# Analysis Data Reviewer's Guide

**R Consortium**

**R Submission Pilot 3**

**ADRG Template Version 2019-07-18**

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# Table of contents

# 1 Introduction

## 1.1 Purpose

This document provides context for the analysis datasets and terminology that benefit from additional explanation beyond the Data Definition document (define.xml). In addition, this document provides a summary of ADaM conformance findings.

## 1.2 Study Data Standards and Dictionary Inventory

| Standard or Dictionary | Versions Used |
| --- | --- |
| SDTM | SDTM Implementation Guide Version 3.1.2 SDTM Version 1.2 |
| SDTM Controlled Terminology | CDISC SDTM Controlled Terminology, 2022-12-16 |
| ADaM | ADaM-IG v1.1 ADaM v2.1 |
| ADaM Controlled Terminology | CDISC ADaM Controlled Terminology, 2022-06-24 |
| Data Definitions | Define-XML v2.0 |
| Medical Events Dictionary | MedDRA version 8.0 |

## 1.3 Source Data Used for Analysis Dataset Creation

The ADaM datasets were derived from SDTM version 1.2. For traceability, the SDTM is publicly available at the PHUSE Github Repository.

Which can be traced back to the original CDISC SDTM & ADaM Pilot Project.

# 2 Protocol Description

## 2.1 Protocol Number and Title

- **Protocol Number:** CDISCPilot1
- **Protocol Title:** Safety and Efficacy of the Xanomeline Transdermal Therapeutic System (TTS) in Patients with Mild to Moderate Alzheimer's Disease

The reference documents can be found here.

## 2.2 Protocol Design in Relation to ADaM Concepts

### 2.2.1 Objectives:

The objectives of the study were to evaluate the efficacy and safety of transdermal xanomeline, $50\text{cm}^2$ and $75\text{cm}^2$, and placebo in subjects with mild to moderate Alzheimer's disease.

### 2.2.2 Methodology:

This was a prospective, randomized, multi-center, double-blind, placebo-controlled, parallel-group study. Subjects were randomized equally to placebo, xanomeline low dose, or xanomeline high dose. Subjects applied 2 patches daily and were followed for a total of 26 weeks.

### 2.2.3 Number of Subjects Planned:

300 subjects total (100 subjects in each of 3 groups)

### 2.2.4 Study schema:
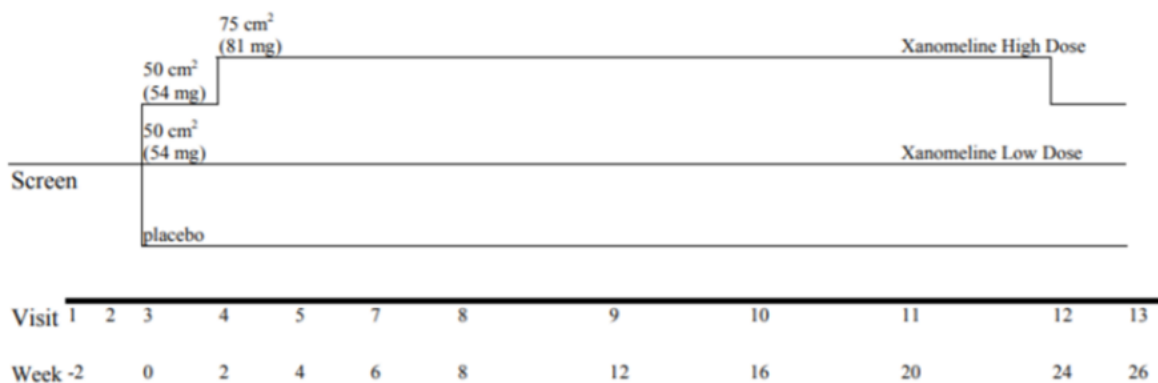
# 3 Analysis Considerations Related to Multiple Analysis Datasets

## 3.1 Core Variables

Core variables are those that are represented across all/most analysis datasets.

| Variable Name | Variable Description |
| --- | --- |
| STUDYID | Study Identifier |
| USUBJID | Unique Subject Identifier |
| SUBJID | Subject Identifier for the Study |
| SITEID | Study Site Identifier |
| SITEGR1 | Pooled Site Group 1 |
| TRTSDT | Date of First Exposure to Treatment |
| TRTEDT | Date of Last Exposure to Treatment |
| AGE | Age |
| AGEGR1 | Pooled Age Group 1 |
| AGEGR1N | Pooled Age Group 1 (N) |
| RACE | Race |
| RACEN | Race (N) |
| SEX | Sex |
| SAFFL | Safety Population Flag |
| ITTFL | Intent-To-Treat Population Flag |
| EFFFL | Efficacy Population Flag |
| COMP24FL | Completers of Week 24 Population Flag |
| DSRAEFL | Discontinued due to AE? |

## 3.2 Treatment Variables

ARM versus TRT01P

```
Are the values of ARM equivalent in meaning to values of TRT01P?

    Yes.
```

ACTARM versus TRT01A

```
If TRT01A is used, then are the values of ACTARM equivalent to values of TRT01A?

    Not applicable - ACTARM is not used.
```

Use of ADaM Treatment Variables in Analysis

```
Are both planned and actual treatment variables used in analysis?

    Yes. Planned treatment variables are used for study population and efficacy
    analyses, whilst actual treatment variables are used for the safety analysis.
    All subjects received the treatment arm to which they were randomised and so
    the planned treatment is equivalent to the actual treatment for all subjects.
```

Use of ADaM Treatment Grouping Variables in Analysis

```
Are both planned and actual treatment grouping variables used in analysis?

    Not applicable - treatment grouping variables are not used.
```

## 3.3 Use of Visit Windowing, Unscheduled Visits, and Record Selection

Was windowing used in one or more analysis datasets?

```
    Yes
```

Were unscheduled visits used in any analyses?

```
    Yes
```

## 3.4 Imputation/Derivation Methods

For ASTDT in ADAE, this date was converted to numeric SAS date from AE.AESTDTC. If the day component is missing, a value of '01' is used. If both the month and day are missing no imputation is performed. See define.xml.

# 4 Analysis Data Creation and Processing Issues

## 4.1 Split Datasets

There were no datasets that required splitting due to size constraints.

## 4.2 Data Dependencies

| Analysis Dataset | Dependent on Following Analysis Datasets |
| --- | --- |
| ADAE | ADSL |
| ADTTE | ADSL, ADAE |
| ADADAS | ADSL |
| ADLBC | ADSL |

## 4.3 Intermediate Datasets

No intermediate datasets were created for this trial.

# 5 Analysis Dataset Descriptions

## 5.1 Overview

The following provides detailed information for each analysis dataset included in the Pilot 3 submission, which were used to generate the outputs in Pilot 1. These ADaM datasets are ADSL, ADAE, ADTTE, ADADAS, ADLBC.

## 5.2 Analysis Datasets

| Dataset - Dataset Label | Class | Efficacy | Safety | Baseline or other subject characteristics | Primary Objective | Structure |
|---|---|---|---|---|---|---|
| ADSL - Subject-Level Analysis Dataset | SUBJECT LEVEL ANALYSIS DATASET | | | x | | One record per subject |
| ADADAS - ADAS-COG Analysis Dataset | BASIC DATA STRUC-TURE | x | | | x | One or more records per subject per analysis parameter per analysis timepoint |
| ADAE - Adverse Events Analysis Dataset | OCCURRENCE DATA STRUC-TURE | | x | | | One record per subject per adverse event |
| ADLBC - Analysis Dataset Lab Blood Chemistry | BASIC DATA STRUC-TURE | | x | | | One or more records per subject per analysis parameter per analysis timepoint |

| Dataset - Dataset Label | Class | Efficacy | Safety | Baseline or other subject characteristics | Primary Objective | Structure |
|---|---|---|---|---|---|---|
| ADTTE - AE Time To 1st Derm. Event Analysis | BASIC DATA STRUCTURE | x | x | | | One or more records per subject per analysis parameter per analysis timepoint |

### 5.2.1 ADSL - Subject-Level Analysis Dataset

The subject level analysis dataset (ADSL) contains required variables for demographics, treatment groups, and population flags. In addition, it contains other baseline characteristics that were used in both safety and efficacy analyses. All patients in DM were included in ADSL. The following are the key population flags are used in analyses for patients:

- SAFFL – Safety Population Flag (all patients having received any study treatment)

- ITTFL – Intent-to-Treat Population Flag (all randomized patients)

### 5.2.2 ADADAS - ADAS-COG Analysis Dataset

ADADAS contains analysis data from the ADAS-Cog questionnaire, one of the primary efficacy endpoints. It contains one record per subject per parameter (ADAS-Cog questionnaire item) per VISIT. Visits are placed into analysis visits (represented by AVISIT and AVISITN) based on the date of the visit and the visit windows.

### 5.2.3 ADAE - Adverse Events Analysis Dataset

ADAE contains one record per reported event per subject. Subjects who did not report any Adverse Events are not represented in this dataset. The data reference for ADAE is the SDTM AE (Adverse Events) domain and there is a 1-1 correspondence between records in the source and this analysis dataset. These records can be linked uniquely by STUDYID, USUBJID, and AESEQ. Events of particular interest (dermatologic) are captured in the customized query variable (CQ01NAM) in this dataset. Since ADAE is a source for ADTTE, the first chronological occurrence based on the start dates (and sequence numbers) of the treatment emergent

dermatological events are flagged (AOCC01FL) to facilitate traceability between these two analysis datasets.

### 5.2.4 ADLBC - Analysis Dataset Lab Blood Chemistry

ADLBC contains one record per lab analysis parameter, per time point, per subject. ADLBC contains lab chemistry parameters and these data are derived from the SDTM LB (Laboratory Tests) domain. Two sets of lab parameters exist in ADLBC. One set contains the standardised lab value from the LB domain and the second set contains change from previous visit relative to normal range values. In some of the summaries the derived end-of-treatment visit (AVISITN=99) is also presented.

### 5.2.5 ADTTE - AE Time To 1st Derm. Event Analysis

ADTTE contains one observation per parameter per subject. ADTTE is specifically for safety analyses of the time to the first dermatologic adverse event. Dermatologic AEs are considered an adverse event of special interest. The key parameter used for the analysis of time to the first dermatological event is with PARAMCD of "TTDE".

# 6 Data Conformance Summary

## 6.1 Conformance Inputs

Were the analysis datasets evaluated for conformance with CDISC ADaM Validation Checks?

```
Yes, Version of CDISC ADaM Validation Checks and software used: Pinnacle 21®
Community 4.0.2
```

Were the ADaM datasets evaluated in relation to define.xml?

```
Yes
```

Was define.xml evaluated?

```
Yes
```

## 6.2 Issues Summary

| Check ID | Diagnostic Message | Dataset | Count (Issue Rate) | Explanation |
|----------|--------------------|---------|--------------------|-------------|
| AD1012 | Secondary custom variable is present but its primary variable is not present | ADSL | 1 (50.00%) | This is a Sponsor Extension to the ADaM Model. The VISNUMEN [End of Trt Visit (Vis 12 or Early Term.)] variable is a integer variable which is not related to any character variable. |

## 6.3 QC Findings and Common Issues

In this Pilot 3 study, our focus was to create a subset of ADaMs based on the CDSICPILOT data, using R. We compared our R generated ADaMs against the CDISCPILOT ADaMs, created in SAS, as a QC step. With these comparisons we listed the QC Findings with explanations as to why these findings exist. We also came across common issues throughout the ADaM generation process, which could be helpful for improvements utilising the CDISC Pilot data in the future. More details can be found in the appendix (Appendix 2 and Appendix 3).

# 7 Submission of Programs

## 7.1 Description

The sponsor has provided all programs for analysis results. They are all created on a Linux platform using R version 4.2.3.

## 7.2 ADaM Programs

The following table contains the list of programs that generate the analysis datasets in Pilot 3. It shows the program file name, the analysis dataset name and the label of the analysis dataset. The recommended steps to execute the analysis results using R are described in the Appendix.

| Program Name | Analysis Dataset Name | Analysis Dataset Label |
| --- | --- | --- |
| adsl.r | adsl.xpt | Subject-Level Analysis Dataset |
| adadas.r | adas.xpt | ADAS-Cog Analysis |
| adlbc.r | adlb.xpt | Analysis Dataset Lab Blood Chemistry |
| adae.r | adae.xpt | Adverse Events Analysis Dataset |
| adtte.r | adtte.xpt | AE Time to 1st Derm. Event Analysis |

## 7.3 Analysis Output Programs

The following table contains a list of programs that generate outputs used in the R consortium R submission Pilot 1. These outputs were rerun in Pilot 3 using the analysis datasets generated by the ADaM programs. It shows the program file names, the related outputs, the input datasets and variables used, and any data selection criteria that need to be applied per Pilot 1.

| Program Name | Output Name | Analysis Datasets & Variables | Selection Criteria |
|---|---|---|---|
| tlf-demographic.r | tlf-demographic-pilot3.out | ADSL.STUDYID<br>ADSL.TRT01P<br>ADSL.ITTFL<br>ADSL.AGE<br>ADSL.AGEGR1<br>ADSL.RACE<br>ADSL.HEIGHTBL<br>ADSL.WEIGHTBL<br>ADSL.BMIBL<br>ADSL.MMSETOT | STUDYID== "CDISCPILOT01"<br>Population:<br>ADSL.ITTFL == "Y"<br>Treatment Groups:<br>ADSL.TRT01P Placebo<br>Xanomeline Low Dose<br>Xanomeline High Dose |
| tlf-primary.r | tlf-primary-pilot3.rtf | ADSL.TRT01P<br>ADSL.USUBJID<br>ADSL.EFFFL<br>ADSL.ITTFL<br>ADADAS.TRTP<br>ADADAS.TRTPCD<br>ADADAS.EFFFL<br>ADADAS.ITTFL<br>ADADAS.PARAMCD<br>ADADAS.ANL01FL<br>ADADAS.AVISIT<br>ADADAS.AVISITN<br>ADADAS.AVAL<br>ADADAS.CHG | STUDYID== "CDISCPILOT01"<br>Population:<br>ADADAS.EFFFL == "Y" ADADAS.ITTFL == "Y"<br>ADADAS.ANL01FL == "Y"<br><br>Treatment Groups:<br>ADSL.TRTP Placebo<br>Xanomeline Low Dose<br>Xanomeline High Dose<br>Parameters:<br>ADADAS.PARAMCD == "ACTOT |

| Program Name | Output Name | Analysis Datasets & Variables | Selection Criteria |
|---|---|---|---|
| tlf-efficacy.r | tlf-efficacy-pilot3.rtf | ADSL.STUDYID ADSL.USUBJID ADSL.ITTFL ADLBC.TRTP ADLBC.TRTPN ADLBC.PARAMCD ADLBC.AVISITN ADLBC.BASE ADLBC.AVAL ADLBC.CHG | STUDYID== "CDISCPILOT01" Population: ADSL.ITTFL == "Y" & ADLBC.TRTPN in (0, 81) & ADLBC.PARAMCD == "GLUC" & ADLBC.AVISITN is not missing<br><br>Treatment Groups: ADLBC.TRTPN Placebo Xanomeline High Dose |
| tlf-kmplot.r | tlf.kmplot-pilot3.pdf | ADSL.STUDYID ADSL.USUBJID ADSL.SAFFL ADSL.TRT01A ADTTE.STUDYID ADTTE.USUBJID ADTTE.PARAMCD ADTTE.AVAL ADTTE.CNSR | STUDYID== "CDISCPILOT01" Population: ADSL.SAFFL == "Y" Treatment Groups: ADSL.TRT01A Placebo Xanomeline Low Dose Xanomeline High Dose Parameters: ADTTE.PARAMCD == "TTDE" |

For reference, below is a description of the analysis programs utilized and outputs generated in Pilot 1.

| Program Name | Output Table Number | Title |
|---|---|---|
| tlf-demographic.r | Table 14-2.01 | Summary of Demographic and Baseline Characteristics |
| tlf-primary.r | Table 14-3.01 | Primary Endpoint Analysis: ADAS Cog (11) - Change from Baseline to Week 24 - LOCF |
| tlf-efficacy.r | Table 14-3.02 | ANCOVA of Change from Baseline at Week 20 |
| tlf-kmplot.r | Figure 14-1 | KM plot for Time to First Dermatologic Event: Safety population |

## 7.4 Proprietary R Packages

| R Package | Package version | Package Description |
|---|---|---|
| pilot3utils | 0.0.2 | The objective of this utility package is to support the R Consortium R submission Pilot 3 Project. It contains all utility functions that were used in the generation of the deliverables: formatting of ADaM variables and analysis results summarize mixed model analysis formatting of layouts |

## 7.5 Open-source R Analysis Packages

| R Package | Package version | Package Description |
|---|---|---|
| admiral | 0.10.1 | A toolbox for programming Clinical Data Interchange Standards Consortium (CDISC) compliant Analysis Data Model (ADaM) datasets in R. ADaM datasets are a mandatory part of any New Drug or Biologics License Application submitted to the United States Food and Drug Administration (FDA). Analysis derivations are implemented in accordance with the "Analysis Data Model Implementation Guide" (CDISC Analysis Data Model Team, 2021, https://www.cdisc.org/standards/foundational/adam/adamig-v1-3-release-package). |

| | | |
|---|---|---|
| cowplot | 1.1.1 | Provides various features that help with creating publication-quality figures with 'ggplot2', such as a set of themes, functions to align plots and arrange them into complex compound figures, and functions that make it easy to annotate plots and or mix plots with images. The package was originally written for internal use in the Wilke lab, hence the name (Claus O. Wilke's plot package). It has also been used extensively in the book Fundamentals of Data Visualization. |
| diffdf | 1.0.4 | Functions for comparing two data.frames against each other. The core functionality is to provide a detailed breakdown of any differences between two data.frames as well as providing utility functions to help narrow down the source of problems and differences. |
| dplyr | 1.1.0 | A fast, consistent tool for working with data frame like objects, both in memory and out of memory. |

| | | |
|---|---|---|
| emmeans | 1.8.5 | Obtain estimated marginal means (EMMs) for many linear, generalized linear, and mixed models. Compute contrasts or linear functions of EMMs, trends, and comparisons of slopes. Plots and other displays. Least-squares means are discussed, and the term "estimated marginal means" is suggested, in Searle, Speed, and Milliken (1980) Population marginal means in the linear model: An alternative to least squares means, The American Statistician 34(4), 216-221 <doi:10.1080/00031305.1980.10483031>. |
| ggplot2 | 3.4.1 | A system for 'declaratively' creating graphics, based on "The Grammar of Graphics". You provide the data, tell 'ggplot2' how to map variables to aesthetics, what graphical primitives to use, and it takes care of the details. |
| haven | 2.5.2 | Import foreign statistical formats into R via the embedded 'ReadStat' C library, <https://github.com/WizardMac/ReadStat>. |
| lubridate | 1.9.2 | Functions to work with date-times and time-spans: fast and user friendly parsing of date-time data, extraction and updating of components of a date-time (years, months, days, hours, minutes, and seconds), algebraic manipulation on date-time and time-span objects. The 'lubridate' package has a consistent and memorable  syntax that makes working with dates easy and fun. |

| | | | |
|---|---|---|---|
| metacore | 0.1.2 | | Create an immutable container holding metadata for the purpose of better enabling programming activities and functionality of other packages within the clinical programming workflow. |
| metatools | 0.1.5 | | Uses the metadata information stored in 'metacore' objects to check and build metadata associated columns. |
| pharmaRTF | 0.1.4 | | Enhanced RTF wrapper written in R for use with existing R tables packages such as 'Huxtable' or 'GT'. This package fills a gap where tables in certain packages can be written out to RTF, but cannot add certain metadata or features to the document that are required/expected in a report for a regulatory submission, such as multiple levels of titles and footnotes, making the document landscape, and controlling properties such as margins. |
| r2rtf | 1.0.1 | | Create production-ready Rich Text Format (RTF) table and figure with flexible format. |

| | | |
|---|---|---|
| rtables | 0.6.0 | Reporting tables often have structure that goes beyond simple rectangular data. The 'rtables' package provides a framework for declaring complex multi-level tabulations and then applying them to data. This framework models both tabulation and the resulting tables as hierarchical, tree-like objects which support sibling sub-tables, arbitrary splitting or grouping of data in row and column dimensions, cells containing multiple values, and the concept of contextual summary computations. A convenient pipe-able interface is provided for declaring table layouts and the corresponding computations, and then applying them to data. |
| stringr | 1.5.0 | A consistent, simple and easy to use set of wrappers around the fantastic 'stringi' package. All function and argument names (and positions) are consistent, all functions deal with "NA"'s and zero length vectors in the same way, and the output from one function is easy to feed into the input of another. |

| | | |
|---|---|---|
| tidyr | 1.3.0 | Tools to help to create tidy data, where each column is a variable, each row is an observation, and each cell contains a single value. 'tidyr' contains tools for changing the shape (pivoting) and hierarchy (nesting and 'unnesting') of a dataset, turning deeply nested lists into rectangular data frames ('rectangling'), and extracting values out of string columns. It also includes tools for working with missing values (both implicit and explicit). |
| Tplyr | 1.1.0 | A traceability focused tool created to simplify the data manipulation necessary to create clinical summaries. |
| visR | 0.3.1 | To enable fit-for-purpose, reusable clinical and medical research focused visualizations and tables with sensible defaults and based on graphical principles as described in: "Vandemeulebroecke et al. (2018)" <doi:10.1002/pst.1912>, "Vandemeulebroecke et al. (2019)" <doi:10.1002/psp4.12455>, and "Morris et al. (2019)" <doi:10.1136/bmjopen-2019-030215>. |
| xportr | 0.2.0 | Tools to build CDISC compliant data sets and check for CDISC compliance. |

# 8 Directory Structure

m1

    cover-letter.pdf

    report-tlf-pilot3.pdf

    response-FDA-IR-pilot3.pdf

m5

    sap-cdiscpilot01.pdf

    datasets

        rconsortiumpilot3

            tabulations

      |     sdtm

      |        blankcrf.pdf

      |        define-v1-updated-html.xsl

      |        define.pdf

      |        define.xml

      |        ae.xpt                 # SDTM datasets in XPT format

      |        cm.xpt

      |        dm.xpt

      |        ds.xpt

      |        ex.xpt

      |        lb.xpt

      |        mh.xpt

      |        qs.xpt

      |        relrec.xpt

      |        sc.xpt

      |        se.xpt

      |        suppae.xpt

      |        suppdm.xpt

```
|        suppds.xpt
|        supplb.xpt
|        sv.xpt
|        ta.xpt
|        te.xpt
|        ti.xpt
|        ts.xpt
|        tv.xpt
|        vs.xpt
   analysis
|      adam
|         programs
|             adadas.r
|             adae.r
|             adlbc.r
|             adsl.r
|             adtte.r
|             tlf-demographic.r
|             tlf-efficacy.r
|             tlf-kmplot.r
|             tlf-primary.r
|             renv.lock
|         datasets
|             adrg.pdf
|             adam-pilot-3.xlsx
|             define.xml
|             adadas.xpt
|             adae.xpt
|             adlbc.xpt
```

|          adsl.xpt

|          adtte.xpt

|          define2-0-0.xsl

# 9 Appendix

## 9.1 Appendix 1 : Pilot 3 Installation and Usage

To install and execute the R programs, follow all of the procedures below. Ensure that you note the location of where you downloaded the Pilot 3 eCTD submission files. For demonstration purposes, the procedures below assume the transfer has been saved to this location: C:\pilot3.

In addition, create a new directory to hold the unpacked Pilot 3 ADaM and tlf programs and files. For demonstration purposes, the procedures below assume the new directory is this location: C:\pilot3-files, where the unpacked files are shown as the m1 and m5 directories.
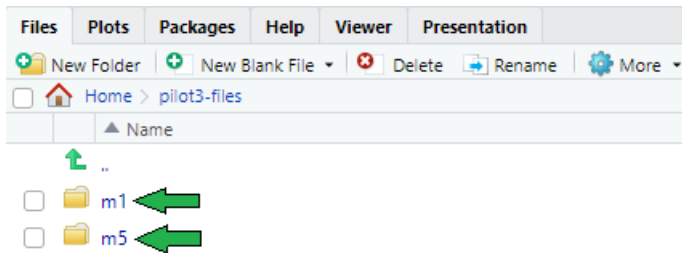


### 9.1.1 Installation of R and R Studio

Download and install R 4.2.3 for Windows from https://cran.r-project.org/bin/windows/base/old/4.2.3/. Then download and run the R-4.2.3-win.exe file. Also download RStudio for Windows by visiting https://dailies.rstudio.com/version/2023.03.1+446.pro1/

### 9.1.2 Create a new R Studio project within the pilot3-files directory

- Open R Studio
- Select File -> New Project
- In the Create Project dialog box, choose Existing Directory
- In the Create Project from Existing Directory dialog box, click the Browse button and navigate to the C:\pilot3-files directory.
- Once the location has been confirmed, click the Create Project button.
- These .Rproj files will be created.
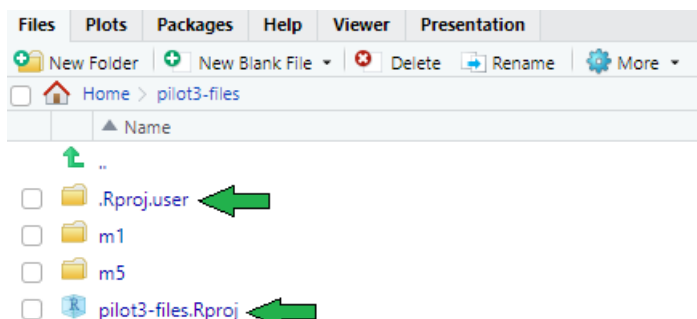
> **i Note**
>
> It is possible that the `.Rproj.user` folder may not have generated for you or or may not be visible as it is a hidden folder. If so, this is fine as it will not be necessary in order to run the analysis programs below.

### 9.1.3 Installation of R Packages

A minimum set of R packages are required to ensure the Pilot 3 analysis programs are successfully run and the custom package environment used for the application is replicated correctly. Please follow these steps below to install these R packages.

1. In the `Files` window pane, ensure that this directory

   `~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis/adam/programs`

   has both the `renv-lock.txt` and `pilot3utils_0.0.2.zip` files.
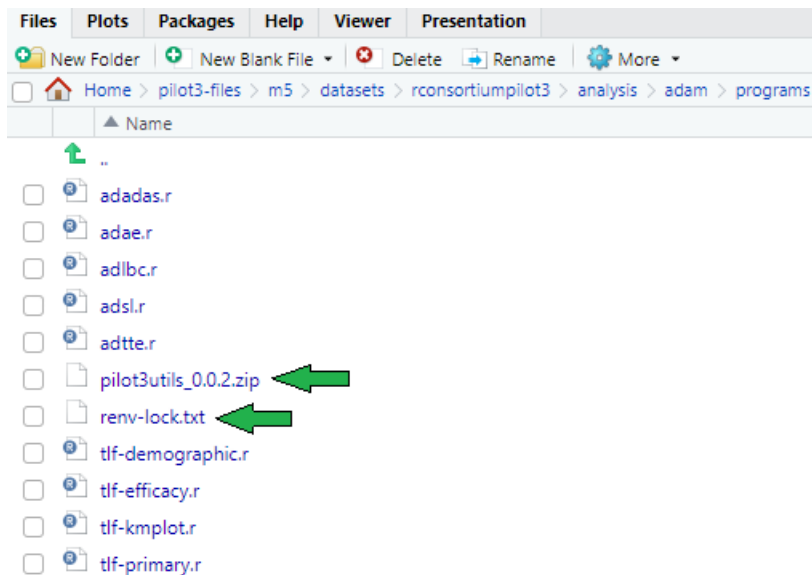
2. In the R Studio console install the {remotes} package:

```
install.packages("remotes")
```

> **ⓘ Note**
>
> - *The console may display a warning message about Rtools being required to build R packages.* **However the Rtools utility is not required to run the programs in this pilot 3 study.**
>
> - *If you receive a warning showing "cannot open URL https://cran.rstudio.com/ src/contrib/PACKAGES"', this is due to the default R Studio option 'Use secure download method for HTTP'. In R Studio, go to Tools → Global Options → Packages, then uncheck the 'Use secure download method for HTTP' option, then retry installation.*

3. Then, install the {renv} package, version 0.17.0:

```
remotes::install_version("renv", version = "0.17.0")
```

> **ⓘ Note**
>
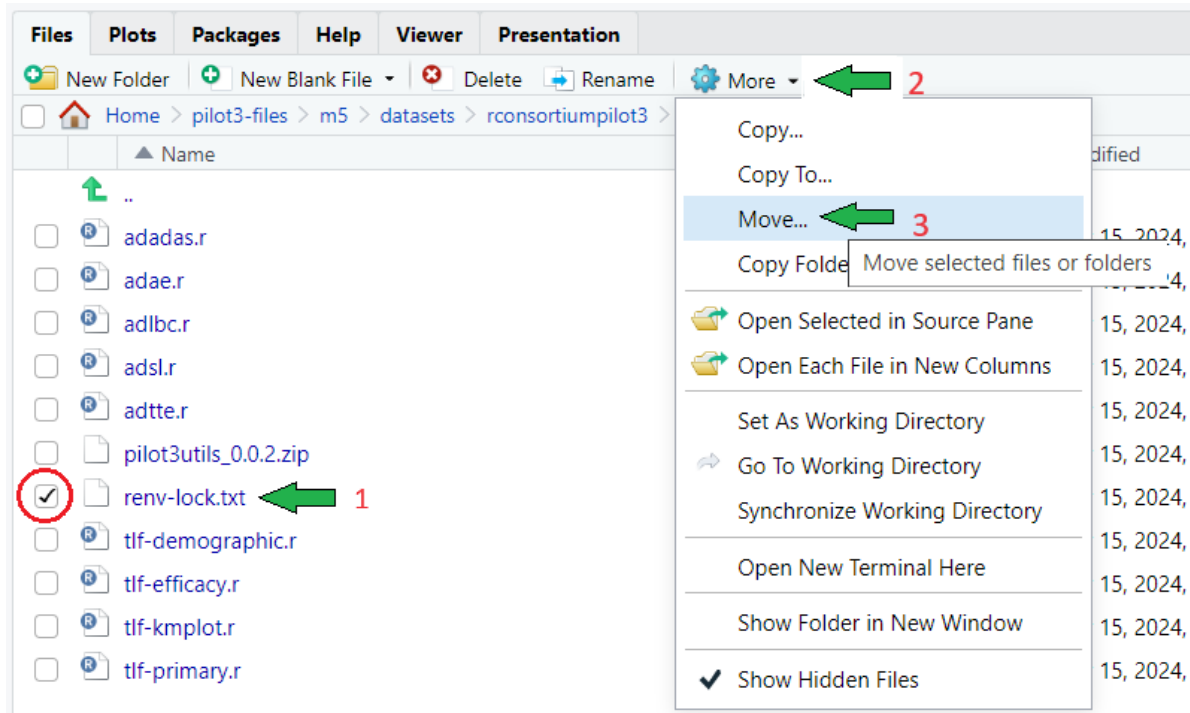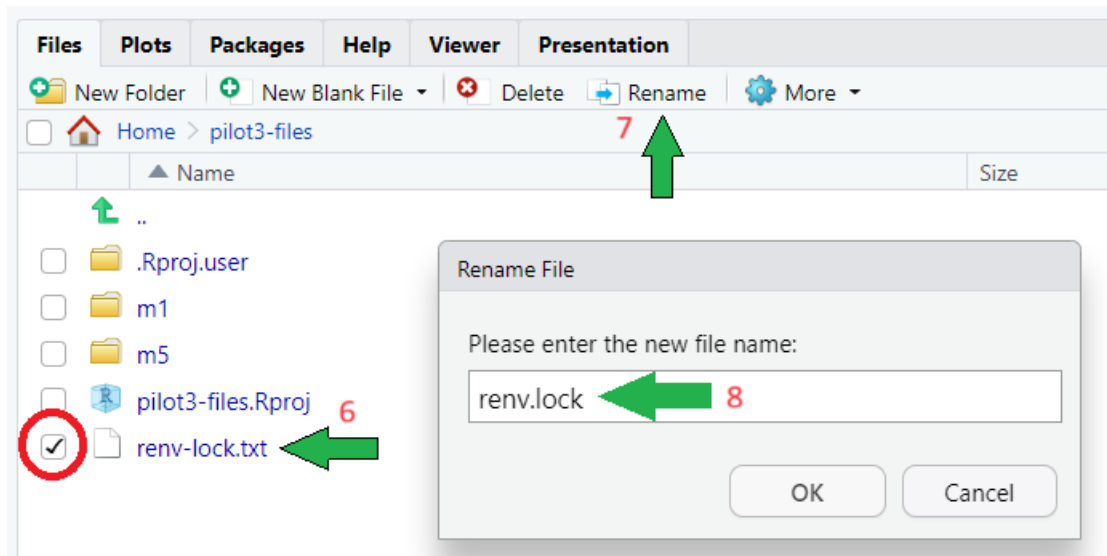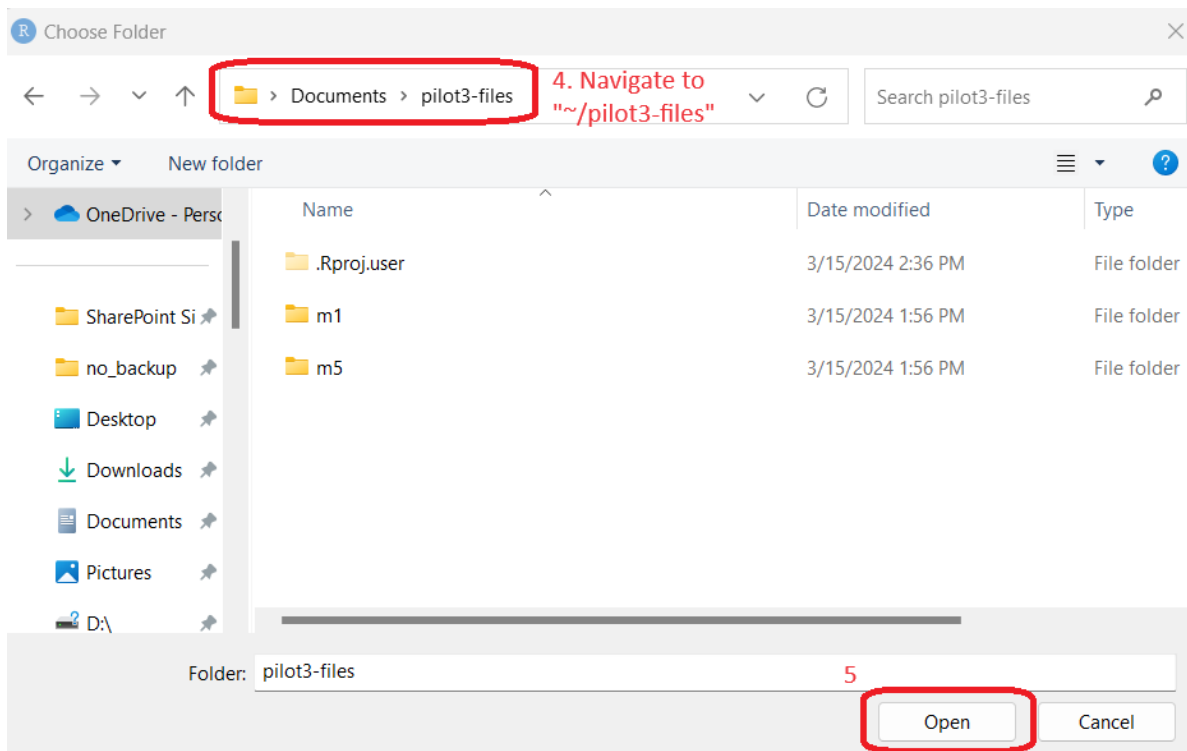> *If not already set, please verify that the working directory is already set to the project folder.*

1. getwd()

2. If not pointing to root project directory then do : `setwd("~/pilot3-files")`

4. Move the 'renv-lock.txt' to the root project directory and rename to 'renv.lock' :

```
./pilot3-files/m5/datasets/rconsortiumpilot3/analysis/adam/programs/renv-lock.txt
--> ./pilot3-files/renv.lock
```

5. Restart the R Session.
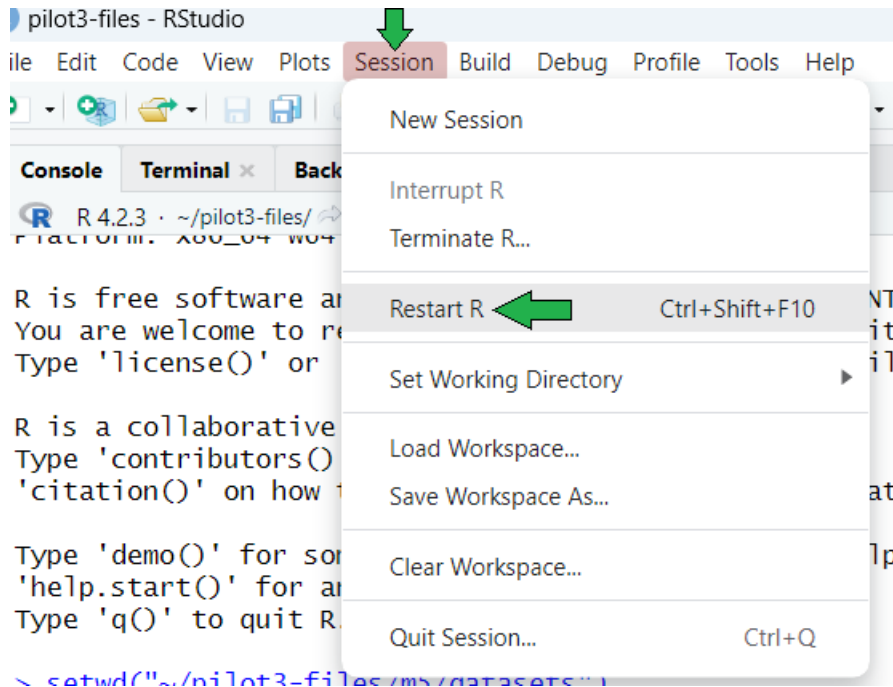
6. Run the code below, then select option 1 :

```
renv::init()
```

```
> renv::init()
This project already has a lockfile. What would you like to do?

1: Restore the project from the lockfile.
2: Discard the lockfile and re-initialize the project.
3: Activate the project without snapshotting or installing any packages.
4: Abort project initialization.

Selection: 1
```

> **ⓘ Note**
>
> - If using {renv} for the first time, you may get a 'Welcome' message describing the renv folder structure and its components. It will also list the packages that will be installed from the `renv.lock` file. At the end it will ask you if you want to proceed. Select 'y'.

```
Do you want to proceed? [y/N]: y
```

> - If after selecting option 1, you may receive a warning such as :

```
Warning: error downloading
```

```
'https://packagemanager.posit.co/cran/2023-03-15/bin/windows/contrib/4.2/
PACKAGES.rds'
['CreateProcess' failed to run 'C:\WINDOWS\SYSTEM32\curl.exe --config
"C:\Users\laxamanj\AppData\Local\Temp\RtmpQrNOy7\renv-download-config-
2e24149c3b5f"']
```

- If so, then run again selecting option 3 instead :

```
> renv::init()
This project already has a lockfile. What would you like to do?

1: Restore the project from the lockfile.
2: Discard the lockfile and re-initialize the project.
3: Activate the project without snapshotting or installing any packages.
4: Abort project initialization.

Selection: 3
```

- This warning will show, which can be ignored :

```
Restarting R session...

* Project '~/pilot3-files' loaded. [renv 0.17.0]
* One or more packages recorded in the lockfile are not installed.
* Use `renv::status()` for more details.
```

- Open the .Rprofile : C:/pilot3-files/.Rprofile and ensure these 2 lines are there :

```
Sys.setenv(RENV_DOWNLOAD_FILE_METHOD = "libcurl")
source("renv/activate.R")
```

  e.g.,
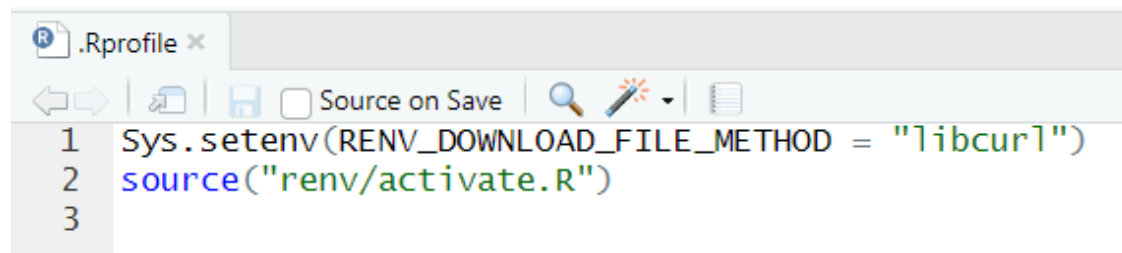


- Restart the R Session (ignoring the warning once more), then run `renv::restore()` and select `y` :

33

```
> renv::restore()
The following package(s) will be updated:

# CRAN ==============================
- MASS              [7.3-58.2 -> 7.3-58.3]
- survival          [3.5-3 -> 3.5-5]
- BH                [* -> 1.81.0-1]
- NLP               [* -> 0.2-1]
- R.cache           [* -> 0.16.0]
- R.methodsS3       [* -> 1.8.2]
- R.oo              [* -> 1.25.0]
- R.utils           [* -> 2.12.2]
- xtable            [* -> 1.8-4]
- yaml              [* -> 2.3.7]
- zip               [* -> 2.2.2]

# GitHub ============================
- xportr            [* -> atorus-research/xportr@main]

# RSPM ==============================
- htmlwidgets       [* -> 1.6.1]
- metacore          [* -> 0.1.2]
- ps                [* -> 1.7.2]
- tibble            [* -> 3.2.0]
- vctrs             [* -> 0.5.2]

Do you want to proceed? [y/N]: y
```

The package installation procedure may take a few minutes or longer depending on internet bandwidth.

7. Upon completion of installing packages using {renv}, please restart your R session.

**i** Note

After restarting the R session at this stage, running `renv::status()` will show us that the only package uninstalled is the {pilot3utils} package.

```
The following package(s) are used in this project, but are not installed:
```

```
    pilot3utils

Consider installing these packages (for example, using `renv::install()`).
Then, use `renv::snapshot()` to record these packages in the lockfile.
Use `renv::dependencies()` to see where these packages appear to be used.
```

We may ignore this as we will be installing the {pilot3utils} package in the following steps.

8. Install the {pilot3utils} package following the steps below :

   - In R Studio, navigate to your `Packages` window pane, then click on `Install`.
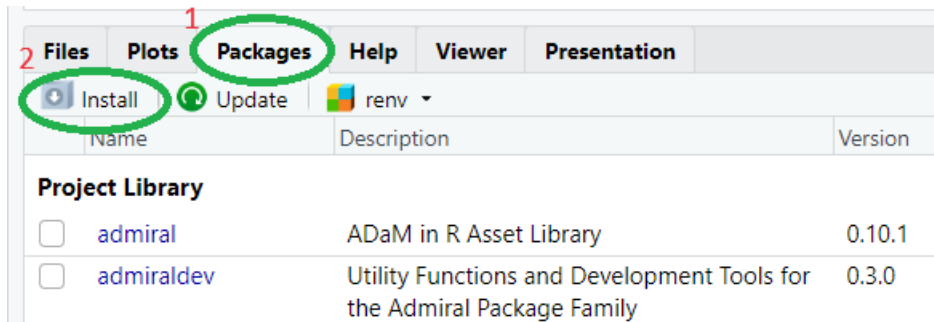


   - A new window called `Install Packages` will show up.

- In the field `Install from:`, click on the drop-down menu and select `Package Archive File (.zip; .tar.gz)`

> **i** Note
>
> This drop-down option is only available on a local Windows installation, not on linux systems.

- In the field `Package Archive`, click on `Browse...` and navigate to this directory to point to the {pilot3utils} package :

`~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis/adam/programs/pilot3utils_0.0.2.zip`



- In the field `Install to Library:`, you may keep this at its default setting.
- Click `Install`.

9. **Set the paths to run the analysis programs**

INPUT path: to rerun the analysis programs, define the path variable

- Path for SDTM data: path$sdtm

- Path to ADaM specifications : path$adam

OUTPUT path: to save the analysis datasets and results, define the path variable

- Path for ADaM data: path$adam

- Path for output TLFs: path$output.

All these paths must be defined before executing the analysis programs. You may do so by first entering the full file path directories to where the SDTM is currently stored and where the ADaMs and Outputs will be generated upon execution of the analysis programs.

> **i Note**
>
> Before executing the example file paths below, first navigate to the `~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis` folder and do this :
>
> 1. Create a copy of the `adam` folder in the same location and rename the new folder copy as `adam-reviewer`. The reason for creating this `adam-reviewer` folder (e.g ../adam-reviewer) is to keep the original ADaM datasets generated by the sponsor (e.g ../adam) so they will not get overwritten upon reviewers' execution of the analysis programs.
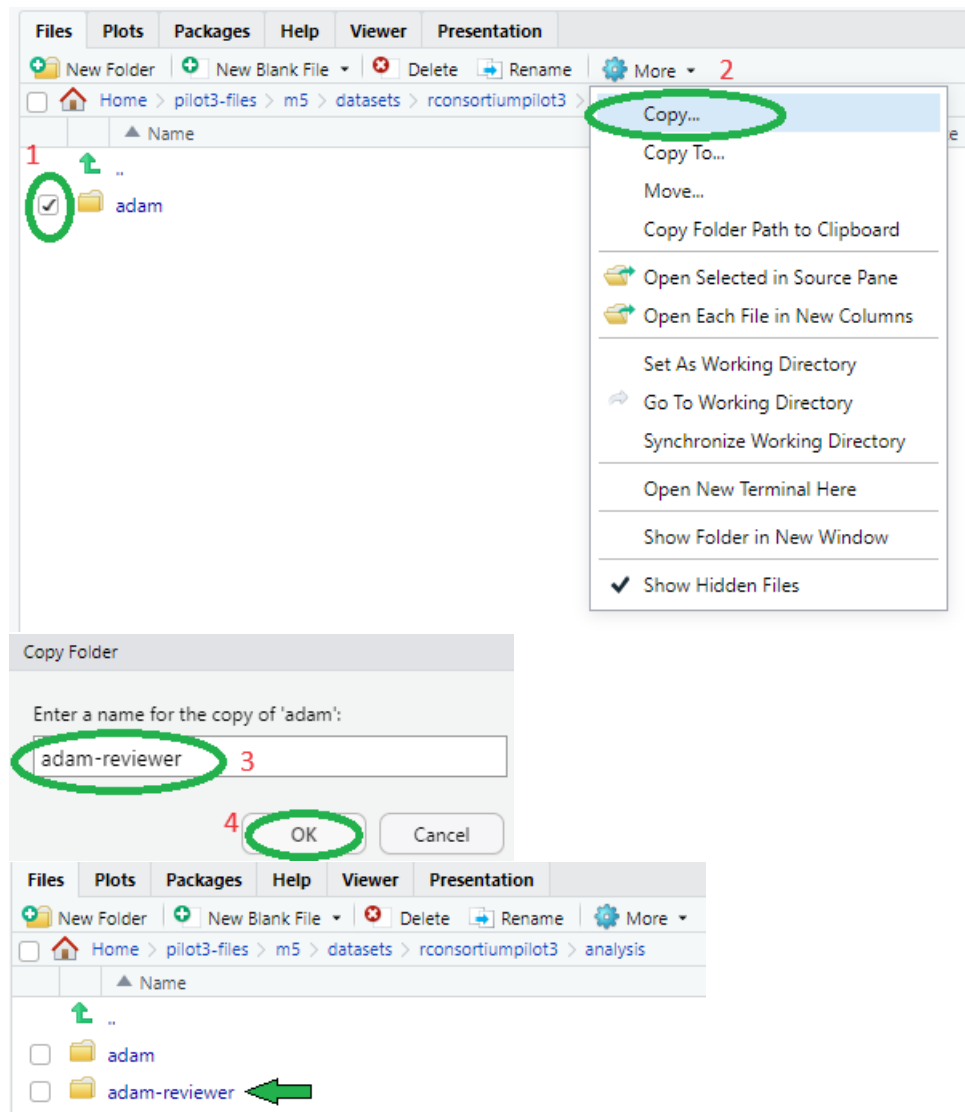
2. In the same location create a new folder called `output` in order to write the outputs in this folder upon reviewers' execution of the analysis output programs.

Files  Plots  Packages  Help  Viewer  Presentation

New Folder  |  New Blank File ▾  | ❌ Delete  | ➡ Rename  | ⚙ More ▾

Home > pilot3-files > m5 > datasets > rconsortiumpilot3 > analysis

1

▲ Name

⬆ ..

☐ 📁 adam
☐ 📁 adam-reviewer

New Folder

Please enter the new folder name

2

output

3  OK    Cancel

Files  Plots  Packages  Help  Viewer  Presentation

New Folder  | ➕ New Blank File ▾  | ❌ Delete  | ➡ Rename  | ⚙ More ▾

Home > pilot3-files > m5 > datasets > rconsortiumpilot3 > analysis

▲ Name

⬆ ..

☐ 📁 adam
☐ 📁 adam-reviewer
☐ 📁 output  ⬅

```
# Modify path to the sdtm, adam and output location
# Output saved in current folder

path <- list(
  sdtm = "Enter full file path to the sdtm data here",
  adam = "Enter full file path to where adam data will be written and
  sourced here",
  output = "Enter full file path to where outputs should be saved here"
  )


# For example

path <- list(
  sdtm = "~/pilot3-files/m5/datasets/rconsortiumpilot3/tabulations/sdtm",
  adam = "~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis/
          adam-reviewer/datasets",
  output = "~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis/output"
  )
```

10. **Execute analysis program**

To reproduce analysis results, rerun the following programs in the order below from `~/pilot3-files/m5/datasets/rconsortiumpilot3/analysis/adam-reviewer/programs`
:

- "adsl.r"
- "adae.r"
- "adadas.r"
- "adlbc.r"
- "adtte.r"
- "tlf-demographic.r"
- "tlf-efficacy.r"
- "tlf-kmplot.r"
- "tlf-primary.r"

## 9.2 Appendix 2 : QC Findings

### 9.2.1 ADSL

The R-generated ADSL matches the original ADSL from CDISC pilot data, besides the following mismatches:

- Subject 01-702-1082 has a missing value for BMIBLGR1 in the R-generated ADSL, whilst BMIBLGR1 = "<25" in the original ADSL. This is an issue with the original ADSL, as this subject's BMI at baseline (BMIBL) is missing and therefore the subject shouldn't be assigned a BMI at baseline group.

### 9.2.2 ADAE

The R-generated ADAE matches the original ADAE from CDISC pilot data, besides the following mismatches: There is an issue with the original CDISC pilot dataset. ADURN is blank, where AESEQ is (5, 6, 7, 8) for the original CDISC dataset for Subject below:

```
> adae_orig %>%
     filter(USUBJID=='01-716-1418') %>%
     select(USUBJID,TRTSDT,ASTDT,AENDT,ADURN,ADURU,AESEQ)

# A tibble: 10 × 7
   USUBJID    TRTSDT     ASTDT      AENDT      ADURN ADURU AESEQ
   <chr>      <date>     <date>     <date>     <dbl> <chr> <dbl>
 1 01-716-1418 2013-05-05 2013-05-05 2013-05-07     3 DAY       1
 2 01-716-1418 2013-05-05 2013-05-05 NA            NA NA        2
 3 01-716-1418 2013-05-05 2013-05-05 2013-05-07     3 DAY       3
 4 01-716-1418 2013-05-05 2013-05-07 NA            NA NA        4
 5 01-716-1418 2013-05-05 2013-07-01 2013-09-26    NA NA        5
 6 01-716-1418 2013-05-05 2013-07-01 2013-10-04    NA NA        6
 7 01-716-1418 2013-05-05 2013-07-01 2013-09-26    NA NA        7
 8 01-716-1418 2013-05-05 2013-07-01 2013-10-04    NA NA        8
 9 01-716-1418 2013-05-05 2013-09-26 2013-11-11    47 DAY       9
10 01-716-1418 2013-05-05 2013-09-26 2013-11-11    47 DAY      10
```

Because it seems the original SDTM.AE.AESTDTC was missing Day, where it seems the original ADAE derivation for ADURN was probably using this date instead of the imputed date. Because day is missing in AESTDTC, ADURN can't derive days.

```
> ae %>% filter(USUBJID=='01-716-1418') %>% select(USUBJID,AESTDTC,AESEQ) %>%
    arrange(AESEQ)
# A tibble: 10 × 3
   USUBJID      AESTDTC     AESEQ
   <chr>        <chr>       <dbl>
 1 01-716-1418 2013-05-05       1
 2 01-716-1418 2013-05-05       2
 3 01-716-1418 2013-05-05       3
 4 01-716-1418 2013-05-07       4
 5 01-716-1418 2013-07          5
 6 01-716-1418 2013-07          6
 7 01-716-1418 2013-07          7
 8 01-716-1418 2013-07          8
 9 01-716-1418 2013-09-26       9
10 01-716-1418 2013-09-26      10
```

but the same records, derived in the Pilot 3 dataset do show a calculation since we are using
the imputed ASTDT, per the define (ADURN=AENDT-ASTDT+1).

```
#AE.AESTDTC, converted to a numeric SAS date. Some events with partial dates
#are imputed in a conservative manner. If the day component is missing, a value
#of '01' is used. If both the month and day are missing no imputation is
#performed as these dates clearly indicate a start prior to the beginning of
#treatment. There are no events with completely missing start dates.

> adae0 %>% filter(USUBJID=='01-716-1418') %>%
    select(USUBJID,TRTSDT,ASTDT,AESTDTC,AENDT,AEENDY,ADURN,ADURU,AESEQ)
# A tibble: 10 × 9
   USUBJID      TRTSDT     ASTDT      AESTDTC    AENDT      AEENDY ADURN ADURU AESEQ
   <chr>        <date>     <date>     <chr>      <date>      <dbl> <dbl> <chr> <dbl>
 1 01-716-1418 2013-05-05 2013-05-05 2013-05-05 2013-05-07      3     3 DAY       1
 2 01-716-1418 2013-05-05 2013-05-05 2013-05-05 NA             NA    NA NA        2
 3 01-716-1418 2013-05-05 2013-05-05 2013-05-05 2013-05-07      3     3 DAY       3
 4 01-716-1418 2013-05-05 2013-05-07 2013-05-07 NA             NA    NA NA        4
 5 01-716-1418 2013-05-05 2013-07-01 2013-07    2013-10-04    153    96 DAY       6
 6 01-716-1418 2013-05-05 2013-07-01 2013-07    2013-10-04    153    96 DAY       8
 7 01-716-1418 2013-05-05 2013-07-01 2013-07    2013-09-26    145    88 DAY       5
 8 01-716-1418 2013-05-05 2013-07-01 2013-07    2013-09-26    145    88 DAY       7
 9 01-716-1418 2013-05-05 2013-09-26 2013-09-26 2013-11-11    191    47 DAY       9
10 01-716-1418 2013-05-05 2013-09-26 2013-09-26 2013-11-11    191    47 DAY      10
```

This latter approach should be the correct approach.

Due to this, we have outlined the expected differences here :

```
> diffdf(adae, adae_orig, keys = c("STUDYID", "USUBJID", "AESEQ"))
Differences found between the objects!

A summary is given below.

There are columns in BASE and COMPARE with differing attributes !!
All rows are shown in table below
```

1. ADURN values will be populated in Pilot 3 (i.e. under BASE), following the latter deriva-
   tion approach (i.e. ADURN=AENDT-ASTDT+1) for Subject 01-716-1418 where AE-
   SEQ is (5, 6, 7, 8) specified in define.

```
All rows are shown in table below


   ============================================================
    VARIABLE    STUDYID       USUBJID     AESEQ  BASE  COMPARE
   ------------------------------------------------------------
     ADURN    CDISCPILOT01  01-716-1418    5     88    <NA>
     ADURN    CDISCPILOT01  01-716-1418    6     96    <NA>
     ADURN    CDISCPILOT01  01-716-1418    7     88    <NA>
     ADURN    CDISCPILOT01  01-716-1418    8     96    <NA>
   ------------------------------------------------------------
```

2. ADURU should be set to 'DAYS' (i.e. under BASE) instead of 'DAY' when ADURN is
   not missing. Updated in Pilot 3 define.

```
First 10 of 718 rows are shown in table below


   ============================================================
    VARIABLE    STUDYID       USUBJID     AESEQ  BASE  COMPARE
   ------------------------------------------------------------
     ADURU    CDISCPILOT01  01-701-1015    3     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1023    1     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1023    4     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1047    1     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1047    2     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1097    2     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1097    3     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1097    5     DAYS   DAY
     ADURU    CDISCPILOT01  01-701-1097    6     DAYS   DAY
```

```
    ADURU    CDISCPILOT01   01-701-1097    7    DAYS    DAY
   ----------------------------------------------------------
```

### 9.2.3 ADLBC

The R-generated ADLBC matches the original ADLBC from CDISC pilot data, besides the following mismatches:

Three variables from R-generated ADLBC have class date while the same variables are numeric in the CDISC ADLBC. We opted to keep the date class in our R-generated ADLB.

```
> diffdf(adlbc, qc_adlbc, keys = c("STUDYID", "USUBJID", "AVISIT", "LBSEQ"))
Differences found between the objects!

A summary is given below.

There are columns in BASE and COMPARE with different classes !!
All rows are shown in table below

   ===================================
    VARIABLE   CLASS.BASE   CLASS.COMP
   -----------------------------------
      ADT         Date       numeric
     TRTEDT       Date       numeric
     TRTSDT       Date       numeric
   -----------------------------------
```

### 9.2.4 ADADAS

The R-generated ADADAS matches original ADADAS from CDISC pilot data, except for the records where `PARAMCD=ACTOT, DTYPE=LOCF`. This is an issue from the CDISC ADADAS.

- CDISC SDTM/QS : 818 records for `QSTESTCD=ACTOT`
- CDISC ADaM/ADADAS : 1040 records for `PARAMCD=ACTOT`, 799 (directly from QS, **should be 818**) + 241 imputed records (`DTYPE=LOCF`)
- ADADAS generated by R: 1040 records for `PARAMCD=ACTOT`, 818 (directly from QS) + 222 imputed records (`DTYPE=LOCF`)

Take a detailed example USUBJID="01-701-1294"

CDISC QS:

```
> qs %>% filter(QSTESTCD=="ACTOT") %>%
+    select(USUBJID, QSSEQ, VISIT, QSTESTCD, QSTEST,QSSTRESN) %>%
+    filter(USUBJID=="01-701-1294")
# A tibble: 4 × 6
  USUBJID       QSSEQ VISIT     QSTESTCD QSTEST                QSSTRESN
  <chr>         <dbl> <chr>     <chr>    <chr>                    <dbl>
1 01-701-1294    5015 BASELINE  ACTOT    ADAS-COG(11) Subscore        9
2 01-701-1294    5030 WEEK 8    ACTOT    ADAS-COG(11) Subscore       14
3 01-701-1294    5045 WEEK 12   ACTOT    ADAS-COG(11) Subscore        6
4 01-701-1294    5060 RETRIEVAL ACTOT    ADAS-COG(11) Subscore        9
```

CDISC ADADAS :

**For the record with `QSSEQ=5045` and `AVISIT=Week 8`, DTYPE is populated as `LOCF` , but this record is directly from `qs` dataset, not imputed.**

```
> qc_adadas %>% filter(PARAMCD=="ACTOT") %>%
+    select(USUBJID, QSSEQ, PARAMCD, AVISITN, AVISIT, VISIT, AVAL, DTYPE,
             ANL01FL, ADT, ADY) %>%
+    arrange(USUBJID, AVISITN) %>% filter(USUBJID=="01-701-1294")
# A tibble: 5 × 11
  USUBJID       QSSEQ PARAMCD AVISITN AVISIT   VISIT      AVAL DTYPE  ANL01FL
  <chr>         <dbl> <chr>     <dbl> <chr>    <chr>     <dbl> <chr>  <chr>
1 01-701-1294    5015 ACTOT         0 Baseline BASELINE      9 ""     "Y"
2 01-701-1294    5030 ACTOT         8 Week 8   WEEK 8       14 ""     "Y"
3 01-701-1294    5045 ACTOT         8 Week 8   WEEK 12      14 "LOCF" ""
4 01-701-1294    5045 ACTOT        16 Week 16  WEEK 12      14 "LOCF" "Y"
5 01-701-1294    5060 ACTOT        24 Week 24  RETRIEVAL     9 ""     "Y"

ADT        ADY
<date>     <dbl>
2013-03-24     1
2013-05-22    60
2013-06-14    83
2013-06-14    83
2013-10-08   199
```

ADADAS generated by R:

DTYPE is not `LOCF` for the record with `QSSEQ=5045` and `AVISIT=Week 8`, as this record is directly from `qs`.

```
> adadas %>% filter(PARAMCD=="ACTOT") %>%
+       select(USUBJID, QSSEQ, PARAMCD, AVISITN, AVISIT, VISIT, AVAL, DTYPE,
                ANL01FL, ADT, ADY) %>%
+       arrange(USUBJID, AVISITN) %>% filter(USUBJID=="01-701-1294")
# A tibble: 5 × 11
  USUBJID      QSSEQ PARAMCD AVISITN AVISIT   VISIT       AVAL DTYPE  ANL01FL
  <chr>        <dbl> <chr>     <dbl> <chr>    <chr>      <dbl> <chr>  <chr>
1 01-701-1294   5015 ACTOT        0 Baseline BASELINE      9 ""     "Y"
2 01-701-1294   5030 ACTOT        8 Week 8   WEEK 8       14 ""     "Y"
3 01-701-1294   5045 ACTOT        8 Week 8   WEEK 12       6 ""     ""
4 01-701-1294   5030 ACTOT       16 Week 16  WEEK 8       14 "LOCF" "Y"
5 01-701-1294   5060 ACTOT       24 Week 24  RETRIEVAL     9 ""     "Y"

ADT          ADY
<date>      <dbl>
2013-03-24      1
2013-05-22     60
2013-06-14     83
2013-05-22     60
2013-10-08    199
```

The same issue occurred for other subjects and resulted in the following discrepancies:

```
There are rows in BASE that are not in COMPARE !!
First 10 of 33 rows are shown in table below


  ==========================================
    USUBJID      PARAMCD   AVISIT       ADT
  ------------------------------------------
  01-701-1294    ACTOT    Week 16   2013-05-22
  01-701-1302    ACTOT    Week 16   2013-10-22
  01-703-1076    ACTOT    Week 16   2013-12-17
  01-703-1076    ACTOT    Week 24   2013-12-17
  01-704-1010    ACTOT    Week 24   2014-06-13
  01-704-1065    ACTOT    Week 16   2013-12-20
  01-704-1065    ACTOT    Week 24   2013-12-20
  01-704-1120    ACTOT    Week 16   2014-01-27
  01-704-1120    ACTOT    Week 24   2014-01-27
  01-705-1310    ACTOT    Week 16   2013-12-26
  ------------------------------------------


There are rows in COMPARE that are not in BASE !!
```

```
First 10 of 33 rows are shown in table below

    =============================================
       USUBJID     PARAMCD   AVISIT       ADT
    ---------------------------------------------
     01-701-1294    ACTOT    Week 16   2013-06-14
     01-701-1302    ACTOT    Week 16   2013-11-05
     01-703-1076    ACTOT    Week 16   2013-12-24
     01-703-1076    ACTOT    Week 24   2013-12-24
     01-704-1010    ACTOT    Week 24   2014-07-09
     01-704-1065    ACTOT    Week 16   2013-12-24
     01-704-1065    ACTOT    Week 24   2013-12-24
     01-704-1120    ACTOT    Week 16   2014-02-03
     01-704-1120    ACTOT    Week 24   2014-02-03
     01-705-1310    ACTOT    Week 16   2014-01-23
    ---------------------------------------------


Not all Values Compared Equal
All rows are shown in table below

    ==============================
      Variable  No of Differences
    ------------------------------
        AVAL            19
         CHG            19
        PCHG            19
       DTYPE            19
    ------------------------------
```

In the CDISC ADADAS, there are 19 subjects whose records have the incorrect `DTYPE=LOCF`
value instead of the expected missing `DTYPE`, resulting IN different `AVAL/CHG/PCHG` values for
these subjects.

```
> diff <- diffdf(adadas, qc_adadas, keys = c("USUBJID", "PARAMCD", "AVISIT", "ADT"))
> count(diff$VarDiff_AVAL, USUBJID)
# A tibble: 19 × 2
   USUBJID          n
   <chr>        <int>
 1 01-701-1294      1
 2 01-701-1302      1
 3 01-703-1076      1
 4 01-704-1065      1
```

```
 5 01-704-1120      1
 6 01-705-1292      1
 7 01-705-1310      1
 8 01-708-1347      1
 9 01-709-1102      1
10 01-709-1259      1
11 01-710-1045      1
12 01-710-1278      1
13 01-710-1300      1
14 01-710-1315      1
15 01-714-1068      1
16 01-715-1107      1
17 01-716-1373      1
18 01-718-1172      1
19 01-718-1250      1
```

### 9.2.5 ADTTE

The R-generated ADTTE matches original ADTTE from CDISC pilot data except for minor
SAS format discrepancies. Since this adtte was generated in R compared to SAS formats, the
columns Type & Length in the define should be sufficient enough to describe the attributes of
these variables.

```
> diffdf(adtte, qc_adtte, keys = c("STUDYID", "USUBJID", "PARAMCD", "SRCDOM", "STARTDT"))
Differences found between the objects!

A summary is given below.

There are columns in BASE and COMPARE with differing attributes !!
First 10 of 20 rows are shown in table below

  =================================================
   VARIABLE  ATTR_NAME   VALUES.BASE  VALUES.COMP
  -------------------------------------------------
     AGE      format.sas     NULL          3
    AGEGR1    format.sas     NULL         $5
   AGEGR1N    format.sas     NULL          3
   EVNTDESC   format.sas     NULL         $25
    PARAM     format.sas     NULL         $32
   PARAMCD    format.sas     NULL         $4
     RACE     format.sas     NULL         $32
```

```
    RACEN    format.sas    NULL            3
    SAFFL    format.sas    NULL           $1
      SEX    format.sas    NULL           $1
    ------------------------------------------------
```

### 9.2.6 Label discrepancies

In Pilot3, variable labels were updated per ADaM IG 1.1, which caused some discrepancies
with original CDISC pilot data label.

| Dataset | Variable | CDISC pilot data label | Pilot3 label |
|---------|----------|------------------------|--------------|
| ADAE | ADURN | Analysis Duration (N) | AE Duration (N) |
| | ADURU | Analysis Duration Units | AE Duration Units |
| | AOCCFL | 1st Occurrence of Any AE Flag | 1st Occurrence within Subject Flag |
| ADADAS | ANL01FL | Analysis Record Flag 01 | Analysis Flag 01 |
| | ITTFL | Intent-to-Treat Population Flag | Intent-To-Treat Population Flag |
| ADTTE | SRCDOM | Source Data | Source Domain |

## 9.3 Appendix 3 : Common Issues

### 9.3.1 Package issue tracking

#### 9.3.1.1 Package issues

- `haven::read_xpt()` Some attributes are dropped after using `haven::write_xpt()` `haven::read_xpt()`, e.g., type, length. to do: further check

- `xportr::xportr_length()` `NA_character_` is considered as length 2 - issue resolved on Dec 14, 2022 to do: to be incorporated in pilot3

#### 9.3.1.2 Potential improvement

- `metatools::build_from_derived()` https://github.com/pharmaverse/metatools/issues/46 Not urgent feature but nice to have - especially when `define.xml` is not in good quality

### 9.3.2 Knowledge sharing

Summary of similarities and differences between packages, to help user identify the best tool that suits the need. Maybe this could go to Bayer SAS2R catalog in the future,

#### 9.3.2.1 `metatools` vs `xportr`

- `metatools::set_variable_labels()` vs `xportr::xportr_label()`

#### 9.3.2.2 `xportr` vs `haven`

- `xportr::xportr_write()` vs `haven::write_xpt()`

#### 9.3.2.3 `diffdf` vs `arsenal`

- `diffdf::diffdf()` vs `arsenal::comparedf()`