

# Introducing the Analysis Results Standard: Project Start Up and Call for Volunteers

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Hansjörg Frenzel, Sr. Principal Clinical Data Standards Consultant, PRA Health Sciences  
Brian Harris, Director, Biometrics Operations and Clinical Data Standards, AstraZeneca  
Bess LeRoy, Head of Standards Development, CDISC  
Kent Letourneau, Executive Director, Global Head, Data Standards, PRA Health Sciences  
Jon Neville, Sr. Standards Developer, CDISC  
Peter Van Reusel, CSO, CDISC



Thursday, 22 OCT 2020  
11:00AM – 12:30PM EDT



## Today's Agenda

1. Housekeeping
2. Presenter Introductions
3. Feature Presentations
4. Question & Answer Session
5. Upcoming Learning Opportunities + Resources



# Housekeeping

# Housekeeping

- You will remain on **mute** for the entirety of the webinar
- There will be a Q&A after all of the presentations are finished
- Audio issues? Shut down and restart the GoToWebinar app
- The slides from the presentation and a recording of this webinar will be available in the Members Only section of the CDISC website
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# Submitting Questions

- To send a question, use the “QUESTIONS” function on your GoToWebinar app. (See red arrow)
- You can submit questions at any time during the presentation, we’ll answer them during the Q&A.
- If you have a question for a specific presenter, please indicate the presenter’s name at the beginning of the question
  - Examples:
    - John: ‘Question’
    - Alana: ‘Question’

A screenshot of the GoToWebinar interface. At the top, there is a dark blue header with a downward-pointing triangle and the word "Questions". Below this is a large white text area. Underneath the text area is a smaller white input field with the placeholder text "Type question here.". At the bottom right of the interface is a grey button with a paper plane icon and the word "Send".



# Content Disclaimer

- The purpose of this webinar is to provide examples of implementation and should not be considered official recommendations by CDISC unless otherwise stated in the presentation.
- This webinar is not an authorized CDISC course, is not developed or delivered under CDISC Operating Procedures, and should not replace a published standard. Please refer to the latest published standards for the most authoritative implementation information.



# Our Presenters

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Thursday, 22 OCT 2020  
11:00AM – 12:30PM EDT



# CDISC Analysis Results Standard Kick-off Meeting

Bess LeRoy  
Head of Standards Development, CDISC

27 October 2020





# Agenda

1. Background
2. Enhancing CDISC ADaM standards
3. Leveraging existing work
4. Scope
5. Timelines

# Background

ADaM currently provides ***standardized inputs*** to enable analysis

- Subject-Level Analysis Dataset (ADSL)
- Basic Data Structure (BDS)
  - Time to Event (TTE)
- Occurrence Data Structure (OCCDS)
  - Adverse Events (ADAE)
- Limited Controlled Terminology



# Background

- Analysis Results Metadata (ARM) *extension to the Define-XML 2.0 model*
  - Provides traceability for a given analysis result to the specific ADaM data that were used as input to generating the analysis result
  - Provides standard metadata fields to represent analysis method used and the reason the analysis was performed

**Table 4.2.2: HbA1c Longitudinal Repeated Measures Analysis Results Metadata**

Metadata Field	Metadata
DISPLAY IDENTIFIER	Table 4.2.1/Figure 4.2.1
DISPLAY NAME	Mean Change from Baseline in HbA1c (Percent) Longitudinal Repeated Measures Analysis, 24-Week Short-term Double-blind Treatment Period, Intention-to-treat Population
RESULT IDENTIFIER	Treatment difference results (LSMean, confidence interval, p-value)
PARAM	HbA1c (%)
PARAMCD	HBA1C
ANALYSIS VARIABLE	CHG (Change from baseline)
ANALYSIS REASON	SPECIFIED IN SAP
ANALYSIS PURPOSE	PRIMARY OUTCOME MEASURE
ANALYSIS DATASET	ADHBA1C
SELECTION CRITERIA	ITTFL="Y" and PARAMCD = "HBA1C" and CHG ne . and ANL01FL = "Y" and DTYPE = " "
DOCUMENTATION	See SAP Section XX for details. Program: t-hba1c-repmeas.sas LS means and 95% CIs are based on repeated measures model adjusting for planned treatment, baseline HbA1c value, avisit, avisit*baseline and avisit*treatment interaction.
PROGRAMMING STATEMENTS	[SAS version 9.2] <pre>PROC MIXED DATA = ADHBA1C;   WHERE ITTFL = "Y" and PARAMCD = "HBA1C" and CHG ne . and ANL01FL = "Y" and DTYPE = " ";   CLASS TRTP AVISIT;   MODEL CHG = TRTP BASE AVISIT BASE*AVISIT AVISIT*TRTP / DDFM=KR;   LSMEANS TRTP / CL DIFF; REPEATED usubjid / subject = USUBJID TYPE=UN; RUN ;</pre>



# Challenges

- ARM provides limited traceability from analysis results to analysis data and does not currently support the capture of actual results
- Limited standardization of analysis results metadata and conceptual layer of TFLs

Enhancing and extending ADaM standards is key to help achieve end to end automation and improve consistent use of the standards

# Enhancing ADaM standards



Add features that support automation of analysis results



Provide guidance on basic analysis structures towards analysis results generation



Provide greater traceability between analysis results and analysis data

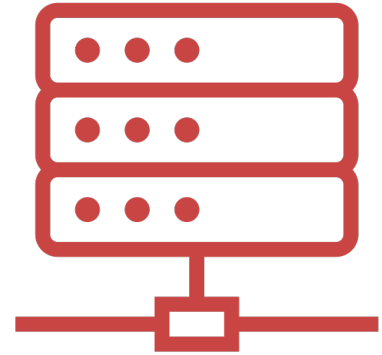
# What could this look like?

- Concept-based standards development for ***generally accepted analyses***
- Analysis dataset examples including relevant controlled terminology
- Expansion of the standardization that is provide by the ARM specification for Define.xml
  - Methodology guidance examples
  - Pseudo code for transformations and derivations
- Standardized analysis results metadata for TFL generation
  - Structure
  - Terminology
  - Enhancing traceability and documentation of the results



## Analysis dataset structure including relevant controlled terminology

- Provide ADaM dataset structure examples that are used to produce TFLs
- Challenges with variation in ADaM dataset that are generated for submission
  - Provide feedback to relevant ADaM teams to work towards a more consistent implementation for biomedical concepts





# Expansion of the standardization that is provide by the ARM specification for Define.xml

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**Analysis Results Metadata Specification  
Version 1.0  
for  
Define-XML Version 2**

Need for standard analysis definition

The ARM specification standardizes the metadata structure for the define.xml



# Standardized analysis results metadata for TFL generation

qb:Observation	qb:Table	dim.population	dim.treatment	dim.parameter	dim.sex	dim.agecat	dim.statistic	analysisResult
1001 dm.summary	enrolled	Treatment.A	param.subjects	sex.ALL	agecat.ALL	stat.freq	100	
1002 dm.summary	enrolled	Treatment.A	param.subjects	sex.F	agecat.ALL	stat.freq	60	
1003 dm.summary	enrolled	Treatment.A	param.subjects	sex.F	agecat.ALL	stat.percent	60	
1004 dm.summary	enrolled	Treatment.A	param.subjects	sex.M	agecat.ALL	stat.freq	40	
1005 dm.summary	enrolled	Treatment.A	param.subjects	sex.M	agecat.ALL	stat.percent	40	
1006 dm.summary	enrolled	Treatment.B	param.subjects	sex.ALL	agecat.ALL	stat.freq	50	
1007 dm.summary	enrolled	Treatment.B	param.subjects	sex.F	agecat.ALL	stat.freq	30	
1008 dm.summary	enrolled	Treatment.B	param.subjects	sex.F	agecat.ALL	stat.percent	60	
1009 dm.summary	enrolled	Treatment.B	param.subjects	sex.M	agecat.ALL	stat.freq	20	
1010 dm.summary	enrolled	Treatment.B	param.subjects	sex.M	agecat.ALL	stat.percent	40	
1011 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.ALL	agecat.ALL	stat.freq	150	
1012 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.F	agecat.ALL	stat.freq	90	
1013 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.F	agecat.ALL	stat.percent	60	
1014 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.M	agecat.ALL	stat.freq	60	
1015 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.M	agecat.ALL	stat.percent	40	
1016 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.freq	100	
1017 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.mean	40.7	
1018 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.stdev	10.7	
1019 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.median	37.0	
1020 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.min	21.0	
1021 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.max	66.0	
1022 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.freq	50	
1023 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.mean	41.2	
1024 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.stdev	10.3	
1025 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.median	36.0	
1026 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.min	23.0	
1027 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.max	67.0	
1028 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.freq	150	
1029 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.mean	40.9	
1030 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.stdev	10.4	
1031 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.median	37.0	
1032 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.min	21.0	
1033 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.max	67.0	

# Standardized analysis results metadata for TFL generation

qb-Observation	qb-Table	dim.population	dim.treatment	dim.parameter	dim.sex	dim.agecat	dim.statistic	analysisResult
1001 dm.summary	enrolled	Treatment.A	param.subjects	sex.ALL	agecat.ALL	stat.freq	✓ 100	
1002 dm.summary	enrolled	Treatment.A	param.subjects	sex.F	agecat.ALL	stat.freq	✓ 60	
1003 dm.summary	enrolled	Treatment.A	param.subjects	sex.F	agecat.ALL	stat.percent	✓ 40	
1004 dm.summary	enrolled	Treatment.A	param.subjects	sex.M	agecat.ALL	stat.freq	✓ 40	
1005 dm.summary	enrolled	Treatment.A	param.subjects	sex.M	agecat.ALL	stat.percent	✓ 40	
1006 dm.summary	enrolled	Treatment.B	param.subjects	sex.ALL	agecat.ALL	stat.freq	✓ 50	
1007 dm.summary	enrolled	Treatment.B	param.subjects	sex.F	agecat.ALL	stat.freq	✓ 30	
1008 dm.summary	enrolled	Treatment.B	param.subjects	sex.F	agecat.ALL	stat.percent	✓ 60	
1009 dm.summary	enrolled	Treatment.B	param.subjects	sex.M	agecat.ALL	stat.freq	✓ 20	
1010 dm.summary	enrolled	Treatment.B	param.subjects	sex.M	agecat.ALL	stat.percent	✓ 40	
1011 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.ALL	agecat.ALL	stat.freq	✓ 150	
1012 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.F	agecat.ALL	stat.freq	✓ 90	
1013 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.F	agecat.ALL	stat.percent	✓ 60	
1014 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.M	agecat.ALL	stat.freq	✓ 60	
1015 dm.summary	enrolled	Treatment.ALL	param.subjects	sex.M	agecat.ALL	stat.percent	✓ 40	
1016 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.freq	✓ 100	
1017 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.mean	✓ 40.7	
1018 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.stdev	✓ 10.7	
1019 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.median	✓ 37.0	
1020 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.min	✓ 21.0	
1021 dm.summary	itt	Treatment.A	param.age	sex.ALL	agecat.ALL	stat.max	✓ 66.0	
1022 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.freq	✓ 50	
1023 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.mean	✓ 41.2	
1024 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.stdev	✓ 10.3	
1025 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.median	✓ 36.0	
1026 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.min	✓ 23.0	
1027 dm.summary	itt	Treatment.B	param.age	sex.ALL	agecat.ALL	stat.max	✓ 67.0	
1028 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.freq	✓ 150	
1029 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.mean	✓ 40.9	
1030 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.stdev	✓ 10.4	
1031 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.median	✓ 37.0	
1032 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.min	✓ 21.0	
1033 dm.summary	itt	Treatment.ALL	param.age	sex.ALL	agecat.ALL	stat.max	✓ 67.0	

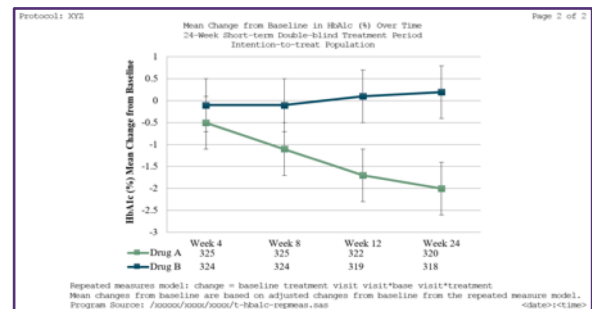
Table 42.1: HBAlc Longitudinal Repeated Measures Analysis - Table Shell

Protocol: XYZ Page 1 of 2

HBAlc (%) Longitudinal Repeated Measures Analysis  
24-Week Short-term Double-blind Treatment Period  
Intention-to-treat Population

	Drug A N=125	Drug B N=125
<b>BASELINE</b>		
Mean (SD)	X.XX ( X.XXXX)	X.XX ( X.XXXX)
<b>WEEK 4</b>		
Mean	X.XX	X.XX
Change from baseline: Mean (SD)	X.XX ( X.XXXX)	X.XX ( X.XXXX)
Adjusted change from baseline: Mean (SD)	X.XX ( X.XXXX)	X.XX ( X.XXXX)
95% Confidence Interval for adjusted mean	(XX.XX, XX.X)	(XX.XX, XX.X)
Difference vs. Drug B (SD)	(XX.XX, XX.X)	(XX.XX, XX.X)
95% Confidence Interval for difference	(XX.XX, XX.X)	(XX.XX, XX.X)
p-value vs. Drug B		X.XXXXX
...		
<b>WEEK 12</b>		
Mean	X.XX ( X.XXXX)	X.XX ( X.XXXX)
Change from baseline: Mean (SD)	X.XX ( X.XXXX)	X.XX ( X.XXXX)
Adjusted change from baseline: Mean (SD)	X.XX ( X.XXXX)	X.XX ( X.XXXX)
95% Confidence Interval for adjusted mean	(XX.XX, XX.X)	(XX.XX, XX.X)
Difference vs. Drug B (SD)	(XX.XX, XX.X)	(XX.XX, XX.X)
95% Confidence Interval for difference	(XX.XX, XX.X)	(XX.XX, XX.X)
p-value vs. Drug B		X.XXXXX

N: the number of subjects in the Intention-to-treat (ITT) Population.  
 nB: the number of subjects in the ITT population with non-missing baseline and non-missing Week t value.  
 Repeated measures model: change = baseline treatment visit visit\*baseline treatment visit\*treatment  
 Program source: %%%%%%%/%%%%%%/%%%%%%/IT-HBAlc-rpmgsa.sas @date=t:ctime@



# What existing work can we leverage?



# JPMA: Commonly used analysis shells and ADaM data for clinical study reports

総括報告書の解析帳票レイアウトと使用する ADaM データの事例

(Commonly used analysis shells and ADaM data for clinical study reports)

日本製薬工業協会 医薬品評価委員会 データサイエンス部会

2019 年度 CDISC タスクチーム

2019 年 8 月

Data Science Expert Committee CDISC Taskforce, Japan Pharmaceutical Manufacturers Association

August, 2019



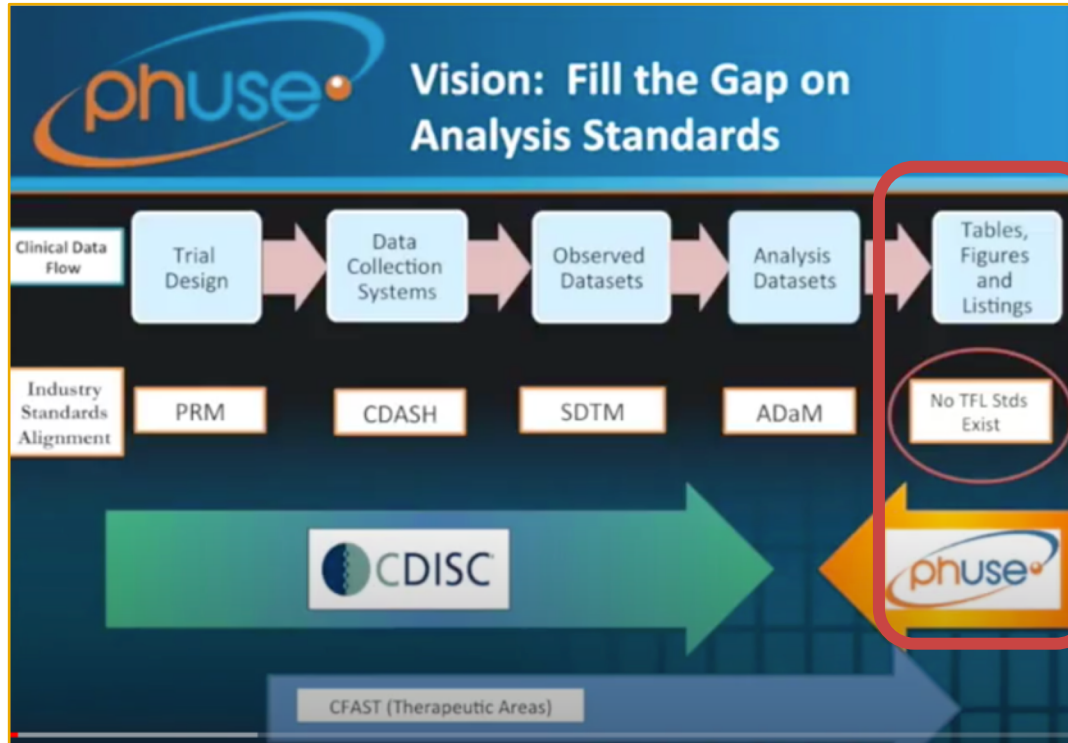
# JPMA: Commonly used analysis shells and ADaM data for clinical study reports

- Data Science Expert Committee CDISC Taskforce of JPMA conducted survey in 2019
- 40 member companies responded to the survey, and the Taskforce identified the standard TFLs commonly used for clinical study reports
- Proposed TFL Shells and ADaM data structures were defined based on the identified standard TFLs
- Document describes analysis shells for clinical study reports with annotation of CDISC ADaM datasets/variables commonly used for statistical analysis of clinical trials
- It will support data science functions in pharmaceutical companies, CROs and academia, etc., when they create statistical analysis deliverables

# Analysis shells for clinical study reports with annotation of CDISC ADaM datasets/variables

Table summary of subject incidence of treatment-emergent adverse events		ADSL.TRTxxP/ADSL.TRTxxA	
		Treatment A	Treatment B
		N=XX	N=XX
ADAE.TRTEMFL (= 'Y')		n(%)	n(%)
TEAE		xx (xxx.x)	xx (xxx.x)
AE related to study treatment	ADAE.AEREL/ADAE.AREL (= 'Y' or '')	xx (xxx.x)	xx (xxx.x)
Serious TEAE	ADAE.AESER (= 'Y')	xx (xxx.x)	xx (xxx.x)
Serious TEAE related to study treatment	ADAE.AESER (= 'Y') and ADAE.AEREL/ADAE.AREL (= 'Y' or '')	xx (xxx.x)	xx (xxx.x)
TEAE leading to death	ADAE.AEOUT (= 'FATAL')	xx (xxx.x)	xx (xxx.x)
AE related to study treatment leading to death	ADAE.AEOUT (= 'FATAL') and ADAE.AEREL/ADAE.AREL (= 'Y' or '')	xx (xxx.x)	xx (xxx.x)
Other important TEAE		xx (xxx.x)	xx (xxx.x)
Other important AE related to study treatment		xx (xxx.x)	xx (xxx.x)
TEAE: Treatment emergent adverse events	ADAE.AESER (= 'N') and ADAE.AEACN (= 'DOSE REDUCED' or 'DRUG WITHDRAWN')		
	ADAE.AESER (= 'N') and ADAE.AEREL/ADAE.AREL (= 'Y' or '') and ADAE.AEACN (= 'DOSE REDUCED' or 'DRUG WITHDRAWN')		

# PHUSE Working Group: Standard Analyses and Code Sharing







# PHUSE Working Group: Standard Analyses and Code Sharing

- Vision: Leverage crowd-sourcing to improve the content and implementation of analyses for medical research, leading to better data interpretations and increased efficiency in the clinical drug development and review processes.
- Goals:
  - Establish and maintain a publicly available repository for storing program code to be used as analytical tools for medical research.
  - Where gaps exist, develop recommendations for analyses and displays in areas that could benefit from crowd-sourcing.
  - Where gaps exist, develop code for recommended analyses and displays that could benefit from crowd-sourcing (to reside in the repository).

# PHUSE analysis & display white papers

	Version 1		Version 2	
	Review	Publish (ed)	Review	Publish (ed)
Vital Signs, Labs, ECG – Central Tendency		Oct 2013 ✓		
Non-Compartmental PK		March 2014 ✓		
Demographics, Disposition, Medications		Oct 2014 ✓	Q4 2017 ✓	Q1 2018 ✓
Vital Signs, Labs, ECG – Outliers / Shifts		Sept 2015 ✓		
QT/QTc Studies		March 2016 ✓		
Adverse Events		Feb 2017 ✓		
General Output Tips and Considerations (Karin)	Q1 2020	Q2 2020		
Treatment-Emergent Definitions (Survey Results)	Q2 2020	Q3 2020		
Labs (Wei)	Q3 2020	Q1 2021		
Hepatotoxicity (Terry)	Q3 2020	Q1 2021		
Questionnaires (Karin)	Q3 2020	Q1 2021		
Listings	Q3 2020	Q4 2020		
Safety Topics of Interest (Brenda)	Q3 2020	Q4 2020		
Vital Signs	Q3 2021	Q4 2021		
ECG's	Q3 2021	Q4 2021		
Treatment-Emergent Definitions (Recommendations on Definition)	Q3 2021	Q1 2022		
Interactive Displays for Clinical Safety Data (Wei)	Q4 2021	Q1 2022		

# CDISC 360: The Art of the Possible

The screenshot displays the CDISC 360 web application interface. At the top, there is a navigation bar with the CDISC 360 logo, the text "Powered by Microsoft", a search bar labeled "Search the CDISC Library", and several utility icons (refresh, user profile, settings, and a user avatar). On the left side, a vertical navigation pane lists six categories: 1. Disease Area (Endocrine), 2. Therapeutic Area (Diabetes - Type 2), 3. Standards Focus (Study Endpoint), 4. Study Endpoint (Analysis of Glycated Hemoglobin), 5. Standard Analyses (Mean Change from Baseline in HbA1c (% Over Time)), and 6. Selection Summary (highlighted with a blue circle). The main content area is titled "Selection Summary" and is divided into three columns: "Study Endpoint", "Analysis", and "Analysis Datasets". The "Study Endpoint" column contains a box for "Analysis of Glycated Hemoglobin" with a description of a Phase III study and a "View details" link. The "Analysis" column contains a box for "Mean Change from Baseline in HbA1c (%) Over Time" featuring a line graph and a "View details" link. The "Analysis Datasets" column contains two boxes: "ADSL" (Analysis Data Subject Level) and "ADHBA1C" (DBS - Structured Dataset), each with links for "View analysis dataset metadata", "View sample analysis data", and "View analysis dataset structure". At the bottom of the main content area, there is a "Back" button and a "Save Selection" button.

Powered by Microsoft

Search the CDISC Library

## Selection Summary

### Study Endpoint

#### Analysis of Glycated Hemoglobin

Analysis of the continuous clinical endpoint of HbA1c. Example: a Phase III, parallel-group study designed to determine efficacy of Drug A for patients with Type II diabetes. The primary endpoint defined as the change in HbA1c from baseline.

[View details](#)

### Analysis

#### Mean Change from Baseline in HbA1c (%) Over Time

Week	Drug A (Mean Change %)	Drug B (Mean Change %)
0	0	0
4	-2	2
8	-4	4
12	-6	6
16	-7	7
20	-7.5	7.5
24	-8	8
28	-8	8
32	-8	8
36	-8	8
40	-8	8
44	-8	8
48	-8	8
52	-8	8

[View details](#)

### Analysis Datasets

#### ADSL

Analysis Data Subject Level

[View analysis dataset metadata](#)

[View sample analysis data](#)

[View analysis dataset structure](#)

#### ADHBA1C

DBS - Structured Dataset

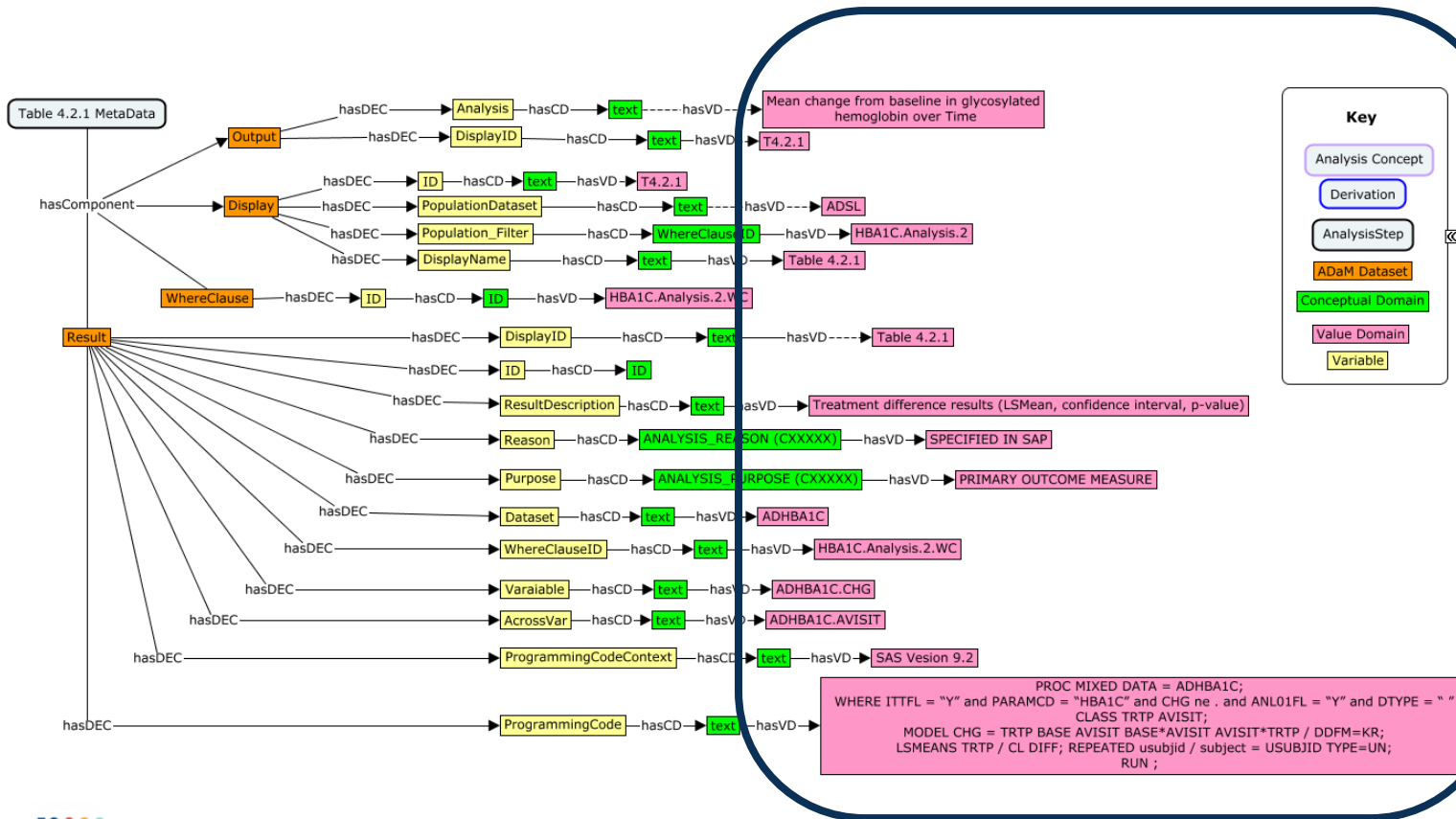
[View analysis dataset metadata](#)

[View sample analysis data](#)

[View analysis dataset structure](#)

[Back](#) [Save Selection](#)

# Analysis Result Concept



# CDISC ARM v1 Metadata

Study - CDISC 360

Table 14.1.1.1  
Demographic characteristics (Safety Population)

Characteristics	METFORMIN (N=XX)	HUMAN INSULIN (N=XX)
<b>Age (years)</b>		
n	XX	XX
Mean	XX.X	XX.X
SD	XX.XX	XX.XX
Min	XX	XX
Q25	XX.X	XX.X
Median	XX.X	XX.X
Q75	XX.X	XX.X
Max	XX	XX
<b>Age Group - n (%)</b>		
15 - <30 years	XX ( XX.X)	XX ( XX.X)
30 - <45 years	XX ( XX.X)	XX ( XX.X)
>=45 years	XX ( XX.X)	XX ( XX.X)
<b>Gender - n (%)</b>		
Male	XX ( XX.X)	XX ( XX.X)
Female	XX ( XX.X)	XX ( XX.X)

Max = Maximum. Min = Minimum. N = Number of subjects in treatment group. n = Number of subjects included in analysis. SD = Standard deviation.

Datasets used - adsl

Executed by <Username> on DDMONYYYY:HH:MM

Result

ResultOID

Description

Reason

Purpose

Dataset

WhereClause

AnalysisVariable

Documentation

ProgrammingCode

Display

DisplayOID

Name

Title

Document

# CDISC ARM v1 Metadata Extensions

## Output (Study, Analysis, Group, Filename/Type, Style)

Result  
Version  
DisplayPattern  
Grouping  
- AnalysisVar  
- ByVar  
CodeReference

Study - CDISC 360

Table 14.1.1.1  
Demographic characteristics (Safety Population)

Characteristics	METFORMIN (N=XX)	HUMAN INSULIN (N=XX)
Age (years)		
n	XX	XX
Mean	XX.X	XX.X
SD	XX.XX	XX.XX
Min	XX	XX
Q25	XX.X	XX.X
Median	XX.X	XX.X
Q75	XX.X	XX.X
Max	XX	XX
Age Group - n (%)		
15 - <30 years	XX ( XX.X)	XX ( XX.X)
30 - <45 years	XX ( XX.X)	XX ( XX.X)
>=45 years	XX ( XX.X)	XX ( XX.X)
Gender - n (%)		
Male	XX ( XX.X)	XX ( XX.X)
Female	XX ( XX.X)	XX ( XX.X)

Max = Maximum. Min = Minimum. N = Number of subjects in treatment group. n = Number of subjects included in analysis. SD = Standard deviation.  
Datasets used - ads1  
Executed by <Username> on DDMONYYYY:HH:MM

## Display

Parent  
Version  
Grouping:  
- Dataset  
- WhereClause  
- AnalysisVar  
- ByVar  
Template  
Title 1..N  
RowLabelHeader  
Header 1..N  
Footer 1..N



# CDISC 360 Enriched TFL Metadata (ARM<sup>++</sup>)

- Based on CDISC ARM v1
- Added OUTPUT & STYLE
- Extended DISPLAY and RESULT
  - Parent
  - Version
  - Grouping and ByVar
  - CodeReference
- Use-cases for production TFL automation

# CDISC 360 Enriched TFL Metadata (ARM<sup>++</sup>): Sample

Study - CDISC 360

Table 14.1.1.1  
Demographic characteristics (Safety Population)

Characteristics	METFORMIN (N=XX)	HUMAN INSULIN (N=XX)
Age (years)		
n	XX	XX
Mean	XX.X	XX.X
SD	XX.XX	XX.XX
Min	XX	XX
Q25	XX.X	XX.X
Median	XX.X	XX.X
Q75	XX.X	XX.X
Max	XX	XX
Age Group - n (%)		
15 - <30 years	XX (XX.X)	XX (XX.X)
30 - <45 years	XX (XX.X)	XX (XX.X)
>=45 years	XX (XX.X)	XX (XX.X)
Gender - n (%)		
Male	XX (XX.X)	XX (XX.X)
Female	XX (XX.X)	XX (XX.X)

Max = Maximum. Min = Minimum. N = Number of subjects in treatment group. n = Number of subjects included in analysis. SD = Standard deviation.  
Datasets used - adsl  
Executed by <Username> on DDMMYYYY:HH:MM

Study	Analysis	Group	Order	DisplayID	DisplayVersion	Filename	Type	StyleID
CDISC	CDISC 360	Safety	1	T14111_SAF_DEMOG	1	tdemog_saf	rtf	table_rtf
CDISC	CDISC 360	Safety	2	T14131_SAF_AE2TIER	1	tae_soc_pt_saf	rtf	table_rtf
CDISC	CDISC 360	Efficacy	3	T1421_EFF	1	tmace_edpt_fas	rtf	table_rtf

DisplayID	DisplayName	DisplayTitle	Title1	Title2	Title3
T14111_SAF_DEMOG	Table 14.1.1.1	Demographic characteristics (SAF)	Study - CDISC 360	Table 14.1.1.1	Demographic characteristics (Safety Population)

ResultDisplayOID	AnalysisResultOID	Version	ResultDescription	DisplayPattern
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	n	xxx
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	Mean	xx.x
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	SD	xx.xx
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	Min	xx
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	Q25	xx.x
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	Median	xx.x
T14111_SAF_DEMOG	T14111_01_SAF_DEMOG	1	Q75	xx.x

WhereClauseOID	Dataset	Variable	Comparator	Value
T14111_02_SAF_DEMOG_01	ADSL	AGEGR1	EQ	15 <= to <30 years
T14111_02_SAF_DEMOG_02	ADSL	AGEGR1	EQ	30 <= to <45 years
T14111_02_SAF_DEMOG_03	ADSL	AGEGR1	EQ	>=45 years
T14111_03_SAF_DEMOG_01	ADSL	SEX	EQ	M
T14111_03_SAF_DEMOG_02	ADSL	SEX	EQ	F



# What content will be the focus?

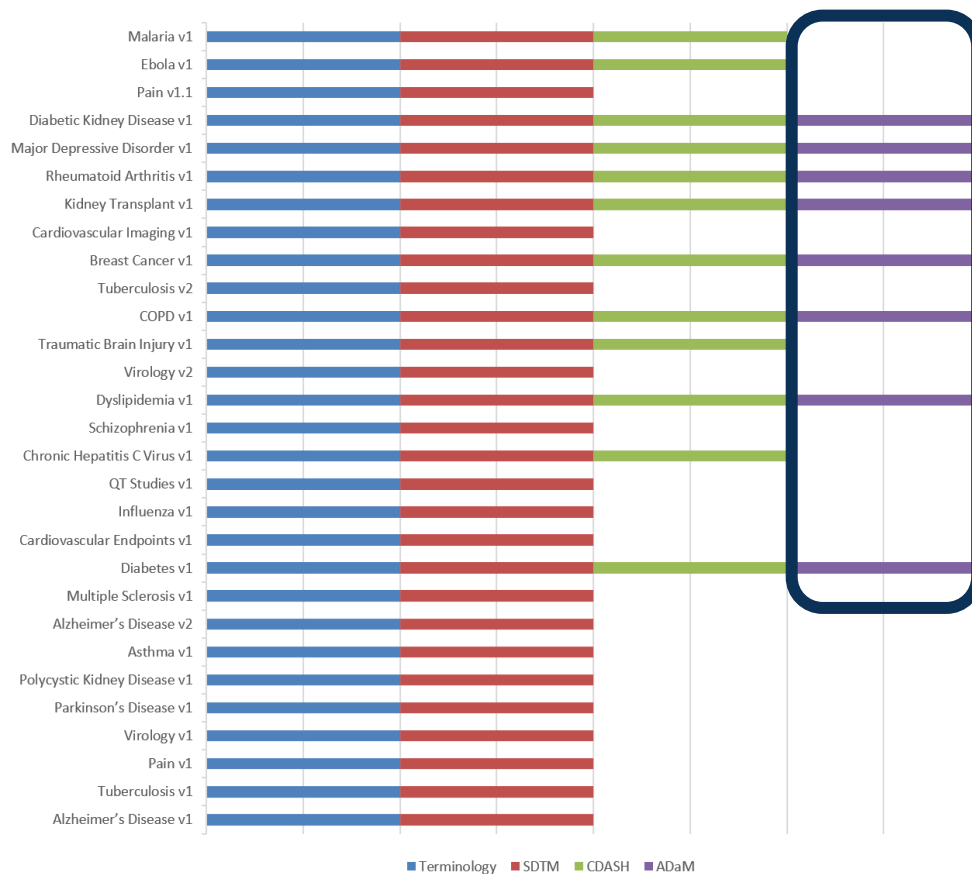
- Most common safety analyses
- TAUGs with analysis components
- TAUGs without analysis components
- Community generated content
- Will not focus on TFL layout
  - Example options for layouts for illustration purposes



# What common safety analyses do we start with?

	Version 1		Version 2	
	Review	Publish (ed)	Review	Publish (ed)
Vital Signs, Labs, ECG – Central Tendency		Oct 2013 ✓		
Non-Compartmental PK		March 2014 ✓		
Demographics, Disposition, Medications		Oct 2014 ✓	Q4 2017 ✓	Q1 2018 ✓
Vital Signs, Labs, ECG – Outliers / Shifts		Sept 2015 ✓		
QT/QTc Studies		March 2016 ✓		
Adverse Events		Feb 2017 ✓		
General Output Tips and Considerations (Karin)	Q1 2020	Q2 2020		
Treatment-Emergent Definitions (Survey Results)	Q2 2020	Q3 2020		
Labs (Wei)	Q3 2020	Q1 2021		
Hepatotoxicity (Terry)	Q3 2020	Q1 2021		
Questionnaires (Karin)	Q3 2020	Q1 2021		
Listings	Q3 2020	Q4 2020		
Safety Topics of Interest (Brenda)	Q3 2020	Q4 2020		
Vital Signs	Q3 2021	Q4 2021		
ECG's	Q3 2021	Q4 2021		
Treatment-Emergent Definitions (Recommendations on Definition)	Q3 2021	Q1 2022		
Interactive Displays for Clinical Safety Data (Wei)	Q4 2021	Q1 2022		

# TAUGs with and without ADaM components



# TAUG Tables, Listings, and Figures

**Table 4.2.1: HbA1c Longitudinal Repeated Measures Analysis - Table Shell**

Protocol: XYZ

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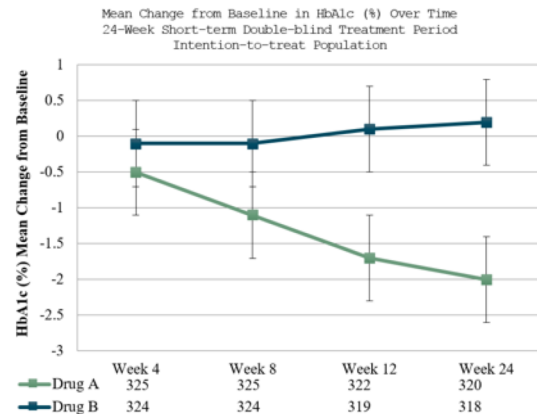
		HbA1c (%) Longitudinal Repeated Measures Analysis 24-Week Short-term Double-blind Treatment Period Intention-to-treat Population	
		Drug A N=125	Drug B N=125
BASELINE	N#	125	125
	Mean (SD)	X.XX ( X.XXX)	X.XX ( X.XXX)
WEEK 4	N#	XXX	XXX
	Change from baseline: Mean (SD)	X.XX ( X.XXX)	X.XX ( X.XXX)
	Adjusted change from baseline: Mean (SD)	X.XX ( X.XXX)	X.XX ( X.XXX)
	95% Confidence interval for adjusted mean	(XX.XX, XX.X)	(XX.XX, XX.X)
	Difference vs. Drug B (SE)		XX.XX ( X.XXXX)
	95% Confidence interval for difference		(XX.XX, XX.X)
	P-value vs. Drug B		X.XXXX
...			
WEEK 12	N#	X.XX ( X.XXX)	X.XX ( X.XXX)
	Change from baseline: Mean (SD)	XXX	XXX
	Adjusted change from baseline: Mean (SD)	X.XX ( X.XXX)	X.XX ( X.XXX)
	95% Confidence interval for adjusted mean	X.XX ( X.XXX)	X.XX ( X.XXX)
	Difference vs. Drug B (SE)	(XX.XX, XX.X)	(XX.XX, XX.X)
	95% Confidence interval for difference		XX.XX ( X.XXXX)
	P-value vs. Drug B		(XX.XX, XX.X)
			X.XXXX

N: the number of subjects in the Intention-to-treat (ITT) Population.  
 N#: the number of subjects in the ITT population with non-missing baseline and non-missing Week t value.  
 Repeated measures model: change = baseline treatment visit visit\*treatment  
 Program Source: %%%%%%%\xxxx\xxxx\t-hb1c-rmrems.sas <date>:<time>

Some examples exist in the TAUGs for various disease areas but not all analysis sections have the same level of detail

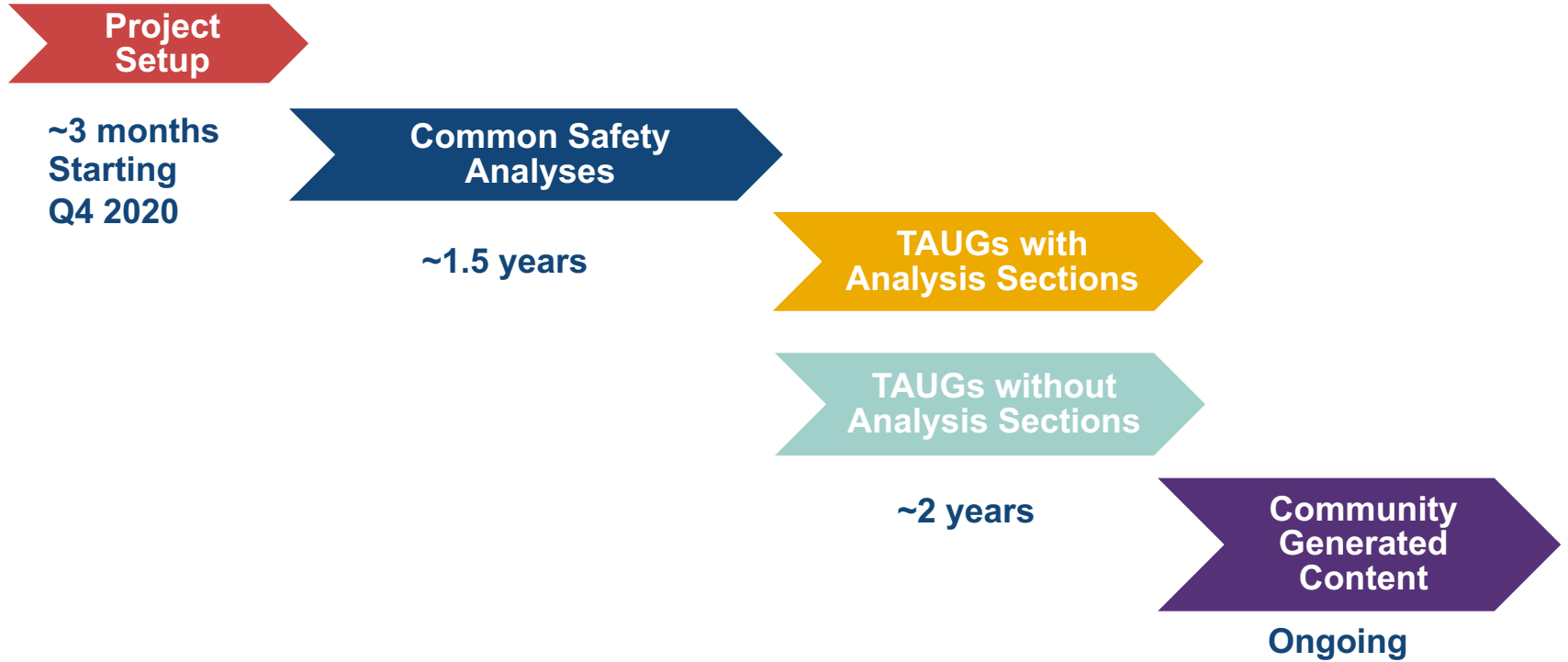
Protocol: XYZ

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Repeated measures model: change = baseline treatment visit visit\*base visit\*treatment  
 Mean changes from baseline are based on adjusted changes from baseline from the repeated measure model.  
 Program Source: /%xxxx\xxxx\xxxx\t-hb1c-rmrems.sas <date>:<time>

# Anticipated Project Timeline



# Interested? Join our team!

- Looking for additional team members
- Meet weekly on Friday at 10:00 am Eastern
- Contact Bess LeRoy at [bleroy@cdisc.org](mailto:bleroy@cdisc.org)



# Thank you to the current team!

- Jeff Abolafia
- Brian Harris
- Nate Freimark
- Mary Nilsson
- Maria Matilde Kam
- Yumiko Asami
- Kent Letourneau
- Hansjoerg Frenzel
- Nancy Brucken
- Bhavin Busa
- Sally Cassells
- Jon Neville
- Peter Van Reusel
- Azusa Tsukida
- Chenoa Conley

# Audience Questions

How can I get involved in the project?





# Audience Questions



The paper by Chris Decker that you mentioned builds on the PhUSE working group: PhUSE Analysis Results Model Project, (2016, Marc Andersen and Tim Williams, [https://www.phusewiki.org/wiki/index.php?title=Analysis\\_Results\\_Model](https://www.phusewiki.org/wiki/index.php?title=Analysis_Results_Model) ).

# Audience Questions

I'm excited to hear about this project. One thing that has always bothered me about the current ARM standard is the one-to-one coupling of results with displays, which leads to unnecessary repetition, e.g. when the same result appears in multiple tables. Will this project consider the whole data model behind ARM, so the relationship between results and displays can be normalised? It sounds like it probably will but confirmation would be great!



# Audience Questions



Why can't ARM currently be used to help generate results. Instead of being produced after results are generated?

# Audience Questions

Nice presentation. Is there an online form to be filled become an volunteer?

Answer:

<https://www.cdisc.org/volunteer>



# Audience Questions



Is a development of ODM-XML-based standard for TLFs (based on ARM/ARM++) is part of the project scope?

# Audience Questions

Is this a CDISC initiative or will the results datasets be requested soon by the FDA?





# Upcoming Learning Opportunities

# 2021 CDISC Upcoming Events

## February 2021 – TechniCon Virtual Events



### TechniCon

- Tuesday, 2 February: Asia-Pacific Rim
- Wednesday, 3 February: EMEA
- Friday, 5 February: India
- Monday, 8 February: Americas

Submit Abstracts Now. Registration Open Soon!

## April 2021 – Europe Virtual Event



### 2021 Europe Interchange

28-29 April

February 2021 – Abstract Submissions and Registration Coming Soon.



# Free Upcoming Webinar Lineup – Registration Open!

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## CDASH SAE v2.0 Public Review

10 NOV 2020, 11:00 AM - 12:30 PM EDT

- CDISC, with support from our partner TransCelerate Biopharma, is developing version 2.0 of the CDASH SAE Supplement, which will capture how to structure serious adverse events (SAE) concepts for regulated clinical trials.

## CDISC Tabulate Certification Launch

16 NOV 2020, 11:00 AM - 12:30 PM EDT

- Announcing the new CDISC Certification program: why you should take it, and how you can do it.

# New Virtual Training Methods

- CDISC Provides Many Ways to Begin or Continue Growing Your Standards Knowledge.
  - Popular self-paced training plus new Blended Learning and Virtual Classroom settings.

## Blended Learning from CDISC

Online Resources  
+ In-Person Instruction  
More Personalized Learning

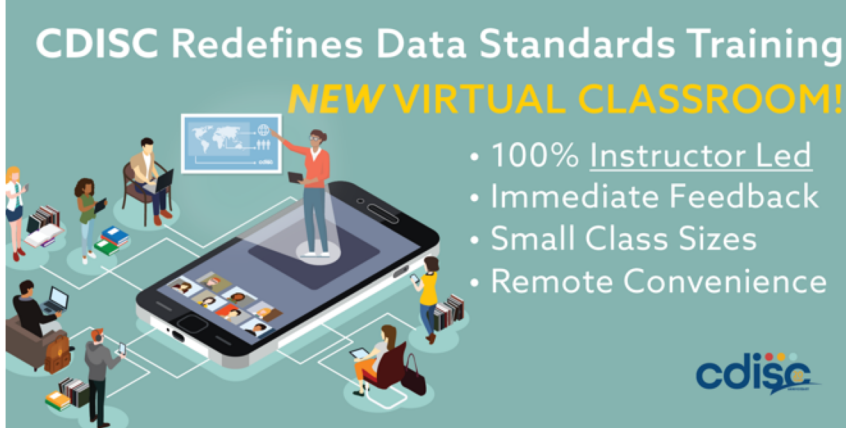


Classes Starting Soon!

## CDISC Redefines Data Standards Training

### NEW VIRTUAL CLASSROOM!

- 100% Instructor Led
- Immediate Feedback
- Small Class Sizes
- Remote Convenience



cdisc



# Thank You!

Questions, comments, concerns? Email [bklinke@cdisc.org](mailto:bklinke@cdisc.org)

Don't forget to fill out the feedback survey!

