences in the distributions of social background indicators between twin and other multiple-child households is important for TwinLife, since it would otherwise be impossible to capture the full range of social structural variation using a twin-based sampling strategy. Moreover, this is also beneficial for generalizing inferences of social structural influences based on the TwinLife sample to the corresponding population at large. If different outcomes in twin and other multiple-child families are not a consequence of different social structural distributions, these varying outcomes indicate different inequality-generating processes for twin and non-twin families. Therefore, if a researcher has reason to assume that there are no different inequality-generating processes for twin and non-twin families, findings based on the TwinLife data can be generalized to all multiple-child families in Germany.

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## Appendix A

### Selectivity correction weighting scheme based on the Microcensus

This appendix contains instructions for constructing a weighting scheme matching the cohort specific highest ISCED by German citizenship distribution of parents on the household level for TwinLife analysis samples with the Microcensus multiple-child sample. The aim of the proposed weighting scheme is to address the selectivity of the TwinLife sample regarding parental education and German citizenship status, particularly in the younger cohorts. We advise using it as a robustness check, i.e., to assess discrepancies in the results between analyses conducted with and without the weighting scheme. Comparable results in both analyses indicate that the conclusions drawn are not influenced by the selectivity.

We construct weights specific to each of the four TwinLife cohorts. First, for a cohort-specific weighting scheme like this, we need to calculate the shares of observations in the TwinLife analysis sample used by highest ISCED and German citizenship of the parents on the household level for each cohort using the categorization presented in Table A1. This share is given by the number of observations in a specific highest ISCED by German citizenship cell ( $J$ ) for a specific cohort divided by the total number of observations in the analysis sample ( $N$ ) for a specific cohort. Second, we need to divide the cell-specific correction factors ( $C$ ) presented in Table A1 by the cohort-specific shares calculated for the analysis sample. The correction factors in Table A1 are based on the cohort-specific shares of observations in the Microcensus multiple-child sample by highest ISCED and German citizenship. Hence, the cohort-specific weights ( $W$ ) assigned to each observation in the analysis sample depending on highest parental ISCED and parental German citizenship on the household level are given conducting the following calculation:

$$W = C/(J/N) = C \times N/J$$

The resulting weighted analysis sample has the same number of observations as the sample without weights in each cohort but its cohort-specific highest ISCED by German citizenship distribution matches the one in the Microcensus multiple-child sample. If the distributions of parental background indicators for a specific analysis sample based on TwinLife do not differ significantly between the household- and the family-level of aggregation this weighting scheme can also be implemented on the family level.

*Table A1* Factors for a selectivity correction weighting scheme based on Microcensus

	Highest educational level (using ISCED) in household			
	1, 2	3a, 3b, 3c	4a, 4b, 5b	5a, 6
<i>Cohort 1</i>				
German citizenship	0.05735661	0.24804655	0.17722361	0.25835412
No German citizenship	0.07547797	0.09293433	0.03142145	0.05918537
<i>Cohort 2</i>				
German citizenship	0.05561700	0.28282509	0.18991942	0.25075051
No German citizenship	0.06794122	0.08547954	0.02938853	0.03807869
<i>Cohort 3</i>				
German citizenship	0.05466035	0.32669826	0.21800948	0.22353871
No German citizenship	0.06082149	0.06650869	0.02085308	0.02890995
<i>Cohort 4</i>				
German citizenship	0.06781795	0.36643281	0.19769743	0.18546501
No German citizenship	0.07609282	0.06817773	0.01978773	0.01852851

*Note:* The correction factors in the table are not the weights. Please read Appendix A for instructions on how to construct weights using these correction factors.

*Sources:* Microcensus 2013, own calculations

