



2023  
EUROPE  
INTERCHANGE  
COPENHAGEN | 26-27 APRIL



*Balancing quality and efficiency - a Novo Nordisk submission example*

Presented by Adrian Czaban, Statistical Programming Specialist,  
Biostatistics 2, Novo Nordisk



# Meet the Speaker

Adrian Czaban

**Title:** Statistical Programming Specialist/International Lead Programmer

**Organization:** Biostatistics 2, Novo Nordisk

- Started programming career in 2015
- Happy to work on new things and try out new solutions
- Lives with wife and 2 daughters in Copenhagen area



# Disclaimer and Disclosures

- *The views and opinions expressed in this presentation are those of the author and do not necessarily reflect the official policy or position of CDISC.*
- *The author has no real or apparent conflicts of interest to report.*



# Agenda

1. Introduction to the project
2. Programming setup
3. Opportunities and challenges
4. Outcome



# Introduction to the project and deliverables

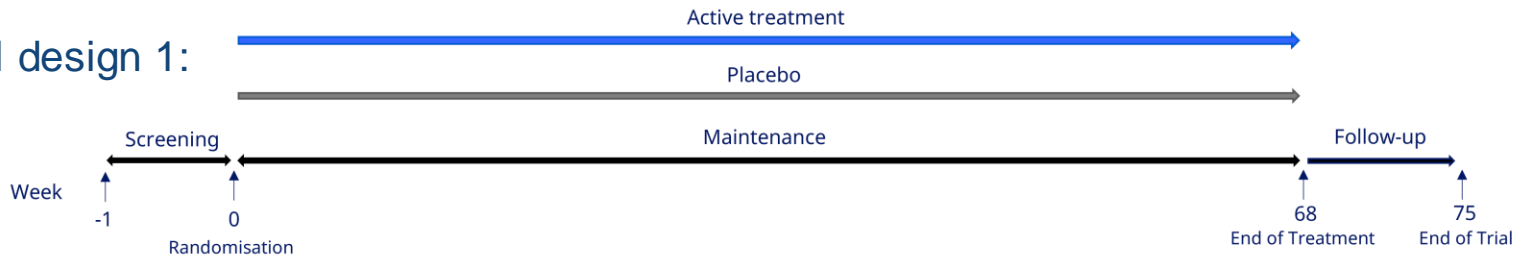
# Large project with the goal of submitting for a NDA in all major markets

4 phase 1 trials

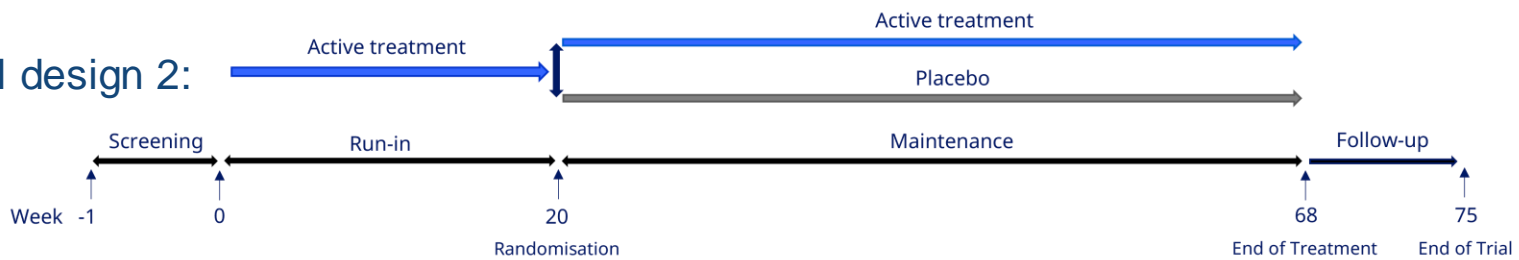
1 phase 2 trial

5 phase 3a trials with 2 types of design

Trial design 1:



Trial design 2:



# Contents of the submission package

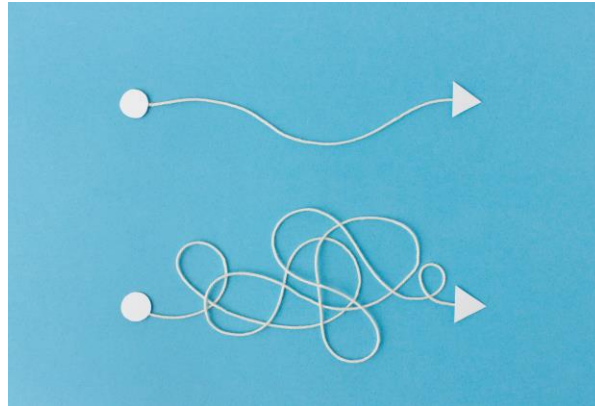
- For each trial and summaries, we planned to include the following:
  - ADRG
  - define.xml with Analysis Results Metadata (ARM)
  - ADaM datasets
  - All programs creating ADaM datasets and all macros used
  - All metadata datasets along with their programs, apart from programming plan specification
  - A subset of output programs where we have defined the ARM. This was split into programs creating the final output as well as programs making the statistical analysis
  - BIMO

# What would we like to achieve?

Programs that are "submission ready": easy to read and understand, and can be easily executed by FDA if required. Consistent both internally and across the project.

ADaM datasets, define.xml and ADRG deliverables conforming with CDISC requirements and in tight agreement with each other.

Make the review process as smooth as possible, by keeping things simple and giving reviewers the tools to find answers themselves.





# What can we do to be more efficient when working in our trials – main focus points

Think in terms of the submission package as a whole, and not a collection of individual trials

Re-use as much of code as possible across the project – with finding a balance between copy-paste and macro usage

Don't ask multiple people to create the same thing

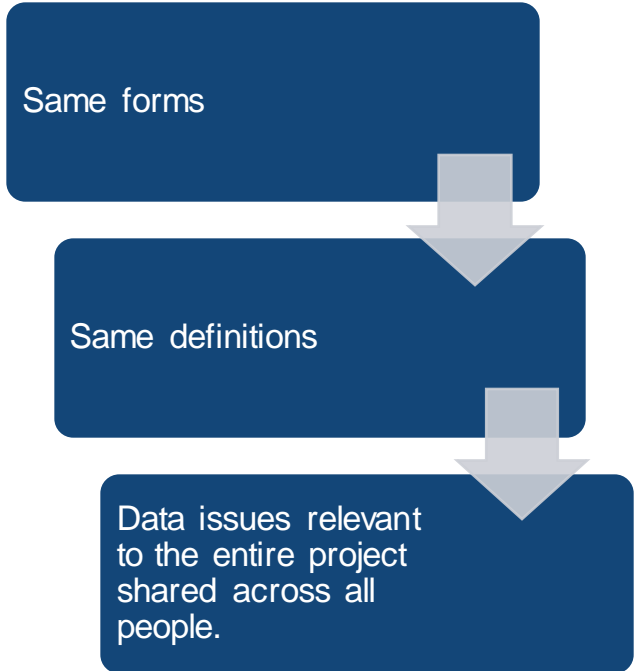
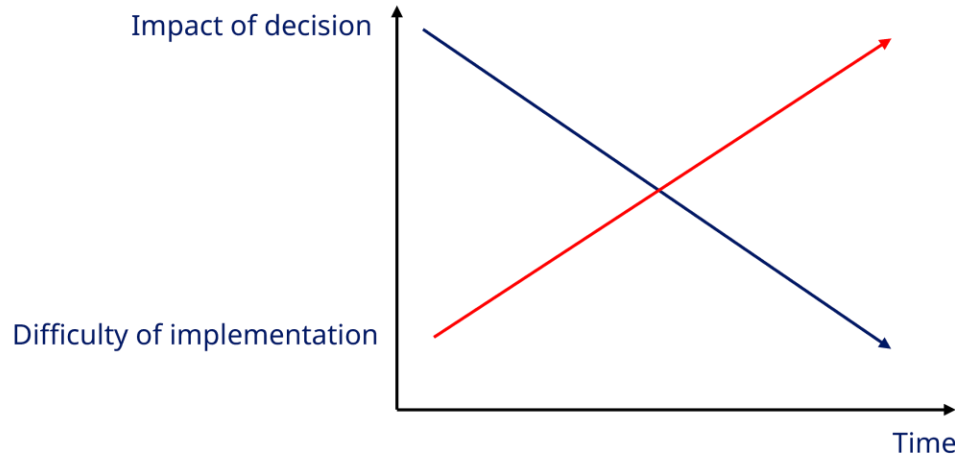
Avoid making the same changes in multiple places

Keep the terminology and methods consistent across the whole project



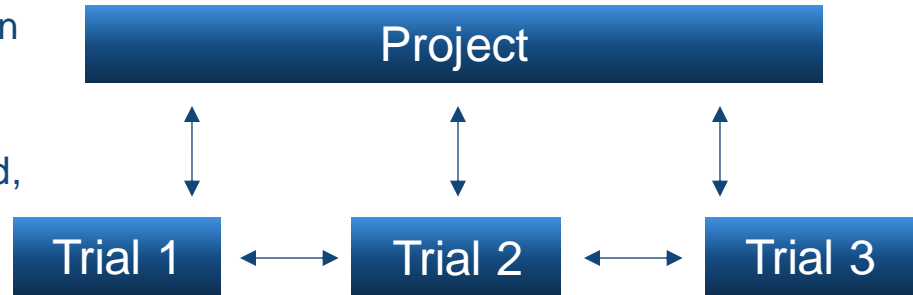
# Programming setup

# Aligning already on the CRF design stage



# Alignment and ease of combining the trials

- All ADaM and output programs first created for Trial nr 1
- All of the programmers assigned their own ADaM programs, that are shared in a common project space
- Once Trial 1 programs have been created, programmers have moved out into their respective trials
- Similarly, output programs have been designed to work across all trials and maintained in the project space



# How do we keep a common dataset content?

Project data content sheet, ensuring the same content definitions are used across all trials

| include_in_Trial1 | include_in_Trial2 | include_in_Trial3 | include_in_Trial4 | include_in_Trial5 | include_in_pooled_database | Table | Column   | Label                             |
|-------------------|-------------------|-------------------|-------------------|-------------------|----------------------------|-------|----------|-----------------------------------|
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | ARMCD    | Planned Arm Code                  |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | ACTARM   | Description of Actual Arm         |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | ACTARMCD | Actual Arm Code                   |
| Y                 | N                 | Y                 | Y                 | N                 | N                          | ADSL  | ACTARMN  | Numeric version of Actual Arm (N) |
| N                 | Y                 | N                 | N                 | N                 | Y                          | ADSL  | ACTARMN  | Numeric version of Actual Arm (N) |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | FASFL    | Full Analysis Set Population Flag |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | FASREA   | Reason for Exclusion from FAS     |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | SAFFL    | Safety Population Flag            |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | SAFREA   | Reason for Exclusion from SAF     |
| Y                 | Y                 | Y                 | Y                 | Y                 | Y                          | ADSL  | PPROTFL  | Per-Protocol Population Flag      |

| algorithm         | algorithm_Trial1 | algorithm_Trial2 | algorithm_Trial3 | algorithm_Trial4 | algorithm_Trial5 | algorithm_pool    |
|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|
| When ANL04FL eq Y |                  |                  |                  |                  |                  | When ANL04FL eq Y |

# Thinking of project instead of trials – pooled database developed alongside other tasks

```
1 /*****  
2 Description: Development of Laboratory Assessments (ADLB) dataset of 7 trials.
```

<Stack datasets>  
<Derive pool-specific variables>

```
156 ****;  
157 **** STEP 6: OUTPUT POOLED ADLB ****;  
158 ****;  
159 %adamensurestruct (  
160     inds                = adlb  
161     , remove_non_specified_cols = Y  
162     , missing_column_severity  = WARN  
163 );
```

## How do we align on output level?

Trial 1 :  
351

Trial 2 :  
371

Trial 3 :  
315

Trial 4 :  
322

Trial 5 :  
383

Summaries  
: 622

**Total: 2364**

# What could go wrong?

Age (years)

```
N
18-<65
65-<75
75-<85
>=85
```



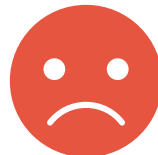
Age (years)

```
N
18-65
65-<75
75-<85
>=85
```



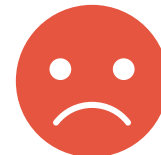
Age (years)

```
N
>=85
75-<85
65-<75
18-<65
```



Age (years)

```
N
18-<75
75-<85
>=85
```





# Strict control of codelists on the project level

Master file:

| include_in_trial_1 | include_in_trial_2 | codelist   | value  | ord | descript |
|--------------------|--------------------|------------|--------|-----|----------|
| Y                  | Y                  | agegrp1skl | N      | 5   | N        |
| Y                  | Y                  | agegrp1skl | 18-<65 | 10  | 18-<65   |
| Y                  | Y                  | agegrp1skl | 65-<75 | 20  | 65-<75   |
| Y                  | Y                  | agegrp1skl | 75-<85 | 30  | 75-<85   |
| Y                  | Y                  | agegrp1skl | >=85   | 40  | >=85     |

Metadata:

| CODELIST   | CODE   | ORDER | DECODE |
|------------|--------|-------|--------|
| agegrp1skl | N      | 5     | N      |
| agegrp1skl | 18-<65 | 10    | 18-<65 |
| agegrp1skl | 65-<75 | 20    | 65-<75 |
| agegrp1skl | 75-<85 | 30    | 75-<85 |
| agegrp1skl | >=85   | 40    | >=85   |

Output:

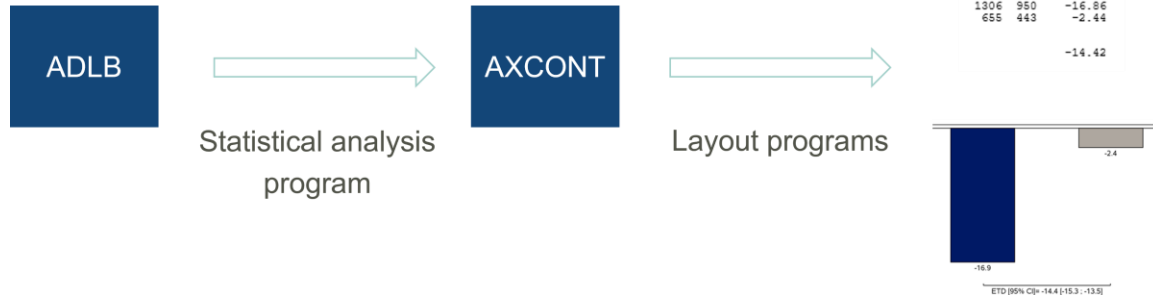
```
Age (years)
N
18-<65
65-<75
75-<85
>=85
```

# Usage of macros

Previous feedback on too many/too complicated macro programs

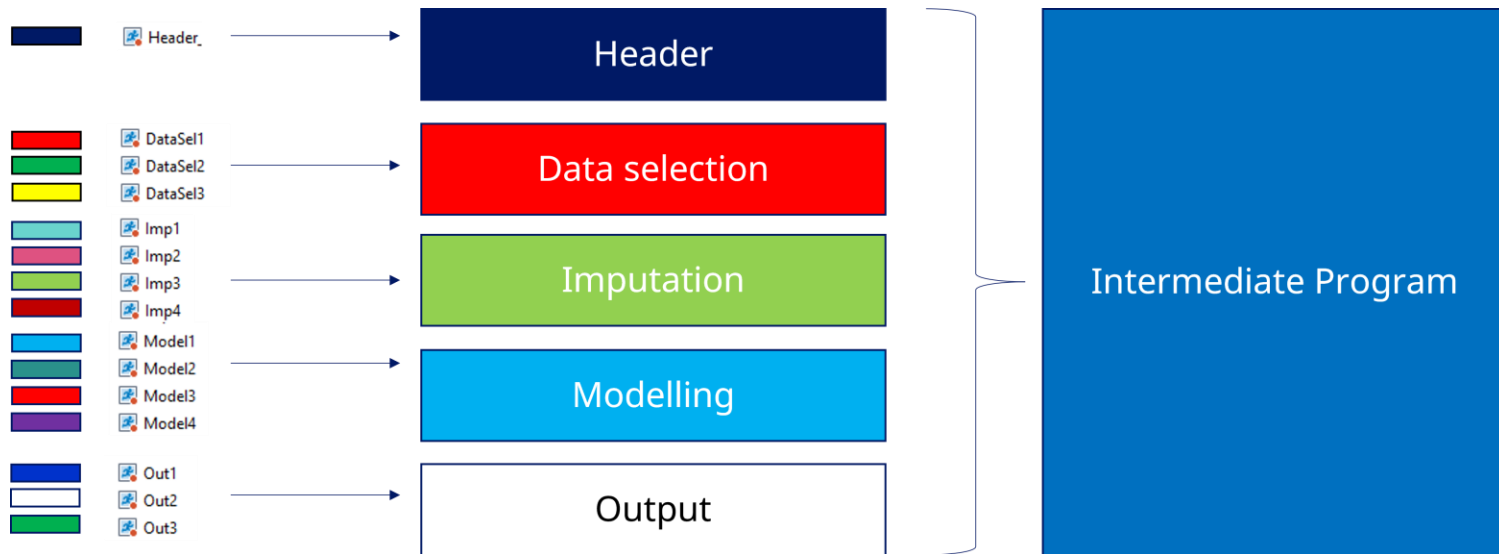
# Statistical analysis without macros – ‘AX programs’ setup

- Programs making statistical analyses are some of the most complex to review and understand.
- However, there is a danger of creating complex macro programs which are hard to debug and take a very long time to execute.
- Introducing an intermediate step and separating the program making the analyses from the one generating the output has many benefits



# Generating programs: 1 analysis – 1 program approach

- All AX programs should be self-contained and submission-ready
- There is a need to generate those programs in a simple and automated way
- Solution – building blocks



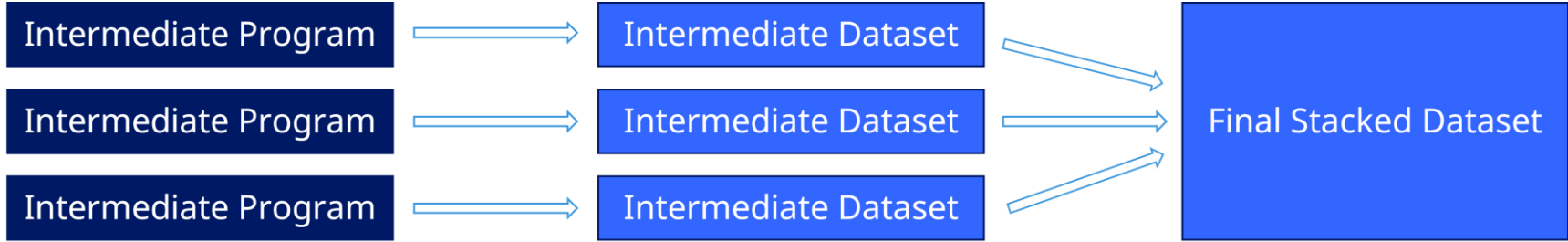
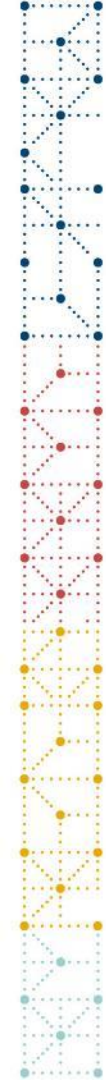
# Two levels of control:

- Which blocks to use

|                       |                   | Header<br>HeaderX |         |         |         | Data selection<br>DataSelX |         |         |         | Imputation<br>ImpX |         |         |         | Modelling<br>ModelX |         |         |         | Output<br>OutX |         |         |         |   |
|-----------------------|-------------------|-------------------|---------|---------|---------|----------------------------|---------|---------|---------|--------------------|---------|---------|---------|---------------------|---------|---------|---------|----------------|---------|---------|---------|---|
| Model/imputation type | Program part-name | TRIAL 1           | TRIAL 2 | TRIAL 3 | TRIAL 4 | TRIAL 1                    | TRIAL 2 | TRIAL 3 | TRIAL 4 | TRIAL 1            | TRIAL 2 | TRIAL 3 | TRIAL 4 | TRIAL 1             | TRIAL 2 | TRIAL 3 | TRIAL 4 | TRIAL 1        | TRIAL 2 | TRIAL 3 | TRIAL 4 |   |
| ANCOVA - RD-MI        | rdmi              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 1                   | 1       | 1       | 1       | 1              | 1       | 1       | 1       | 1 |
| LR - RD-MI            | lrdmi             | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 2                   | 2       | 2       | 2       | 2              | 2       | 2       | 2       | 2 |
| ANCOVA - J2R-MI       | j2rmi             | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 2                   | 2       | 2       | 2       | 1              | 1       | 1       | 1       | 1 |
| LR - J2R-MI           | lj2rmi            | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 2                   | 2       | 2       | 2       | 2              | 2       | 2       | 2       | 2 |
| ANCOVA - S1-SI        | s1                | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 3                   | 3       | 3       | 3       | 3              | 3       | 3       | 1       | 1 |
| LR - S1-SI            | lrs1              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 3                   | 3       | 3       | 3       | 4              | 4       | 4       | 4       | 2 |
| ANCOVA - S2-SI        | s2                | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 3                   | 3       | 3       | 3       | 3              | 3       | 3       | 1       | 1 |
| LR - S2-SI            | lrs2              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 3                   | 3       | 3       | 3       | 4              | 4       | 4       | 4       | 2 |
| ANCOVA - TP-MI        | tpmi              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 1                   | 1       | 1       | 1       | 5              | 5       | 5       | 5       | 3 |
| LR - TP-MI            | lrtpmi            | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 1                   | 1       | 1       | 1       | 6              | 6       | 6       | 6       | 4 |
| MMRM1                 | mrm1              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | NA                  | NA      | NA      | NA      | 7              | 7       | 7       | 7       | 1 |
| LR - MMRM1            | lrmrm1            | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 4                   | 4       | 4       | 4       | 4              | 4       | 4       | 4       | 2 |
| MMRM2                 | mrm2              | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | NA                  | NA      | NA      | NA      | 7              | 7       | 7       | 7       | 1 |
| LR - MMRM2            | lrmrm2            | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 4                   | 4       | 4       | 4       | 4              | 4       | 4       | 4       | 2 |
| LR - NR               | lrrnr             | 1                 | 1       | 1       | 1       | 1                          | 1       | 1       | 1       | 1                  | 1       | 1       | 1       | 5                   | 5       | 5       | 5       | 4              | 4       | 4       | 4       | 2 |
| LR - RD-MI - CO       | lrdmico           |                   |         |         |         |                            |         |         |         |                    |         |         |         |                     |         |         |         |                |         |         |         | 5 |
| LR - MMRM2 - CO       | lrmrm2co          |                   |         |         |         |                            |         |         |         |                    |         |         |         |                     |         |         |         |                |         |         |         | 5 |

- Make slight changes to individual blocks

| model          | estimand         | param1                   | param2 | dataset1 | dataset2 | chgtype1 | chgtype2 | impfactors                  |
|----------------|------------------|--------------------------|--------|----------|----------|----------|----------|-----------------------------|
| ANCOVA - RD-MI | Treatment policy | Body Weight (kg)         |        | ADVS     |          | PCHG     |          | SEX BMIG3BL STRAT1V STRAT2V |
| LR - RD-MI     | Treatment policy | Body Weight (kg)         |        | ADVS     |          | PCHG     |          | SEX BMIG3BL STRAT1V STRAT2V |
| LR - RD-MI     | Treatment policy | Body Weight (kg)         |        | ADVS     |          | PCHG     |          | SEX BMIG3BL STRAT1V STRAT2V |
| LR - RD-MI     | Treatment policy | Body Weight (kg)         |        | ADVS     |          | PCHG     |          | SEX BMIG3BL STRAT1V STRAT2V |
| ANCOVA - RD-MI | Treatment policy | Waist Circumference (cm) |        | ADVS     |          | CHG      |          | SEX BMIG3BL STRAT1V STRAT2V |
| ANCOVA - RD-MI | Treatment policy | Body Weight (kg)         |        | ADVS     |          | PCHG     |          | SEX BMIG3BL STRAT1V STRAT2V |
| ANCOVA - RD-MI | Treatment policy | HbA1c (%)                |        | ADLB     |          | CHG      |          | SEX BMIG3BL STRAT1V STRAT2V |
| ANCOVA - RD-MI | Treatment policy | HbA1c (mmol/mol)         |        | ADLB     |          | CHG      |          | SEX BMIG3BL STRAT1V STRAT2V |



- mk900lrtpmibw5
- mk900mmrm1bw
- mk900mmrm2bw
- mk900rdmibiohscrp
- mk900rdmibiopai1c
- mk900rdmibw
- mk900rdmidbp
- mk900rdmifpg
- mk900rdmifpgsi

- tmmrm1bw
- ~~tmmrm2bio\_hscrp~~
- ~~tmmrm2bio\_lept~~
- ~~tmmrm2bio\_pai1\_c~~
- ~~tmmrm2bio\_slept~~
- tmmrm2bmi
- tmmrm2bw

mk905axcomb

- axcat.xpt
- axcont.xpt
- axstrat.xpt
- axtp.xpt

# Define.xml presentation

|   |  |
|---|--|
| <b>Data References (incl. Selection Criteria)</b> | <p><a href="#">ADVS</a> [<a href="#">FASFL</a> = "Y" and <a href="#">ANL01FL</a> = "Y" and <a href="#">ANELFL</a> = "Y" and <a href="#">PARAM</a> IN ("Body Fat Mass (kg)", "Body Fat Percentage (%)", "Lean Body Mass (kg)", "Lean Body Mass in % (%)", "Visceral Fat Mass (kg)", "Visceral Fat Mass in % (%)") ]</p> <p><a href="#">AXCONT</a> [<a href="#">ESTIMAND</a> = "TREATMENT POLICY" and <a href="#">POPVAR</a> = "DXAFL" and <a href="#">MODEL</a> = "ANCOVA - J2R-MI" and <a href="#">PARAM</a> IN ("Body Fat Mass (kg)", "Body Fat Percentage (%)", "Lean Body Mass (kg)", "Lean Body Mass in % (%)", "Visceral Fat Mass (kg)", "Visceral Fat Mass in % (%)") and <a href="#">CHGTYPE</a> = "CHG"]</p> <p>Results presented in table are selected from the AX data set. Results in the data set AX are based on imputation/modelling of data in the AD data set.</p> |
|---|--|

|                               |   |
|-------------------------------|---|
| <b>Programming Statements</b> | <p>[SAS version 9.4]</p> <p>Imputation of missing data and modelling/estimation was done using mk9xxx.txt referenced below. Estimates were added to the AXCONT data set, wherefrom estimates were selected when presenting estimates in the table using tstatancova.txt.</p> <p>Imputation of missing AVAL was done using PROC MI. Imputation was based on available values within imputation group where each combination of treatment arm and treatment status (on-/off-drug status) at landmark visit defined an imputation group. Last available observation on treatment is denoted LAO_OT.</p> <pre>proc mi data = {data with missing results} out = {output data set} nimpute= 1000;   by TRTP {treatment status};   class SEX BMIG3BL {LAO_OT time interval};   var SEX BMIG3BL {LAO_OT time interval} {AVAL at baseline} LAO_OT AVAL;   monotone regression (AVAL = SEX BMIG3BL {LAO_OT time interval} {AVAL at baseline} LAO_OT); run;</pre> <p>Modelling of change and consecutive estimation was done using PROC MIXED.</p> <pre>proc mixed data = {data with missing replaced by imputed results};   by PARAM _IMPUTATION_;   class TRTP;   model CHG = TRTP {AVAL at baseline};   lsmeans TRTP/diff=control('Placebo') obsmargins at means cl; run;</pre> <p>Results presented in table:</p> <pre>proc print (using selection as specified in Data References);   var MGROUP CGROUP NOBSPOP NOBST EST CFB CONTR CONTRLL CONTRUL PROBSUP; run;</pre> <p><a href="#">mk900j2rmidxabw.txt</a> @</p> <p><a href="#">mk900j2rmidxabwkg.txt</a> @</p> <p><a href="#">mk900j2rmidxalbm.txt</a> @</p> <p><a href="#">mk900j2rmidxalbmg.txt</a> @</p> <p><a href="#">mk900j2rmidxatfm.txt</a> @</p> <p><a href="#">mk900j2rmidxatfmkg.txt</a> @</p> <p><a href="#">mk900j2rmidxavfm.txt</a> @</p> <p><a href="#">mk900j2rmidxavfmkg.txt</a> @</p> <p><a href="#">tstatancova.txt</a> @</p> |
|-------------------------------|---|



# Combined ADRG and define.xml templates

Review of define.xml and ADRG is part of developing and reviewing the ADaM program

One template project document to be used for all trials





# Integrated summaries (ISS, ISE and pro questionnaires)

Subgroup analysis made very easy due to a solid integrated database foundation

Most of the programs are re-used from trial level, both the output and the statistical analysis



# Opportunities and challenges

# Doing analyses across the projects - challenges

Increased maintenance and rigidity – single updates required a lengthy process

Different definitions for Trial nr. 4 variables forced many changes in both ADaM and TFL

Quality of TFL programming could be improved

3 separate analysis pools, each with their own set of variables: phase3a, dose escalation, non-diabetic

Keeping everyone in the loop was critical

Adding new trial to the existing pools required general updates – losing backwards compatibility

PMDA submission requirements different from FDA

# Different requirements for the PMDA submission

FDA:

Table 1-2 Versions of standards and dictionaries used

| Standard or Dictionary | Version(s) Used   |
|------------------------|---|
| SDTM                   | SDTM v1.4<br>SDTM IG v3.2.  |
| ADaM                   | ADaM Model Document 2.1<br>ADaM Implementation Guide v1.1<br>ADaM Structure for Occurrence Data (OCCDS) 1.0 |
| Controlled Terminology | ADaM 2018-12-21   |
| Data Definitions       | define.xml v2.0   |

PMDA:

Table 1-2 Versions of standards and dictionaries used

| Standard or Dictionary | Version(s) Used   |
|------------------------|---|
| SDTM                   | SDTM v1.4<br>SDTM IG v3.2.  |
| ADaM                   | ADaM Model Document 2.1<br>ADaM Implementation Guide v1.0<br>ADaM Structure for Occurrence Data (OCCDS) 1.0 |
| Controlled Terminology | ADaM 2018-12-21   |
| Data Definitions       | define.xml v2.0   |

# Things that were appreciated:

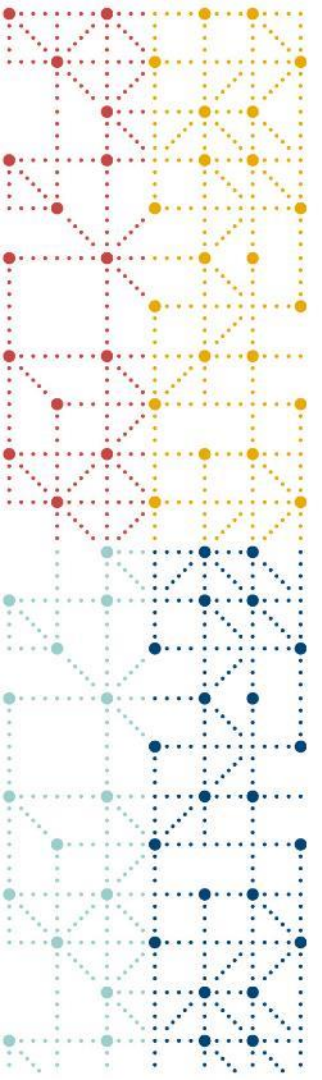
A large number of high quality, submission ready programs have been created

Repetitive programming has been largely eliminated

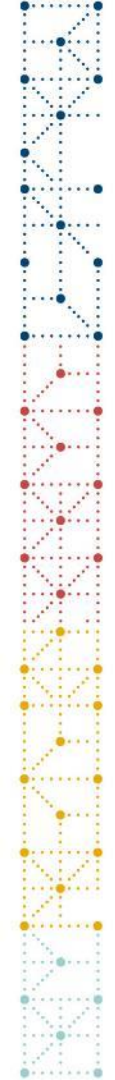
Making subgroups or slight modifications to programs and reviewing them was quite easy, consistent and transparent

Analysis Results Metadata was describing all programs used to create an individual output, making life easy for the reviewers

We have been asked multiple times during the Q&A to provide programs we've created in order to answer the reviewer's questions. Having all our programs at a high 'submission-ready' level made this much easier



**Outcome**



FDA response to a pre-NDA meeting: "Yes, your proposal appears acceptable. However, we may request additional datasets or programs if needed during the review process."



Submission made without any technical issues



No questions to Biostatistics deliverables in the Q&A phase – neither in the FDA nor the PMDA side!



The Project was a team effort of many skilled Programmers and Statisticians – thank you all!





**Thank You!**



CDISC 2023 Europe Interchange | #CDISCEU #ClearDataClearImpact



# Questions?

