

Harmony and Melody - The Role of Metadata Standards in Improving Machine Learning Efficiency



Meet the Speaker

Steve Ross

Title: Director, Statistics and Life Sciences Consultancy Organization: Beaconcure

Steve has worked in clinical research for more than 25 years, in statistics and programming roles for Big Pharma, Small Pharma, CROs, Biotech, and Consultancy. In his current role at Beaconcure, Steve works with clients to reduce obstacles to TLF production, streamline statistics and programming processes, and reduce deliverable timelines.



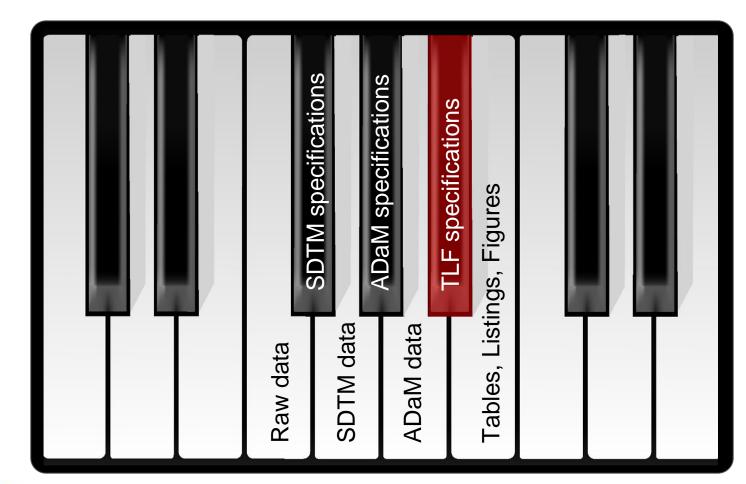
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 The views and opinions expressed in this presentation are those of the author(s) and do not necessarily reflect the official policy or position of CDISC.





Current State of TLF Production and Validation
 The Problem: What Lies Between ADaM and TLFs
 Future State: CDISC to the Rescue!





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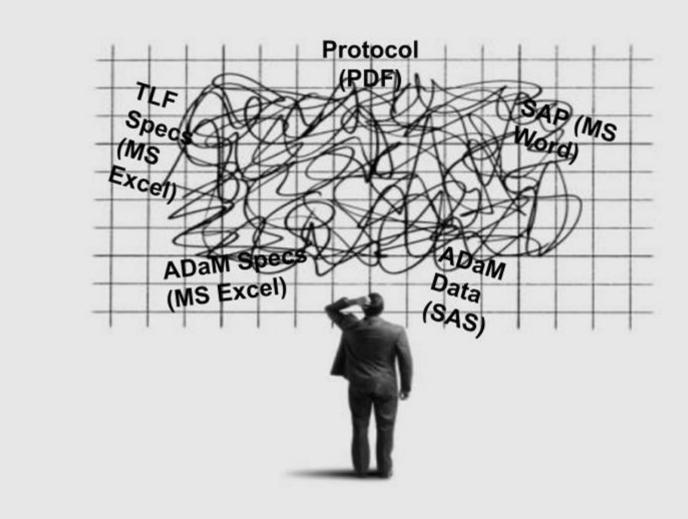


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- Tables, Listings, and Figures are then generated using...





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The Problem: What Lies Between ADaM and TLFs

• Obstacles to effective TLF development

General instructions in the protocol

9.1.2. Vital Signs

Vital signs assessments will include respiratory rate (breaths per minute), systolic and diastolic BP (mmHg), heart rate (HR) (beats per minute [bpm]) and body temperature, which will be measured after a participant has rested for at least 5 minutes in the supine or recumbent position, as age appropriate and feasible and will be collected as per Table 1, Table 3, Table 4, and Table 6.

Any clinically significant abnormal vital sign assessment requires at least one repeat measurement.

Vital signs abnormalities that are (1) considered clinically significant initially and on confirmation, (2) require a participant to be discontinued from the study, (3) require a participant to receive treatment, or (4) require a change or discontinuation from the study drug (if applicable) will be recorded as AEs.



Programming/Statistics Notes in SAP

Table of Contents

3.6 Study Specific Programming Instructions

3.6.1 Baseline

1.	Purpose	Variable	Baseline Visit
2.	Programming Used to Produce Data Presentations	Laboratory tests	The baseline value is defined as the last non-missing
3.	Functional Specifications		measurement collected prior to the first administration of study drug at Day 1. For the lab values, if the calculated study day
3.1	Operating System, SAS Version Number, and Version Control		for the labelled baseline visit is not study Day 1 but falls
3.2	General Specifications		within 28 days before the start of the study dosing, then that data should be used for the baseline instead of leaving baseline
3.3	Treatment Labels		data should be used for the buseline instead of leaving buseline
3.3 3.4 3.5	Standard Directory Structure Naming Conventions for Programs, Data sets, Variables, and Data Presenta	Concomitant Medications	Baseline for systemic steroid, NSAIDs and opioids is defined as on stable dose at least 4 weeks prior to the first dose of study drug and analysis end time after date of first exposure.
3.6	Study Specific Programming Instructions		Baseline for anti-malarial is defined as treated on Day 1. Start time before the first dose of study drug and analysis end time after date of first exposure.
	3.6.2 Algorithms		
4.	 3.6.2.1 General Algorithms for Prior and Concomitant Medications Tables 3.6.2.2 General Algorithms for Disposition Tables	model cfb repeated tim Ismeans vis	rt (ref="Control") time (ref="2"); = base time trt time*trt time*base / ddfm=kr; e /subject= id type= un; it*trt / pdiff at base= &basemean alpha=0.10 cl; fs= dlancova lsmeans= dlancova;
5.	Patient ID (PID) Lists and/or Patient Profiles	set dlancova;	
6.	Review and Approval of the A&R Plan Analysis Specifications		trt="Control") & (time=_time));

Programming Notes in Standard TLF Specs

General Notes:

1.	A "Missing" row will be added if there are unreported results for any
	category.
2.	For tables and listings where patients are stratified by MP500 dose,
	patients will also be stratified by treatment with corticosteroid
	premedication.
3.	MP500 single agent dose escalation tables, listings, and figures shells
	are included. Upon initiation of the MP500 + Standard of <u>Care(</u> SOC) dose
	escalation, MP500 + SOC Dose Escalation treatment arms and Total columns
	will be added to the outputs. Duplicate table, listing, and figure shells
	will be added if needed as noted in the programming notes. Additionally,
	shells specific to SOC, crossover, or dose expansion have not been
	included at this time: they are available in the TOC.
4.	Only cohorts that have subjects will be included in the TLFs. No dummy
1.	columns or rows will be presented for cohorts that do not yet have
	subjects or data.
	subjects of data.



Now We're getting somewhere...

Title1	Miracle Pharmaceuticals			<dry draft="" fi<="" run="" th=""><th>NAL/CSR1/CSR2/DM</th><th>C></th></dry>	NAL/CSR1/CSR2/DM	C>	
Title2	PROTOCOL: MP-XXX-XXXX (<data cut<="" td=""><td>off/Last Subject Out></td><td>DDMMMYYYY)</td><td></td><td>Page x of</td><td>y ADSL.STUDYID</td></data>	off/Last Subject Out>	DDMMMYYYY)		Page x of	y ADSL.STUDYID	
Title3							
able 15.1.2.x Title4			Table 15.1.2.x				
Title5			Analysis Sets				
Title6			(Enrolled Analysis S	et)		ADSL.ENRLFL='Y'	
		Placebo	<miracle drug=""></miracle>	<active comparator=""></active>	Total	ADSL.TRT01P	
		(N=xx)	(N=xx)	(N=xx)	(N=xx)	_	
	All Enrolled				xx (xx.x)	ADSL.ENRLFL = 'Y'	
	Number of Screen Failures				xx (xx.x)	ADSL.SCRNFL= 'Y'	
	Randomized Analysis Set	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	ADSL.RANDFL = 'Y	
	Safety Analysis Set	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	ADSL.SAFFL='Y'	
	Full Analysis Set	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	ADSL.FASFL='Y'	
	Per Protocol Analysis Set	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	ADSL.PPROTFL='Y'	
	Completer Analysis Set	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	ADSL.COMPLFL = "	
Footnote1	1 <add appear="" define="" footnotes="" in="" populations="" subject="" table="" that="" this="" to=""></add>						
Lastfoot	/compound/study//tables/xxxx	XXXXX			DDMMMYYYY xx:	xx	



Current State Obstacles to Effective Programming

• Each of these documents is bespoke, tailored to the requirements of the protocol that governs the trial.



Current State: Obstacles to Effective Programming

- Each of these documents is bespoke, tailored to the requirements of the protocol that governs the trial.
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- Each of these documents appears to have structure, but natural variability in study purposes results in **limited carryover from study to study** within a compound's development, and **even from table to table** within the same study.



Current State: Obstacles to Effective Programming

- Each of these documents is bespoke, tailored to the requirements of the protocol that governs the trial.
- Each of these documents takes multiple weeks to develop and is continually updated (save for the protocol) and refined right up until database lock.
- Each of these documents appears to have structure, but natural variability in study purposes results in **limited carryover from study to study** within a compound's development, and **even from table to table** within the same study.
- Study level metadata and results data are generated post-hoc (in the define.xml); however, it does not facilitate automation, repeated use, and reflects the lack of standardization found in the source documents.





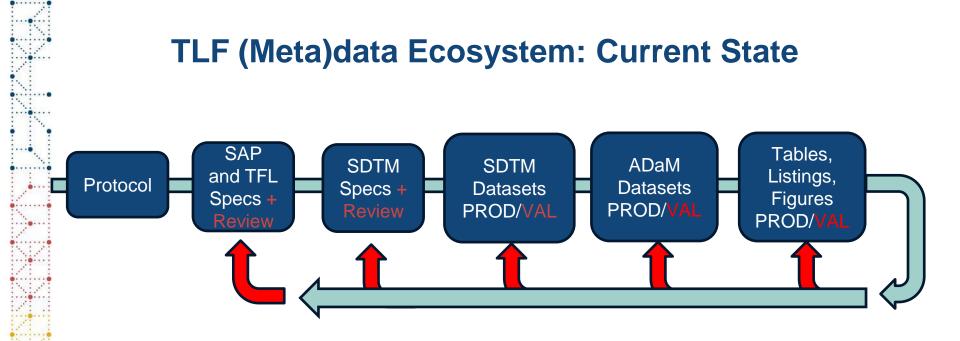
Even within these 'standard documents' the metadata and results data *are not standardized.*

How do we know this?

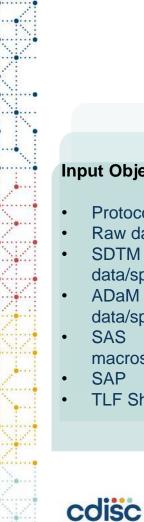


Future State: CDISC to the Rescue!

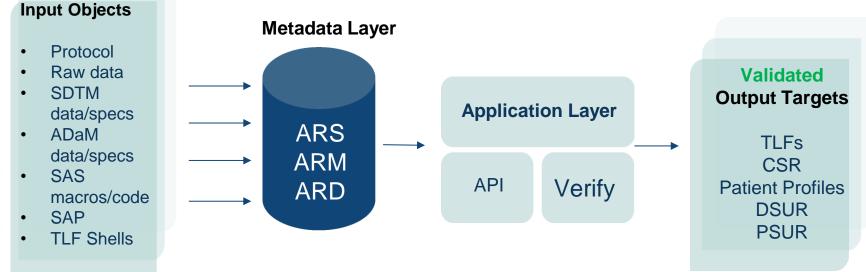
Refining the metadata layer between ADaM and TLFs with Analysis Results Standards (ARS) and Analysis Results (Meta)data (ARD)



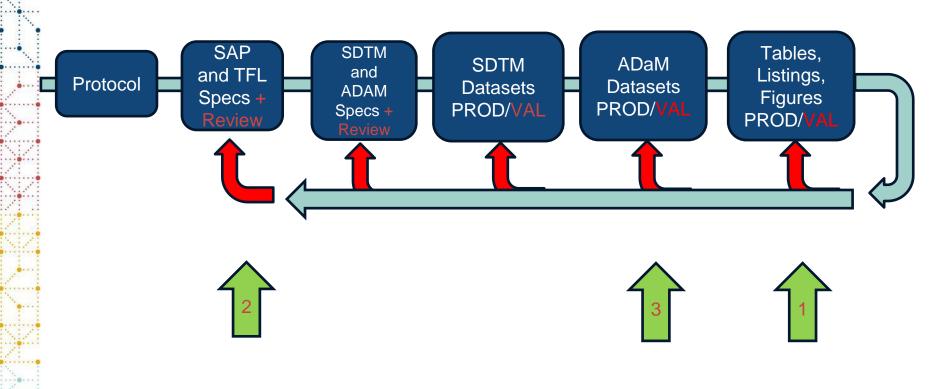




TLF (Meta)data Ecosystem: Future State



TLF (Meta)data Ecosystem: Current State



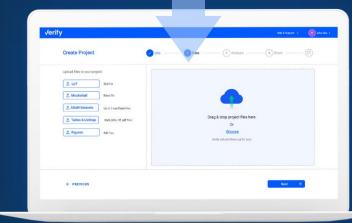


Model data ingestion

- Either upload all your delivery files(TLFs, Table of Contents, TLF shell documents) to Verify application, or link directly through an API
- Application parses your files, deconstructing down to the cell level, categorizing and linking objects

Table 14-1-1-16 ng in >5% of Subjects in at least One Treatment Group in S Class and Preferred Term (Safety Population Drug J Drug B (N=119 (N=117) 61 (51.3% 69 (59.03 stro Disorder 53(32.8%) 48 (41.0% Diarrhea 25 (21.08 35 (29.98 Vomiting 20 (16.8% 0 (25.61 10 (8.5% 10 (8.5% and Mediastinal Disorde 10 (8.5% 29 /24.41 62 / 538 (1.7%) 8 (6.83) 30 (25.68 20 (16.8% 2 (27.48 2(1.7% 5 (4.3%) 1 (0.8%) etabolism and nutrition disorders 12 (10.1%) 45 (38.58 2 (1.7%) 5 (4.2%) 7 (5.9%) 9 (7.6%) 10 (8.58 14 (12.0% 20 (17.1% 1 (0.8%) olydipsia 1 (0.8%)
1 (0.8%)

Docs Xis Html Pdf Rtf Sas

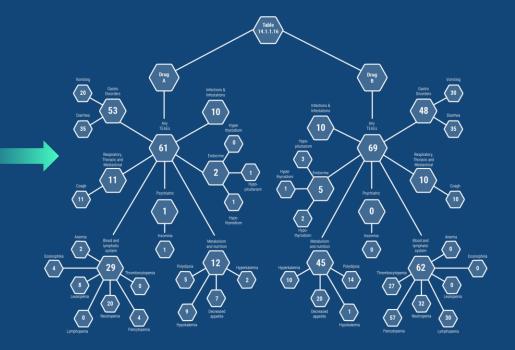




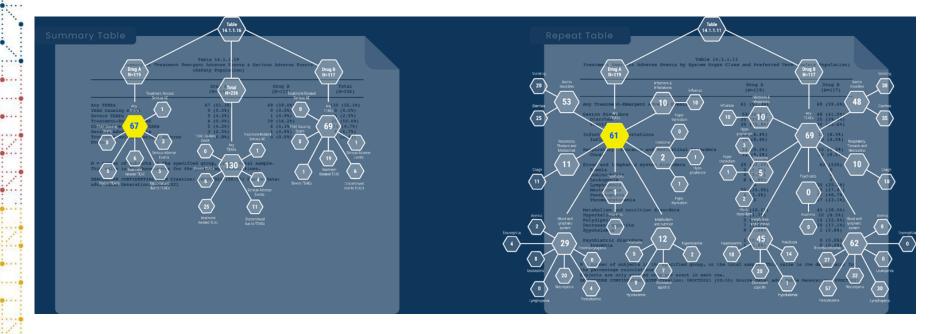
Al-Enabled Conversion of TLFs into a Robust Structured Database

	Drug A (N=119)	Drug B (N=117)
ny TEAEs	61 (51.3%)	69 (59.0%)
astro Disorders Diarrhea Vomiting	53(32.8%) 25 (21.0%) 20 (16.8%)	48 (41.0%) 35 (29.9%) 30 (25.6%)
nfections & Infestations	10 (8.4%)	10 (8.5%)
espiratory, Thoracic and Mediastinal Disorders Cough	11 (9.2%) 11 (9.2%)	10 (8.5%) 10 (8.5%)
lood and lymphatic system disorders hnemia Eosinophilia Leukopenia Lymphopenia Pancytopenia Pancytopenia Thrombocytopenia	$\begin{array}{cccc} 29 & (24.48) \\ 2 & (1.78) \\ 4 & (3.48) \\ 8 & (6.88) \\ 0 \\ 20 & (16.88) \\ 4 & (3.48) \\ 0 \\ \end{array}$	62 (53%) 0 0 30 (25.6%) 32 (27.4%) 57 (48.7%) 27 (23.1%)
ndocrine disorders Hyperthyroidism Hypopituitarism Hypothyroidism	2(1.7%) 0 1 (0.8%) 1 (0.8%)	5 (4.3%) 1 (0.8%) 3 (2.6%) 2 (1.7%)
etabolism and nutrition disorders Hyperkalaemia Polydippia Decreased appetite Hypokalaemia	12 (10.1%) 2 (1.7%) 5 (4.2%) 7 (5.9%) 9 (7.6%)	45 (38.5%) 10 (8.5%) 14 (12.0%) 20 (17.1%) 1 (0.8%)
sychiatric disorders	1 (0.8%) 1 (0.8%)	0

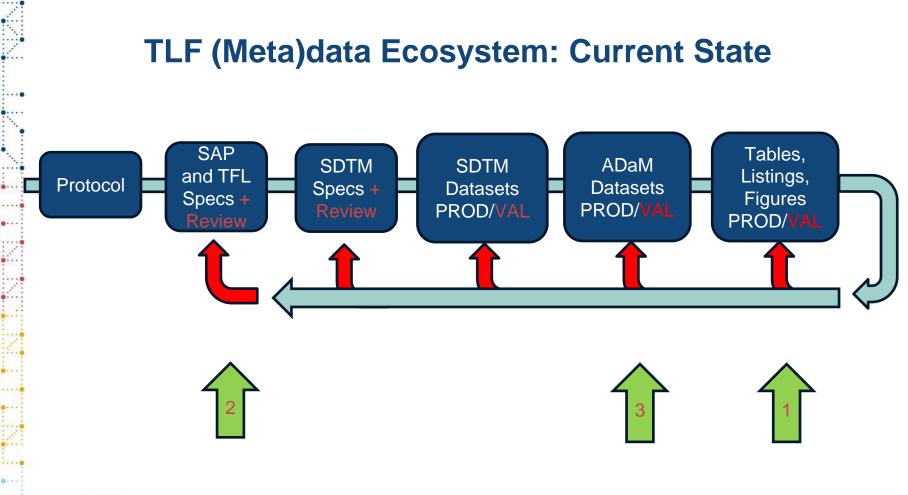
Psychiatric disorders Insomnia	1 (0.8%) 1 (0.8%)	0
Metabolika and nutrition disorders Ryperkalaenia Polydigala Decreased appetite Hypokalaenia	$\begin{array}{c} 12 & (10,18) \\ 2 & (1,78) \\ 5 & (4,28) \\ 7 & (5,98) \\ 7 & (5,98) \\ 9 & (7,68) \end{array}$	



Fully parsed data facilitates semantic understanding of different tabular data.









Standard Demographics Table

Miracle Pharmaceuticals Protocol No.: MP500-1001--Data Cutoff Date:21Nov2021 Page 1 of 5

Tabl	e	15		1	•	4		1	
Dem	og	ra	p	h	i	С	s		
Safety	An	a]	3	Į2	3	is	5	S	е

	1	4P500 Single Age	nt Dose Escalatio	n
Characteristic	MP500 8 ug/kg (N=3)	MP500 16 ug/kg (N=5)	MP500 16 ug/kg + 1 DEX (N=3)	MP500 16 ug/kg + 2 DEX (N=3)
Age (years) [a]				
nge (years) [a]	3	5	3	3
Mean (SD)	66.7 (6.11)	70.6 (5.81)	57.3 (11.68)	57.0 (8.89
Median	68.0	68.0	55.0	54.0
Min, Max	60, 72	65, 80	47, 70	50, 67
Age categories [a] [n (%)]				
18 to 64	1 (33.3)	0	2 (66.7)	2 (66.7)
65 to 84	2 (66.7)	5 (100)	1 (33.3)	1 (33.3)
85 or above	0	0	0	0
Sex [n (%)]				
Male	3 (100)	5 (100)	2 (66.7)	2 (66.7)
Female	0	0	1 (33.3)	1 (33.3)
Missing	0	0	0	0
Ethnicity [n (%)]				
Hispanic or Latino	0	1 (20.0)	1 (33.3)	0
Not Hispanic or Latino	3 (100)	4 (80.0)	2 (66.7)	3 (100)
Not Reported	0	0	0	0

DEX = Dexamethasone

[a] Age is calculated as the integer part of (Date of informed consent - Date of birth) / 365.25.

[b] Body Mass Index is defined as weight(kg) / [height (m)]2.

Standard Demographics Table

acle Pharmaceuticals	Data <u>Sutoff</u> Date:21Nov20	Table 15.1.4.1 Demographics Safety Analysis So		entifiers	Page 1
Characteristic	Group Vars	MP500 8 ug/kg (N=3)	1P500 Single Agen MP500 16 ug/kg (N=5)	nt Dose Escalatio MP500 16 ug/kg + 1 DEX (N=3)	n MP500 16 ug/kg + 2 DEX (N=3)
Age (years) [a] n Mean (SD) Median Min, Max	Result Vars	3 66.7 (6.11) 68.0 60, 72	5 70.6 (5.81) 68.0 65, 80	3 57.3 (11.68) 55.0 47, 70	3 57.0 (8.89) 54.0 50, 67
Age categories [a] [n (18 to 64 65 to 84 85 or above	%)]	1 (33.3) 2 (66.7) 0		CS 2 (65.7) 1 (33.3)	2 (66.7) 1 (33.3) 0
Sex [n (%)] Male Female Missing		3 (100) 0 0	5 (100) 0 0	2 (66.7) 1 (33.3) 0	2 (66.7) 1 (33.3) 0
Ethnicity [n (%)] Hispanic or Latin Not Hispanic or I Not Reported		0 3 (100) 0	1 (20.0) 4 (80.0) 0	1 (33.3) 2 (66.7) 0	0 3 (100) 0

DEX = Dexamethasone

[a] Age is calculated as the integer part of (Date of informed consent - Date of birth) / 365.25.[b] Body Mass Index is defined as weight(kg) / [height (m)]2.



/bios/MP500/studies/1001/dryrun/tables/t15.1.4.1-demo

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Standard Demographics Table Shell

T DEM			1	1		
Title1	_					
_ Title1	Miracle Pharmaceuticals			<dry draft="" fi<="" run="" th=""><th>NAL/CSR1/CSR2/DMC></th><th></th></dry>	NAL/CSR1/CSR2/DMC>	
 Title3	PROTOCOL: MP-XXX-XXXX (<data cutoff="" last="" subject<="" th=""><th>Out>: DDMMMYYYY)</th><th></th><th></th><th>Page x or y</th><th>ADSL.STUDYID</th></data>	Out>: DDMMMYYYY)			Page x or y	ADSL.STUDYID
Table 15.1.4.x Title4			Table 15.1.4.x			
Title5		Demographic C	haracteristics by	Prestment Group		
 Title6			ed Set/Safety Set/An			<adsl.randfl='y' *fl="Y" saffl="Y"></adsl.randfl='y'>
		(criterio onite	ca bee, bareey bee, im	119010 00077		ADSLINANDIL- TYSAITL- TY TL- TZ
-			MP500	<active< th=""><th></th><th>ADSL.TRT01A</th></active<>		ADSL.TRT01A
-		Placebo	Drug xx mg>	Comparator xx mg>	Total	
-	Characteristic	(N=xx)	(N=xx)	(N=XX)	(N=xx)	
1						
1	Age (years) [a]					ADSLAGE
	n	xx	XX	XX	xx	
	Mean (<sd>)</sd>	xx.x (xx.xx)	xx.x (xx.xx)	xx.x (xx.xx)	xx.x (xx.xx)	
]	Median	xx.x	xx.x	xx.x	xx.x	
	Q1, Q3	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	
	Min, Max	xx, xx	xx, xx	xx, xx	xx, xx	
]						
	Age Categories (n[%])					non-missing unique values for ADSL.AGEGRy
	< xx	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	
	xx - xx	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	
	xx - xx	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	
	> XX	xx (xx.x)	xx (xx.x)	xx (xx.x)	xx (xx.x)	



Analysis Results (+) Metadata

	Identifiers	Group Vars		Result Vars			Statistics		
Number	Title	Dataset	Variable	Value	Variable	Label	Value	Name	Label
15.1.4.1	Demographics Safety Analysis Set	ADSL	TRT01a	MP500 8 ug/kg (n=3)	AAGE	Age (years) [a]	3	Count	N
15.1.4.1	Demographics Safety Analysis Set	ADSL	TRT01a	MP500 8 ug/kg (n=3)	AAGE	Age (years) [a]		Mean (standard deviation)	Mean (SD)
15.1.4.1	Demographics Safety Analysis Set	ADSL	TRT01a	MP500 8 ug/kg (n=3)	AAGE	Age (years) [a]	68	Median	Median
15.1.4.1	Demographics Safety Analysis Set	ADSL	TRT01a	MP500 8 ug/kg (n=3)	AAGE	Age (years) [a]	60, 72	Minimum, Maximum	Min, Max



Future State of TLF Development

- ARS-standardized TLF metadata enables rapid TLF identification and selection from a growing database of displays of all shapes and sizes
- Where new displays are required, software will make suggestions based on input parameters.
- Where existing metadata are not sufficient for production or validation tasks, Humans-in-the-loop provide last-mile input once to complete
- As metadata store grows at an organization, the AI algorithms become more efficient and more accurate, making better suggestions and requiring less human-in-the-loop interventions



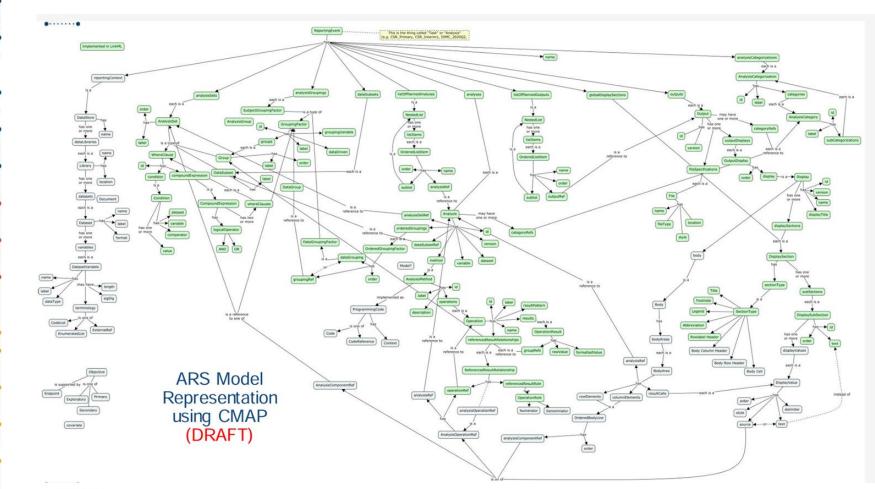
Summary

Analysis Results Standards (ARS) provide a framework to capture structural aspects of the displays, as well as the results data in the body of the TLFs.

This common structure of ARS data facilitates:

- Rapid development of TLFs during the statistical analysis design phase
- Consistency in TLF design across compounds/phase/TAs/organizations
- Linkages back to ADaM datasets, creating automated validation pathways, opportunities for data reuse





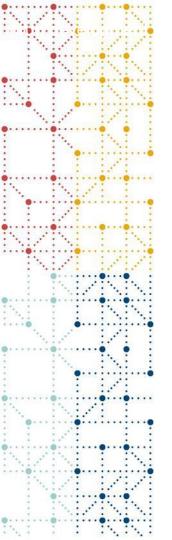


References

Large-scale TFL Automation for regulated Pharmaceutical trials using CDISC Analysis Results Metadata (ARM); Malcolm

Pre-launching CDISC Analysis Results Standards PHUSE US Connect 2023; Busa, LeRoy





Thank You!

