MRC Epidemiology Unit

UNIVERSITY OF CAMBRIDGE

MRC Epidemiology Unit
Standard Operating Procedures

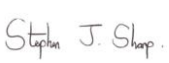
Title	**Standard Operating Procedure for Good Analytical Practice**
Filename/ Directory location	V:\Unit_Work_Processes\Unit SOPs
Document Status (Draft/ Approved/ Superseded)	Approved

SOP Reference number (Approver to assign)**: MRC Epi_SOP005** **Associated Risk Assessment number(s): N/A** **Version Number: 4.0**	**Effective date:** 21 January 2022 **Review date:** 21 January 2024

SOP Author

Name	***Position***	***Signature***	***Date***
Jennifer Furman	Senior Study Trial Manager		21/01/2022

SOP Approver

Name	***Position***	***Signature***	***Date***
Stephen Sharp	Senior Statistician		21/01/22
Tony Webb	Senior Data Manager		21/01/22

1. Table of contents

1. **Table of contents** 1
2. **Purpose & scope** 2
3. **Responsibilities & safety precautions** 2
4. **Equipment & reagents** 2
5. **Definitions & abbreviations** 2
6. **Procedure** 3
7. **Study specifications** 6

8. Date added to site SOP folders/ Intranet.....6
9. Other related procedures & documents.....6
10. Revision History.....6

2. Purpose & scope

This Standard Operating Procedure (SOP) applies to all employees, students and visitors affiliated to any of the research programmes described here https://www.mrc-epid.cam.ac.uk/about-us/organisation/ who perform any type of analysis using data and generate outputs for which the MRC Epidemiology Unit has primary responsibility, including, but not limited to CETU work. Examples of outputs include papers, reports, PhD theses, MPhil project reports, conference presentations.

The rationale of this SOP is to ensure that all analytical work is clearly justified, accurate, transparent and reproducible.

Benefits from compliance with the requirements and recommendations in this SOP include the following:

- all outputs can be easily linked back to an analysis plan, data source(s) and analysis programs used to generate the results reported in the output.
- authors of an output should be able to locate analysis programs/datasets long time after the analyses were first performed, and address external queries or requests for data/results.
- individuals working on similar types of analysis should be able to share their analysis programs with each other.
- there will be increased transparency in how the results presented in an output have been obtained, thus increasing the opportunity for other co-authors on an output to identify and correct errors prior to an output being submitted or published.

3. Responsibilities

It is the joint responsibility of each member of staff/student and their supervisor/line manager to ensure adherence to the requirements of this SOP. The Chief Investigator (CI) of the project has ultimate responsibility to ensure adherence to this SOP.

In situations where analysis is performed for other collaborators who are primarily responsible for the output, this SOP should also be followed as closely as possible.

4. Equipment & reagents

N/A

5. Definitions & abbreviations

Definition/Abbreviation	Description
CI	Chief Investigator
CSV	Comma-Separated-Values – a simple file format used to store tabular data
GCP	Good Clinical Practice

RCT	Randomised Controlled Trial
SOP	Standard Operating Procedure
SRD	Secure Research Drive/Domain – the safe haven space within the MRC Epidemiology Unit.
SAP	Statistical Analysis Plan
CETU	Cambridge Epidemiology & Trials Unit

6. Procedure

6.1 Statistical Analysis Plan (SAP)

For all analyses, a Statistical Analysis Plan (SAP) should be written, agreed with co-authors/collaborators, and saved in an appropriate folder (see section 7) prior to analyses being performed.

The following is the type of information that should be included in the SAP:

- Date when SAP was finalised. Dates of and justifications for any subsequent revisions.
- Name of SAP author and SAP reviewers.
- Statistical software to be used.
- Objectives and hypotheses.
- Descriptive analyses.
- Outcomes.
- Exposures.
- Potential confounders and effect modifiers.
- Statistical methods.
- Modelling strategy.
- Sensitivity analyses (i.e. analyses that assess the sensitivity of the results to the model assumptions).

Some of the above sections may be less relevant if the SAP relates to genetic discovery analyses which are hypothesis-free.

The level of detail to be included in a SAP will vary between different projects. At a minimum, the SAP should contain the information that would be included in the "Statistical Analysis" section of a results paper.

For clinical trials, a more formal and detailed template has been developed based on guidelines published in Gamble et al, JAMA. 2017;318(23):2337-2343. See section 9 for the location of this template.

6.2 Analysis software

Where possible, analytical work should be performed using either Stata or R (or both). Python may also be considered, preferably only if at least some co-authors also have experience in using this package. Other specialised software may be needed (e.g. for genetics analyses); this should be documented in the SAP.

If a software package is required that is not available on the network, please email helpdesk@mrc-epid.cam.ac.uk ; the cost of purchasing such software would usually need to be met by the grant or research programme that requires it. If someone (e.g. a visiting worker) does not have an MRC-EPID account and needs remote access to core Unit software, their line manager should discuss with the IT department.

6.3 Analysis programs

All analysis programs should be written and annotated in such a way that co-authors could use them to replicate the analysis. Analysis programs should be text format files which include the following information:

- name of study/project.
- brief description of the specific purpose of the analysis program.
- name of the person who has written the analysis program.
- version of the software being used.
- names of any add-on packages that need to be installed before the program can run, e.g. user-written Stata commands from the Statistical Software Components (SSC) archive, R libraries.
- command to change working directory to a relevant folder, so that any outputs from the program are saved in that folder rather than on the hard disk of the PC or some other system folder.
- command to read in the relevant dataset.
- comments throughout the file to aid understanding of what each section of code is doing.

Line spacing/indentation can enhance clarity. A "master" program which runs all the analysis programs in sequence can be useful, rather than including all analyses in a single program, which can quickly become very large and hard to navigate.

The name of the analysis program should be a concise description of its main purpose.

In some situations it may be useful to retain previous versions of programs for a particular analysis. If this is the case, the version number of each program should be included at the start of the file; previous versions should be moved to a clearly labelled sub-folder, so they are not confused with the current/final versions.

6.4 Datasets

Original data sources (e.g. internal data releases or externally provided data) should be stored in an appropriate network folder. They should not be moved or copied to other folders. Appropriate approvals and agreements should be in place for externally provided data (i.e. Data Sharing Agreements or Collaboration Agreements), and it also should be ensured that there is ethical approval for sharing of data.

Prior to undertaking any analysis, a program should be written, whose purpose is to create a dataset for analysis based on the original data

source(s), and also keep a record of relevant information related to the data source(s).

If the data source(s) are from within the MRC Epidemiology Unit, the release IDs of the original data source(s) and any updates, together with the title and date of the original data request, should be included at the start of the file. If the data source(s) are from outside the Unit, similar information should be recorded where possible.

Examples of tasks that could be performed by this program include:

- remove potentially personally identifiable data (these data should already have been removed from internal data releases).
- merge or append any other relevant data.
- generate any new variables required for the analysis (e.g. a variable representing BMI categories based on values of a continuous BMI variable).
- rename and/or label variables.
- label values of variables (e.g. if there is a variable coded 1/2 for men and women, these can be replaced with value labels M and F).
- reshape data to wide or long format.
- set up data for e.g. survival analysis.

This "analysis dataset" can then be saved under a different name from the original data source, and used for all subsequent analyses. Once an output is published, the analysis dataset, not the raw data source, will usually be the most appropriate "data" to be provided externally if required (with a Data Sharing Agreement, as needed).

6.5 Location of analysis work related to an output

All analysis work relating to an output (SAP, analysis programs, analysis datasets, outputs) should be saved in appropriately located folders on a network (Windows or Linux) drive (not a personal drive or memory stick). Any analyses of personally identifiable data should be performed and saved in folders on the SRD. To mitigate risks of over-writing data, analysis work should not be saved in the same folder as the original data release.

Multiple copies of the original data source(s) should not be made. If a dataset has been provided from a source external to the unit, then a single copy of this dataset should be saved. Datasets should not be stored as attachments to emails. Data should additionally not be sent without prior agreement/authorisation.

There should be sufficient information in the analysis programs to enable the original data sources to be easily identified (see section 6.4).

6.6 Internal peer review of analysis work

Peer review of analysis work (especially analysis programs) within the Unit is encouraged whenever feasible. This increases the chance of identifying any errors prior to submission, and facilitates sharing of good practice. This could be done by co-authors of a particular output or other members of the same research programme. Making analysis work easy to find and understand will help to facilitate this.

6.7 Statistical and outcome data reports

Results of all analyses defined in the SAP should be collated in a single outcome data report, alongside a statistical report that provides any further statistical information that is relevant to the understanding of the results, and will refer back to specific sections of the SAP. These reports should be saved in a study folder (see section 6.5) and shared with collaborators and potential co-authors before or at the same time as the first draft of the output that is being prepared.

6.8 When an output is published

As soon as possible after an output is published, the analysis work relating to this output should be tidied up, removing any unnecessary or old versions of programs, temporary datasets etc. The location (i.e. folder path) of the analysis work for a particular output should be sent to dmt@mrc-epid.cam.ac.ukso that a central repository of this information can be maintained.

6.9 Leaving the Unit

Analysis work for Unit research projects should remain on the network after a member of the Unit has left. The line manager and/or corresponding author is responsible for ensuring that this is the case. The leaver has a responsibility to ensure that to the best of their knowledge and ability, they have left their analysis work for projects as well as relevant scripts, notebooks, etc.

7. Study specifications

Not applicable.

8. Date added to site SOP folders/ Intranet

17 June 2021

9. Other related procedures & documents

Template for analysis plan for a clinical trial
Unit V: drive: Functional_Groups\Statistics\Clinical trial SAP template

In-house exemplar Stata do files for specific analytical tasks
Unit V: drive: Functional_Groups\Statistics\Stata resources\In-house do files

In-house Stata commands for genetics analyses on Linux
Within Stata (on Linux), type:
net from /genetics/data/GWA/jianan/ado/myprogs
and then click on the program you wish to install.

10. Revision History

Version Number	Date	Changes	Author
1.0	August 2015	Initial document	Stephen Sharp
2.0	July 2018	Minor changes and updates to initial document	Stephen Sharp

3.0	17 June 2021	Moved to SOP template, minor changes to formatting, added requirements for ethical and legal approval for working on data	Jennifer Furman
4	21 January 2022	Added information on statistical and outcome data reports (section 6.7)	Stephen Sharp