FAMILY

"Running in the FAMILY – Understanding and predicting the intergenerational transmission of mental illness"

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Deliverable D2.1

Data management plan

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V1	17/03/2023	First version		
V2*	17/06/2024	Second version: added SOPS, DTA, Knowledge Base and Data Dictionary. Updated PIF.		
V3	02/04/2025	Third version: updated hyperlinks to documents and resources referenced in the text,		

Open Issues

No:	Date	Issue	Resolved
1	17/03/2023	Complete appendices 1b-1i	**yes**
2	17/03/2023	Creation Data access committee	**Yes**
3	27/03/2023	Development of long-term data management plan	**No**

SUMMARY

This is the third version of the data management plan of the FAMILY consortium.

**This is a living document that is under continuous revision. It is uploaded at regular*

intervals to Keyways after substantial changes and approval by relevant stakeholders (e.g., work package leads).

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1 INTRODUCTION

The FAMILY consortium aims to deepen our understanding of the intergenerational transmission of mental illness, focusing on mood and psychotic disorders. For this purpose, FAMILY is set to explore the mechanisms of intergenerational transmission of psychiatric disorders, from the genetic, epigenetic, environmental and neuroimaging perspectives, and build novel prediction models that encompass the familial context. Hence, FAMILY will gather the largest population and high-risk offspring cohorts along with animal models and will implement state-of-the art approaches to integrate and analyze the data. Moreover, the consortium will investigate the bioethical and social issues risk prediction brings. Ultimately, the FAMILY consortium will help unravel the target of preventive strategies and contribute to ameliorating the effects of the intergenerational transmission of mood and psychotic disorders by identifying susceptibility and resilience markers.

Due to its interdisciplinary and translational nature, the FAMILY consortium will employ and generate large quantities of multimodal human data, which is subjected to strict ethical and GDPR regulations and must be handled in conformity with Standard Operating Procedures (SOPs).
The purpose of this data management plan is to establish a framework that adheres to the strictest data protection requirements and standards while guaranteeing data findability, accessibility, interoperability and reuse.

1.1 Definitions, Abbreviations and Acronyms

Table 1 List of Abbreviations and Acronyms

Abbreviation/ Acronym	DEFINITION
CHUV	Centre Hospitalier Universitaire Vaudois
DRE	Digital research environment
DTA	Data Transfer Agreement
EMC	Erasmus Universitair Medisch Centrum Rotterdam
FAIR	Findable, Accessible, Interoperable, and Re-usable
FCRB	Fundacio Clinic per a la Recerca Biomedica
FIBHGM	Fundacion para la Investigacion Biomedica del Hospital Gregorio Maranon
GDPR	General Data Protection Regulation
miRNA	micro Ribonucleic acid
NA	Not applicable
NIPH	Folkehelseinstituttet - Norwegian Institute of Public Health
RegionH	Region Hovedstaden
RNA	Ribonucleic acid
SNP	Single nucleotide polymorphisms
SOPs	Standard operating procedures
UCL	University College London

2 DATA SUMMARY

2.1 Purpose of the data collection/generation and its relation to the objectives of the project

FAMILY aims to improve causal understanding and gain prediction power of mental illnesses from the family context and address key bioethical and social issues raised by the concept of intergenerational risk transmission and risk prediction.

The specific objectives of the project are:

1. To understand the intergenerational transmission of risk:
    i. Estimate the contribution of genetic and environmental routes of intergenerational transmission of risk from parent to offspring throughout the life course.
    ii. Identify causal factors underlying genetic and environmental routes of risk transmission and resilience.
2. To predict the risk and resilience of mental illness in a familial context:
    i. Identify and validate genetic, epigenetic and brain imaging biomarkers of risk or resilience to mental disease in the family.
    ii. Develop and validate a multimodal risk prediction model and a normative modelling framework to predict, at the individual level, who is at risk of developing a mental disorder.
3. To create societal impact and end-user engagement:
    i. Map and evaluate social and ethical consequences of risk prediction for clinical use.
    ii. Increase awareness and foster active engagement of families and translate new discoveries to patients and mental healthcare professionals.

Within this framework, the FAMILY consortium will collect and analyse multimodal human and animal-model data to establish mental disorder risk and resilience mechanisms as well as analyse potential use of risk prediction tools and ethical and social aspects of their development and application.

2.2 Specify the types and formats of the data generated/collected.

a. MRI imaging data: digital (DICOM, NIfTI format).
b. Blood: biological.
c. Saliva: biological.
d. Data drawn from biological samples: digital (gene SNPs, miRNA).
e. Qualitative interviews: audio (mp4) and textual digital data and paper informed consent forms.
f. Questionnaires: paper and/or digital
g. Surveys: digital.

Biological data will be stored at local biobanks. Storage of analogue data will be in locked cabinets at the site where they were originally obtained and will be kept separated from personal data. Audio data from qualitative interviews will further be transcribed and digitalised. Storage of raw analogue and audio data will be organized in accordance with local guidelines. Once analogue data is transferred to a digital format or audio recordings are transcribed in a digital format and checked for accuracy by the interviewer and, in the case of audio data, also by the interviewee, the audio and analogue data will be destroyed or temporarily and securely stored. All data are stored securely per GDPR and specific local requirements. Digital data will be stored in a secured digital research environment (DRE) to allow for centralized analyses, conditional on appropriate data transfer and data processing agreements between Erasmus MC and FAMILY partners.

2.3 Specify if existing data is being reused and how.

FAMILY will use existing data from the population studies and high risk-offspring cohorts detailed in Table 1.

Cohort name	Partner	Cohort N	Available data	Additional Information
Population studies				
Gen R	EMC	9778	Phenotype, Genetics, epigenetics and MRI	Appendix 1a
COPSYCH/COPSAC	RegionH	650	Phenotype, Genetics, epigenetics and MRI	Appendix 1b
ALSPAC	University of Bristol	15589	Phenotype, Genetics, epigenetics	Appendix 1c
MoBa	NIPH	114500	Phenotype, Genetics, epigenetics	Appendix 1d
MCS	UCL	18818	Phenotype, Genetics	Appendix 1e
UK Biobank	*NA*	70000	Phenotype, Genetics	Appendix 1f
ABCD	*NA*	11878	Phenotype, Genetics, MRI	Appendix 1g
HCP	*NA*	1206	Phenotype, Genetics, MRI	Appendix 1h

PNC	*NA*	9500	Phenotype, Genetics, MRI	Appendix 1i
Familial high-risk cohorts				
BRIDGE	EMC	208	Phenotype, Genetics, MRI	
KBO	EMC	140	Phenotype, Genetics	
MARIO	EMC	500	Phenotype, Genetics	
BASYS	FCRB	60	Phenotype, Genetics, MRI	
	FIBHGM	60	Phenotype, Genetics, MRI	
LG	CHUV	389	Phenotype, Genetics, MRI	
VIA	RegionH	522	Phenotype, Genetics, epigenetics, MRI	

Table 1: Data available to the FAMILY consortium.

2.4 Data origin.

The existing population and high-risk offspring cohort information have various origins as described in Table 1. The data collection within the family consortium is specified in Table 2.

Cohort name	Partner	Estimated N to collect	Types of data
BASYS	FCRB	105	Phenotype, Genetics, MRI
BASYS	FIBHGM	62	Phenotype, Genetics, MRI
LG	CHUV	150	Phenotype, Genetics, MRI
BRIDGE	EMC	450	Phenotype, Genetics, MRI
KBO	EMC	*NA*	Phenotype, Genetics
MARIO	EMC	*NA*	Phenotype, Genetics

Table 2: Data collected in the FAMILY consortium

2.5 Data size.

The full amount of data cannot be precisely addressed since it depends on data format and cohort. Nevertheless, the FAMILY consortium currently includes data from population cohorts and familial high risk cohorts (see Table 1), and is expected to gather and generate a vast quantity of multidimensional data (see Table 2).

2.6 Data utility.

Consortium members will use the FAMILY data to elucidate the mechanisms of intergenerational transmission of mental illness, develop risk assessment tools and study the ethical implications of risk prediction.
Further, the data produced by FAMILY will be made available to other researchers and clinicians to develop and implement ethically informed preventive strategies that strengthen resilience and improve clinical outcomes in individuals at risk.

3 FAIR MANAGEMENT OF THE DATA

3.1 Making data findable, including provision for metadata

As part of deliverable 2.2 we have developed a knowledge base, which provides a platform where researchers and the general public can find important information regarding the data collected within the consortium, its management and secure storage, deliverables and milestones reported in the consortium and dissemination and educational activities.
Within the knowledge base, a data dictionary has been developed that contains information on the data modalities collected in FAMILY and the metadata associated with them. Currently the full version of this data dictionary is only available for consortium members on Keyways. Nevertheless its code is available at the consortium's GitHub page.

3.1.1 Are the data produced and/or used in the project discoverable with metadata, identifiable and locatable by means of a standard identification mechanism (e.g., persistent and unique identifiers such as Digital Object Identifiers)?

All data produced by FAMILY will be discoverable through detailed and descriptive metadata. When possible it will be associated with persistent identification mechanisms, such as DOI.

3.1.2 What naming conventions do you follow?

FAMILY will use harmonized variable names based on existing international/EU standards linked to metadata in the data dictionary and according to the Data Harmonization Plan. The naming conventions are being defined in the data harmonization plan.

3.1.3 Will search keywords be provided that optimise possibilities for re-use?

Yes.

3.1.4 Do you provide clear version numbers?

All files will be marked with explicit dates (YYYY–MM–DD) and version numbers, where appropriate.

3.1.5 Do you provide clear version numbers?

The metadata that will be created is the standard for each data type and will be marked with explicit dates (YYYY–MM–DD) and version numbers, where appropriate.

3.2 Making data openly accessible

3.2.1 Which data produced and/or used in the project will be made openly available as the default? If certain datasets cannot be shared (or need to be shared under restrictions), explain why, clearly separating legal and contractual reasons from voluntary restrictions. Note that in multi-beneficiary projects it is also possible for specific beneficiaries to keep their data closed if relevant provisions are made in the consortium agreement and are in line with the reasons for opting out.

Since the consortium will be operating with sensitive pseudo-anonymised human data, the principles of open science must be balanced with the need for data protection and privacy. Standard Operating Procedures (SOPs) for human data are specific to each cohort. Hence, there can be different procedures for data sharing or data accessibility.
We have established a series of SOPs within the consortium, which can be found in Keyways. These procedures ensure that all projects conducted within the consortium are feasible, that all partners providing data are asked for consent and that the requesting parties have access to the data. First, FAMILY members who want to use pseudonymized raw data must request access to the data access committee through a *project initiation form* (PIF), which can be found here. Once the data access committee verifies the PIF is complete, it does not overlap with other projects and the data requested in it is available in the consortium, the PIF will be distributed to stakeholders and steering committee members to ask for their approval. When all explicit approvals and/or comments from the stakeholders and steering committee members have been addressed, the data requesters will be notified. Next, DRE resources will be accommodated for the project (i.e. workspaces, software, permissions). Afterwards, the data will be uploaded to the DRE and made available only to the consortium members specified in the PIF.

All FAMILY results, pipelines and scientific publications will be made openly available to every consortium member through the DRE and the FAMILY intranet (Keyways) and will be published in open-access journals and repositories (as far as possible).

3.2.2 What methods or software tools are needed to access the data? Is documentation about the software needed to access the data included? Is it possible to include the relevant software (e.g., in open source code)?

To access the data, FAMILY members will need access to the DRE, where all software needed for data access and analysis will be pre-installed. DRE access manuals can be found here. These software tools will depend on data and analysis types. The use of open-source software and code will be encouraged. Documentation about the software will be included when appropriate (e.g., when the software is developed within FAMILY and no documentation is available online so far).

3.2.3 Where will the data and associated metadata, documentation and code be deposited? Preference should be given to certified repositories which support open access where possible. Have you explored appropriate arrangements with the identified repository?

Where relevant, FAMILY's metadata, methodology, code and documentation will be made available on the FAMILY consortium GitHub page and on the FAMILY website. For data storage, see sections 2.2 and 5.1.

3.2.4 If there are restrictions on use, how will access be provided?

See section 3.2.1.

3.2.5 Is there a need for a data access committee?

As stated in sections 2.3 and 2.4 of this document, the data analyzed within the FAMILY consortium comes from several sources. Thus, a data access committee (composed of WP2 members) has been created in order to address data requests, which will be articulated through the PIFs.

3.2.6 Are there well-described conditions for access (i.e. a machine-readable license)?

This depends on the cohorts and will be overseen by the data access committee.

3.2.7 How will the identity of the person accessing the data be ascertained?

Each consortium member has a personal and non-transferable username and password for both the FAMILY intranet and the DRE. This also includes a logging system tracking (i.e., audit trails) what specific data is accessed/used by whom.

3.3 Making data interoperable

3.3.1 Are the data produced in the project interoperable, that is allowing data exchange and re-use between researchers, institutions, organizations, countries, etc. (i.e. adhering to standards for formats, as much as possible compliant with available (open) software applications, and in particular facilitating re-combinations with different datasets from different origins)?

The DRE provides a flexible, scalable cloud-based platform where researchers have access to and can work with the data, methods and tools that are available in FAMILY. The environment is secure, self-serviced, capable of real-time collaboration, provides data and process audit trails, and complies with all laws and regulations (D4LS, Feb 2017). The DRE operates on the Microsoft Azure platform (which has been accredited to ISO 27001 and numerous other certifications such as CSA STAR), and the hardware is located within the EU. Microsoft Azure respects the intellectual property (IP) of the researcher. The DRE facilitates FAMILY researchers to collaborate on research projects in a safe, yet flexible computing and storage environment. The architecture of the DRE allows researchers to use a solution within the boundaries of data management rules and regulations. Alongside the DRE, consortium partners will have access to the Dutch National Supercomputer ("Snellius") when high performance computing is required. In situations where a partner's data privacy protections prohibit these resources from being used, singularity containers will be implemented to safeguard against pipeline and platform-dependent biases from being introduced and in particular facilitating re-combinations with different datasets from different origins. Proper guidelines for the use of these containers will be posted on FAMILY's wiki.

3.3.2 What data and metadata vocabularies, standards or methodologies will you follow to make your data interoperable? Will you be using standard vocabularies for all data types present in your data set, to allow inter-disciplinary interoperability?

Harmonization of datasets will leverage existing efforts and plans already in place with large, EU-funded consortia using similar data types and structures (e.g., LifeCycles (Jaddoe et al., 2020) and Early Cause (Mariani et al., 2021)), which jumpstarts the harmonization process. In nonstandard cases where differing measures/instruments have been used, a team of experts from the different sites will inventory and evaluate all phenotypic data collected across the consortium to identify the best options for harmonization. Project groups (i.e. those that have an interest and are motivated in

using the data) can be linked to experts for guidance on e.g. how harmonisation is done, resulting variables, and description of use cases.
To facilitate sharing and long-term inter-disciplinary use of FAMILY's data, the following file formats will be chosen: pdf, txt, csv, sql, dat (SPSS), RData, DICOM, NIfTI. All files will be marked with explicit dates (YYYY–MM–DD) and version numbers where appropriate, and provenance information will be documented in the Knowledge Base. FAMILY will use standardized variable names linked to metadata in a data dictionary. In cases where possible, metadata will be included inside of files (e.g., attributes within RData structures). Industry-standard data structures will be utilized for brain imaging data and standardized processing pipelines will be applied to imaging and -omics data, in many cases within Singularity containers to ensure consistent and reproducible processing is applied uniformly to all data.

3.3.3 In case it is unavoidable that you use uncommon or generate project specific ontologies or vocabularies, will you provide mappings to more commonly used ontologies?

Yes.

3.4 Increase data re-use

3.4.1 How will the data be licensed to permit the widest re-use possible?

There will be a long-term data re-use plan (deliverable D2.3, month 48) that will provide detailed guidelines to guarantee the widest re-use possible.

When will the data be made available for re-use? If an embargo is sought to give time to publish or seek patents, specify why and how long this will apply, bearing in mind that research data should be made available as soon as possible.

The data will be made available for within-project re-use as soon as it is processed, analyzed and inspected to make sure it complies with the quality standards. Consortium members who are interested in re-using data will be required to follow the SOPS and submit the corresponding PIF. In the long-term, data re-use will be made available in accordance with the data re-use plan.

3.4.2 Are the data produced and/or used in the project usable by third parties, in particular after the end of the project? If the re-use of some data is restricted, explain why. How long is it intended that the data remains re-usable?

The long-term data re-use plan (deliverable D2.3) will be split into two generic categories: those which do not require access to original data, and those which do require access to original data. For the former, normative models will be made available via standard open access platforms (e.g., GitHub) for broad dissemination and use. For the latter, the DRE will be utilized. Resources will be

identified to maintain the storage of the data within the DRE and outline a plan for coordinating with each consortium partner on data requests. Importantly, this strategy also allows for new groups to incorporate their data into the DRE, expanding the potential of this resource.

In accordance with local guidelines and regulations, participant data will be retained for at least 10 years upon completion of the FAMILY studies at the site where they are originally obtained and preferably at the DRE (if local legislation allows transfer of data to the DRE).

3.4.3 Are data quality assurance processes described?

Each partner is responsible for the quality control of the data collected within its own cohort.
Standard quality control procedures will be applied to processed data.

4 ALLOCATION OF RESOURCES

4.1 Estimate the costs of FAIR data and describe how we intend to cover these costs

Each partner has a specific fund devoted to the cost associated with FAIR data, where expenses like publishing in open-access journals and data management costs are contemplated. DRE costs associated with the FAMILY project are covered by the consortium, and WP2 can provide assistance with data management or data harmonization.

4.2 Clearly identify responsibilities for data management

The data management (data handling and data analysis) in FAMILY is the responsibility of the Coordinator (EMC), integrated within WP2 (FCRB), supported by WP7 (RUMC) with respect to infrastructure and by WP8 (LU) for issues related to research ethics. Procedures are based on the data management plan developed as part of WP2 (FCRB).
Furthermore, the Data Transfer Agreement (DTA) defines the data-related processes and operating procedures within the consortium, including access to key knowledge (WP1, Concentris). In all cases, each FAMILY partner will be responsible for the databases from cohorts that they host or collect new data from (which is the case in four familial high-risk cohorts, EMC, FCRB, FIBHGM, CHUV) as well as for keeping records of the experiments undertaken, in line with good research practice and the FAIR principles. In FAMILY, all processing of data (when local regulations allow) will be implemented on a dedicated research infrastructure and implement the strictest data protection standards (GDPR). Importantly, partners from non-EU countries have a security of information agreement with the EU (USA, Switzerland, UK, and Norway). The activities will be supported by WP2 and facilitated through the DRE infrastructure (WP2/7) and web portal (WP9).

4.3 Describe costs for long term preservation

A long-term data (re)use financial plan will be developed by the 48th month of the project.

5 DATA SECURITY

5.1 What provisions are in place for data security (including data recovery as well as secure storage and transfer of sensitive data)? Is the data safely stored in certified repositories for long term preservation and curation?

Biological data will be securely stored at local biobanks. All digital data will be stored and managed through the DRE. The environment is secure and compliant with all laws and regulations (D4LS, Feb 2017). Access is handled via WP2. For a given *data provider*, workspace will be created for the data, and the GDPR controller of the data will be given GDPR-controller rights for the workspace (e.g., monitor download requests). The GDPR controller also is responsible for granting access to their data to GDPR processors within the consortium. This is done via a web-based user interface. Access to the DRE requires Multifactor Authentication (MFA) for security. Only individuals authenticated via MFA who also have permission for a given workspace will be able to access the stored data. All operations of the DRE/workspace are logged, and thus a full detailed track-record/history of activities in a workspace are recorded and can be accessed/retrieved if needed. The Z-drive of the DRE (where data is stored) is backed up every day at 23:00 NL time with snapshots, and a 30 day history is recorded. Note, the DRE is not intended as the permanent or primary storage for data, and thus each individual site/data contributor is responsible for ensuring proper backup/copies of their data.

6 ETHICAL ASPECTS

6.1 Are there any ethical or legal issues that can have an impact on data sharing? These can also be discussed in the context of the ethics review. If relevant, include references to ethics deliverables and ethics chapter in the Description of the Action (DoA).

FAMILY involves human participants, including minors and potentially vulnerable groups and individuals (children in families with intergenerational risk of mental illness).

The research involving human subjects will comply with the WMA Declaration of Helsinki, the CoE Oviedo Convention, and other international documents on human subject research. The non-EU countries being partners in tasks involving human subject research will comply with the EU regulations in addition to their country's regulation. Both for medical and social sciences research involving human participants, ethics approval has been or will be applied for and obtained from respective research ethics committees in advance in each country.

All consortium members and researchers in FAMILY are committed to the highest research ethics and integrity standards. They will conform to the applicable international and EU law, Horizon Europe

standards, and to national law in the countries where the project will be carried out. Consortium members will constantly seek advice from ethics experts involved in the consortium, external ethics experts (in the Scientific and Ethical Advisory Board [SEAB]), specialised ethics departments at their institutions and national ethics bodies, compliance managers, research ethics committees and DPOs. WP8 (work package 8: ethical aspects and social consequences of intergenerational transmission of risk and prediction of mental illness) will have the responsibility to coordinate handling previously identified, as well as any new ethical issues arising from the project. Given that ethical regulation might slightly differ between consortium member states and institutions, WP8 will also take responsibility for reviewing and advising on ethics issues if brought up by any one of the partners. The Steering Committee will evaluate ethical issues and decide upon actions at least bi-annually but more frequently when needed. This will be achieved by following the Standard Operating Procedures (SOPS), which can be found here.

6.2 Is informed consent for data sharing and long term preservation included in questionnaires dealing with personal data?

The clinical studies that are part of FAMILY are each performed following local ethical requirements that are in place at each site. The studies are longitudinally ongoing and as part of FAMILY, a follow-up assessment has been made possible. Thus, ethics were already in place given the previous assessments. Before sharing data, all sites are responsible to check each individual's informed consent for approval.

For the follow-up assessments within already existing cohorts, every participant will be informed about the planned research and will receive an information sheet in their language. Potential research participants will have an opportunity to ask questions about the research project and get them answered. If potential participants agree to participate in research, they will be asked to sign an informed consent form. Participation will be entirely voluntary, free, and fully informed consent will be obtained from all research participants. For children, parental consent and child's assent will be obtained according to the legal regulations in each country.

In case of retraction of consent by a study participant, coupled with the wish to delete their personal data, all personal data of the participant will be deleted. This will be handled by the site hosting the cohort in which the participant participated, where data deleted within the DRE takes immediate effect for all partners with access.

For social sciences research (qualitative interviews) performed in WP8, every potential participant will be informed about the planned research and use of data and will receive an information sheet. Potential research participants will have an opportunity to ask questions about the research project and get them answered. If potential participants will agree to participate in interviews, they will be asked to sign an informed consent form. Participation will be entirely voluntary, free, and fully informed consent will be obtained from all research participants. For anonymous survey, an introductory part at the beginning of the questionnaire will be included, explaining the purpose of the survey, anonymity and rights of research participants.

7 Literature references

Jaddoe, V. W., Felix, J. F., Andersen, A. M. N., Charles, M. A., Chatzi, L., Corpeleijn, E., ... & Duijts, L. (2020). The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. European journal of epidemiology, 35, 709-724.

Mariani, N., Borsini, A., Cecil, C. A., Felix, J. F., Sebert, S., Cattaneo, A., ... & Lekadir, K. (2021). Identifying causative mechanisms linking early-life stress to psycho-cardio-metabolic multi-morbidity: The EarlyCause project. Plos one, 16(1), e0245475.

8 APPENDICES

Appendix 1a. Generation R Data Requests

Access to Generation R Data for FAMILY-related projects follows a multi-step process.

1.) A brief project proposal must be drafted (see Appendix 1).
2.) The project proposal is first sent to the data access committee via WP2. It will be briefly discussed at the SC meeting,
3.) One approved by the data access committee and SC, the data access request can proceed to the Generation R MT.
4.) Once approved by the GenR MT, access can be granted to the DRE workspace with GenR data by the GenR data manager (J Krikeb) once it has been confirmed that the partner has a.) filled in the consortium agreement addendum related to data access within the consortium and b.) each user who will be granted access has signed the Generation R confidentiality agreement.
5.) Access is granted for a period of XX months. If the project has not yet completed, access can be renewed with an addendum to the project proposal.

Appendix 1b. COPSYCH/COPSAC Data Request - Pending

Appendix 1c. ALSPAC Data Request

All FAMILY partners (and their known research teams) who have signed the consortium agreement as of MM-DD-YYYY (and the data access addendum) have been added to the ALSPAC data request, and can request data access via the data access committee with a brief project proposal. See Appendix 1 for info on the project proposal. After discussion by the SC, access will be granted to ALSPAC data by WP2.

For research staff not listed in the original ALSPAC data request, an addendum must be filed. We will file addendums twice per year, unless it is urgently necessary to file an extra addendum sooner. Contact WP2 staff if you have new research staff not listed in the original ALSPAC data request. The list can be found on the intranet (in development).

Appendix 1d. MoBa Data Request - Pending

Appendix 1e. MCS Data Request - Pending

Appendix 1f. UK Biobank Data Request - Pending

Appendix 1g. ABCD Data Request - Pending

Appendix 1h. HCP Data Request - Pending

Appendix 1i. PNC Data Request - Pending

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