



TwinLife Technical Report Series

No. 11, June 2025

***TwinLife* ShortGuide**

V1.5.0

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TwinLife ShortGuide v1.5.0

TwinLife Technical Report Series No. 11
Project TwinLife “Genetic and social causes of life chances”
Bielefeld, June 2025

TwinLife Technical Report Series

General Editors: Martin Diewald, Christian Kandler, Rainer Riemann, and Frank M. Spinath

ISSN 2512-403X

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This publication has been funded by the German Research Foundation (DFG).

TwinLife Technical Reports are refereed scholarly papers. Submissions are reviewed by the general editors before a final decision on publication is made.

The Technical Report Series is a forum for presenting technical works (e.g., data documentation, field reports) in progress. Comments on the manuscript should be addressed directly to the author(s).

The papers can be downloaded from the project website:

<https://www.twin-life.de/twinlife-series>

TwinLife “Genetic and social causes of life chances”

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June 2025

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The ShortGuide is intended to give both an overview of the longitudinal twin family study TwinLife and a short instruction on how to use the TwinLife data.

It corresponds to the contents of the data documentation website of TwinLife (www.twinlife.de/documentation).

The following pages contain information about the project and links to various helpful documents that should facilitate the first steps into working with the TwinLife data. For a very quick description of everything you need to get started with the TwinLife data set, see 'getting started' section below.

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0. Getting started

TwinLife – A genetically informative, longitudinal study about the development of social inequality

Design

- An overview of the theoretical and empirical background, the study design and content as well as the implementation of the study can be found in the [TwinLife reference papers](#) ([Hahn et al., 2016](#); [Mönkediek et al., 2019](#); [Rohm et al., 2023](#)).

Data

- The TwinLife data are described and archived in the [GESIS data catalogue](#).
- To get access to the TwinLife data, please fill in the Data Use Agreement which you can find under 'Actions' in the GESIS data catalogue. All data sets are available with English and German labels in SPSS and Stata formats. You can also follow the direct link to the [Data Use Agreement](#).

Variables

- The codebooks for each data collection (ZA6701_cod_wid\$.pdf)¹ provide a complete description of the variables, including variable and value labels, filter conditions, references, question texts, univariate frequency distributions, and an explanation of variable-specific peculiarities, if applicable. The codebooks are available on the [TwinLife data documentation website](#).
- A list of all variables (including their frequencies), their corresponding question text, answer options, and filter conditions can be found on the metadata documentation platform paneldata.org/twinlife.

Questionnaires and Technical Reports

- The questionnaire files include the implemented questionnaires. These files are only available in the original language of the study (German). The original questionnaires are available in the [downloads section](#) of the TwinLife data documentation website.
- The [Technical Reports Series](#) are scientific contributions dealing with technical aspects of data presentation (e.g., sampling design and data collection, data documentations, field reports, etc.) as well as methodical questions. They also include various reports on how to work with selected constructs and variables.

Citation

Please acknowledge the use of the TwinLife data in your work by citing both the [dataset](#) (e.g., Diewald et al., 2024) and one of the [reference papers](#) ([Hahn et al., 2016](#); [Mönkediek et al., 2019](#); [Rohm et al., 2023](#)).

¹ Here and in the remainder of the text, „\$“ is a placeholder for the numeric referring to the survey wave (wid). For example, ZA6701_cod_wid1.pdf refers to the codebook of wid = 1.

Funding statements

Please use the appropriate funding statements listed below for the data that was used in your publication to correctly acknowledge the usage of the TwinLife data.

- **TwinLife data:**

The TwinLife study was funded by the German Research Foundation (DFG) (Grant number 220286500, <https://gepris.dfg.de/gepris/projekt/220286500>). Funding was awarded to Martin Diewald, Christian Kandler, Frank M. Spinath, and Rainer Riemann. The funder had no role in the study design, data collection and analysis, the decision to publish, or the preparation of the manuscript.

- **TwinSNPs data:**

The molecular genetic extension project of TwinLife was funded by the German Research Foundation (DFG; Grant number 428902522, <https://gepris.dfg.de/gepris/projekt/428902522>). Funding was awarded to Martin Diewald, Peter Krawitz, Markus M. Nöthen, Rainer Riemann, and Frank M. Spinath. The funders had no role in the study design, data collection and analysis, the decision to publish, or the preparation of the manuscript.

- **TECS data:**

The epigenetic change satellite project of TwinLife was funded by the German Research Foundation (DFG; Grant number 458609264, <https://gepris.dfg.de/gepris/projekt/458609264>). Funding was awarded to Elisabeth Binder, Martin Diewald, Andreas J. Forstner, Christian Kandler, Markus M. Nöthen, and Frank M. Spinath. The funders had no role in the study design, data collection and analysis, the decision to publish, or the preparation of the manuscript.

Ethics statements

In case an ethics statement for the data use is needed for your publication, please use the respective ethics statements provided below.

- **Survey data:**

The TwinLife study was reviewed and approved by the German Psychological Society (Deutsche Gesellschaft für Psychologie; protocol number: RR 11.2009).

[Use this paragraph when using COVID-19 supplementary data]

The COVID-19 supplementary questionnaires were reviewed and approved by the Ethics Committee of the University of Bielefeld (Application No. 2020-106).

All participants were informed in writing about the aims of the TwinLife study, the incentives, and that their participation was voluntary and could be withdrawn at any time. In addition, in all face-to-face surveys, participants received a two-page leaflet summarizing the procedures concerning data protection and privacy and their rights to demand the deletion of all data collected in line with German data integrity laws. Written material was sent to participants before all interviews. At the beginning of each interview, informed verbal consent was obtained from participants (and the participants' legal guardians when the participants were underage) and documented. Following the national legislation and the

institutional requirements, written informed consent was not required to participate in this study. Nevertheless, for all supplementary online surveys, written informed consent was obtained from all participants.

- **Saliva samples:**

The Ethics Committee of the Medical Faculty of the University of Bonn (No. 113/18) reviewed and approved the protocols for the genetic sampling via saliva samples.

Prior to the genetic sampling, the participants received extensive written information on, e.g., the sampling procedures, the scope of the study, their right to refuse participation, and their right to withdraw their consent at any given time. For sampling genetic data, written informed consent was obtained from all participants and the participant's legal guardian or next of kin (for minors).

Change log

v1.5.0

- Update to the release of the latest data collection F2F 5 (v9-0-0) and (planned) release dates
- Addition of the new reference papers that were published after 2016 (chapters 0, 6.2, and 7)
- Update of the dataset citation to v9.0.0 (chapters 0 and 6.2)
- Update of the University of Bremen logo (title page)
- Update of the funding statement on the second page
- Addition of funding and ethics statements (chapter 0)
- Addition of polygenic score description as part of "Biological factors" (chapter 1.1)
- Update of Figure 2 to show all panel waves (chapter 1.2)
- Addition of complete *wid* variable information (chapter 3.4)
- Added K2ID information (chapter 3.1 and 3.4)
- Updated Figure 2 to include K2ID survey
- Update and reformatting of code examples; added R code (chapter 3.9)
- Overall reformatting of tables and boxes
- Overall check of consistency of abbreviations

v1.4.0

- Update to the release of the latest data collections F2F 4 and CATI 4 (v8-0-0) and (planned) release dates
- Update of the "Basic Concept" section (chapter 1.1) to the new structure of TwinLife's domains
- Addition of example syntax for the definition of the analysis sample using the TwinLife master file (chapter 1.2)
- Addition of new data file Children of twins (ZA6701_cot_v\$) in chapter 3.1 "Data Formats and Data Files"
- Addition of several generated variables in chapter 5.1 "Generated Variables"

v1.3.0

- Update to the release of the latest data collections CATI 3 and Cov 3 (v7-0-0) incl. correction of the (planned) release dates and corresponding information (dataset citation, etc.)
- Update of the “Study Design and Sample Structure” section (chapter 1.2) (survey modes and drop-out policy)
- Update of the “Data Formats and Data Files” section (chapter 3.1) (data set description)
- Inclusion of Technical Report No. 15 “TwinLife Survey Weights” in chapter 3.7 “Survey Weights”
- Update of the description of migration variables in chapter 5.1 “Generated Variables”

v1.2.0

- Correction of the planned release dates
- Chapter 3.10 about Matching information from the parent-about-child questionnaire to the child's data set was added

v1.1.0

- Update to the release of the latest data collections CATI 2 and Cov 1 (v5-0-0) incl. correction of the release date
- Addition of Corona supplementary survey to the description of the data structure and data files (chapter 3.1) and correction of the file name structure
- Minor correction of SPSS syntax in chapter 3.9 (generalization of file path)
- Revision of chapter 5 “Generated variables and scales”: shortening of the generation description, insertion of the generation description of the mig variables, insertion of a reference to the documentation website, linking of Technical Report No. 06
- Addition of the citation reference to use the current DOI

1. About TwinLife

TwinLife is a longitudinal, interdisciplinary twin family study on the development of social inequality. It takes a genetically informed life course perspective on social inequalities that acknowledges the importance of both genetic and social influences, social structure, and individual agency. The combination of genetically sensitive data, the survey design, multiple indicators of social success or failure, and a variety of environmental variables enables a fine-grained investigation of the complex interplay between nature and nurture concerning social inequality.

1.1 Basic Concept

To better understand how social inequality arises, TwinLife examines not only various causal factors but also various indicators of personal and social success or failure.

Figure 1 provides an overview of the relevant characteristics. On the conditioning side (left), both genetic predispositions and aspects of the environment in which children and young people grow up and live are considered. On the impact side (right), not only objective but also subjective information about a person's individual development are taken into account. For example, education and access to the labour market, participation in social, cultural and political life and subjective assessments of quality of life are examined. Children are influenced by their environment, but they can react differently to this environment depending on their individual characteristics. They can also interact with it and shape it. To be able to look more closely at this reciprocal process, the characteristics shown in Figure 1 are recorded over an 8-year period. This makes TwinLife broader than most comparable twin studies and should be understood more like a classic social science study. It thus examines many life domains, outcomes and possible causes of social inequality.

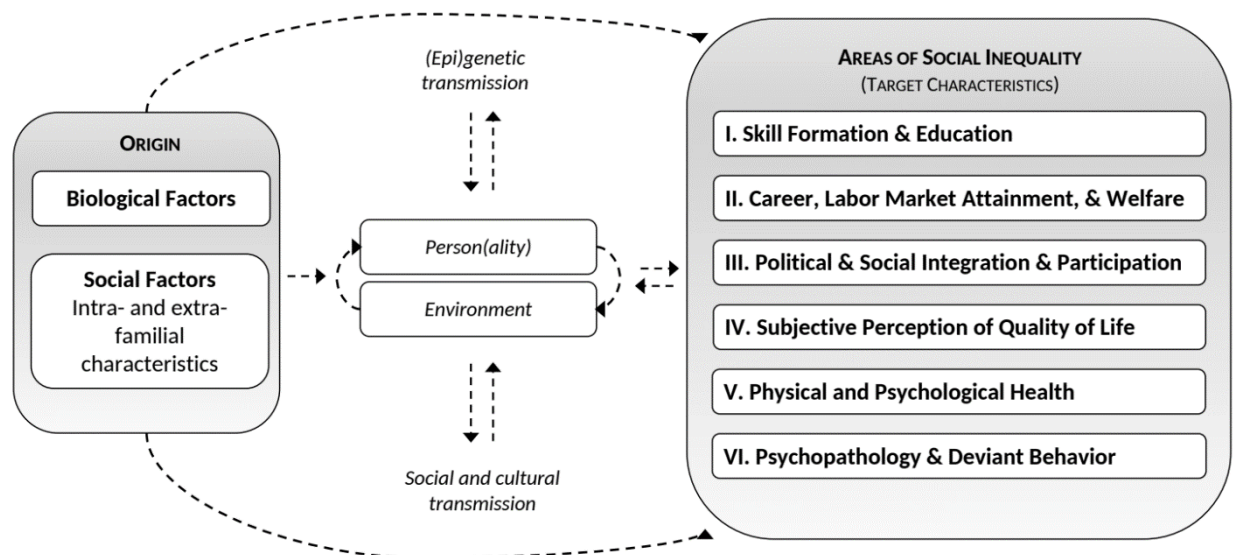


Figure 1: The basic concept and main domains of social inequality.

Biological factors

Information from monozygotic and dizygotic twins can be used to determine the significance of genetic differences for many developmental indicators, such as behavior. Furthermore, in the satellite project [TwinSNPs](#), polygenic scores were developed based on saliva samples. These summarize the estimated effect of many genetic variants on individual phenotypes. To achieve this, large genome-wide association studies, or GWAS, analyze which genetic variants are associated with certain phenotypes. GWAS summary statistics can then be used to calculate polygenic scores for different samples such as the TwinSNPs subsample of TwinLife. Data requests can be sent to: twinlife@uni-bielefeld.de

Social factors

In addition to biological characteristics, environmental characteristics are considered, such as socioeconomic status, family environment and structure, relationships between family members, and neighborhood characteristics.

Epigenetic transmission

Certain genes in a person can be “turned on” or “turned off” by environmental influences. This plays a role, for example, in the development of disease and can explain why, e.g., identical twins may have the same genetic makeup for Alzheimer's disease, but not both develop it. We investigate epigenetic interactions in our satellite project [TECS](#).

Person

The term “person” refers to the individual and his/her behavior, as well as his/her characteristic behavioral tendencies, which in psychology are called “personality”. A person's personality influences his or her behavior in almost every area of life. The [“Big Five”](#) model can be used to provide a comprehensive description of personality. It includes traits such as extraversion, openness, and conscientiousness. Other traits, such as self-efficacy, self-confidence, and coping styles, also play a role.

Environment

The environment includes all external influences. This includes, for example, whether a person grows up in the city or country, the area they live in, the school or workplace they attend, or the income a family has at its disposal. The special importance of environmental influences is addressed in the [TwinLife Environment satellite project](#).

Person-Environment Interaction

This refers to the fact that the environment and the person influence each other, i.e. they interact with each other. On the one hand, the environment affects the people in it. But at the same time, people also create the environments around themselves and for others. For example, an extroverted person creates an environment with lots of friends. Or growing up on a farm makes a person more likely to love animals. Culture in the broader sense (see “Social and Cultural Transmission”) also plays a role.

Social and cultural transmission

The social and cultural transmission of social inequalities describes the shaping of people's perceptions and behavior by socially and culturally shaped norms and values. These influence the opportunities, behaviors, and ultimately the experiences of people within society. They can thus contribute to the creation or perpetuation of social inequalities.

Social inequality can be described from different perspectives that reach from education and labor market attainment to health, psychopathology, and deviant behavior:

- I. Skill formation and education**
This area includes, for example, educational attainment, educational aspirations and achievement motivation, as well as cognitive skills and their development.
- II. Career, labor market attainment, and welfare**
This domain includes perceived job security, job satisfaction, work engagement, current occupation and position, and income or receipt of social benefits.
- III. Political and social integration and participation**
The characteristics of each person's social environment, such as support from family, friends and spouses, are covered in this area. In addition, social and political commitment and social resources are of particular interest.
- IV. Subjective perception of quality of life**
This category includes, for example, overall satisfaction with life as well as satisfaction in specific areas, life goals, and subjective perceptions of inequality.
- V. Physical and psychological health**
This area includes assessments of general health in terms of illness, subjectively perceived impairment, and information on health behaviors.
- VI. Psychopathology and deviant behavior**
Criminal or delinquent behavior and the degree of internalizing and externalizing problem behavior are assessed in this domain.

1.2 Study Design and Sample Structure

Data collection began in 2014 with a population-based sample of 4,096 twin families. The cross-sequential survey design (see Figure 2) contains four twin birth cohorts with ~1,000 same-sex (both monozygotic and dizygotic) twin pairs.

Face-to-face interviews (*F2F*) within the households take place every other year², and telephone interviews (*CATI*) are conducted in the consecutive years. In the *F2F* interviews, data was collected using a mixed-mode design: Participants were surveyed by an interviewer (computer-assisted personal interview; *CAPI*), by means of questionnaires on a tablet or laptop (computer-assisted self-interview; *CASI*), via a paper-and-pencil interview (*PAPI*), and/or via online questionnaires (computer-assisted web interview; *CAWI*).

On the one hand, these mixed modes ensured the most suitable assessment strategy for each question type, i.e., more sensitive topics were covered via *CASI*. On the other hand, they allowed a certain degree of flexibility for the interviewer in order to minimize the total interview duration in the households.

School reports and developmental check-up reports were scanned as part of the *CAPI* and encoded afterwards.

² Due to the COVID-19 pandemic, a new interview mode *CAPI-by-Phone* was introduced for the *F2F* interviews. This means that the interviewer, who normally conducts the interview with the family *F2F*, conducted the interview via phone. In *F2F4*, this was the only interview mode available. In *F2F5*, respondents could choose between *CAPI-by-Phone* and a *F2F* interview in the household.

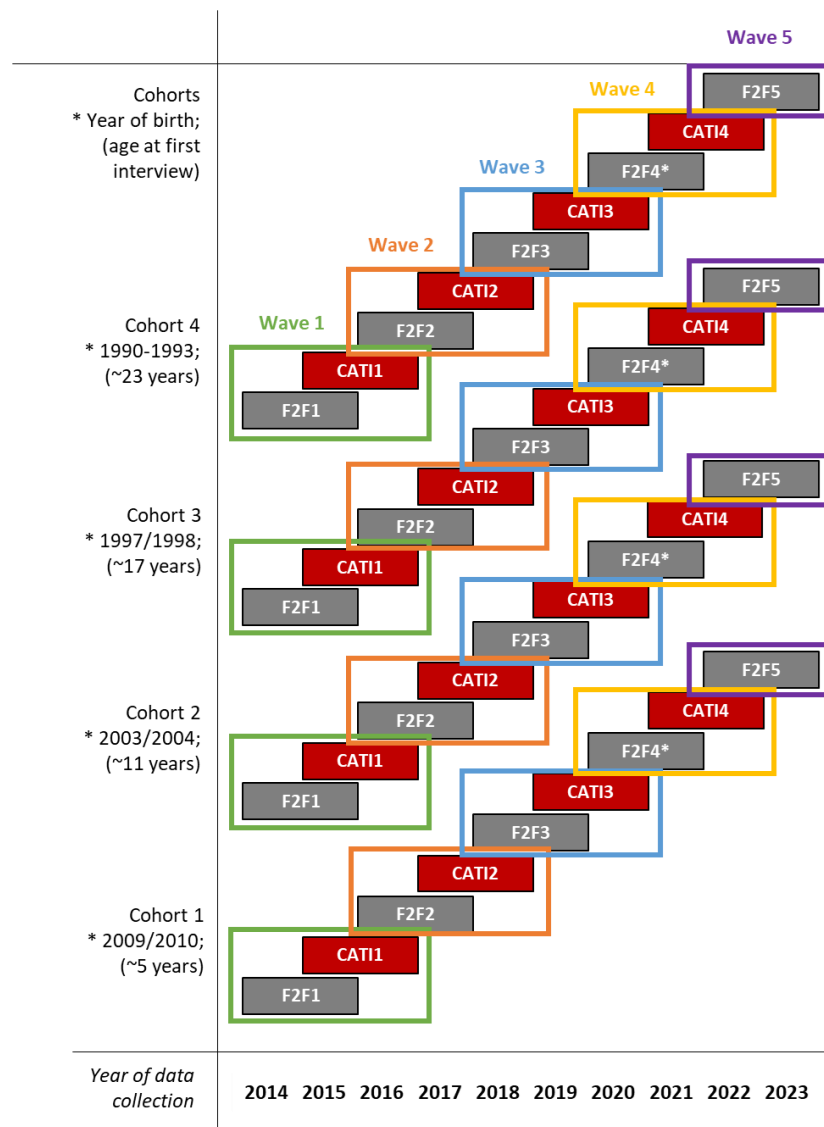


Figure 2: Cross-sequential survey design.

The cross-sequential structure is combined with an Extended Twin Family Design (ETFD, see Figure 3). The sample contains not only monozygotic and dizygotic twins, but also their biological, adoptive or foster parents, one biological, adoptive, or foster sibling (if available), as well as (if applicable) stepparents and partners of the twins. Thus, the ETFD captures both the biological family of the twins as well as the environment the twins live in.

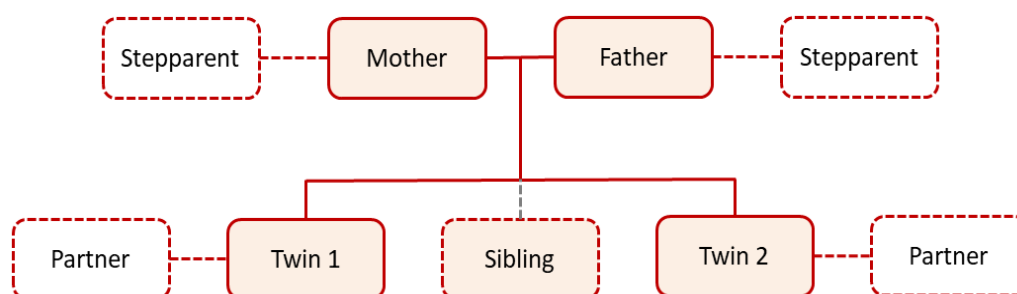


Figure 3: ETFD sample structure.

There are two characteristics of data collection and sample composition, which are briefly explained here.

First characteristic: Two subsamples

When the study was implemented, two subsamples of the initial age cohorts (consisting of twins aged about 5, 11, 17, and 23 years) were drawn, which were born in consecutive years (see Figure 2). This was necessary to achieve a sufficiently large sample size for TwinLife based on the target population of twin families in Germany.

As a result, the first subsample (Subsample a) consists of twins born in 1990/91, 1997, 2003 and 2009 and the second subsample (Subsample b) consists of twins born in 1992/93, 1998, 2004 and 2010. The subsample a) was interviewed for the first time in 2014 while subsample b) was interviewed first in 2015. Together, subsamples, a) and b) form the complete sample of TwinLife.

Identifiers for the two subsamples are recorded in variable *wav0100*.

Second characteristic: Two data collections are one survey wave

F2F interviews are carried out biennially in TwinLife. In the year between, a part of the sample is surveyed via CATI interviews. The main purposes of the CATI interviews are: **(1)** keeping in touch with the participants, **(2)** updating the contact information of the families (tracking), **(3)** collecting some complementary data that could not be surveyed in the F2F interview due to time restrictions, and **(4)** keeping track of important life events and transitions. Therefore, each F2F data collection together with the consecutive CATI data collection including both subsamples a) and b) is defined as one survey wave.

The identifiers for the survey waves are recorded in variable *wav0200* and the identifiers for the type of data collection (F2F or CATI) are recorded in variable *wav0300*. The consecutive numbering for each data collection is recorded in variable *wid* (see Table 1 for an overview).

wav0200	wav0300	wid	wav0100	(planned) release date
Wave 1	F2F 1	Data collection 1	Subsample a Subsample b	Autumn 2017
	CATI1	Data collection 2	Subsample a Subsample b	January 2019
Wave 2	F2F 2	Data collection 3	Subsample a Subsample b	Spring 2020
	CATI 2	Data collection 4	Subsample a Subsample b	Spring 2021
Wave 3	F2F 3	Data collection 5	Subsample a Subsample b	Spring 2022
	CATI 3	Data collection 6	Subsample a Subsample b	Spring 2023
Wave 4	F2F 4	Data collection 7	Subsample a Subsample b	Spring 2024
	CATI 4	Data collection 8	Subsample a Subsample b	Spring 2024
Wave 5	F2F 5	Data collection 9	Subsample a Subsample b	Summer 2025

Table 1: Survey and sample structure.

In TwinLife, a person or family who does not participate in one or more waves is considered a temporary drop-out until they finally refuse to participate. They will then be excluded from the following waves. Each person that was ever part of a TwinLife family is stored in the master file with the respondent status on the personal, the household, and the family level. The master file should always be the starting point for the sample selection of each analysis. You can find an example syntax (Stata and R) for the sample definition in the [Downloads section](#) of the TwinLife documentation website ("Example Syntax").

Usually, there is one data release each year, including new data of either a F2F or a CATI data collection for both subsamples.

For further information about the TwinLife sample and sampling design, please take a look at the [methodology report of the first wave](#) (Brix et al., 2017) and the corresponding [article](#) (Lang &

Kottwitz, 2020). Methodology reports of all data collections including a fieldwork description and outcomes can be found in the [Downloads section](#) of the TwinLife documentation website.

1.3 Where and how to get the Data

To receive the TwinLife data, please fill in the [Data Use Agreement](#) which you can find under 'Actions' in the [GESIS data catalogue](#). All data sets are available in both English and German and in SPSS and Stata formats.

2. Documentation of the Study

There are various ways of getting informed about the data sets and variables. A first overview of the TwinLife data can be found and downloaded [here](#).

2.1 Data Documentation Website and ShortGuide

The central [documentation website](#) of TwinLife gives the user a quick overview of the study, its structure and documentation and provides information on how to handle the data. It largely corresponds to the contents of the ShortGuide. In addition to the ShortGuide, the documentation website provides all documents mentioned in the ShortGuide in the [Downloads section](#), including questionnaires, methodology reports as well as helpful syntax files, and wave-specific and longitudinal overviews. The tables contained in the latter describe specific facets of the main study domains surveyed in each year. They also include information on the family members and age groups that were questioned as well as information on the sources of the items and scales. Furthermore, the download section contains documentation of changes between the different data releases.

2.2 Documentation within the Data Sets

Stata users can find several information on variables within the notes attached to the dataset. Use the command `-note varname-` in order to get the following information:

- filter condition in Stata language
- question and item text in German and English
- the data collections in which the variable has been surveyed

2.3 paneldata.org

The platform paneldata.org documents the data sets and meta data of various German panel studies. At <https://paneldata.org/twinlife> you can find a brief study description of TwinLife, information on the survey methods, topics and the data access. Furthermore, detailed information on variables and instruments are available: Use the keyword search or the topic list in order to find your variable of interest. By clicking on the variable, you receive information on

- labels
- categories
- frequencies
- related instrument(s) and variables

At <https://paneldata.org/twinlife> you will also find all questionnaires and the question wording for each variable including the input filter of the question in English and in German.

2.4 Codebooks

The [codebooks](#) give an overview of the variables included in the current data release of the person files of the data collections (for the structure of the delivered data, see chapter 3.1) and their frequencies. The variables are sorted alphabetically within content-related chapters. The codebooks document the following information for these variables:

- variable name
- variable label (also includes information on age groups and person types surveyed)
- question text
- categories (including the value labels) and frequencies
- the waves the variable was surveyed in
- filter conditions based on the instruments used for the variable
- sources for additional information

The codebooks for all data collections can be found in the [Downloads section](#) of the TwinLife Data Documentation website.

2.5 Technical Report Series, Methodology Reports, and Working Paper Series

The TwinLife Technical Reports (ISSN: 2512-403X) are scientific contributions dealing with both technical aspects of data presentation (e.g., sampling design and data collection, data documentations, etc.) and methodological questions. The version number of a technical report consists of three digits separated by dots (e.g., *v1.0.0*). The first digit marks significant changes (major release), the second digit designates extensions and additions (minor release), and the 3rd digit contains only bug fixes (revision level).

The Methodology Reports (first-authored by the survey institutes) contain detailed information on the data collection and the instruments included in each survey wave and are part of the Technical Report Series.

The TwinLife Working Papers (ISSN 2512-4048) are refereed scholarly papers that provide a forum for presenting work in progress.

All Technical Reports (including the Methodology Reports) and Working Papers are available [here](#).

Are you using the TwinLife data? The TwinLife Working Paper Series and the TwinLife Technical Report Series are open for your submission! Contributions are reviewed by the editors before a decision on publication is made. Please submit your manuscript to submission.twinlife@uni-bielefeld.de.

3. Data Structure

The following chapter describes the data sets, the data format, and the data structure itself.

3.1 Data Formats and Data Files

The TwinLife data is available free of charge and can be accessed via GESIS after filling in the [Data Use Agreement](#). The data delivery consists of a certain number of data files in SPSS and Stata format:

- Master data (ZA6701_master_v\$): Includes information on the gross sample, such as consistency checked variables that are stable over time (e.g., sex, year of birth, relation to the twins, zygosity, migration background) and wave-specific variables (e.g., person type, response status, family composition) about all individuals included in TwinLife in each wave. The master file includes all persons who have ever been recorded in TwinLife. This includes the target persons of the twin families, but also household members not relevant for the survey.
- Survey data in person format (ZA6701_person_wid\$_v\$): There is one data set for each data collection. Each surveyed person has one data row. The data collection identifier is the variable *wid*. The survey file of a data collection includes all persons that belong to a household of which at least one person participated in that data collection. Families that (temporarily or permanently) refused to participate as a whole, are not included.
- Data of the COVID supplemental surveys (ZA6701_person_cov\$_v\$): There is one data set for each COVID supplemental survey. Each surveyed person has one data row. The data collection identifier is the variable *cov*. But each of the supplemental surveys has also a value in the variable *wid*, namely 10, 11, or 12.
- Survey data in family format (ZA6701_family_wide_wid\$_v\$): There is one data set for each data collection. Each family has one data row with information of each participating person in the family being stored in separate variables/columns). See chapter 3.3 for more detailed information. Person format and family format data sets contain the same data using different structures.
- Survey weights (ZA6701_weights_v\$): A data file containing the survey weights (design, nonresponse and panel weights).
- Children of twins (ZA6701_cot_v\$): A data file containing information about the children of the twins, collected from the twins during the F2F4 data collection (*wid* 7).
- K2ID (ZA6701_k2id_v\$): A data file containing information about the early childhood education center (ECEC) of the twins in cohort 1.
- Twin zygosity assessment (ZA6701_zygosity_v\$): A data file with information of the twin zygosity assessment in F2F 1.
- Survey mode (ZA6701_mode_wid1_v\$): A data file with information on the survey mode for each variable in F2F 1.
- Unadjusted data of all variables collected in the PAPI survey mode (ZA6701_person_unadj_wid\$_v\$): One data file for each data collection with data

unadjusted for filter errors for all constructs/variables that were at least partly surveyed in the PAPI mode. See chapter 4.2 for further details.

All data is provided with English and German variable descriptions. In Stata, these languages are included in one data set while in SPSS, these are separate data files. The data are checked for inconsistencies and adjusted for filter errors (for details see chapter 4).

3.2 Person Types

According to the Extended Twin Family Design (ETFD), multiple persons in the family are surveyed. Each type of person in the family has a specific letter and a code that are displayed in the variable names of proxy-questions and the variable *ptyp*. The characters are specified in Table 2.

Letter in variable name	Person	Code in variable <i>ptyp</i>
t	twin 1	1
u	twin 2	2
s	surveyed sibling - full, half or step; for details see variable <i>fpr0107</i>	200
p	partner of twin 1	110
q	partner of twin 2	120
m	mother of the twins - biological, adoptive, or foster; for details see variable <i>fpr0107</i>	300
n	partner of the twins' father / 'stepmother'	600
f	father of the twins - biological, adoptive, or foster; for details see variable <i>fpr0107</i>	400
g	partner of the twins' mother / 'stepfather'	500

Table 2: Person codes. Please note: Additionally, non-participating siblings (*ptyp* 201 – 2xx) and other household-members (*ptyp* 700 – 7xx, 800) are coded in the variable 'ptyp'.

By using the variable *ptyp*, the data can be restricted to a certain sample of person types that are of interest for the analysis. The variable *fpr0107* describes the relation to the twins in more detail, e.g., it differentiates full siblings, half siblings and stepsiblings, etc.

Please note: The person type of twins in *ptyp* is always identical to the person type in the first data collection and always corresponds with the last three digits of the person ID *pid*. If the information on the relation to the twins was corrected in one of the most recent surveys, the variable *fpr0107* in the master data set was adjusted accordingly. Thus, the information differs between *ptyp* and *fpr0107* in very rare cases. For instance, if one twin was declared as the 'first-born twin' in the first data collection, but this was corrected to 'second-born twin' in a more recent data collection, the twin is longitudinal-consistently treated as the first-born twin in *ptyp*, but files as second-born twin in *fpr0107*. Thus, the birth order of the twins is documented in *fpr0107*, not in *ptyp*. Please keep this in mind when using the variables for sample selection or analyses.

3.3 System of Variable Names

Generally, the variable name is a composite of the variable stem (three letters), the item block (two digits), and the item number (two digits). Furthermore, depending on the person- or family-format of the data sets, person code letters in variable names indicate that proxy information is given from and/or about a certain family member (see chapter 3.2 for person codes).

Examples

1. What information is in the variable name *edu0100* in the 'person format' ('long' dataset)?

edu is the variable stem (type of education – self-report), *0100* is 'school attendance' within the facet 'type of education'.

2. What information is in the variable name *pas0100m* in the 'person format' ('long' dataset)?

pas is the variable stem (parental style – child report), the four digits *0100* are the item number within the construct. In most cases, for scale variables the first two digits are the item block within the construct (*01*, parental style) and the last two digits are the item number (*00*, shows affection); the variable extension *m* is the person code (statement about the mother). Thus, this item assesses the child's rating of parental style, more precisely on how much affection the parent, here the mother, shows.

3. What further information is in the variable names in the 'family format' ('wide' dataset), e.g., *pas0100m_s_1*?

_s is the person code of the person who provides the information (sibling), *_1* is the data collection code (first data collection). Thus, this item assesses the child's rating of parental style, more precisely on how much affection the parent (in this case mother) shows – rated by the sibling in the first data collection.

In the family format, two particularities have to be mentioned:

First, information on the households get the code *_1* to *_x* (x= maximum number of households within families) instead of a person code.

- For example, *ptyp_hq_1_1* provides information on the **type of respondent** for the **household questionnaire** in **data collection one** for the **first household which belongs to the family**.
- The variable *pih_\$_\$* shows the household number of a person (e. g. *pih_t_1* is the household number of the first-born twin in data collection 1).

Second, information given by a parent about their children is not filed under the type of person of the interviewed parent. Instead, the letter suffix reflects for which person information was given.

- For example, the variable name *eca0300t_1* shows that the statement was made for the first-born twin, but provides no information about the parent who filled in the questionnaire.
- Instead, the variable *ptyp_cp_1* indicates which parent completed the questionnaire about their children in data collection 1.

Variable labels contain a short description of the variable content and information about filter conditions (e.g., which person types and which age groups have answered the question). Generated variables are marked with '(gen)'; labels of variables with differing age filters over time include the minimum age of respondents across data collections.

3.4 ID Variables, Wave and Data Collection Identifiers

In TwinLife, various ID variables/identifiers are available. Each person belongs to a family that has a unique family ID (*fid*) and to a household that has a unique household ID which is wave-specific (*hid*; a composite of the family ID and an indicator for the household).³ Additionally, each person has a unique person ID (*pid*, which is a composite of the family ID and the person type). Although the person types except for the twins can change (i.e. '700 - other person' might change to '110 - partner of twin', or '200 - surveyed sibling' might change to '201 - non-surveyed sibling'), the person ID is invariable over time. Additionally, in the K2ID survey, the kindergartens of the cohort 1 twins were surveyed during 2015/16. Here, *kid* is the kindergarten ID, while *gid* is the identifier for the groups within one kindergarten.

The family ID consists of six digits: the first digit indicates the twin birth cohort (e.g., 1 for the first cohort; note that information about birth cohort is also coded in variable *cgr*); the other five digits are assigned randomly. ID variables are particularly important when different data files have to be combined. To match data of different survey waves in the family-wide-format, the variable *fid* needs to be used; to match the master data set with the person-format, the variable *pid* has to be used. Please note that time variable information in the master data set need to be reshaped into the long format in order to match the data with the person-format of the survey data. Before matching the master data set with the family format, the master data set has to be restructured to family format.

Furthermore, the variables with variable stem *wav* exactly describe in which survey wave (*wav0200*, *wav0300*) and subsample (*wav0100*) the data was assessed. The variable *wid* is the data collection identifier. The wave identifier (*wid*) is consecutively numbered, while the F2F and CATI waves (as well as the COVID-19 supplementary surveys) follow their own consecutive numbering, which results in the following denominations that are not to be confused (also see Table 1):

- *wid* == 1 stands for the first F2F household survey (F2F 1, surveyed in 2014–16)
- *wid* == 2 stands for the first telephone survey (CATI 1, surveyed in 2015–17)
- *wid* == 3 stands for F2F 2 (2016–18)
- *wid* == 4 stands for CATI 2 (2017–19)
- *wid* == 5 stands for F2F 3 (2018–20)
- *wid* == 6 stands for CATI 3 (2019–21)
- *wid* == 7 stands for F2F 4 (2020–22)
- *wid* == 8 stands for CATI 4 (2021–23)
- *wid* == 9 stands for F2F 5 (2022–24)
- *wid* == 10 stands for the first COVID-19 supplementary survey (Cov1; summer 2020)
- *wid* == 11 stands for the second COVID-19 supplementary survey (Cov2; winter 2020–21)
- *wid* == 12 stands for the third COVID-19 supplementary survey (Cov3; summer 2021)

³ The indicator for the household and therefore the household ID itself are linked to the information whether the twins live in this household or not. It is possible that in two consecutive years two households with different household compositions have the same household ID. Therefore, *hid* should not be used for longitudinal analyses.

- wid == 15 stands for the K2ID supplementary survey (K2ID; surveyed in 2015-16)

3.5 Missing Types

In TwinLife, missing values are delivered in a differentiated way. Table 3 gives an overview of the standard missing codes and a short explanation of their meaning.

Value	Value label	Explanation
-99:	not specified (refused to answer)	The respondent has explicitly refused to answer the question.
-98:	don't know	The respondent has explicitly stated not to know what to answer.
-96:	mixed missing values – e.g., don't know / not specified	Here, the instrument has not differentiated between two or more types of missings. This is mostly the case in the paper and pencil questionnaires of the first survey wave.
-95:	doesn't apply (screened out)	It indicates that the question was not intended for the respondent based on the filter conditions, for instance, due to the respondent's age.
-94:	technical error	In most of these cases, the filter condition of the question was programmed incorrectly so that respondents have falsely received or not received a certain question.
-93:	unclear classification of system missing (only for paper-and-pencil questionnaires)	Here, it is not possible to determine what the reason for a missing value is (whether it does not apply, the respondent does not know or whether they do not want to reply).
-92:	no participation in survey module	The respondent has not participated in the survey module / questionnaire, either because the questionnaire did not apply for the respondent or they refused to participate.
-90:	no participation in data collection	The person has participated in past data collections or may participate in future data collections, but not in the current one (all variables have the missing -90 in this wave for this person).
-87:	multiple answers	The person has given multiple answers in questions where only one answer is possible (usually in paper and pencil questionnaires).
other -80s:		... have different meanings and can contain valid information (see below)

Table 3: Missing codes.

Please note that the missing codes -80 to -89 (except for -87) have special meanings that can differ between variables and can be of importance for analyses. Generally, they contain 'valid' information but the answers are not direct answers to the question and are therefore coded as negative missings.

One example is the variable *emp0800* in wid == 3 (data collection F2F 2) "When did you leave your last job?" – The answer that the interviewee *has not been employed until now* is not a direct answer to the question but contains valid information and is therefore coded as a negative missing (-81).

In contrast, the answer "I already have children" on the question "Having children: How likely do you think you are to achieve this goal in your lifetime?" (*lgd0204*) in wid == 3 (data collection F2F 2) is a valid and analyzable answer to the question and is therefore coded with a positive code outside the actual answering scale (96).

You should check all variables for positive and negative meaningful missing values before using them for analyses.

3.6 Delivered Para Data

Para data are administrative data about the survey that are collected besides the actual survey data. In TwinLife, mainly month and year, in which an interview was conducted, is delivered as para data. Time stamps of questions or thematic blocks are recorded as well, but not delivered in the Scientific Use File. Under certain circumstances, it is possible for researchers to get access to the time stamps (e.g., for methodological research). Please contact info@twin-life.de if you are interested in using these data.

3.7 Survey Weights

There are three types of survey weights for the TwinLife data: design weights, nonresponse weights, and panel weights. While design weights address unequal sampling probabilities due to the sampling design, nonresponse weights account for a selective response pattern in F2F1. Panel weights for the waves from CATI 1 and onwards account for selective panel attrition. You will find a detailed documentation of the survey weights in the [Technical Report No. 15 “TwinLife Survey Weights”](#).

3.8 Peculiarities of Data

Peculiarities concerning families or persons are coded in the variable *pec* in the master data set. It records cases which in some way deviate from the sampling design, and which should, therefore, be considered when analyzing the data. For instance, this is the case when the twins are in fact part of triplets. Other examples are that the twins are orphans or, in very rare cases, the twins do not belong to the target birth cohorts defined within the sample design.

3.9 How to Match the Data Files

For longitudinal studies, the data sets of different survey data collections need to be combined. The single data sets can easily be appended as variable names and categories have already been harmonized across all data collections. For the person long format, different matching strategies can be chosen, depending on the desired data structure of the combined dataset ('long': several rows per person (one for each data collection) and one column per variable vs. 'wide': one row per person and a column for each data collection of variables). In the following we provide syntax for Stata and SPSS for both cases. Especially for the family wide format, it is strongly recommended to only use and merge the variables that are needed for the analyses in order to limit the size of the final data set.

Matching data files in Stata and R

1. Person long format, 'long' (one row per data collection for each person and one column per variable). The following example for combining the first two F2F data collections can be customized.

Stata:

```
cd "path" // navigate into the data directory
use ZA6701_person_wid1_v9-0-0.dta // load wid1 person dataframe
```

```

append using ZA6701_person_wid3_9-0-0.dta // append wid3 person dataframe
append using ZA6701_person_wid3_9-0-0.dta // append wid3 person dataframe
append using ZA6701_person_wid$9-0-0.dta // append ... person dataframe

* Combine all F2F waves
use ZA6701_person_wid1_v9-0-0.dta // load wid1 person dataframe
append using ZA6701_person_wid3_v9-0-0.dta ZA6701_person_wid5_v9-0-0.dta
ZA6701_person_wid7_v9-0-0.dta ZA6701_person_wid9_v9-0-0.dta

* Combine all CATI waves
use ZA6701_person_wid2_v9-0-0.dta // load wid1 person dataframe
append using ZA6701_person_wid4_v9-0-0.dta ZA6701_person_wid6_v9-0-0.dta
ZA6701_person_wid8_v9-0-0.dta

* Combine all waves except Covid surveys
cd "path" // navigate into the folder where the data is stored
use ZA6701_person_wid1_v9-0-0.dta
append using ZA6701_person_wid2_v9-0-0.dta ZA6701_person_wid3_v9-0-0.dta
ZA6701_person_wid4_v9-0-0.dta ZA6701_person_wid5_v9-0-0.dta ZA6701_person_wid6_v9-0-0.dta
ZA6701_person_wid7_v9-0-0.dta ZA6701_person_wid8_v9-0-0.dta
ZA6701_person_wid9_v9-0-0.dta

```

R:

```

library(haven) # package to read dta files
library(tidyverse) # package for data wrangling

path <- "..." # save data directory

person_files <- list.files(path) %>% # list all files in data directory
  str_extract(pattern = ".*_person_(w|c).*") %>% # extract person files
  discard(is.na) %>% # drop non-matches
  str_c(path, ., sep = "/") # append directory to file name

df_full <- person_files %>%
  map(read_dta) %>% # read all person files
  bind_rows() # bind by row

# Combine all F2F waves

person_files_f2f <- list.files(path) %>% # list all files in data directory
  str_extract(pattern = ".*_person_wid(1|3|5|7|9).*") %>% # extract f2f
files
  discard(is.na) %>% # drop non-matches
  str_c(path, ., sep = "/") # append directory to file name

df_f2f <- person_files %>%
  map(read_dta) %>% # read all person files
  bind_rows() # bind by row

# Combine all CATI waves

person_files_cati <- list.files(path) %>% # list all files in data directory
  str_extract(pattern = ".*_person_wid(2|4|6|8).*") %>% # extract f2f
files
  discard(is.na) %>% # drop non-matches
  str_c(path, ., sep = "/") # append directory to file name

df_cati <- person_files %>%
  map(read_dta) %>% # read all person files

```

```

        bind_rows() # bind by row

# Combine all waves except Covid

person_files_nocov <- list.files(path) %>% # list all files in data directory
  str_extract(pattern = ".*_person_w.*") %>% # extract person files
  discard(is.na) %>% # drop non-matches
  str_c(path, ., sep = "/") # append directory to file name

df_nocov <- person_files %>%
  map(read_dta) %>% # read all person files
  bind_rows() # bind by row

```

You can select the variables you are interested in while reading in the data.

Stata:

```

cd "path" // navigate into the data directory
use varlist using ZA6701_person_wid1_v$-0-0.dta // varlist is a placeholder for the
list of variables

```

R:

```

path <- "..."
df <- read_dta(file = str_c(path, "/ZA6701_person_wid_v$-0-0.dta"), col_select =
varlist) # varlist is a string vector containing the variables

```

2. Person long format, 'wide' (one row per person over all data collections and one column for each data collection and variable).

Stata:

```

cd "path"
use ZA6701_person_wid1_v9-0-0.dta
append using ZA6701_person_wid3_v9-0-0.dta

local varselect "varlist" // select list of variables to be converted from long to
wide
rename (`varselect') = _ // add suffix
reshape wide *_ , i(pid) j(wid) // reshape from long to wide format

```

R:

```

path <- "..."
df_wide <- read_dta(file = str_c(path, "/ZA6701_person_wid1_v9-0-0.dta")) %>%
  bind_rows(read_dta(file = str_c(path, "/ZA6701_person_wid3_v9-0-0.dta"))) %>%
  pivot_wider(values_from = varlist, # varlist = string vector with columns to
be reshaped
              names_from = "wid",
              names_sep = "_")

```

3. Family wide format, 'wide' (one row per family over all data collections and separate columns for variables per person and data collection).

For analyses using the family wide format with Stata, use the -merge- command with the family identifier *fid*.

Stata:

```
cd "path"
use varlist using ZA6701_family_wide_wid1_v9-0-0.dta // varlist is list of variables
merge 1:1 fid using ZA6701_family_wide_wid3_v9-0-0.dta, keepusing(varlist)
```

R:

```
path <- "...
df1 <- read_dta(str_c(path, "/ZA6701_family_wide_wid1_v9-0-0.dta")) %>%
  full_join(read_dta(str_c(path, "/ZA6701_family_wide_wid3_v9-0-0.dta")))
```

Matching data files in SPSS

1. Person long format, 'long' (one row per data collection for each person and one column per variable). The following example for combining the first two F2F data collections can be customized:

```
add files
/file= 'path\ZA6701_en_person_wid1_v9-0-0.sav'
/file= 'path\ZA6701_en_person_wid3_v9-0-0.sav'.
save outfile= 'path\en_person_wid13_match.sav'.
exe.
```

2. Person long format and Family wide format, 'wide' (one row per person/family and one column for each data collection and variable; one row per family over all data collections and separate columns for variables per person and data collection).

If the combined data need to be in wide format, it is important that all variables (except for the matching variables) in every dataset have a data collection-specific suffix. In the person format, this suffix has to be created for all variables except *pid* before matching. In the family format, wave-specific suffixes are already provided (except for the variables *wav0100*, *cgr* and *zyg0102*, which are time stable and therefore identical in all waves). Variable suffixes can be easily created using the python plugin. The following code can be customized to do this:

```
begin program.
variables = 'all' # define the variables which should get a suffix, you can use e.g.,
'all', 'x, y, z'; 'x to y'.
suffix = '_1' # enter the chosen suffix.
import spss,spssaux
oldnames = spssaux.VariableDict().expand(variables)
newnames = [varnam + suffix for varnam in oldnames]
spss.Submit('rename variables (%s=%s).'%( '\n'.join(oldnames), '\n'.join(newnames)))
end program.
```

When each dataset has data collection-specific suffixes, all datasets must be sorted by the matching variable; datasets in person format by the *pid*, datasets in family format by the *fid* (see chapter 3.5). To finally combine two data sets, the following code can be customized:

```
sort cases by pid.
match files
/file= 'path\ ZA6701_en_person_wid1_v9-0-0.sav'
/file= 'path\ ZA6701_en_person_wid2_v9-0-0.sav'
/by pid.
save outfile= 'path\en_person_wid12_match.sav'.
```

3.10 Matching Information from the Parent-About-Child Questionnaire to the Child's Data Set

For younger children (under 10 years of age), many information is requested from parents in the so-called parent-about-child questionnaires. This information can be recognized by the information stored in the data rows of the parents and the variable name refers by a suffix to the child about whom the information is given (t for twin 1, u for twin 2, s for sibling). For example, the school attendance of twin 1 is requested from the mother, father, stepmother or stepfather and then stored with that person in the variable edu0100t. However, such parent-about-child information can also be alluded to the data row of the child in question. You can find an example syntax for the variable edu0100t in the [Downloads section of the documentation website](#).

4. Check Routines and Data Adjustment

There is a range of quality check routines that were carried out by the survey institute and the TwinLife team in order to ensure the consistency and plausibility of the data. Furthermore, the data are adjusted for filter inconsistencies.

4.1 Check Routines

The following types of checks are carried out by the TwinLife team or the survey institute:

1. Longitudinal consistency
 - variable pid, sex identical to prior waves
 - body height and weight
 - variable coding longitudinally consistent
2. Identity checks
 - match of sex, first name, date of birth, relationship to twins between preload and survey
 - checks for duplicates (persons included several times in the sample?)
 - change of surveyed sibling identified and corrected
 - household composition
3. Logical relations
 - age of twins vs. cohort
 - age vs. ptyp
 - age and sex of (biological) parents
 - twins' age and sex identical
 - body height and weight
4. Completeness
 - starting sample vs. realized sample (on personal, household, and family level)
 - instrument/questionnaires vs. delivered variables
5. Instrument
 - completeness and correctness of preload variables and generated filter variables
 - filter conditions
6. Variables
 - correctness of variable labels and value labels

- correctness of missing values

4.2 Data Adjustment

The TwinLife data have been adjusted for some filtering inconsistencies that occur when a respondent answers the filter entry question and the following question(s) in an inconsistent manner with regard to the previous answer. This is mainly a phenomenon in the paper-and-pencil questionnaires (PAPI) that are filled by the respondents without interviewer assistance. In rare cases, there can be programming errors in the CAPI/CASI modules as well which can lead to filter inconsistencies.

The TwinLife data are adjusted for this kind of inconsistency, which means that entries or answers not meeting the filter conditions are deleted. This procedure assumes that the filter entry question was answered correctly whereas the following questions were answered incorrectly.

The constructs that are mainly affected by the adjustment are discrimination (dis), dia (diagnoses), hbe and doc (health-related behavior), spa (academic self-concept), del (delinquent behavior), net (social networks), imo (motivation), sat (domains of life satisfaction), sop (social participation), and mus (cultural capital) because they were at least partly surveyed in a paper-and-pencil questionnaire and included (more or less complex) filter conditions. For all constructs/variables that were at least partly surveyed in the PAPI mode the unadjusted data are released in the data sets ZA6701_person_unadj_wid\$_v\$. Users should carefully consider whether and how to use the data to answer their specific research questions. The [TwinLife Technical Report No. 07](#) proposes a way how to treat the unadjusted variables that belong to the discrimination construct which is particularly affected by filter inconsistencies.

Please note: The adjustment was not carried out for the igf-variables (intelligence test) in the second F2F interview, where some of the participants were falsely treated as new members of the sample and took the test a second time. Therefore, the igf-variables of the F2F2 data contain values for participants who should not have filled in the test again. Please consider this when analyzing the igf-variables.

5. Generated Variables and Scales

Below is a brief description of some of the generated variables available in the SUF and how to create user-defined scales. A more detailed description of the generated variables and scales is provided in the [online documentation](#) of the survey.

5.1 Generated Variables

In the course of data processing, some variables were generated based on the raw variables that are surveyed in the field.

Household and personal income manipulation (inc0110, inc0401)

In order to guarantee the twin families' anonymity, we applied a bottom- and top-coding strategy for the (household and personal) income variables inc0100, inc0101 and inc0400 following the recommendations of Wirth (1992)⁴.

Net equivalent household income (inc0411)

We generate and provide the net equivalent household income using the [modified OECD scale](#). Here, the net household income is weighted according to household size and age composition, taking scale effects for bigger and younger households into account. For more information about the concept, see OECD (2011).⁵

ISCED-1997 (eca0106, eca0107, eca0108) and CASMIN (eca0109)

Drawing on the highest reported educational qualification, the International Standard Classification of Education (ISCED) measures the individual education, ranging from 0 (pre-primary education) to 6 (second stage of tertiary education). For more information about the ISCED classification see OECD (1999).⁶ CASMIN (Comparative Analysis of Social Mobility in Industrial Nations) is a hierarchically structured educational scale that is classified on the basis of general school education and vocational qualifications. For more information on the CASMIN classification, see Brauns et al. (2003) and Brauns & Steinmann (1999)⁷.

Classifications of occupation and occupational activity: ISCO-08 (eca0205, emp0503, emp0513, emp0553, bpa0\$08), KldB-2010 (eca0203, emp0501), SIOPS (eca0208, emp0506), ISEI (eca0207, emp0505), EGP (emp0507), ESeC (emp0515)

The International Standard Classification of Occupations (ISCO) from 2008 classifies occupations based on the required skill level and the degree of skill specialization. TwinLife delivers the two-digit ISCO codes. For more information about the ISCO codes visit the [ILO website](#).

SIOPS (Standard Index of Occupational Prestige Scala) is a classification for a prestige ranking of occupations ranging from 0 to 100 based on the ISCO-88 classification. For more information see Ganzeboom & Treiman (1996).⁸

ISEI (International Socio-Economic Index of Occupational Status) is a measure for the socio-economic status of a person ranging from 12 to 90 based on the ISCO-88 classification. For more information see Ganzeboom & Treiman (1996).

⁴ Wirth, H. (1992). Die faktische Anonymität von Mikrodaten: Ergebnisse und Konsequenzen eines Forschungsprojektes. [The factual anonymity of microdata: results and consequences of a research project]. ZUMA Nachrichten 16, 30, 7 - 65.

⁵ OECD (2011). What Are Equivalence Scales? OECD Project on Income Distribution and Poverty.

⁶ OECD (1999). Classifying educational programmes: Manual for ISCED-97 implementation in OECD countries. Organisation for Economic Co-operation and Development.

⁷ Brauns, Hildegard, Scherer, S., & Steinmann, S. (2003). The CASMIN Educational Classification in International Comparative Research. In J. H. P. Hoffmeyer-Zlotnik & C. Wolf (Eds.), *Advances in Cross-National Comparison: A European Working Book for Demographic and Socio-Economic Variables* (pp. 221-244). Springer US. Brauns, Hildegard, & Steinmann, S. (1999). Educational reform in France, West-Germany and the United Kingdom: Updating the CASMIN educational classification. ZUMA Nachrichten, 23(44), 7-44.

⁸ Ganzeboom, H. B. G., & Treiman, D. J. (1996). Internationally comparable measures of occupational status for the 1988 International Standard Classification of Occupations. *Social Science Research*, 25 (3), 201-239.

EGP class typology (Erikson-Goldthorpe-Portocarero classes) is a scheme of social classes. For more information, see Ganzeboom & Treiman (1996).

The ESeC (The European Socio-economic Classification) is a scheme provided for the whole adult population, but is mainly occupationally based classification. It was developed from the EGP (Erikson-Goldthorpe-Portocarero) scheme. The categories of the ESeC summarize occupations according to their position in the labor market and the type of labor regulation. For more information, visit the website of the [German Federal Institute for Vocational Education and Training bibb](#).

Body Measurement: Body Mass Index and flags (bdy0300, bdy1001, bdy1002, bdy1003)

Height and weight are measured in each F2F data collection. The Body Mass Index (bdy0300) is calculated on the basis of these information. The flags document peculiarities in those three measures (bdy1001 peculiarities in height, bdy1002 peculiarities in weight, and bdy1003 peculiarities in BMI). For more information, see the [Technical Report No. 06 "Documentation TwinLife Data: Height, Weight, and BMI"](#).

Housing conditions and household type (liv0210, liv0410)

The housing conditions were surveyed on the household level. The variable liv0210 provides information about the housing conditions from the twins' perspective on a personal level. The variable liv0410 provides information about the household type on a personal level.

Regional variables (ewi, gkpol_r)

Due to data privacy reasons, regional information are only provided in an aggregated form. Whether a household lives in East or West Germany is stored in the variable ewi, while the variable gkpol provides information about the (political) community size.

Country of birth (mig2000/mig3000, mig2100/mig3100, mig2200/mig3200), Born in the GDR (mig2001, mig2101, mig2201), Migration background (mig4000, mig4100), German citizenship (mig0520)

The information about the country of birth was collected by providing a list as well as the opportunity to give an open answer. For data privacy reasons the answers were recoded into country groups⁹ and stored in generated variables. The self-reports are stored in the variables mig2000 (respondent's country of birth), mig2100 (respondent's mother's country of birth) and mig2200 (respondent's father's country of birth). Cross-information by other persons (proxy-reports) are additionally processed in the variables mig3000, mig3100 and mig3200 which leads to user-friendly country of birth variables that integrate all information that are available and cleaned.

Persons for whom at least one information about the country of birth of their parents (mig3100 and mig3200) is available have a value in the variable mig4100 (migration background: none, 1st or 2nd generation). For twins or siblings that have information about the country of birth of at least one parent and one grandparent there is a value in the variable mig4000 as well (migration background: none, 1st, 2nd, 3rd).

Whether a person was born in the GDR is generated on the basis of the country of birth and considers whether the person was born during the existence of the GDR between 7/10/1949 and 2/10/1990.

⁹ A list of the country groups can be found at the [Downloads section](#) of the documentation website under "Documentation of Generated Variables".

The variable mig0520 includes all available information on the personal level and displays whether the individual has the German citizenship or not, using self-reports and proxy information.

Report cards / certificates (cer variables)

School performance data based on photographs of the children's report cards are stored in the *cer* variables. For more information, please see the [TwinLife Technical Report No. 04 "Documentation TwinLife Data: Report Cards"](#).

5.2 Generated Scales

For some constructs, the TwinLife data includes generated scales (e.g., intelligence or zygosity), taking possible pitfalls of the data into account. The recoding process is documented in the [TwinLife Technical Report No. 01 "Documentation TwinLife Data: Zygosity"](#) and [TwinLife Technical Report No. 02 "Documentation TwinLife Data: Cognitive Abilities"](#). For more information about other commonly used scales and constructs in the social sciences included in the TwinLife data, please refer to the [scales manual](#).

6. Publications and Citation

6.1 Publications and Literature Database

The TwinLife team puts great effort in preparing the data and making it available for the open science community. Every publication provides important insights into the forming of social inequalities and is highly appreciated.

Publications based on the TwinLife data are documented and can be found on the [TwinLife website](#). Those lists are updated regularly and cover the following sections:

The [TwinLife Bibliography](#) contains the bibliographic information on all known publications related to TwinLife. All researchers who publish results based on the TwinLife data are kindly asked to provide information about their publication to twinlife@groups.uni-bremen.de so that their publications can be listed. We appreciate your compliance.

The [Conference contributions](#) contain a list of already presented contributions to national and international conferences.

[TwinLife Working Papers](#) are refereed scholarly papers that provide a forum for presenting work in progress. Submissions can be sent to submission.twinlife@uni-bielefeld.de and are reviewed by the general editors before a final decision on publication is made.

[TwinLife Technical Reports](#) are scientific reports on technical data presentation (e.g., data documentation, field reports, etc.) and methodical issues.

6.2 Citation

When preparing a publication based on TwinLife data, we kindly request you to mention our study in your publication. Please acknowledge our work by citing both the [dataset](#) itself (e.g., Diewald et al., 2024) and one of the [reference papers](#) ([Hahn et al., 2016](#); [Mönkediek et al., 2019](#); [Rohm et al., 2023](#)) and. Please keep in mind that the citation of the dataset may change as the study progresses and

newer versions become available. To check the latest citation version, see the [study's entry in the GESIS Data Catalogue](#). Older versions of the data and the related DOI's can also be found there.

Correct citation of the dataset (version 9.0.0) (APA 7):

Diewald, M., Kandler, C., Mönkediek, B., Riemann, R., Spinath, F. M., Andreas, A., Baier, T., Bartling, A., Baum, M. A., Deppe, M., Eichhorn, H., Eifler, E. F., Gottschling, J., Hahn, E., Hildebrandt, J., Hufer-Thamm, A., Instinske, J., Kaempfert, M., ... & Weigel, L. (2025). *TwinLife*. GESIS Data Archive, ZA6701. Data file Version 9.0.0.
<https://doi.org/10.4232/1.14531>

Correct citation of the TwinLife reference papers (APA 7):

Hahn, E., Gottschling, J., Bleidorn, W., Kandler, C., Spengler, M., Kornadt, A. E., Schulz, W., Schunck, R., Baier, T., Krell, K., Lang, V., Lenau, F., Peters, A.-L., Diewald, M., Riemann, R., & Spinath, F. M. (2016). What drives the development of social inequality over the life course? The German TwinLife Study. *Twin Research and Human Genetics*, 19(6), 659–672. <https://doi.org/10.1017/thg.2016.76>

Mönkediek, B., Lang, V., Weigel, L., Baum, M. A., Eifler, E. F., Hahn, E., Hufer, A., Klatzka, C.H., Kottwitz, A., Krell, K., Nikstat, A., Diewald, M., Riemann, R., & Spinath, F.M. (2019). The German Twin Family Panel (TwinLife). *Twin Research and Human Genetics*, 22(6), 540–547. <https://doi.org/10.1017/thg.2019.63>

Rohm, T., Andreas, A., Deppe, M., Eichhorn, H., Instinske, J., Klatzka, C. H., Kottwitz, A., Krell, K., Mönkediek, B., Paulus, L., Piesch, S., Ruks, M., Starr, A., Weigel, L., Diewald, M., Kandler, C., Riemann, R., & Spinath, F. M. (2023). Data from the German TwinLife Study: Genetic and Social Origins of Educational Predictors, Processes, and Outcomes. *Journal of Open Psychology Data*, 11(1), 1–15. <https://doi.org/10.5334/jopd.78>

7. Useful Links

- TwinLife Data Documentation:
<https://www.twin-life.de/documentation/>
- Download of all additional documents mentioned in the ShortGuide and on the documentation website:
<https://www.twin-life.de/documentation/downloads>
- Meta data documentation via paneldata.org:
<https://paneldata.org/twinlife>
- TwinLife reference papers:
[Hahn et al. \(2016\)](#)
[Mönkediek et al. \(2019\)](#)
[Rohm et al. \(2023\)](#)
- Technical Report on sampling design and socio-demographic structure of the first wave of the TwinLife (Lang & Kottwitz, 2017):

- <https://pub.uni-bielefeld.de/record/2913250>
- Dataset citation:
https://search.gesis.org/research_data/ZA6701
- GESIS data catalogue:
https://search.gesis.org/research_data/ZA6701
- Data Use Agreement:
https://www.twin-life.de/documentation/images/TwinLife/Downloads/Data_Use_Agreement_TwinLife.pdf
- TwinLife Technical Reports and TwinLife Working Paper Series:
<https://www.twin-life.de/twinlife-series>
- TwinLife Bibliography:
<https://www.twin-life.de/publikationen>
- TwinLife conference contributions:
<https://www.twin-life.de/konferenzbeitraege>