The Data Machinery Behind Exploratory Biomarkers

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2026 Europe Interchange

THE FUTURE IS CONNECTED: STANDARDS AND AI POWERING DIGITAL TRANSFORMATION

The Data Machinery Behind Exploratory Biomarkers

MILAN, ITALY | MAIN CONFERENCE: 20-21 MAY | TRAININGS & WORKSHOPS: 18, 19, & 22 MAY

Tom Smeets, Clinical & Biomarker Programmer
Ine Wolfs, Clinical & Biomarker Data Standards Manager

Speakers

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OCS Life Sciences

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Clinical & Biomarker Data Standards Manager
argenx

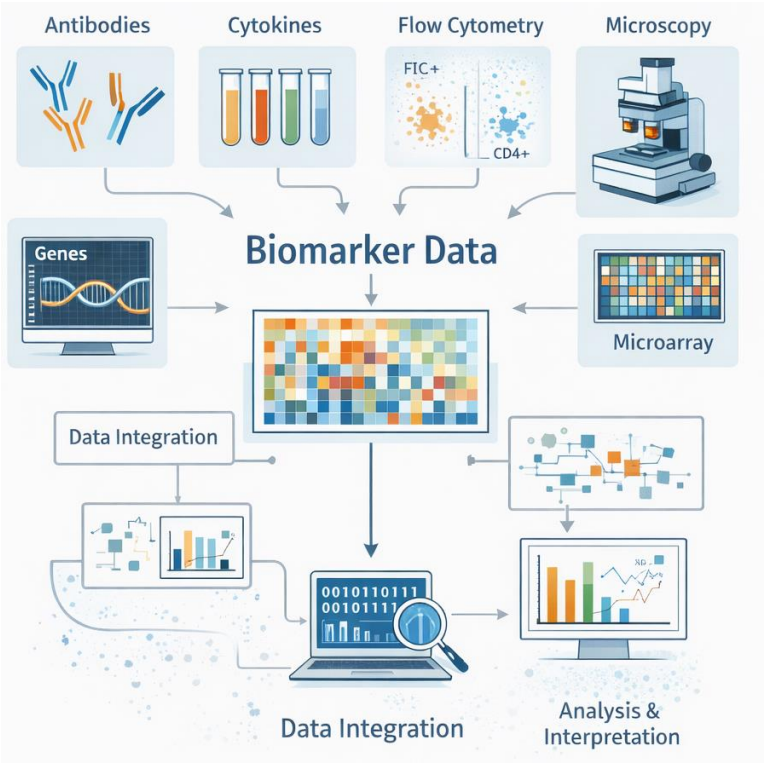
Agenda

1. What are exploratory biomarkers (EBM)?
2. Challenges of exploratory biomarker data
3. The argenx way of handling exploratory biomarker data
4. The future of exploratory biomarkers at argenx

What are Exploratory Biomarkers (EBM)?

Clinical exploratory biomarkers are scientifically driven measurements designed to address key research questions, including:

- understanding of drug mode of action
- disease biology
- variability in treatment response



BUT

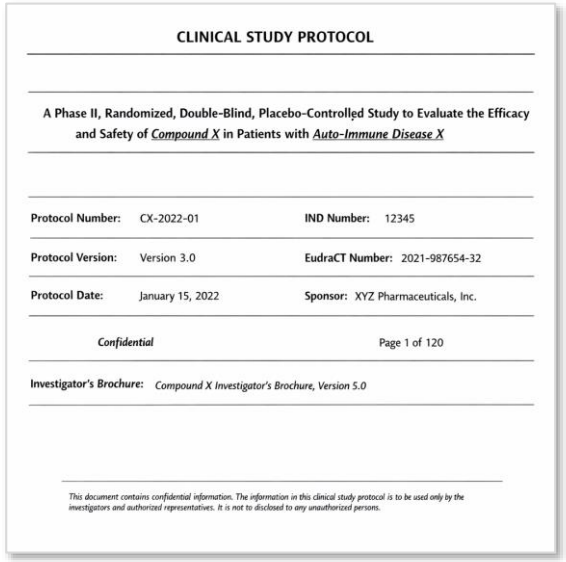
Although part of the study specific biomarker strategy and measured on clinical study samples...

EBM are NOT

- **clinically validated parameters for diagnosis, disease progression and/or treatment response**
- **tied to primary or secondary endpoints**
- **part of the submission package**

Challenges of Exploratory Biomarkers

Protocol | Data | Analysis



CLINICAL STUDY PROTOCOL

A Phase II, Randomized, Double-Blind, Placebo-Controlled Study to Evaluate the Efficacy and Safety of *Compound X* in Patients with *Auto-Immune Disease X*

Protocol Number:	CX-2022-01	**IND Number:**	12345
Protocol Version:	Version 3.0	**EudraCT Number:**	2021-987654-32
Protocol Date:	January 15, 2022	**Sponsor:**	XYZ Pharmaceuticals, Inc.

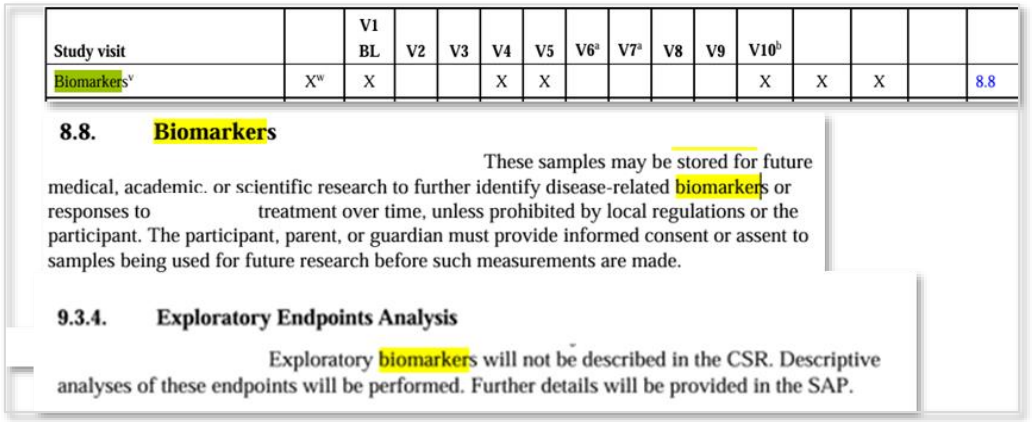
Confidential Page 1 of 120

Investigator's Brochure: *Compound X Investigator's Brochure, Version 5.0*

This document contains confidential information. The information in this clinical study protocol is to be used only by the investigators and authorized representatives. It is not to disclosed to any unauthorized persons.

"Biomarker data will be collected for exploratory research."

- Which EBMs will be measured, often not explicitly mentioned in the protocol
- No details on analysis specifications



Study visit		V1 BL	V2	V3	V4	V5	V6[a]	V7[a]	V8	V9	V10[b]				
Biomarkers[v]	X[w]	X			X	X					X	X	X		8.8

8.8. Biomarkers

These samples may be stored for future medical, academic, or scientific research to further identify disease-related biomarkers or responses to treatment over time, unless prohibited by local regulations or the participant. The participant, parent, or guardian must provide informed consent or assent to samples being used for future research before such measurements are made.

9.3.4. Exploratory Endpoints Analysis

Exploratory biomarkers will not be described in the CSR. Descriptive analyses of these endpoints will be performed. Further details will be provided in the SAP.

Challenges of Exploratory Biomarkers

Protocol | **Data** | Analysis

Complex assays
(e.g. array's; -omics; flow cytometry, etc)

Many biomarkers per study
(typically 4-8 per study)

Data is sent via email, BOX, etc

Vendors provide data without subject ID or other link to the subject

Vendor datasets not always easily machine readable (e.g. empty columns, rows, free text)

EBM data is potentially unblinding!

Many vendors with different capabilities (university labs to Central Lab)

Same biomarker shared differently by different vendors

Vendor 1

Subject ID	Analyte	Result (%)	Visit
1001	PROTEIN A	5	1
1001	PROTEIN B	1	1
1003	PROTEIN A	6,2	1
1003	PROTEIN B	2,3	1

Vendor 2

Subject	PROTEIN A (%)	PROTEIN B (%)	ACCESS ID
1001	5	1	1234567890
1003	6,2	2,3	2233445566

Vendor 3

ID	A (Fr)	B (Fr)	BARCODE
1001	0,05	0,01	123456789001
1003	0,062	0,023	223344556601

Even datasets from same vendor look different in multiple studies

Vendor 1

Study	Subject ID	Analyte	Result (%)	Visit
ARGX 1	1001	PROTEIN A	5	1
ARGX 1	1001	PROTEIN B	1	1
ARGX 1	1003	PROTEIN A	6,2	1
ARGX 1	1003	PROTEIN B	2,3	1

Vendor 1

Study ID	Patient	Protein	ORRES (%)	Visit
ARGX 2	2001	A	5	V1
ARGX 2	2001	B	1	V1
ARGX 2	2005	A	6,2	V1
ARGX 2	2005	B	2,3	V1

Challenges of Exploratory Biomarkers

Protocol

Data

Analysis

Clinical study SAP does not provide details

Analysis datasets are created without standardization

Analysis performed on raw datasets is not quality controlled

Biomarker (derivations) added upon updates in research questions

Longitudinal analyses on data from original and OLE study

Biomarker X

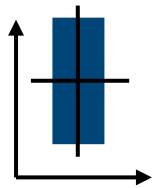
Study 1

Raw dataset 1

Subject	PROTEIN A (%)	PROTEIN B (%)	ACCESS ID
1001	5	1	1234567890
1003	6,2	2,3	2233445566

Study specific data processing and analysis

Study specific analysis dataset 1



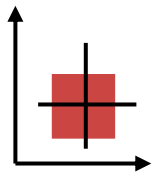
Study 2

Raw dataset 2

ID	A (Fr)	B (Fr)	ACCESS ID
2001	0,075	0,011	112233445
2003	0,054	0,032	9876543210

Study specific data processing and analysis

Study specific analysis dataset 2

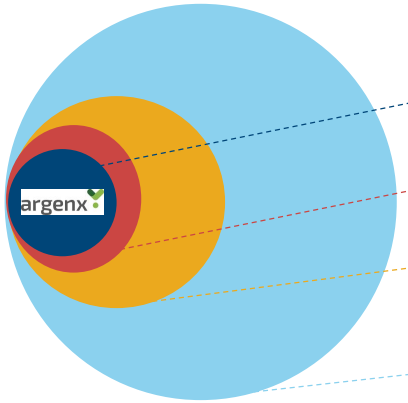


Analyses performed without standardization

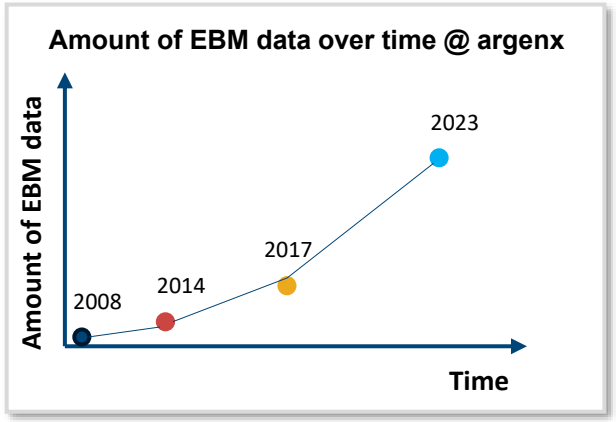
- not reproducible
- not allowing pooling or comparison across indications/compounds,
- not allowing future data-catalogue-ing

The Exploratory Biomarker journey at argenx

argenx: a global BioTech company built on a strong vision to translate scientific breakthroughs in immunology into transformative medicines for patients with severe autoimmune diseases.



- Founded in 2008, Science at its core, only a handful of staff
- 2014-2016, first clinical phase, set-up of first Data Management specializations.
- 2017-2022, late clinical phase & submission, professionalization of Data Management. Scattered biomarker specializations.
- 2023 -...: commercialization and strong portfolio growth



Strongly investing in exploratory biomarkers to deepen disease understanding and predict future treatment responses - **more (complex) biomarkers, assays and vendors**

→ **need for a sustainable process: standardization & dedicated expert team**

The argenx Way of Handling Exploratory Biomarkers

argenx EBM Data Repository & raw-to-end data standardization

FAIR — Data Usability

"Can people find and use this data?"

- **F** Findable
- **A** Accessible
- **I** Interoperable
- **R** Reusable

ALCOA++ — Data Integrity

"Can you trust this data?"

A L C O A Attributable, Legible, Contemporaneous, Original, Accurate

+ Complete

+ Consistent

+ Enduring / Available

Study 1

Raw dataset 1

Subject	PROTEIN A (%)	PROTEIN B (%)	ACCESS ID
1001	5	1	1234567890
1003	6,2	2,3	2233445566

Study 2

Raw dataset 2

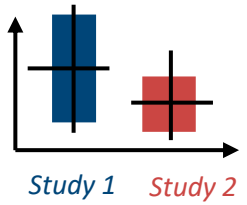
ID	A (Fr)	B (Fr)	ACCESS ID
2001	0,075	0,011	112233445
2003	0,054	0,032	9876543210

argenx raw-to-end data standardization process

Standardized study Analysis dataset 1

Standardized study Analysis dataset 2

Standardization allows
- data pooling
- data comparison across indications and/or compounds
- future data-catalogue-ing



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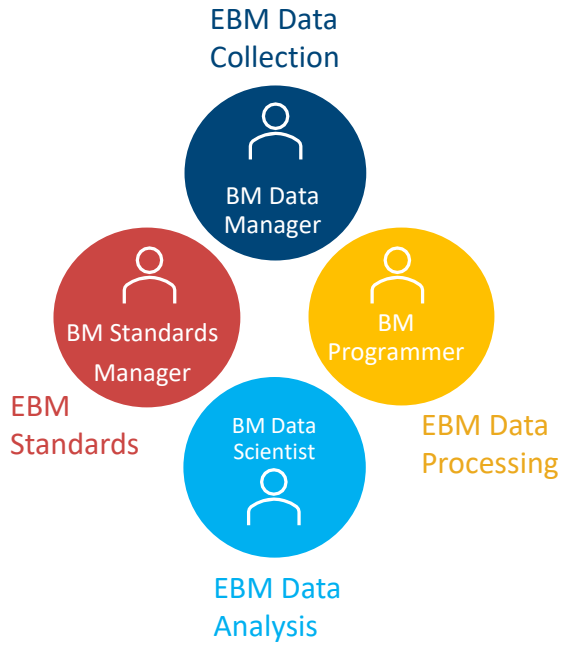
* EBM: Exploratory Biomarkers

The argenx Way of Handling Exploratory Biomarkers

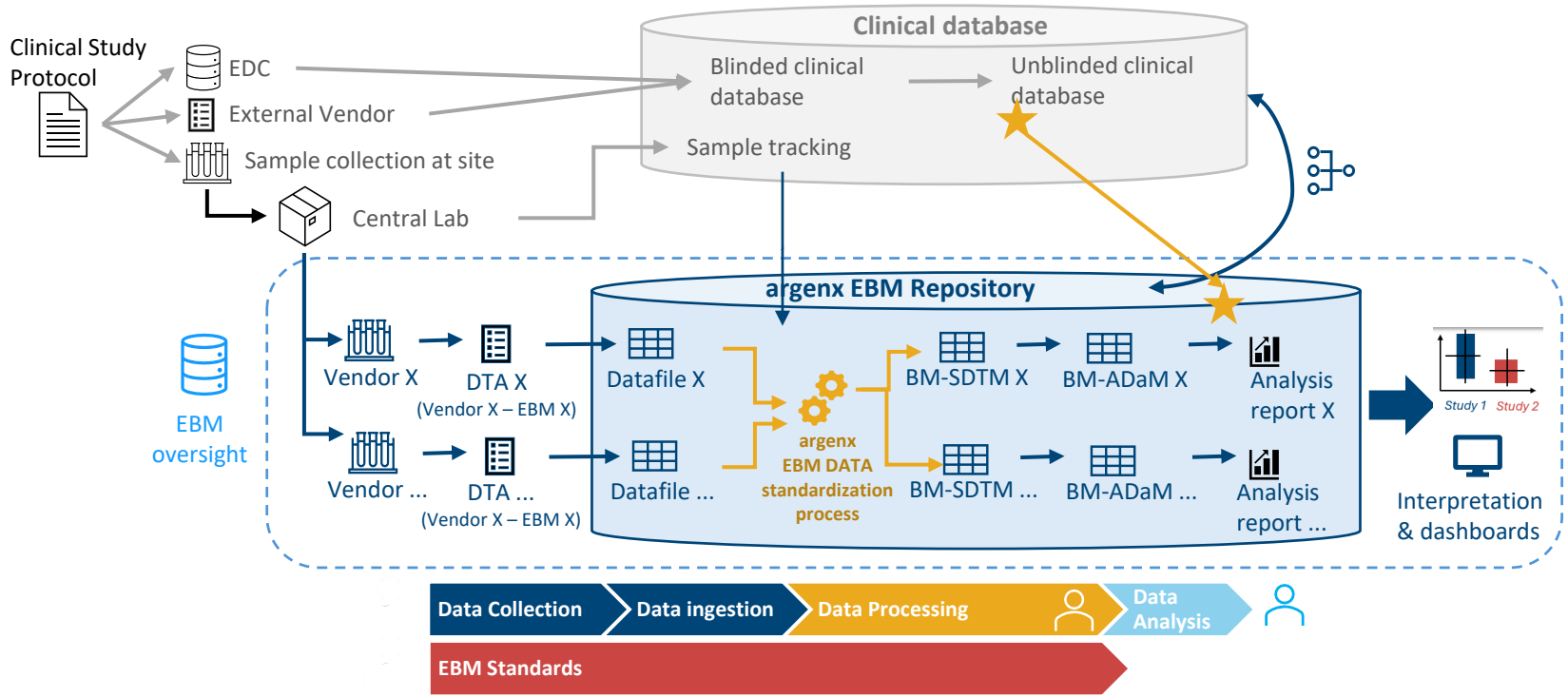
The EBM 'DATA TEAM'

Specialized team with scientific & data expertise - linking the science with the data!



Co-Creation argenx OCS LIFE SCIENCES

The EBM 'DATA PROCESS'



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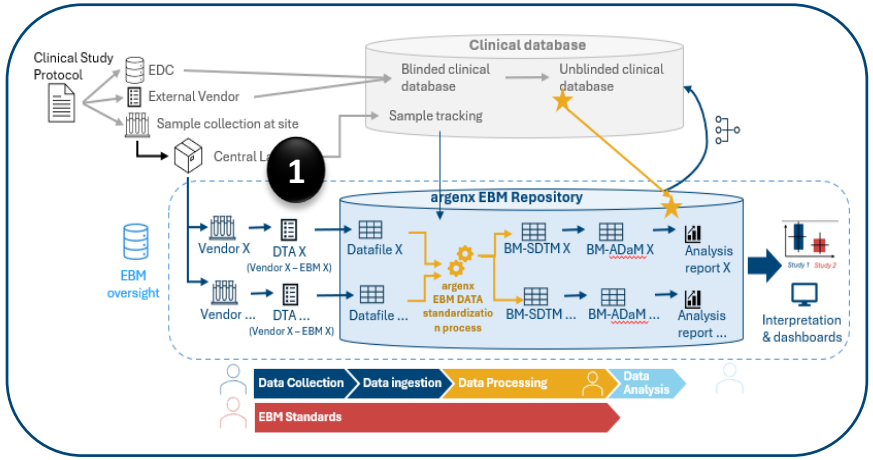
* EBM: Exploratory Biomarkers

The argenx Exploratory Biomarker DATA PROCESS

Data Transfer Agreements (DTA)



ARGENX SOLUTION

- **Biomarker DM**
  - both scientific and data management expertise
- **DTA template**
  - Machine readable
  - For any vendor and data type
  - Documents structure and content 'as collected'
  - Contains EBM-specific additions to ensure result reporting is properly discussed and documented

The argenx Exploratory Biomarker DATA PROCESS

Data Transfer Agreements (DTA)

General | Sample Metadata | Result Reporting | Transfer Specifications | Transfer Specifications_IDENT | Codelists | **Test Identifiers**

Format, frequency, file name, type of transfer, etc

Unique sample identifier information

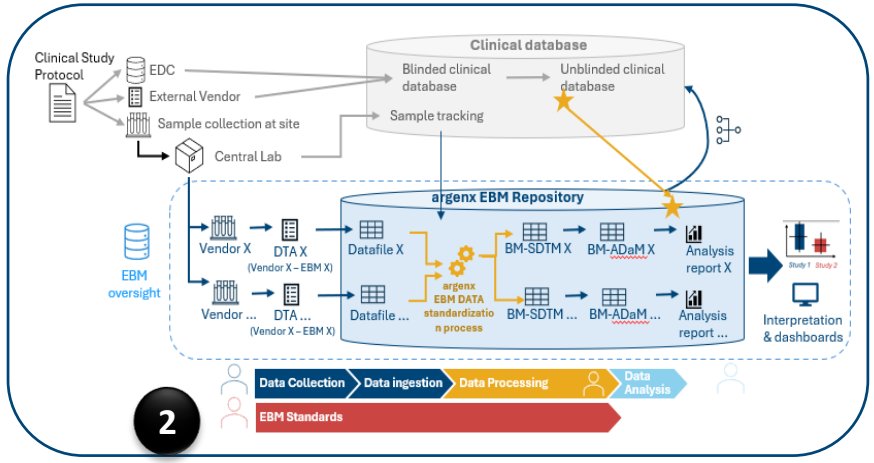
Samples received but not analyzed
Sample re-testing
Comments about Samples status
Unreliable results
Other comments/flags about results

Transfer variable name	Transfer variable label	Format	Length	Allowed values	Test Identifiers	Codelists	Visit and/or Timepoint	Description of variable	use	Unblinding Parameters
STUDYID	Study ID	Char	250							
SUBJID	Subject ID	Char	50					*e.g., 0310003-XXX*		
BARCODE	Barcode	Char	50					*e.g. 12345678910*		
VISIT	Visit	Char	60				X	e.g. D1		
ANALYTE	Analyte	Char	9		X					
RESULT	Result	Char	50					numeric or '<LLOQ'		X
UNIT	Unit	Char	10		X					
MATRIX	Matrix	Char	50		X					
METHOD	Methodology	Char	50		X					

ANALYTE	UNIT	MATRIX	METHOD
BIOMARKER X	ng/mL	Serum	Elisa

The argenx Exploratory Biomarker DATA PROCESS

EBM Data Standards



CHALLENGES

Many different assays and vendors + datafiles in a different structure and format → jungle of data!

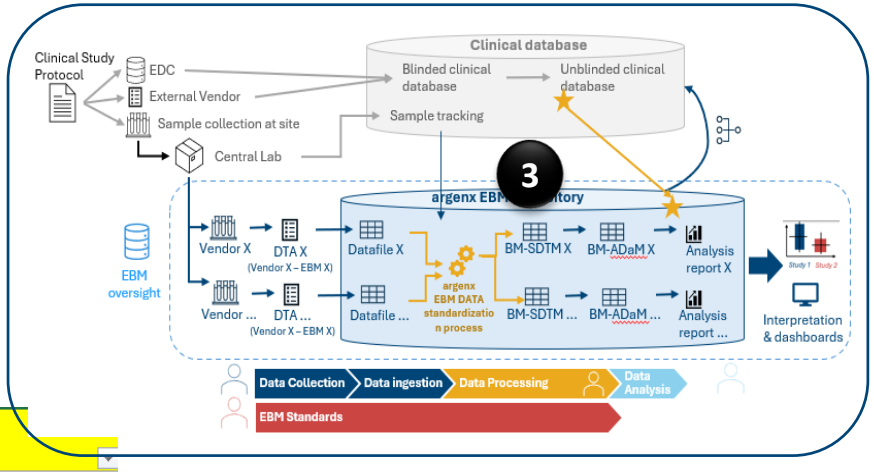
- laborious for data analysis
- difficult to compare or pool data across studies
- does not allow future advanced analytics and AI/ML
- not scalable for future growth and vision of argenx

ARGENX SOLUTION

Invest in end-to-end standards: **EBM Standards**

- **BM-SDTM model**
- **Biomedical Concept (BC) dictionaries/specializations**
- **Annotated DTA (aDTA) library**
- **BM-ADaM model**

The argenx Exploratory Biomarker DATA PROCESS



BM-SDTM model

Order	Dataset	Variable	Label	Data Type	Length	Codelist	Origin	Source	Role	SDTM DOMAIN	VARIABLE IMPLEMENTATION INSTRUCTION
1	BM	STUDYID	Study Identifier	tex	13		Protocol	Sponsor	Identifier	LB, CP, IS, MB, MI	contains the study or study number as defined in the protocol
2	BM	DOMAIN	Dom				Assigned	Sponsor	Identifier		Populate with "BM"
3	BM	USUBJID	Unic Iden				Predecessor		Identifier	LB, CP, IS, MB, MI	A subject number (SUBJID) is assigned for every screened subject. This means that subjects that re-screen, get a new SUBJID. The Previous Subject ID is collected on the CRF and is mapped to SUPPDC (QNAM=PRVSBJID). Only the
4	BM	SUBJID	Subj				Predecessor		Identifier	LB, CP, IS, MB, MI	SUBJID: is a derived variable; it is a concatenation of [STUDYID], [last SUBJID]
5	BM	NHOID	Non-host Organism ID	text	200		Collected	Vendor	Identifier	IS	Variable us variable is u testing.
6	BM	SEQ	Sequence Number	integer	3		Derived	Sponsor	Identifier	LB, CP, IS, MB, MI	uniquely ide
7	BM	GRPID	Group ID	text	200		Collected	Vendor	Identifier	LB, CP, IS, MB, MI	Variable is that is assigned by SDTM programmer to group related records of a sample within the same dataset.
8	BM						Collected	Vendor	Identifier	LB, CP, IS, MB, MI	Variable to map the Sample's unique identifier i.e. the barcode or requisition ID as present on the sample manifest. If the barcode AND the req ID are available, map the Req ID to --REFID and the barcode to '--CNTRID.
9	BM						Assigned	Sponsor	Identifier	LB, CP, IS, MB, MI	Variable to map the transfer file name to.
10	BM					CL_LBTESTCD_DEFINE CL_ISTESTCD_DEFINE CL_MBTESTCD_DEFINE CL_CPTESTCD_DEFINE	Assigned	Sponsor	Topic	LB, CP, IS, MB, MI	Al A ch nu s studies. a max length of 8 d only contain letters,
11	BM	TEST	Test or Examination Name	text	40	CL_LBTEST_DEFINE CL_ISTEST_DEFINE CL_MBTEST_DEFINE CL_CPTEST_DEFINE	Assigned	Sponsor	Synonym Qualifier	LB, CP, IS, MB, MI	The --TEST values are considered labels and are stored in title case (title case means to capitalize the first letter of every word except for articles, prepositions, and conjunctions) with a max length of 40, containing letters, numbers and special characters within the ASCII range 32-126.

Variables and their metadata are in sync with SDTM

Use SDTM IG variable implementation rules

Map all to 1 argenx custom “BM” domain

Maintain the link with CDISC SDTM

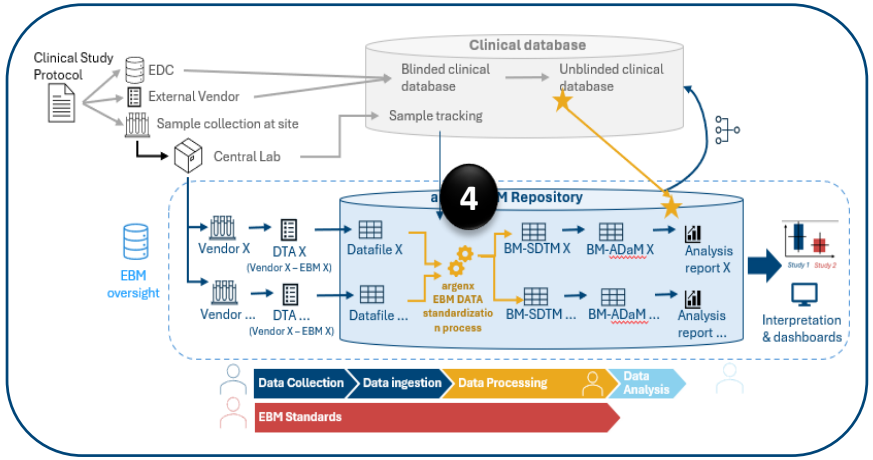
ARGENX SOLUTION

Consistent data standardization model between clinical (CSR) & exploratory biomarkers:

→ Easy conversion of biomarkers between clinical and exploratory datasets

→ Part of the clinical standards, mapping & programming can be easily re-used (and vice versa)

The argenx Exploratory Biomarker DATA PROCESS



EBM Biomedical Concepts (BC) / specializations

ARGENX SOLUTION

- Translate the science in SDTM
- Standardization & reproducibility

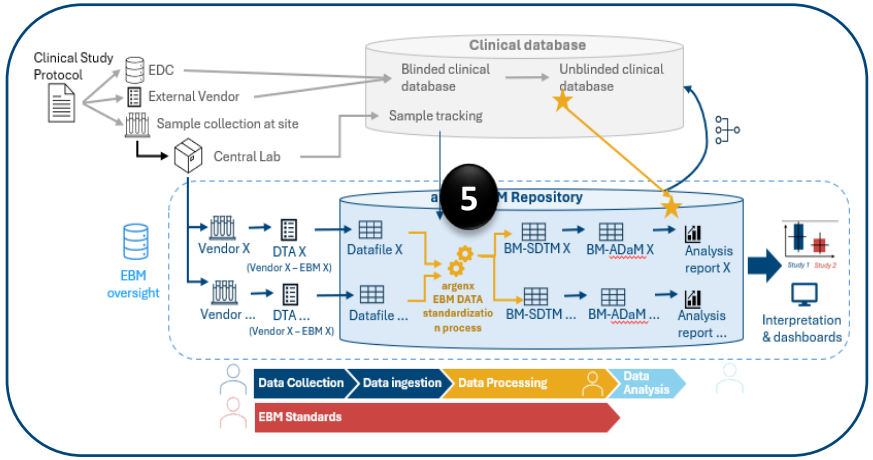
Dataset	VL Code	TESTCD	TEST	CAT	SCAT	SPEC	METHOD	ORRESU	SI-UNIT	Conversion Factor (SI UNIT)	CONV-UNIT	Conversion Factor (ConV UNIT)	RESTYP	RESSCL	MRKSTR	BDAGNT	TSTDTL
IS	VL1247	ATAB	Autoantibody	SEROLOGY		SERUM	CELL BASED BIOASSAY						PRESENCE OR THRESHOLD	NOMINAL		BIOMARKER 1	INTERPRETATION
IS	VL1254	ATAB	Autoantibody	SEROLOGY		SERUM	ELISA						PRESENCE OR THRESHOLD	NOMINAL		BIOMARKER 1	INTERPRETATION
IS	VL1399	ATAB	Autoantibody	SEROLOGY		SERUM	CELL BASED BIOASSAY						PRESENCE OR THRESHOLD	NOMINAL		BIOMARKER 2	INTERPRETATION
IS	VL827	ATAB	Autoantibody					U/mL	U/mL	1	U/mL	1	CATALYTIC CONCENTRATION	QUANTITATIVE		BIOMARKER 3	
LB	VL131	C2	Complement C2					mg/dL	ug/mL	1	mg/dL	1	MASS CONCENTRATION	QUANTITATIVE			
LB	VL7	C2	Complement C2	IMMUNOLOGY	COMPLEMENT	SERUM		Eq/mL	Eq/mL	1	Eq/mL	1	ARBITRARY CONCENTRATION	QUANTITATIVE			
CP	VL1525	BLYCELY	B-Lymphocytes/Lymphocytes	IMMUNOPHENOTYPING	WBC	BLOOD	FLOW CYTOMETRY	%	fraction of 1	0,1	%	1	RATIO	QUANTITATIVE	CD3-CD19+		
CP	VL1511	TLYHTLY	TLym Help/Tlym	IMMUNOPHENOTYPING	WBC	BLOOD	FLOW CYTOMETRY	%	fraction of 1	0,1	%	1	RATIO	QUANTITATIVE	CD3+CD4+		
CP	VL1521	TLCLY	TLym Cytx/Lym	IMMUNOPHENOTYPING	WBC	BLOOD	FLOW CYTOMETRY	%	fraction of 1	0,1	%	1	RATIO	QUANTITATIVE	CD3+CD8+		

--TEST/CD with other attributes that make the scientific concept

Amend with argenx CT if not available (yet)

Use CDISC CT if available

The argenx Exploratory Biomarker DATA PROCESS



aDTA (library)

ARGENX SOLUTION

- Raw to BM-SDTM mappings are documented in **annotated DTA (aDTA)**
  - Machine readable format
  - Vendor, biomarker and assay specific
- EBM **aDTA Standards library** for consistency and reproducibility

Raw data

Raw to SDTM mapping

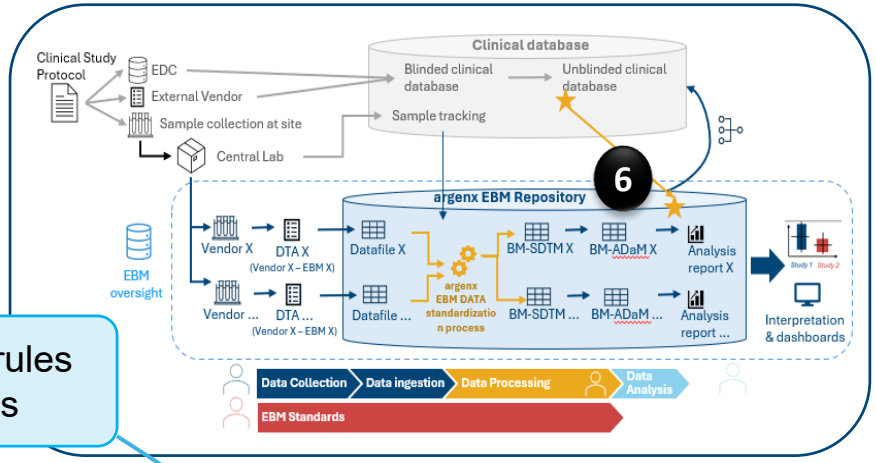
TRANSFER SPECIFICATIONS						BM-SDTM			
Transfer variable name	Transfer variable label	For mat	Anticipated maximum length	Allowed values	Populate for all records	TARGET_ DOMAIN	TARGET_ VARIABLE	MAPPING SPECIFICATIONS	Link to specific Test Concept (if applicable)
STUDYID	Study Identifier	text	200		X	LB	STUDYID	Copy	
SUBJID	Subject ID	text	200		X	LB	SUBJID	Copy (aligns with screenID) and convert to USUBJID format	
REFID	Reference ID	text	200		X	LB	REFID	Copy	
TESTCD	Test Short Name	text	8	see section Test Identifiers	X	LB	TESTCD	controlled terminology	see test identifiers tal
Analyte	Test Name	text	40	see section Test Identifiers	X	LB	TEST	controlled terminology	see test identifiers tal
ORRES	Result	text	200	<numeric result> or see section Codelists	X	LB	ORRES	Copy numeric results and NR, ALQ and BLQ into ORRES, leave empty when "NA" or "INS" If ORRES is "NA" or "INS" assign description to REASND (see Codelist)	

The argenx Exploratory Biomarker DATA PROCESS

BM-ADaM model

List of expected variables

General derivation rules for all BM ADaMs



ARGENX SOLUTION

- Exploratory Biomarker SAP entailing all information needed for analyses
  - Timing/windowing
  - Flagging
  - Biomarker specific derivations
- **BM-ADaM Common Data Model**
- Vendor – assay – biomarker code library

Order	Dataset	Variable	Label	Data Type	Format	Origin	Predecessor	VARIABLE IMPLEMENTATION INSTRUCTION
1	ADBM	STUDYID	Study Identifier	text		Predecessor	SDTM.BM	
2	ADBM	USUBJID	Unique Subject Identifier	text		Predecessor	SDTM.BM	
3	ADBM	SUBJID	Subject Identifier	text		Predecessor	SDTM.BM	
4	ADBM	INDIC	Indicator	text		Derived		Copy from BM._IND_ when available. Set to "hv" when healty volunteers samples are present.
9	ADBM	ADTM	Analysis Datetime	integer	DATETIME	Derived		Copy from BM.BMDTC and convert to numeric with the datetime format when BM.BMDTC contains date and time.
10	ADBM	ADT	Analysis Date	integer	DATE9	Derived		Copy date part of BM.BMDTC and convert to numeric with Date9 format.
12	ADBM	ADY	Analysis Relative Day	integer		Derived		Copy from BM.BMDT or calculate as ADSL.TRTSDT - ADT when ADT is on or after TRTSDT or calculate as ADSL.TRTSDT - ADT + 1 when ADT is before TRTSDT.
15	ADBM	AVISIT	Analysis Visit	text		SAP		
16	ADBM	AVISITN	Analysis Visit Numeric	float		SAP		
17	ADBM	AVISIT2	Analysis Visit 2	text		Derived		Derivation is done per SAP or remarks from statistician
18	ADBM	AVISIT2N	Analysis Visit 2 Numeric	float		Derived		Numeric counterpart of AVISIT2
21	ADBM	ANCHRDT	Anchor Date	integer	DATE9	SAP		
22	ADBM	AWTARGET	Analysis Window Target	text		SAP		
23	ADBM	AWTDIFF	Analysis Window Diff from Target	integer		Derived		Calculated as ADY - AWTARGET
24	ADBM	AWLO	Analysis Window Beginning Timepoint	integer		SAP		
25	ADBM	AWHI	Analysis Window Ending Timepoint	integer		SAP		
26	ADBM	AWADY	Analysis Relative Day for Windowing	integer		Derived		Calculated as ADT - ANCHRDT
28	ADBM	APHASE	Analysis Phase	text		SAP		
29	ADBM	APHASEN	Analysis Phase Numeric	integer		SAP		
30	ADBM	APERIOD	Analysis Period Numeric	integer		SAP		
31	ADBM	APERIODC	Analysis Period Character	text		SAP		
42	ADBM	PARAM	Parameter	text		Derived		Concatenation of all SDTM variables needed to create a unique test parameter, such as BM.BMTEST, BM.BMSTRESU, BM.BMBDAGNT, BM.BMTSTDTL, BM.BMSYM
43	ADBM	PARAMCD	Parameter Code	text		Derived		Abbreviated PARAM code, matching the input of PARAM to give a 1:1 relation between PARAM and PARAMCD, preferably less than 8 characters

The argenx Exploratory Biomarker DATA PROCES

SDTM data machinery

SOURCE_DS	SOURCE_VAR	TARGET_	TARGET_VA	SPECIFICATION	FUNCTION
LAB.VENDOR1	REQUISITION_ID	BM	BMREFID	Copy from source data	COPY
LAB.VENDOR1	SCREEN_ID	BM	SUBJID	Copy from source data	COPY
LAB.VENDOR1	VISIT	BM	VISIT	Copy from source data	COPY
LAB.VENDOR1	COLLECTION_DATE	BM	BMDTC	Copy from source data	COPY
LAB.VENDOR1		BM	STUDYID	Assign STUDYID to 'CDISC-ST001'	ASSIGN [CDISC-ST001]
LAB.VENDOR1		BM	SCRDOM	Assign SRCDOM to 'LB'	ASSIGN [LB]
LAB.VENDOR1	BARCODE	BM	ENTPID	Copy from source data	COPY
LAB.VENDOR1	PLATE_ID	BM	BMRUNID	Copy from source data	COPY
LAB.VENDOR1	DELAY_SAMPLE_STORAGE_MIN	BM	DSTIM	Copy from source data	COPY
LAB.VENDOR1	TIME_BETWEEN_SAMP_ANALYS	BM	CATIM	Copy from source data	COPY
LAB.VENDOR1	COMMENTS	BM	RSDSC	Copy the first 200 characters of COMMENTS to BMRSDSC	FUNCTION [if length(strip(#SOURCE#)) <= 200 then #TARGET# = strip(#SOURCE#); else if length(strip(#SOURCE#)) > 200 then #TARGET# = substr(strip(#SOURCE#), 1, 200);]
LAB.VENDOR1	COMMENTS	BM	RSDSC1	Copy characters 201-400 of COMMENTS to BMRSDSC1	FUNCTION [if 200 < length(strip(#SOURCE#)) <= 400 then #TARGET# = substr(strip(#SOURCE#), 201); else if length(strip(#SOURCE#)) > 400 then #TARGET# = substr(strip(#SOURCE#), 201, 200);]
LAB.VENDOR1	BM1_AUML	BM	BMORRES	Copy from source data	STACK1 [#COPY#;]
LAB.VENDOR1	BM1_AUML	BM	BMSTAT	When BM1_AU_ML is missing, assign BMSTAT to 'NOT DONE'	STACK1 [IF missing(#SOURCE#) THEN #TARGET# = "NOT DONE";]
LAB.VENDOR1	BM1_AUML	BM	BMREASND	When BM1_AU_ML copy COMMENT to BMREASND	STACK1 [IF missing(#SOURCE#) THEN #TARGET# = comments;]
LAB.VENDOR1	BM1_AUML	BM	BMTESTCD	Assign BMTESTCD to 'BM1'	STACK1 [#ASSIGN[BM1]#;]
LAB.VENDOR1	BM1_AUML	BM	BMTEST	Assign BMTEST to 'Biomarker 1'	STACK1 [#ASSIGN[Biomarker 1]#;]
LAB.VENDOR1	BM1_AUML	BM	BMORRESU	Assign BMORRESU to 'AU/mL'	STACK1 [#ASSIGN[AU/mL]#;]
LAB.VENDOR1	BM99_AUML	BM	BMORRES	Copy from source data	STACK2 [#COPY#;]
				When BM99_AUML is missing, assign BMSTAT to 'NOT DONE'	STACK2 [IF missing(#SOURCE#) THEN #TARGET# = "NOT DONE";]
				When BM99_AUML is missing, assign BMSTAT to 'NOT DONE'	STACK2 [IF missing(#SOURCE#) THEN #TARGET# = comments;]
				Assign BMTESTCD to 'BM99''	STACK2 [#ASSIGN[BM99]#;]
				Assign BMTEST to 'Biomarker 99'	STACK2 [#ASSIGN[Biomarker 99]#;]
				Assign BMORRESU to 'AU/mL'	STACK2 [#ASSIGN[AU/mL]#;]

VENDOR 1

ELISA = IS

TEST	TESTCD	TSTDTL	BDAGNT	CAT	SCAT	ORRES	ORRESU	STRESC	METHOD	SPEC	SPCCND	GRPID
IgG Autoantibody	ATIGGAB	TITER	BM1	SEROLOGY	AUTOANTIBODY	3444	titer		ELISA	SERUM		SAMPLEID
IgG1 Autoantibody	ATIGG1AB	INTERPRETATION	BM1	SEROLOGY	AUTOANTIBODY	+		POSITIVE				
IgG2 Autoantibody	ATIGG2AB	INTERPRETATION	BM1	SEROLOGY	AUTOANTIBODY	-		NEGATIVE				
IgG Autoantibody	ATIGGAB	OPTICAL DENSITY	BM1	SEROLOGY	AUTOANTIBODY	1,327						
IgG1 Autoantibody	ATIGG1AB	OPTICAL DENSITY	BM1	SEROLOGY	AUTOANTIBODY							
IgG2 Autoantibody	ATIGG2AB	OPTICAL DENSITY	BM1	SEROLOGY	AUTOANTIBODY							
Autoantibody	ATAB	INTERPRETATION	BM1	SEROLOGY	AUTOANTIBODY	Positive		POSITIVE				
Autoantibody	ATAB	INTERPRETATION		SEROLOGY	AUTOANTIBODY	NF155						

IHC = CP

TEST	TESTCD	TSTDTL	BDAGNT	CAT	SCAT	ORRES	ORRESU	STRESC	METHOD	SPEC	SPCCND	GRPID
Autoantibody	ATAB	LOCALIZATION		AUTOIMMUNITY		*TEXT*			IHC	NERVE	TEASED	SAMPLEID
Autoantibody	ATAB	ISOTYPE		AUTOIMMUNITY		*TEXT*						

CBA = IS

TEST	TESTCD	TSTDTL	BDAGNT	CAT	SCAT	ORRES	ORRESU	STRESC	METHOD	SPEC	SPCCND	
Autoantibody	ATAB	INTERPRETATION	BM1	SEROLOGY	AUTOANTIBODY	-		NEGATIVE	CELL BASED ASSA	SERUM		
Autoantibody	ATAB	ISOTYPE		SEROLOGY	AUTOANTIBODY	IgG2						

VENDOR 2

ELISA

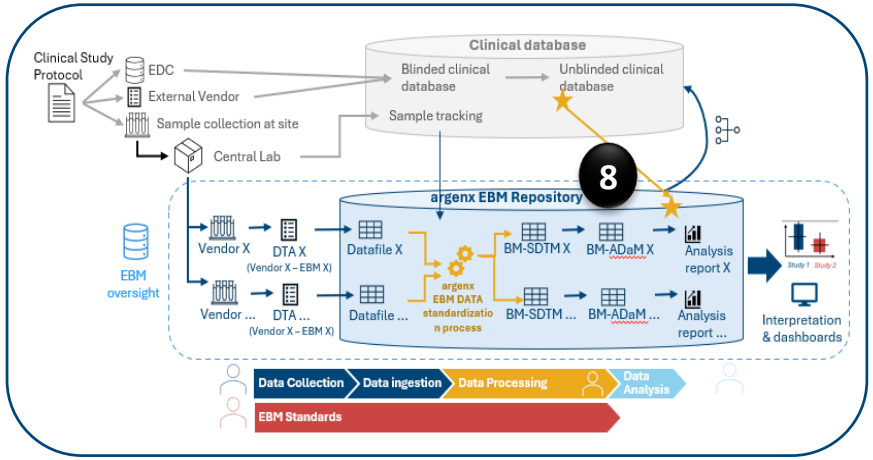
TEST	TESTCD	TSTDTL	BNDAGNT	CAT	SCAT	ORRES	ORRESU	STRESC	METHOD	SPEC	SPCCND	GRPID
IgG Autoantibody	ATIGGAB		BM99	SEROLOGY	GLYCOLIPID	3444	FIU	3444	GLYCOLIPID ARRA	SERUM		SAMPLEID
IgM Autoantibody	ATIGMAB			SEROLOGY								
IgA Autoantibody	ATIGAAB			SEROLOGY								

ARGENX SOLUTION

- Mapping engine to create BM-SDTM in SAS LSAF
- Variable SRCDOM
- Clinical DM, SV and TV
- Taking into account EBM specific information
  - Sample storage time
  - Analysis datetime
- Combination of domains

The argenx Exploratory Biomarker DATA PROCESS

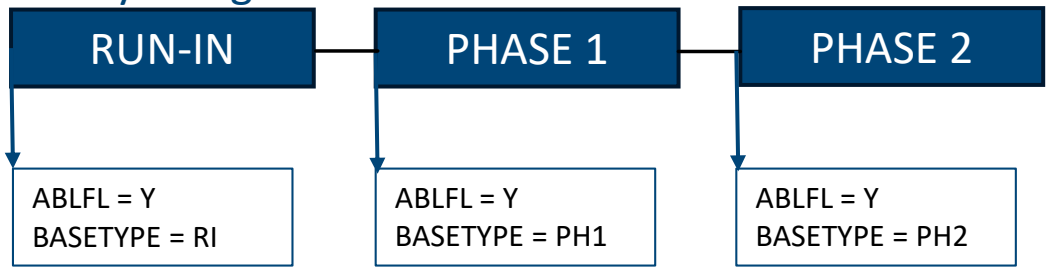
ADaM data machinery



ARGENX SOLUTION

- Consistent derivation analysis flags across studies / biomarkers
- Clinical ADSL to derive timing variables
- Multiple baselines (BASETYPE)
- Multiple AVISIT variables
- Re-use code from clinical ADaMs
- Splitting of BM-ADaM dataset

Study Design:

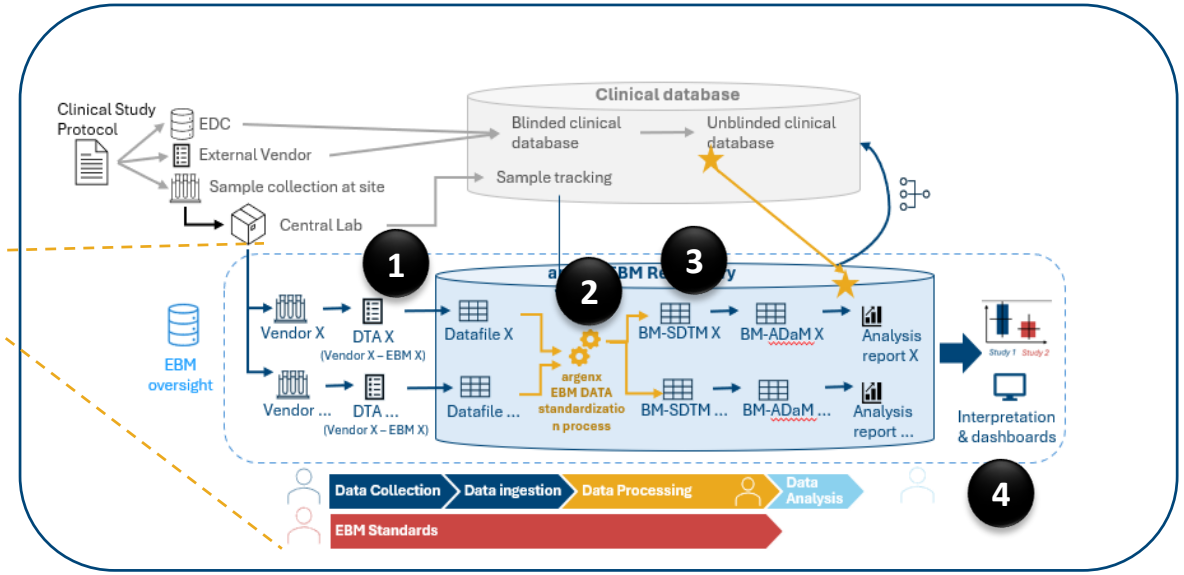


Biomarker	VISIT	AVISIT	AVISIT2	AVISIT3
BM1	Screening	Baseline	Baseline	Baseline
BM1	VISIT 10	Week 20	Week 24	
BM99	End of Run In	Baseline	Baseline phase 1	Baseline phase 1
BM99	VISIT 10	Week 20	Start of phase 2	Baseline phase 2

The future of Exploratory Biomarkers at argenx

Build automation in this non-clinical EBM dataflow

argenx raw-to-end EBM data standardization process and tools



1
- Standardized data file structure for re-used vendor/biomarker combo's
- Automated data ingestion checks of test/production file with the DTA.

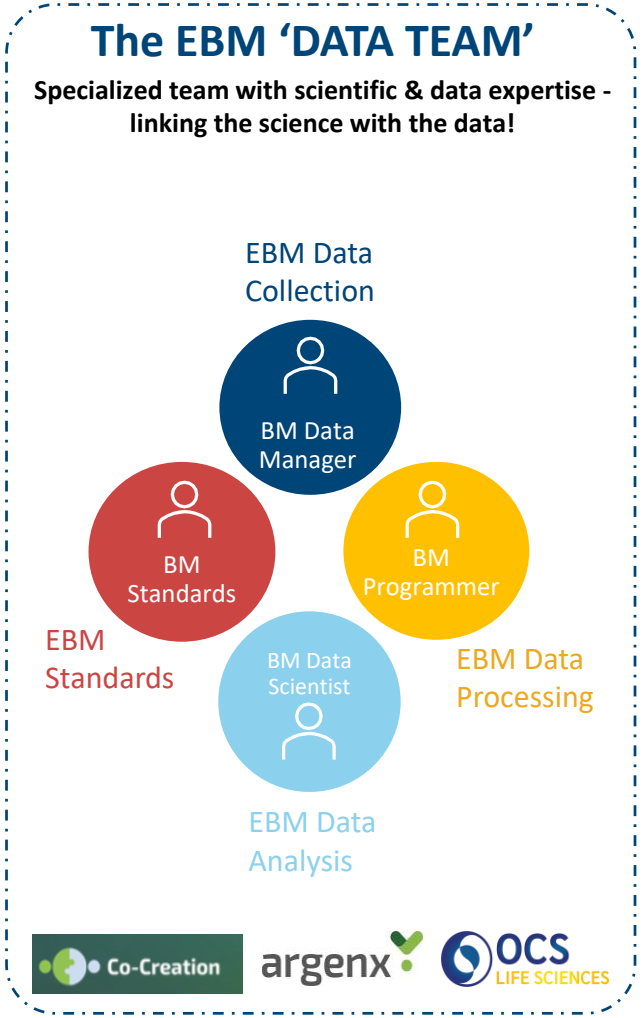
2
- Automated population of mapping engine by reading aDTA library → (semi) automated raw to BM-SDTM mapping
- aDTA library: future use in AI/ML BM-SDTM mapping predictions for new biomarkers and vendors

3
- As BM-SDTMs continue to be more standardized → ADaM programming can be more automated

4
- Standardized data input files allow for EBM data dashboards for data scientist/end-users

Summary and take-home messages

- When we started working with exploratory biomarkers there was no structure in:
  - Collection
  - Storage
  - Conversion
  - Analyses
- Need for standardized process was clear
  - More biomarkers are coming
  - Need for ALCOA++ and FAIR data
- Exploratory biomarker team was set up along with
  - EBM repository
  - Standardized DTA template
  - Annotated DTA (+ library)
  - BM-SDTM + BC concepts
  - BM-ADaM
- Achieved a lot, and ready for the future!
  - More automation and standardization



Thank You!

Acknowledgements

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