



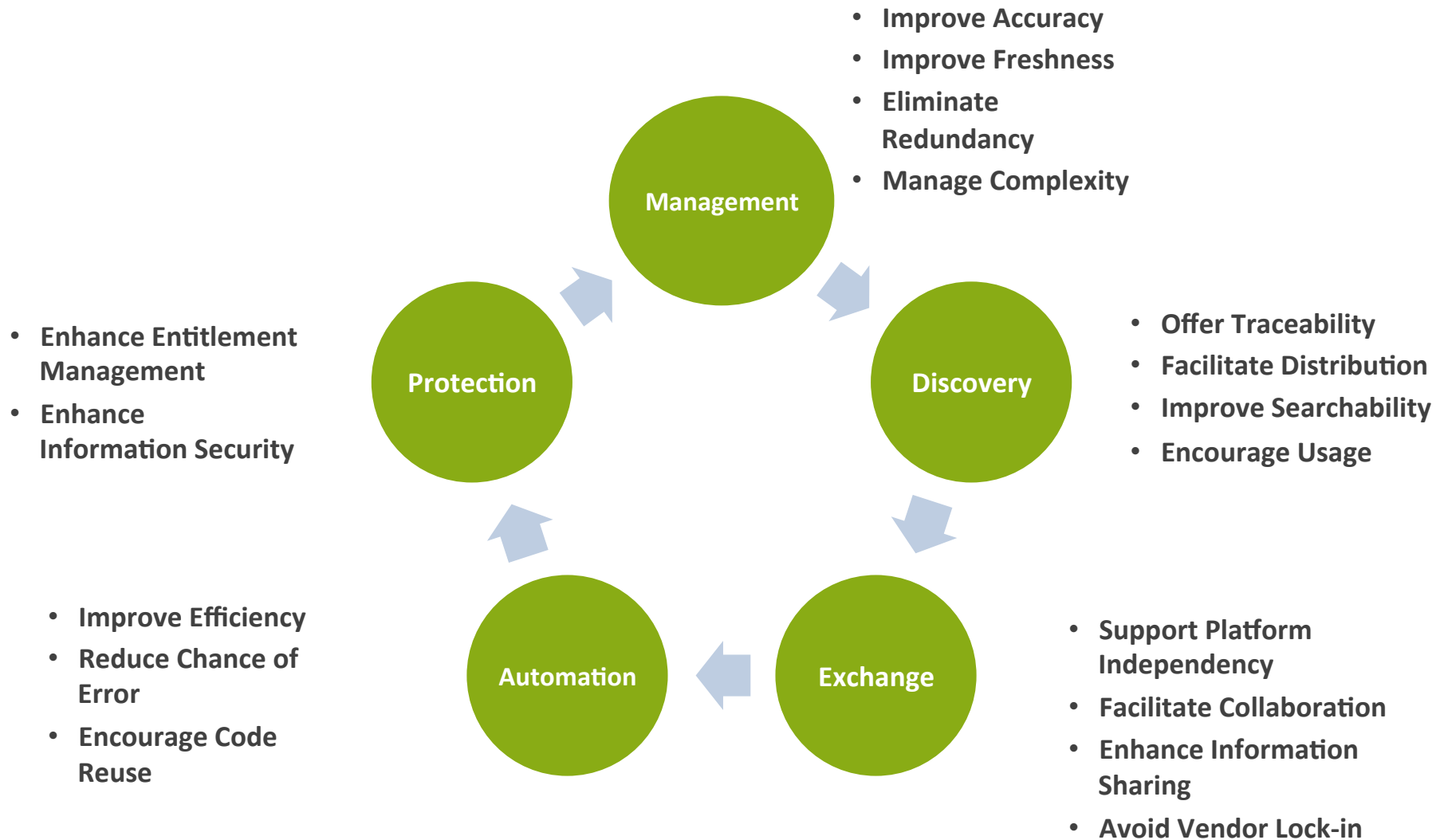
How do companies use metadata driven programming for SDTM, ADaM, and Define XML Creation?

PhUSE Single Day Event - Bridgewater

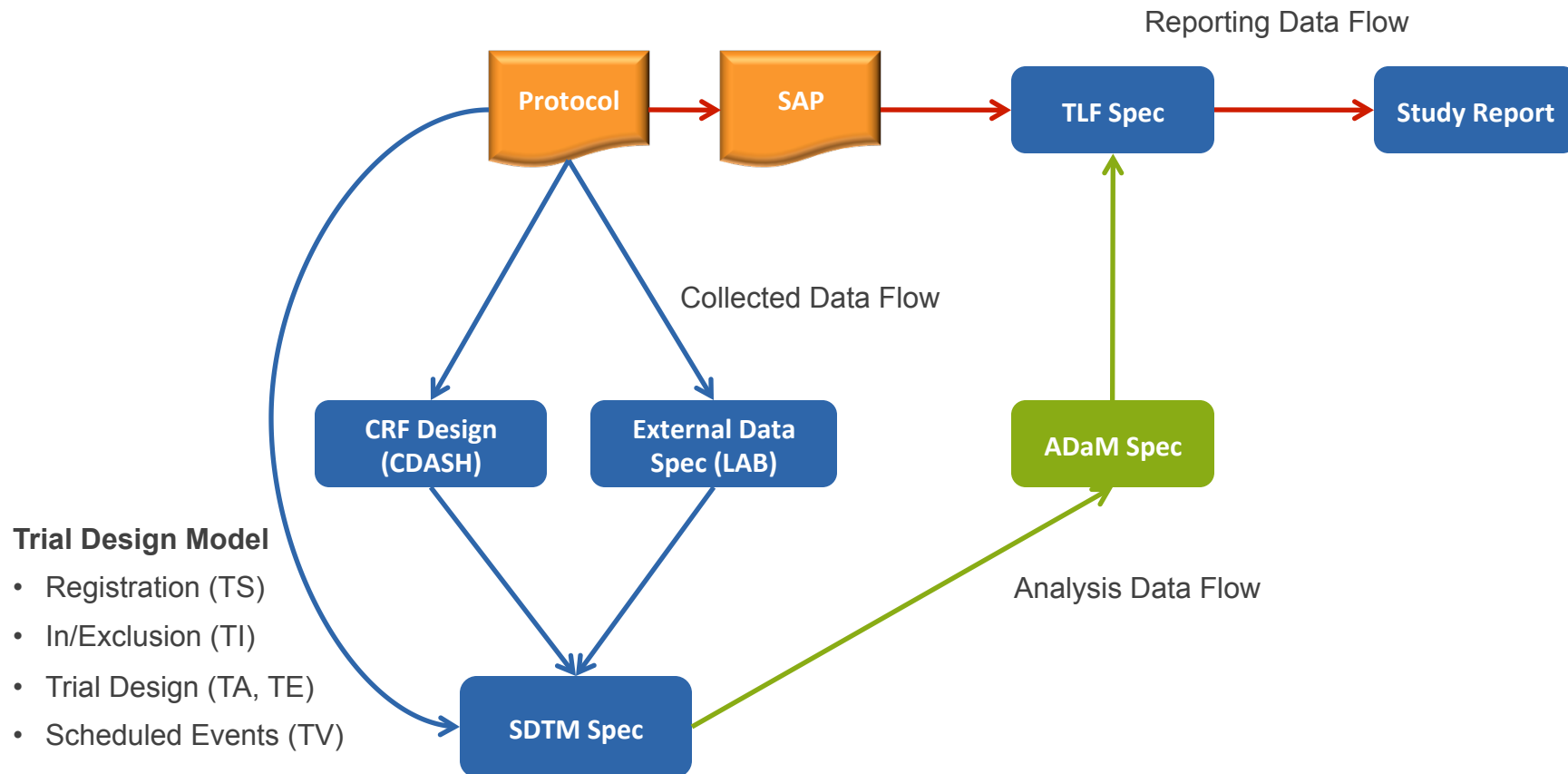
- **Traceability and Metadata**
- **Metadata Flow**
- **Metadata Development**
- **Metadata Enabled Data Processing**
 - Legacy Data Conversion
 - End-to-End Data Management
- **Metadata Management**
- **Implementation Example**
- **Discussion**

- Traceability is a major concern for the FDA. Traceability means understanding the relationship between the results and the source. It facilitates transparency and is an essential component for building confidence in all stages of clinical information processing.
- Building traceability is establishing the path between an element and its immediate predecessor.
- **Metadata Traceability:** provides an explanation of how any downstream information has been created from its predecessors by describing **the algorithms and deviations used**.
- **Data Point Traceability:** provides **data lineage** of how downstream records are related to the predecessor records(s): are the records originating from source or are these derived records.

IMPORTANCE OF METADATA



METADATA FLOW IN CLINICAL TRIAL DATA PROCESSING



METADATA DEVELOPMENT FRAMEWORK

Standards

- Establish Conceptual Models
- Establish CRF, SDTM, and ADaM Standards
- Store in MDR
- Governed and Maintained

Library

- Establish Libraries at Different Levels in Different Areas
- Library would grow to incorporate new scenarios
- CRF Libraries, SDTM Templates, ADaM Templates, TLF Templates

Design

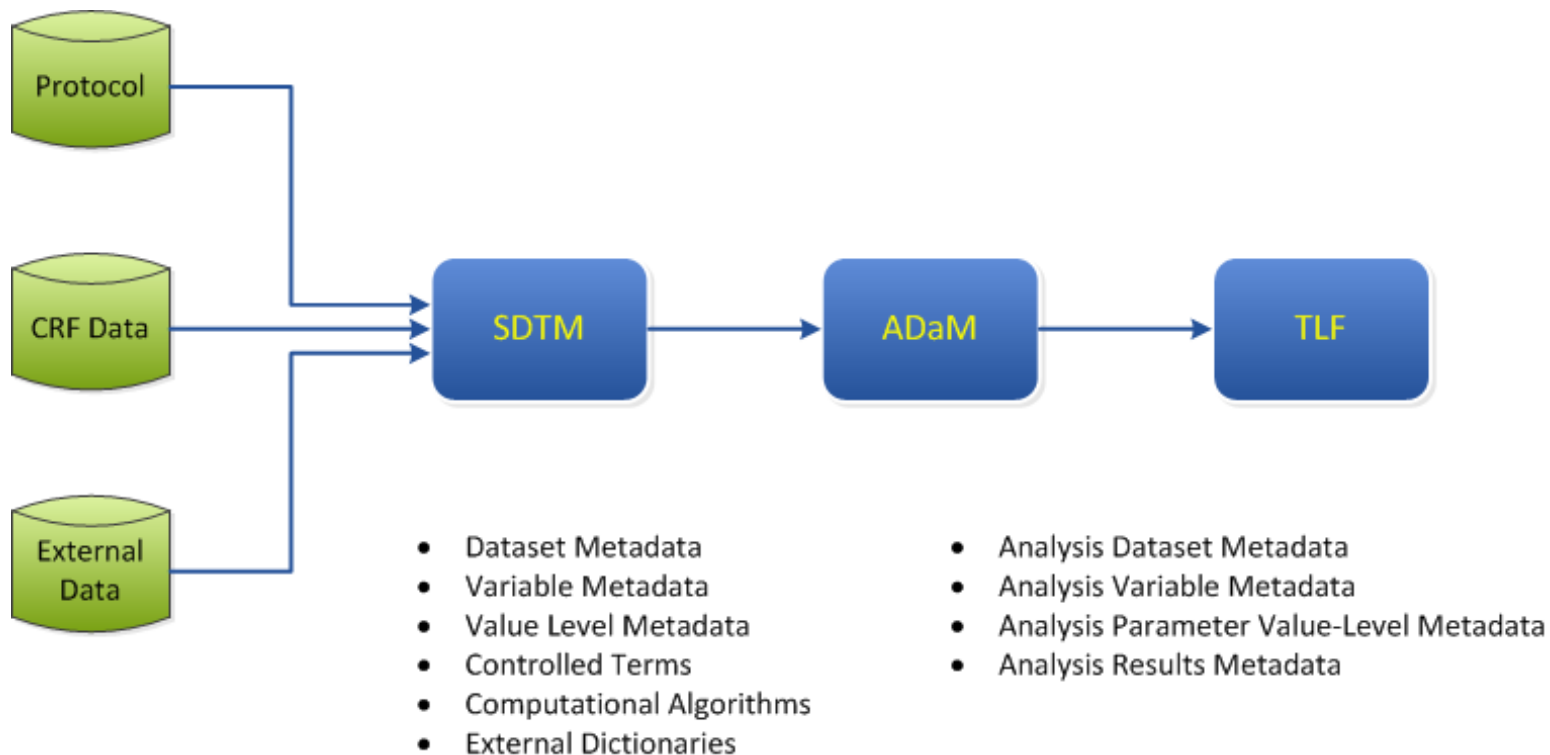
- Extract Metadata from Protocol and SAP
- Study Activities drive CRF Design
- Study Endpoints drive Variable Derivation
- Study Analysis drives TLF Design, ADaM Structure

Customize

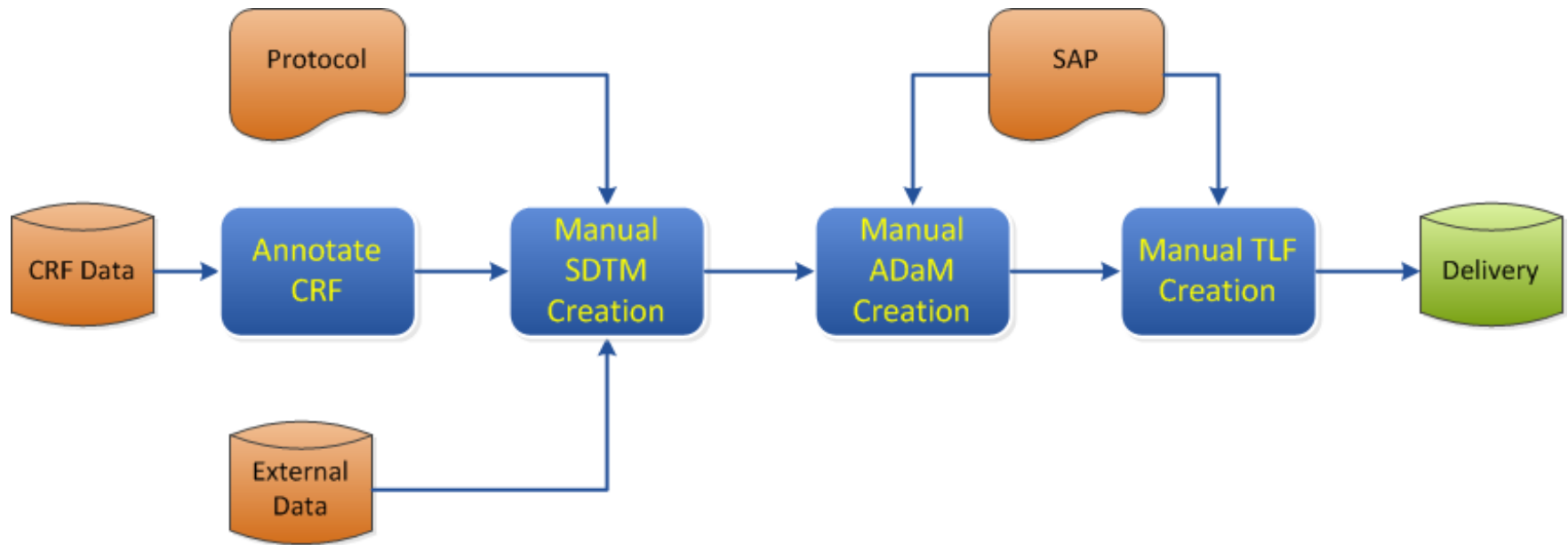
- Study Specific Configuration
- Conformance and Deviation can be monitored
- Mechanism exists to publish to Library

- **Legacy Data Conversion**
 - Convert existing studies to follow CDSIC standards
 - Lessor initial efforts, lessor disruption of existing processes
 - Lessor dependency on CDISC standards during study startup
 - Lessor control over metadata lineage
 - More manual and repeated work to develop metadata
- **End-to-End Metadata Management**
 - Ideal situation, but requires significant initial efforts
 - Depends on CDISC standard development
 - Study Design -> Study Conduct -> Study Analysis -> Study Submission
 - Best utilization of metadata
 - Consistency
 - Accuracy
 - Efficiency

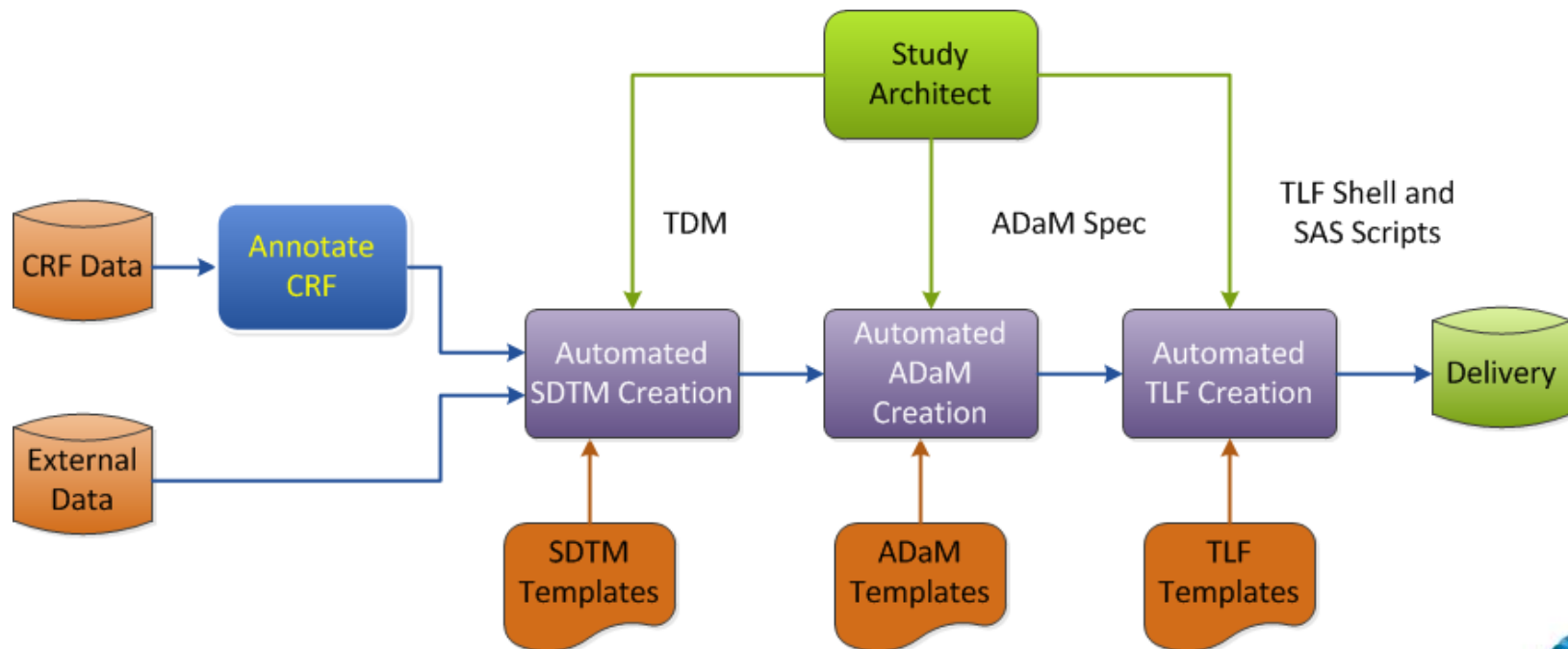
REQUIRED METADATA – LEGACY DATA CONVERSION



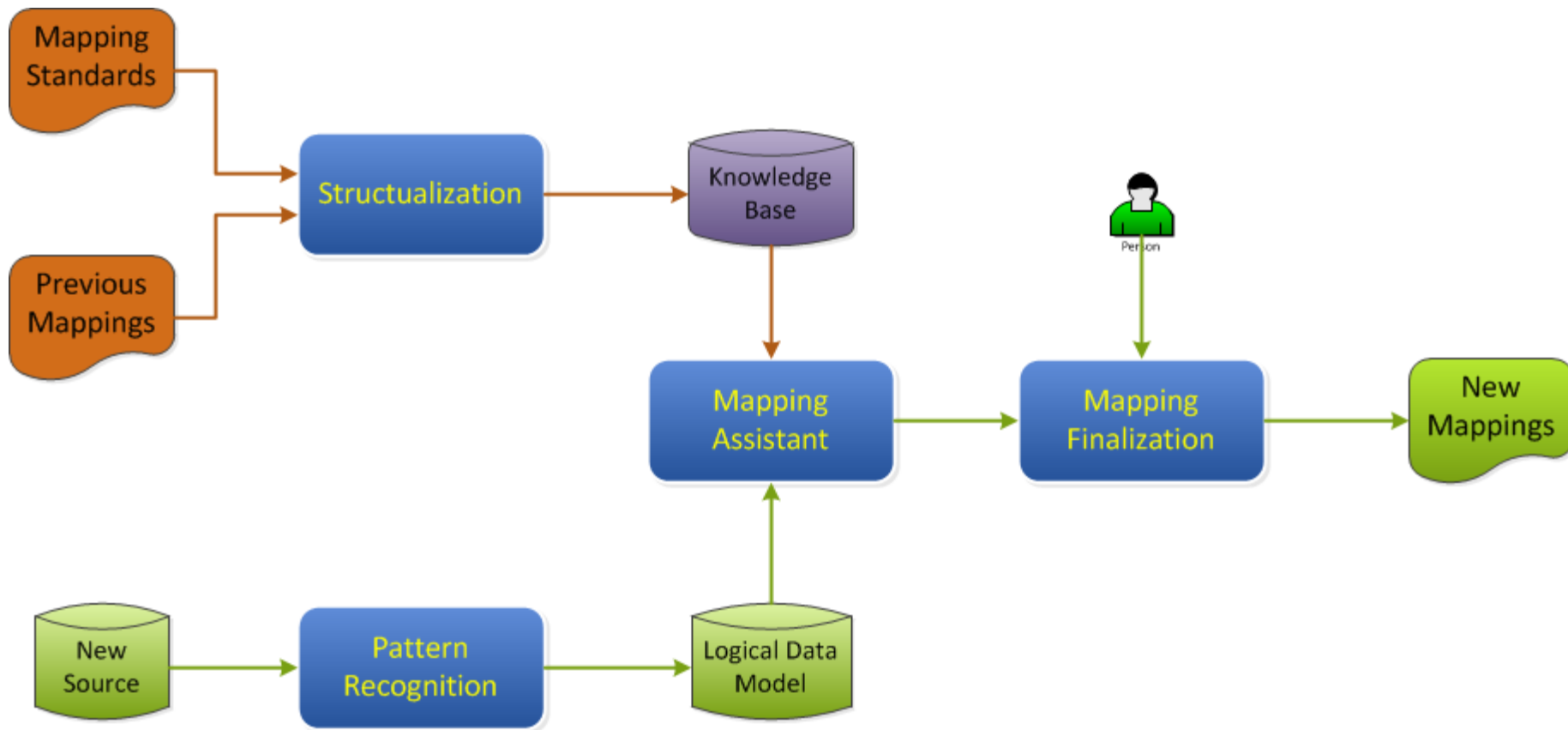
TYPICALLY IT'S A MANUAL PROCESS



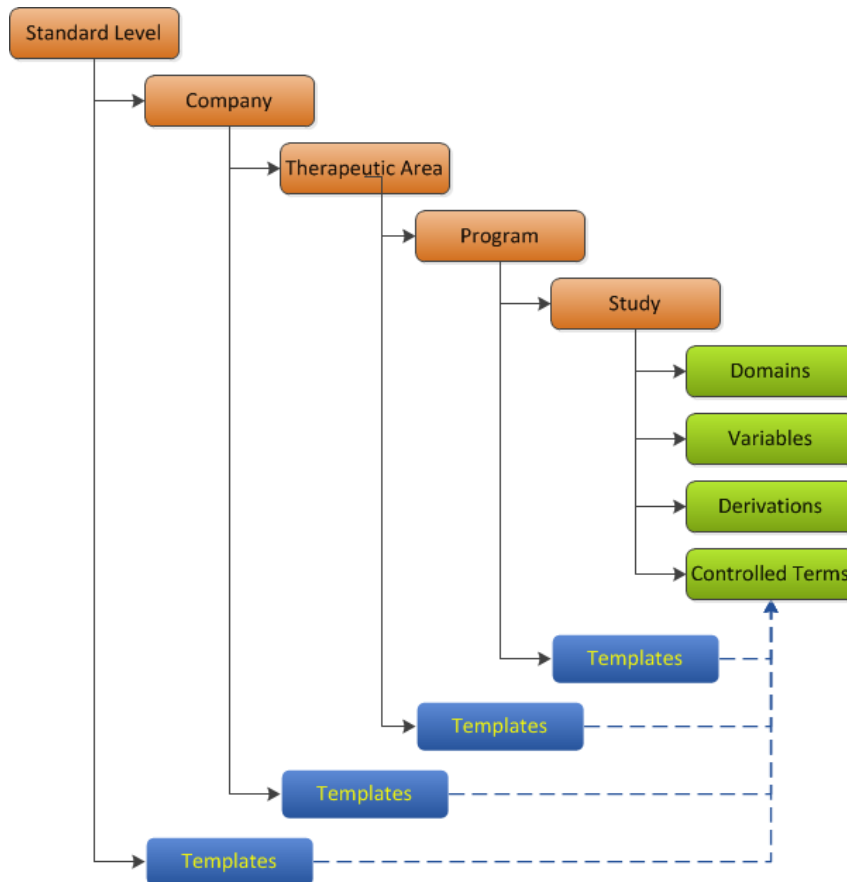
METADATA EMPOWERED LEGACY DATA CONVERSION



KNOWLEDGE-BASE ASSISTED DATA STANDARDIZATION



METADATA MANAGEMENT



Metadata Repository Structure

- Templates can be used for mapping reuse
- Hierarchical structure help to provide granular standardization while maintain consistency
- New derivations can be generated based on auto-matching of standards/templates at different levels
- Metadata need to be managed by dedicated team and governing processes

SDTM ANNOTATED CRFs

The screenshot displays the 'Mapping sCRF' application interface, which is used for mapping clinical trial data from a source CRF to a target SDTM CRF.

Main Window: Mapping sCRF

Top Menu Bar: Undo, Redo, CT&FT, DV&DF, RelRec, Save, Summary, Submit.

Left Panel: Annotated CRF

Right Panel: SDTM CRF

Bottom Panel: Domain View

Domain View Hierarchy:

- DM<Mapper1/Working>
 - \$ STUDYID
 - \$ DOMAIN
 - \$ USUBJID
 - \$ SUBJID
 - \$ RFSTDT
 - \$ RFENDTC
 - \$ RFXSTDT
 - \$ RFXENDTC
 - \$ RFICDT
 - \$ RFPENDTC
 - \$ DTHDT
 - \$ DTHFL
 - \$ SITEID
 - \$ INVID
 - \$ INVNAM
 - \$ BRTHDT
 - \$ AGE
 - \$ AGEU
 - \$ SEX
 - \$ RACE
 - \$ ETHNIC
 - \$ ARMCD
 - \$ ARM
 - \$ ACTARMCD
 - \$ ACTARM
 - \$ COUNTRY
 - \$ DMDTC
 - \$ DMDY
- DS<Mapper1/Working>

Form Comparison:

39755 : Demographics (Demog) DOMAIN - DM

39755 : Demographics (Demog)

Fields:

- Screening Number (read-only) Z_SCRNUM
- Randomization Number (Subject ID from IVRS) (hidden) Z_RADNUM
- Subject/Screening ID (hidden) (all datasets) SUBJID
- Initials SUBJINIT
- Date of Birth BRTHDTN, BRTHDTC
- Gender SEX
- Date of Informed Consent CONSDTN, CONSDTC
- Ethnicity ETHNIC
- Primary Race RACE

Footer: Ready

DATA FLOW CONSTRUCTION

The screenshot displays the 'Data View & Data Flow' application window. On the left, a 'Raw Data Structure' pane lists source datasets: AE, CM, DA, DC, DEATH, DM, DS, EG, EX, HU, IE, IM, INVCRF, IXRS, IXRS_RAW, LB, LBCRF, MH, PE, PERF, QLAB, SG, SS, STRATA, SU, SV, and VS. The main canvas shows a 'Data Flow' diagram with a 'ProcessArea' set to 'DM'. It includes a toolbar with various processing icons, a 'Build' button, and an 'Execute' button. The diagram shows data flowing from source datasets through intermediate processing steps (DM_AG_EX, DM_AG_IXRS, DM_JN) to a final 'DM' dataset. Red callout boxes highlight key features: 'Source Datasets' (pointing to the left pane), 'Comprehensive processing types' (pointing to the toolbar), 'Drag & Drop to design canvas' (pointing to the diagram area), 'Intermediate testing' (pointing to the 'Execute' button), 'Data Flow Diagram defines dataset level relationships' (pointing to the diagram flow), and 'Preview of data' (pointing to the data table at the bottom).

Source Datasets

Comprehensive processing types

Drag & Drop to design canvas

Intermediate testing

Data Flow Diagram defines dataset level relationships

Preview of data

No.	STUDYID	SUBJID	SITEID	VISIT	VISITNUM	VISITDTN	DOMAIN	Z_AEYN	AESQ	AETERM	AEDECOD
1	207	207-5001-101	5001	ALL VISITS	95		AE	YES	1	ANXIETY	ANXIETY
2	207	207-5001-101	5001	ALL VISITS	95		AE	YES	2	COUGH	COUGH
3	207	207-5001-101	5001	ALL VISITS	95		AE	YES	3	FEVER	PYREXIA
4	207	207-5001-101	5001	ALL VISITS	95		AE	YES	4	SPLIT LIM PRODUCTION	PRODUCTIVE COUGH

VARIABLE LEVEL TRANSFORMATION DEFINITION

The screenshot displays the Target Designer (DM) interface for defining variable-level transformations. The interface is divided into three main sections:

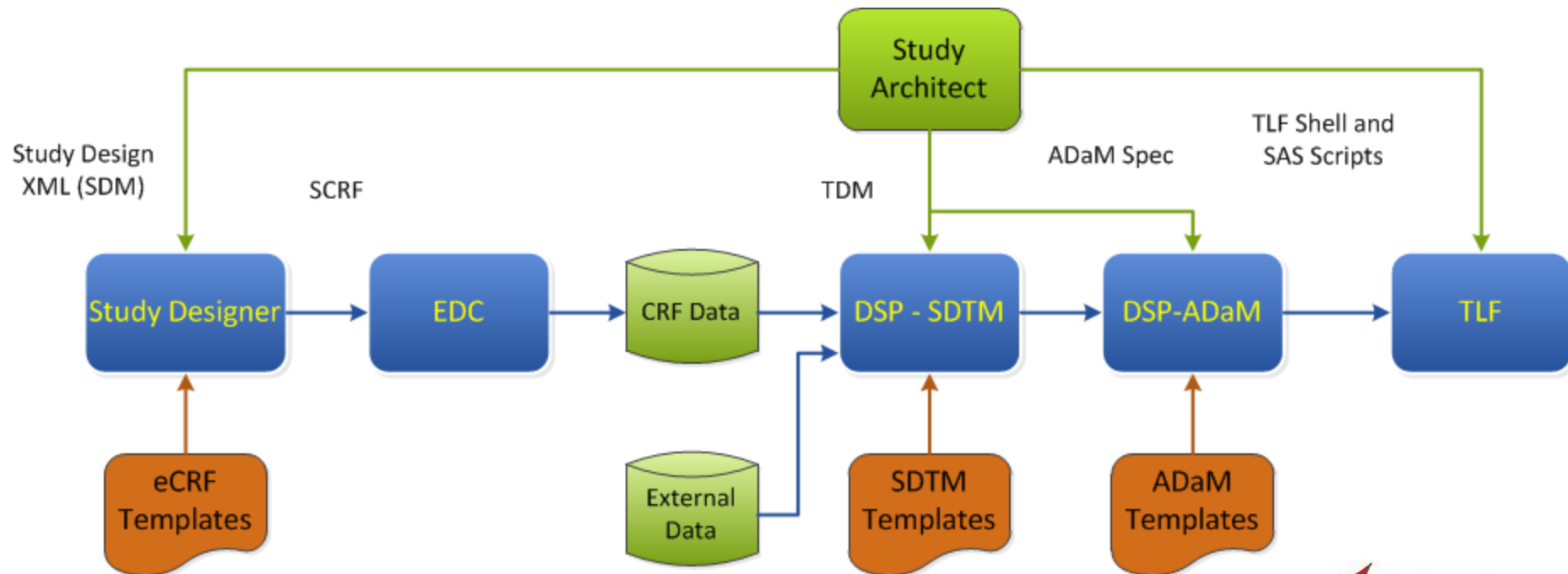
- Source Elements:** A list of source data elements on the left, including STUDYID, DOMAIN, USUBJID, SUBJID, RFSTDTC, RFENDTC, RFXSTDTC, RFXENDTC, RFICDTC, RFPENDTC, DTHDTC, DTHFL, SITEID, INVNAM, BRTHDTC, AGE, and AGEU. The element RFXSTDTC is selected.
- Mapping Rule Editor:** A central pane showing a list of derivation rules. The selected rule is:


```
1 if(Idm.DM.RFXSTDTC != "") Idm.DM.RFXSTDTC else
2 Idm.DM.RFICDTC
```

 Below the list, the 'Warning' tab is active, showing the rule name 'RFXSTDTC' and the rule text 'if(Idm.DM.RFXSTDTC != "") Idm.DM.RFXSTDTC'. The 'Error message' field is empty.
- Target Elements:** A list of target data elements on the right, including STUDYID, DOMAIN, USUBJID, SUBJID, RFSTDTC, RFENDTC, RFXSTDTC, RFXENDTC, RFICDTC, RFPENDTC, DTHDTC, DTHFL, SITEID, INVNAM, BRTHDTC, AGE, and AGEU. The element RFSTDTC is selected.

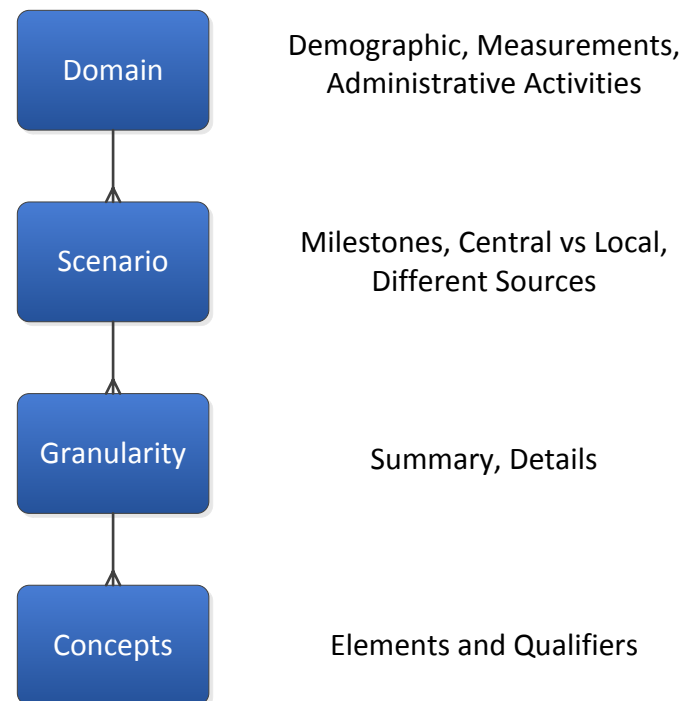
At the bottom of the interface, there are 'OK' and 'Cancel' buttons. A red box labeled 'Element and rule property window' points to the 'Warning' tab in the Mapping Rule Editor.

METADATA EMPOWERED END-TO-END METADATA Flow

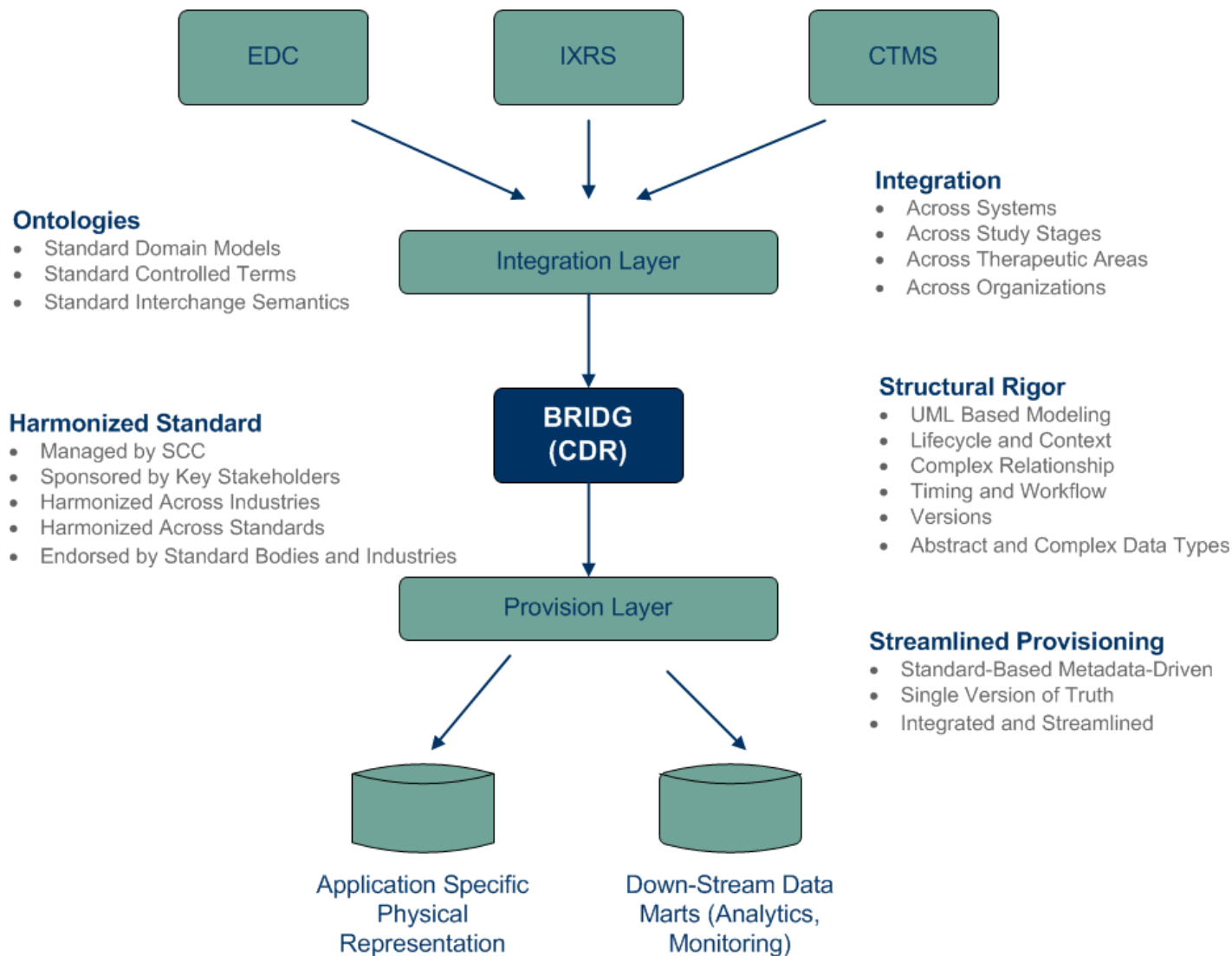


STEP 1 – ESTABLISH STANDARDS

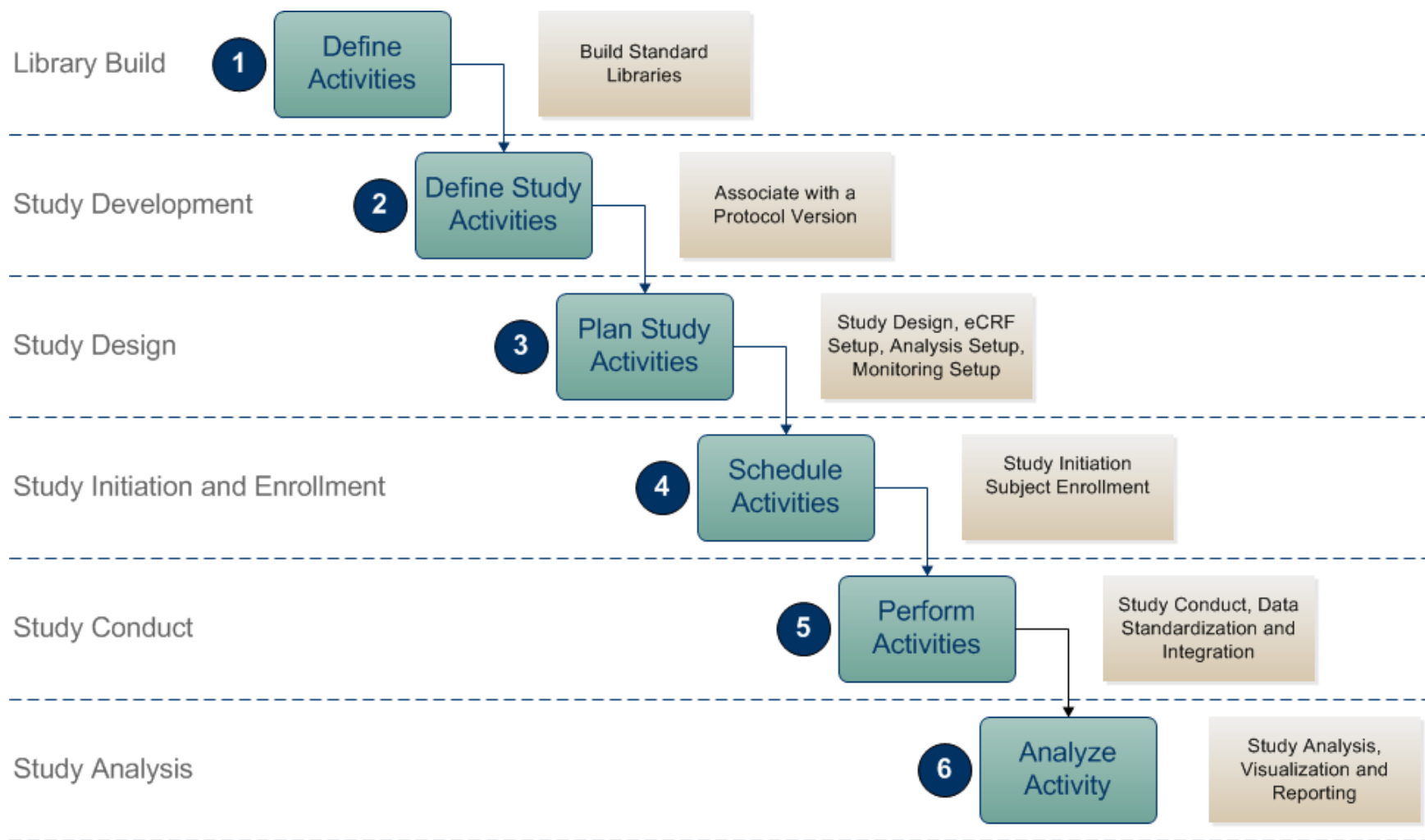
- **Define Conceptual Model**
 - Leverage BRIDG concept
 - Cover all data origins
 - Trial Design
 - Protocol
 - Collected Subject Data
 - Derived Subject Data
 - Cover all trial stages
 - Study Design (TDM -> SDTM)
 - Study Conduct (CDASH -> SDTM)
 - Study Analysis (ADaM)
 - Study Reporting (TLF)
 - Use Controlled Term to add semantics
- **Define CRF, SDTM, and ADaM Standards**



WHY BRIDG?



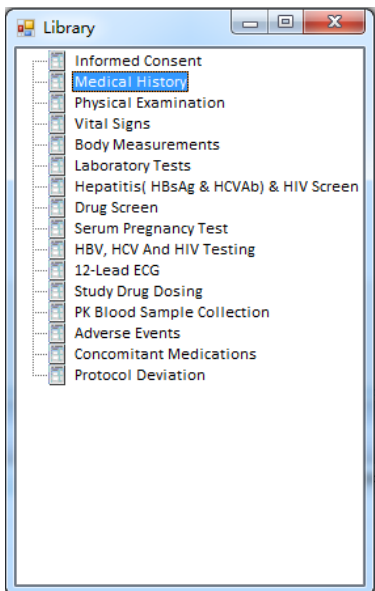
MANAGING STUDY USING BRIDG



STEP 2 – DEVELOP LIBRARIES

- **Libraries at Different Levels**
 - Company
 - Therapeutic Area
 - Program
- **CRF Library**
 - Standard CRFs
 - Cover different scenarios
- **SDTM Template**
 - Standard Structure
 - Standard raw -> SDTM mapping
- **ADaM Template**
 - Standard Structure
 - Standard Derivations
- **TLF Template**
 - Break-down to Standard Units

STEP 2 : CREATE COMMON LIBRARIES – eCRF & TLF



eCRF:

- Common Activities
- Associated Forms
- BRIDG or CDASH Mappings

MEDICAL HISTORY

Does the subject have any past clinically significant medical conditions?

- ☐ Yes
☐ No

MH Number	Diagnosis/Procedure	Start Date (DD/MM/YYYY)	End Date (DD/MM/YYYY)	Ongoing
				☐

Select template

Please select a template:

	TRT A	TRT B
Analysis Variable	XXX	XXX
N	XXX.X (XX.X)	XXX.X (XX.X)
Mean (Std)	XX.X (XX.X)	XX.X (XX.X)
Min, Max	XX, XX	XX, XX

Statistic Formats Setting

Statistic Unit Type: Summary

Simple Statistics:

Statistic	SAS Name	Display Caption	Precision	Shell Text
N	n	N	0	xxxx

Complex Statistics:

Statistic	Name	Display Caption	Expression
MeanStd	MeanStd	Mean (SD)	Mean (Std)

TLF Professional

Sample Table 1

Number of Participants by Study

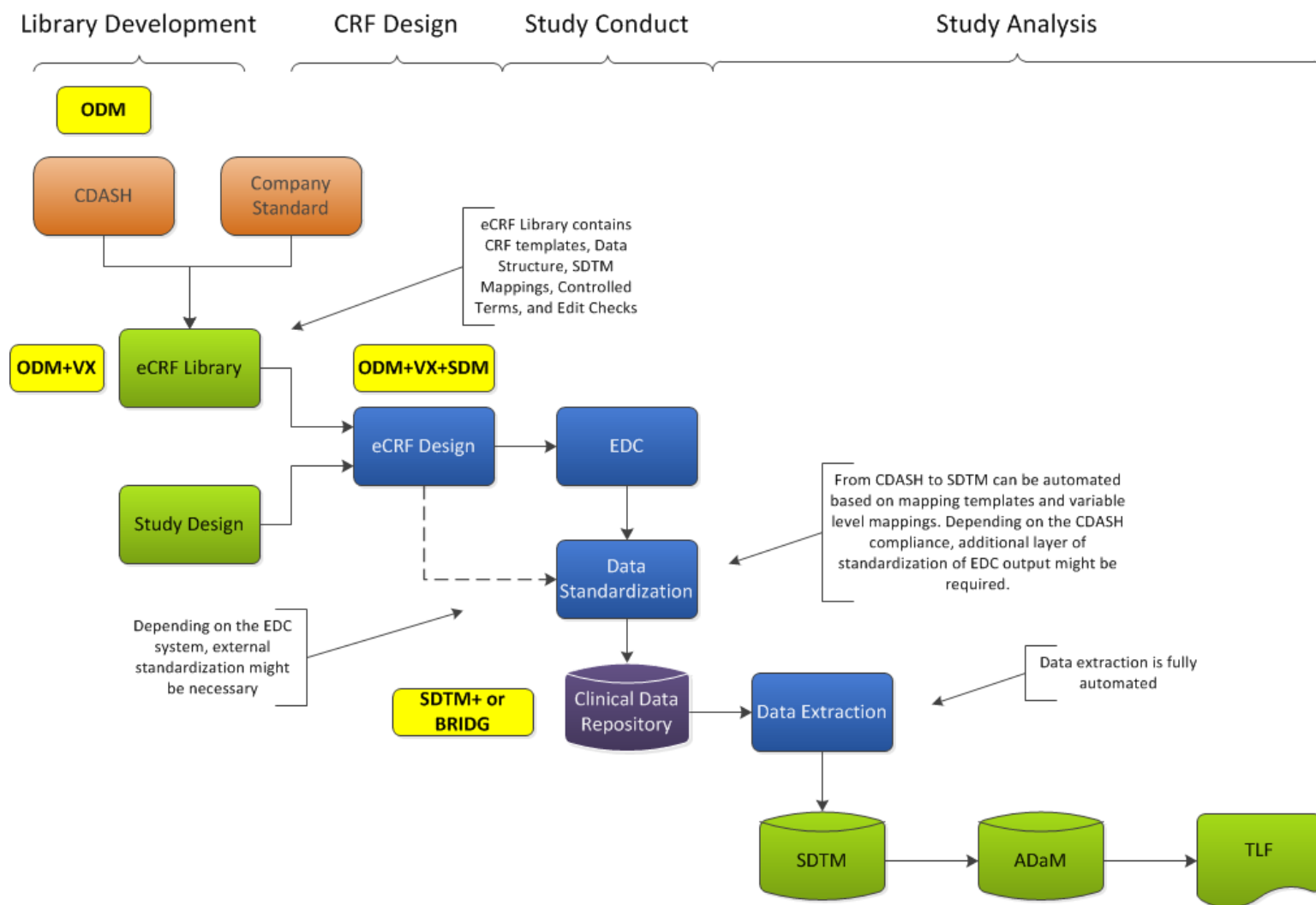
All Participants

	Study 1	Study 2	Study 3	Total
StudyID	Study 1	Study 2	Study 3	Study 1
Study 1	Study 1	Study 2	Study 3	Study 1
Study 2	Study 1	Study 2	Study 3	Study 1

TLFs

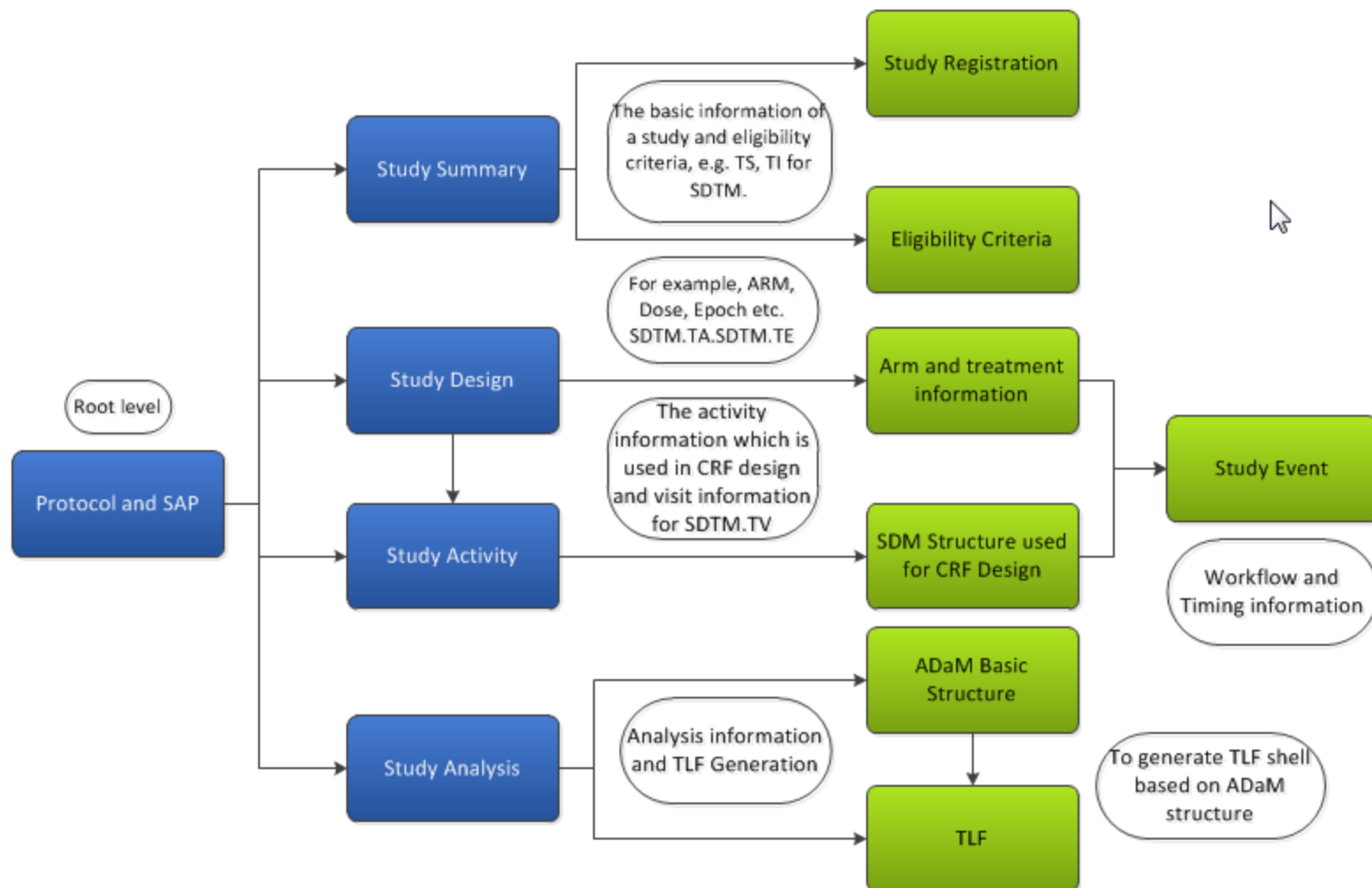
- Common Endpoints
- Reporting Templates
- BRIDG or ADaM Mappings

FLOW FROM DATA COLLECTION TO STUDY ANALYSIS



STEP 3 – STUDY DESIGN USING STUDY ARCHITECT

Study Architect Structure



STEP 3 : STUDY DEVELOPMENT - PROTOCOL

1.0 PROTOCOL SYNOPSIS

Study Title:	A Phase 1, Open-Label, Two-Period, Crossover Study to Evaluate the Relative Bioavailability of a New Tablet Formulation Versus the Current Capsule Formulation of PPI-668 Administered in Healthy Adult Volunteers
Protocol Number:	PPI-668-103
Study Phase:	Phase 1
Study Objectives:	Primary Objective: - To compare the relative bioavailability of PPI-668 when administered as a single oral dose in a tablet formulation vs. in a capsule formulation Secondary Objective: - To evaluate the safety and tolerability of single oral doses of PPI-668 in healthy subjects
Study Design and Duration of Treatment:	This will be an open-label, single-center, single-dose, crossover study. A total of 24 healthy subjects will be enrolled. On Day 1, under a 1:1 randomization scheme eligible volunteers, 12 subjects will receive a single oral dose of PPI-668 in the form of the current capsule formulation and 12 subjects will receive a single oral dose of the test tablet formulation of PPI-668, under fasted conditions. After a one week wash period, on Day 8, subjects will receive under fasted conditions the alternate PPI-668 formulation to the one they received on Day 1. Study medication will be administered approximately 0800 hours on Days 1 and 8 after an overnight fast of at least 10 hours. Screening will take place within 28 days before Study Day 1. Eligible subjects will be screened for eligibility and safety before the study.

Registration

- Titles and Background Info
- Sponsors
- Study Design

Titles and Background Info

Organization's Unique Protocol ID * FDAA XXX-XXX-XXX

Brief Title * FDAA A Phase 1, Open-Label, Two-Period, Crossover Study to Evaluate the Relative Bioavailability of a New Tablet

SAP Name

Rulebook Name

Study Type * FDAA Interventional

Brief Summary * FDAA

Detailed Description

Previous Next OK Cancel

Table 7-1 Schedule of Study Procedures

	Screening ^a	Day -1	Day 1	Day 2	Day 3	Wash-out	Day 7	Day 8	Day 9	Day 10	Day 15 ± 3 days Follow-up
Written Informed Consent	X										
Medical History	X										
Complete Physical Examination	X										X
Brief Physical Examination		X					X				
Vital Signs ^b	X	X			X		X			X	X
Height	X										
Weight	X	X					X				
Hematology ^c	X	X					X				X
Chemistry ^d	X	X					X				X
Urinalysis	X	X					X				X
Urine Drug and Breath Alcohol Screening	X	X					X				
Pregnancy	X	X					X				X

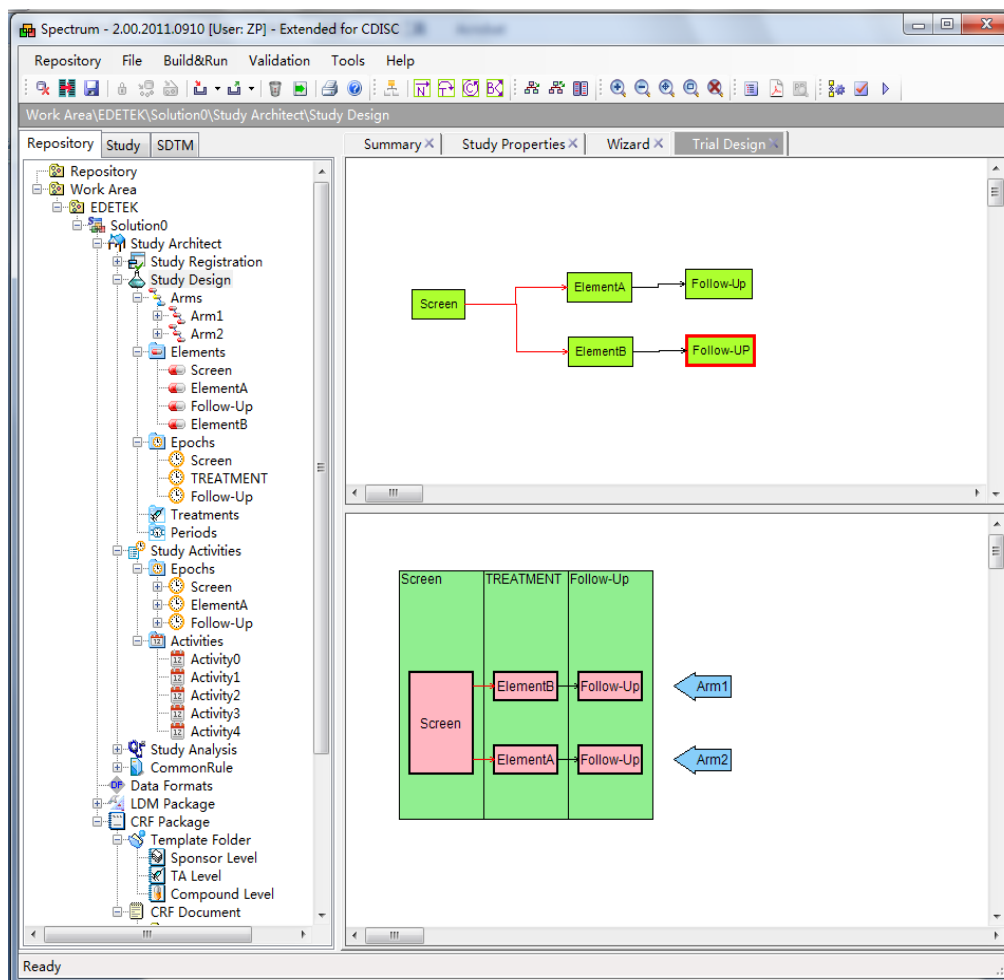
Study Protocol Versions are developed, and are associated with Defined Activities

STEP 3 : STUDY DESIGN – DATA COLLECTION

- Define Arms
- Define Epochs
- Define Segments
- Define Cells
- Define Study Events
- Define Workflow



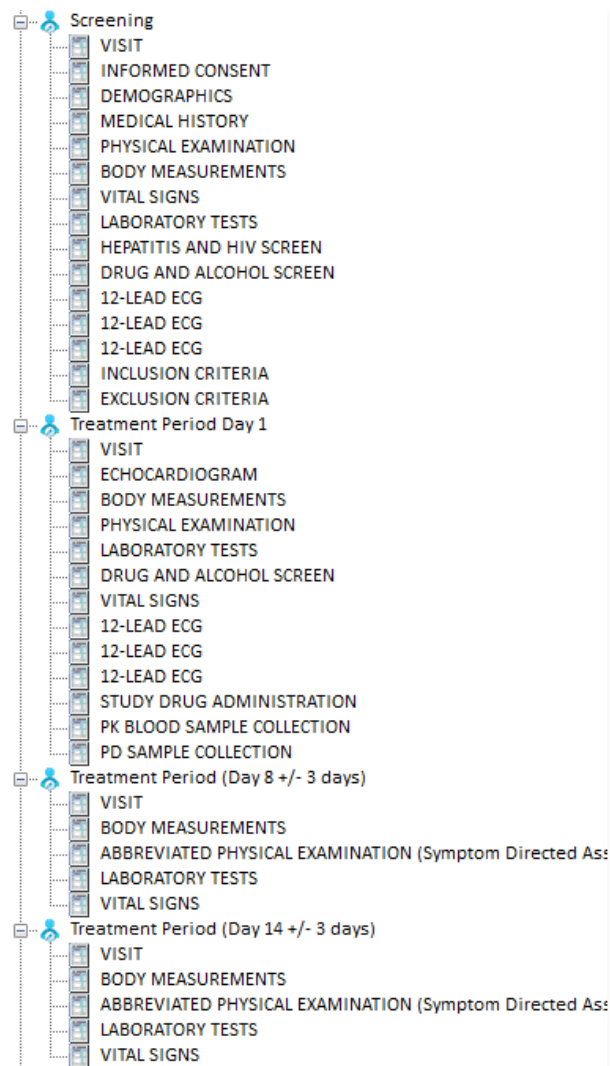
Study Design Model (SDM)



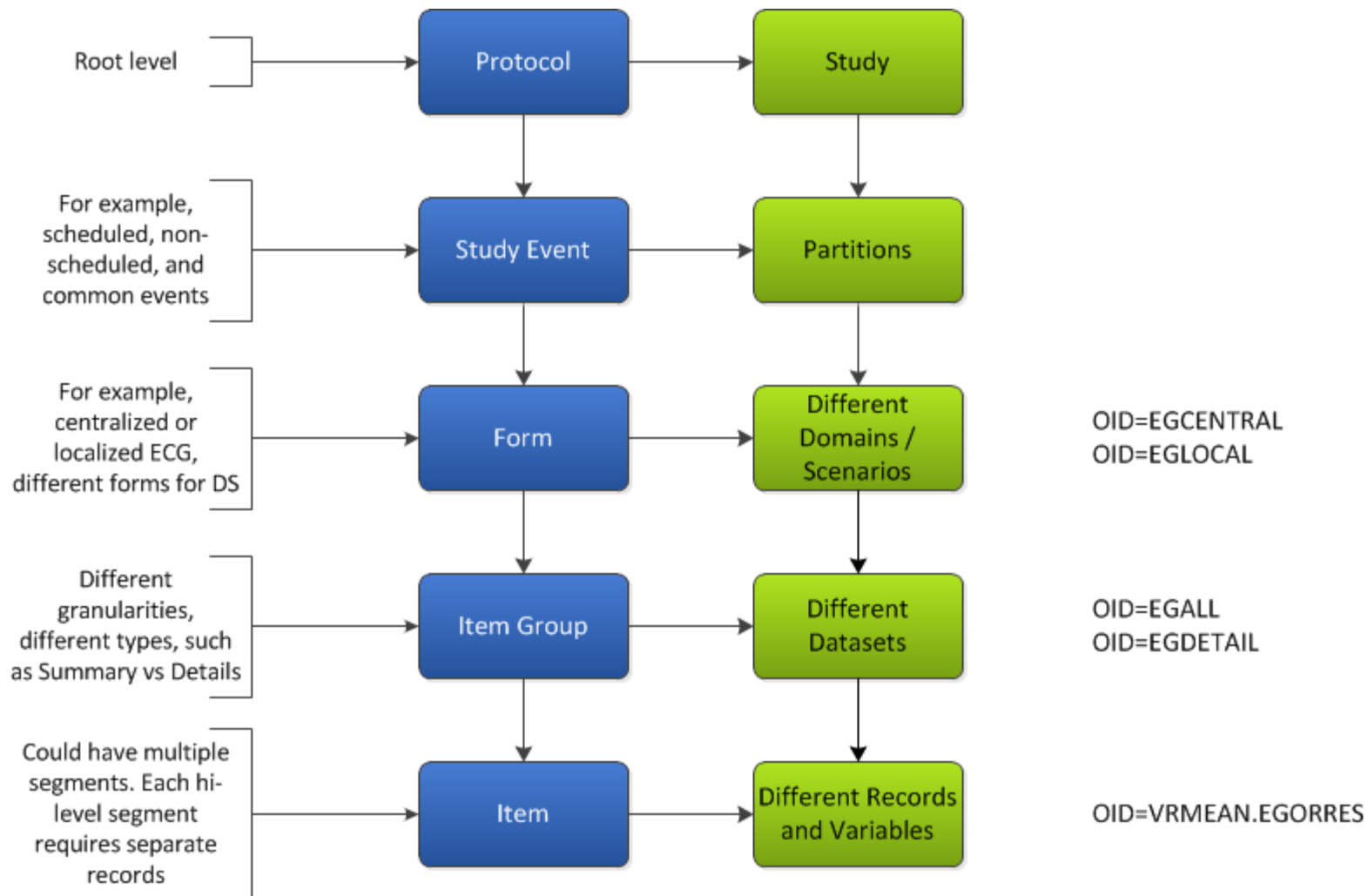
STUDY ACTIVITY FROM SA TO CRF

Epoch	Screening						
Activity/Event	Screening	Treatment Period Day 1	Treatment Period (Day 8 +/- 3 days)	Treatment Period (Day 8 +/- 3 days)	Treatment Period (Day 14 +/- 3)	Treatment Period (Day 21 +/-3)	Treatment Period (Day 28 +/- 3 day)
INFORMED CONSENT	X						
DEMOGRAPHICS	X						
MEDICAL HISTORY	X						
PHYSICAL EXAMINATION	X	X					
BODY MEASUREMENTS	X	X	X	X	X	X	X
VITAL SIGNS	X	X	X	X	X	X	X
LABORATORY TESTS	X	X	X	X	X	X	
HEPATITIS AND HIV SCREEN	X						
DRUG AND ALCOHOL SCREEN	X	X					X
12-LEAD ECG	X	X					
INCLUSION CRITERIA	X						
EXCLUSION CRITERIA	X						
ECHOCARDIOGRAM		X					
STUDY DRUG ADMINISTRATION		X					
PK BLOOD SAMPLE COLLECTION		X					X
ABBREVIATED PHYSICAL EXAMINATION (Symptom Directed Assessment)		X	X	X	X	X	X
PD SAMPLE COLLECTION		X					X
STUDY COMPLETION							
ADVERSE EVENTS							
CONCOMITANT MEDICATIONS							

CRF DESIGN STRUCTURE FROM SA



STANDARDIZED CDASH OUTPUT STRUCTURE



- **Map to unique scientific concepts (logical model element)**
- **Item Group (IG) defines datasets**
 - Develop standard naming convention to cover different scenarios
 - Each name should represent unique set of contents
- **Item defines variable names and hierarchies**
 - Leveraging multiple segment names
 - Category, Sub-category, Test Code, Variable Name
 - Use CDISC Controlled Terminology to convey semantic information

DM CRF DESIGN

DEMOGRAPHICS

OID=F.DM

OID=IG.DM

Date of Birth

 - -

Day

Month

Year

OID=I.BRTHDAT

Sex

☐

Male

OID=I.SEX

☐

Female

Race (Check all that apply)

☐

White

☐

Black/African-American

OID=I.RACE

☐

Asian

☐

Native Hawaiian/Other Pacific Islander

☐

American Indian/Alaska Native

☐

Other Specify

OID=I.RACEOTH

Ethnicity

☐

Hispanic

OID=I.ETHNIC

☐

Not Hispanic

CDASH DM DATASET OBTAINED

BIRTHDAT	ETHNIC	RACE1	RACE2	RACE3	RACE4	RACE5	RACE6	RACEOTH	SEX
23-MAR-1968	2					1			M
27-DEC-1982	2					1			M
15-DEC-1987	2			1					M
06-JAN-1976	2			1					M
14-AUG-1990	2					1			M
13-JAN-1986	1					1			M
20-SEP-1994	2			1					M
25-JUL-1976	2			1					F

EG CRF DESIGN

12-LEAD ECG

OID=F.EG

In triplicate after 5 minutes of resting in the supine position.

OID=IG.EGPERF

☐ Not Done

OID=I.EGPERF

OID=IG.EGDETL Date of ECG	Day Month Year	OID=I.EGDAT
Actual Time	Hour Minute	OID=I.EGTIM
Ventricular Rate	(beats/min)	OID=I.VRMEAN.EGORRES
PR Interval	(msec)	OID=I.VRMEAN.EGORRES
RR Interval	(msec)	OID=I.RRMEAN.EGORRES
QRS Interval	(msec)	OID=I.QRSDUR.EGORRES
QT Interval	(msec)	OID=I.QTC.EGORRES
QTcF Interval	(msec)	OID=I.QTcF.EGORRES

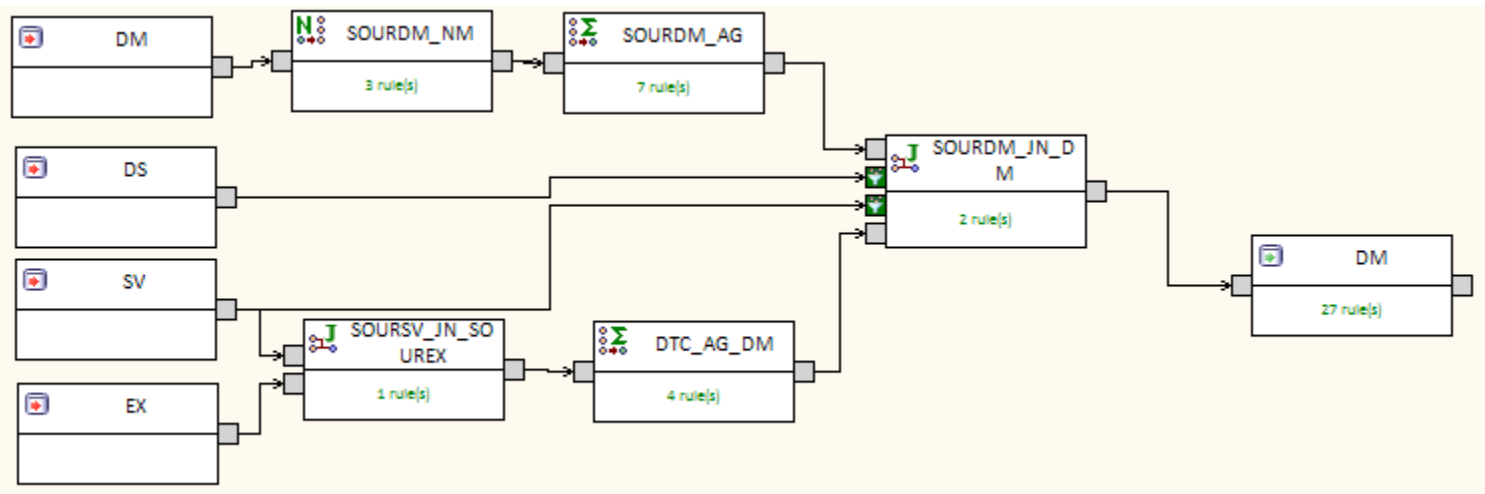
CDASH EG DATASET OBTAINED

EGDAT	EGORRES	EGORRESN	EGORRESU	EGTEST	EGTIM
28-MAR-2014		165	(msec)	PR Interval	0918
28-MAR-2014		985	(msec)	RR Interval	0918
28-MAR-2014		90	(msec)	QRS Interval	0918
28-MAR-2014		410	(msec)	QT Interval	0918
28-MAR-2014		412	(msec)	QTcF Interval	0918
28-MAR-2014	1	.			0918
28-MAR-2014		60	(beats/min)	Ventricular Ra	0918
28-MAR-2014		178	(msec)	PR Interval	0920
28-MAR-2014		966	(msec)	RR Interval	0920
28-MAR-2014		88	(msec)	QRS Interval	0920
28-MAR-2014		411	(msec)	QT Interval	0920
28-MAR-2014		415	(msec)	QTcF Interval	0920
28-MAR-2014	1	.			0920
28-MAR-2014		62	(beats/min)	Ventricular Ra	0920
28-MAR-2014		170	(msec)	PR Interval	0922
28-MAR-2014		979	(msec)	RR Interval	0922
28-MAR-2014		86	(msec)	QRS Interval	0922
28-MAR-2014		407	(msec)	QT Interval	0922
28-MAR-2014		409	(msec)	QTcF Interval	0922
28-MAR-2014	1	.			0922
28-MAR-2014		61	(beats/min)	Ventricular Ra	0922

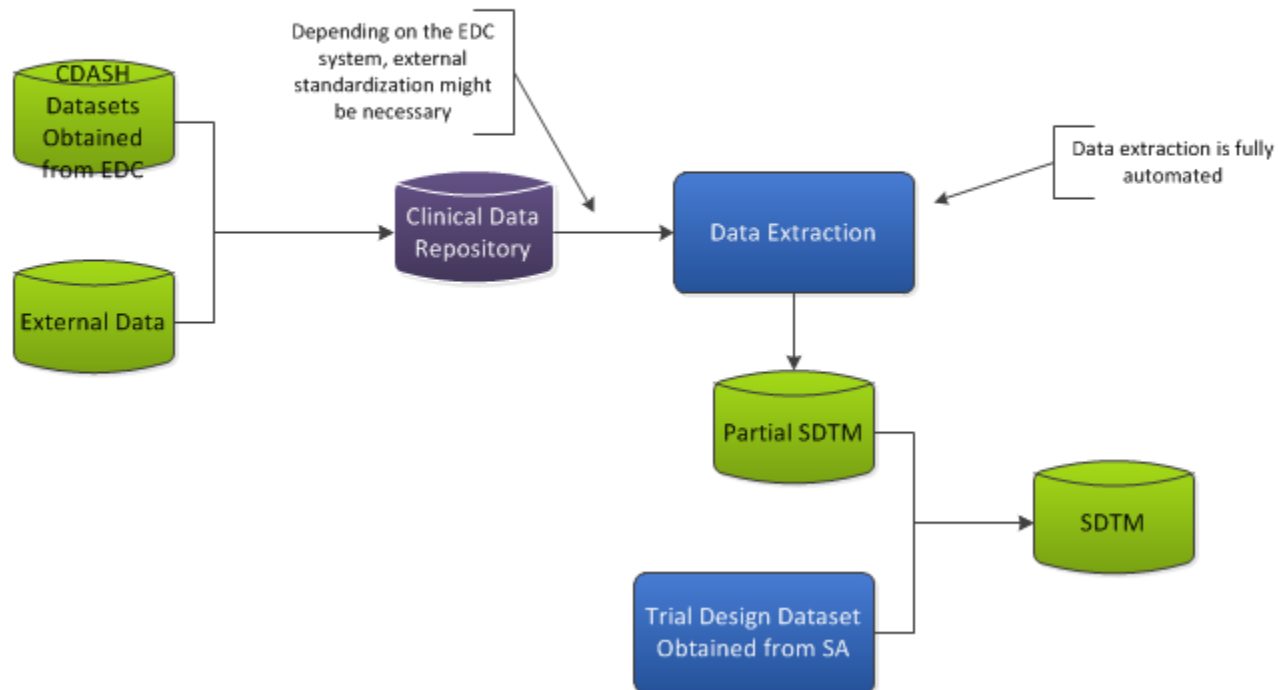
- **Match IG-based EDC Output with Partition-Level Templates**
 - Scenario based templates
 - Auto-matching based on available IG-based outputs
 - Auto-Pruning of extra template variables
- **Match Domain-Level Templates**
 - All partitions are merged together
 - Merged results are matched against domain-level templates
 - Finalization stage is applied based on domain class
 - Baseline calculation
 - --SEQ assignment
 - SUPPQUAL creation

- **Non-standard derived variables have to be defined based on SAP or mapping standards.**
 - Baseline Definition
 - Default: Last non-missing observation before dosing
 - Average of repeated measurements
 - Reference Dates
 - First Dose/Last Dose Dates
 - Treatment Emergent AE
 - Last Participation Date
 - Unit Systems for Lab Standardization
- **Variables of Protocol Origin have to be defined**
 - Trial Design
 - Other protocol specified information not available elsewhere
- **These are specified at study design**

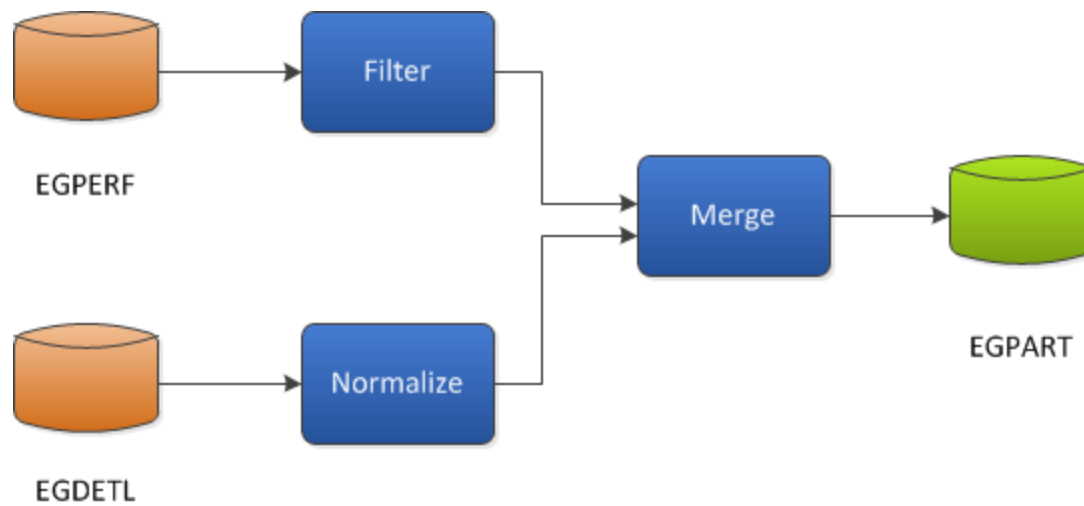
CREATING SDTM/ADAM TEMPLATES



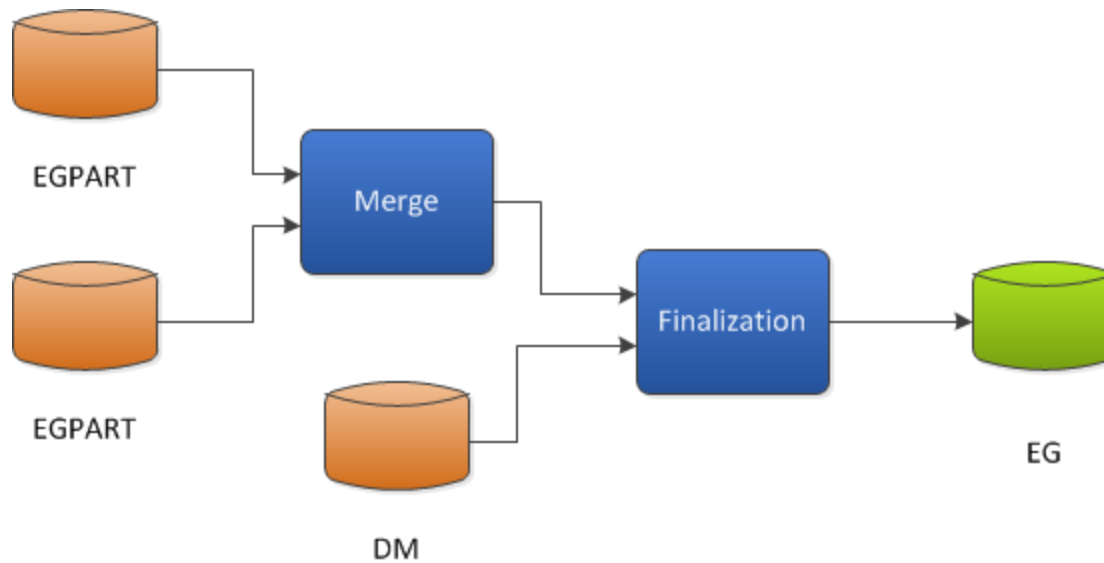
CDASH - SDTM Dataset Generation



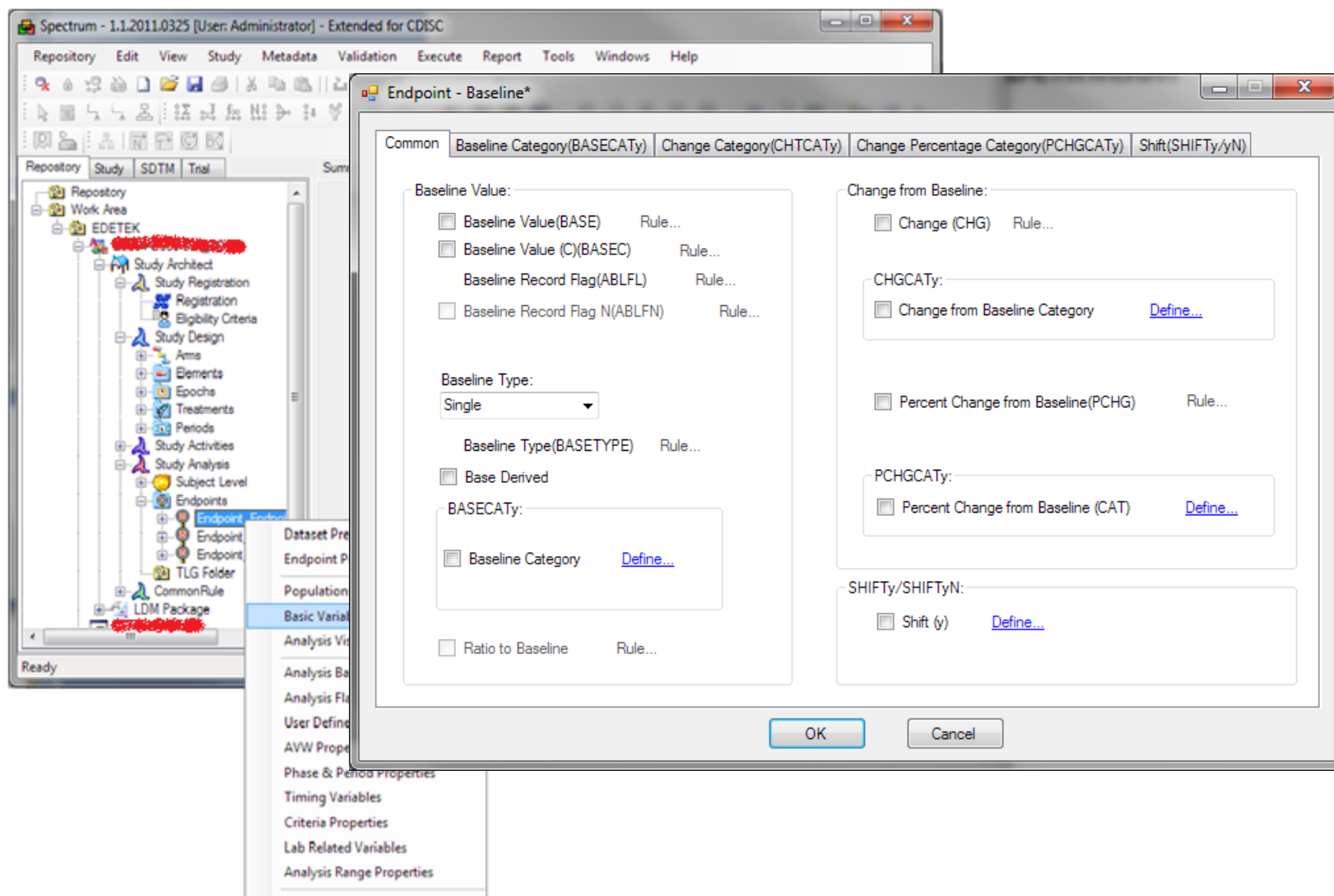
PARTITION LEVEL TEMPLATES



DOMAIN LEVEL TEMPLATES



STEP 3 : STUDY DESIGN - ANALYSIS



STUDY 3 : STUDY DESIGN - REPORTING

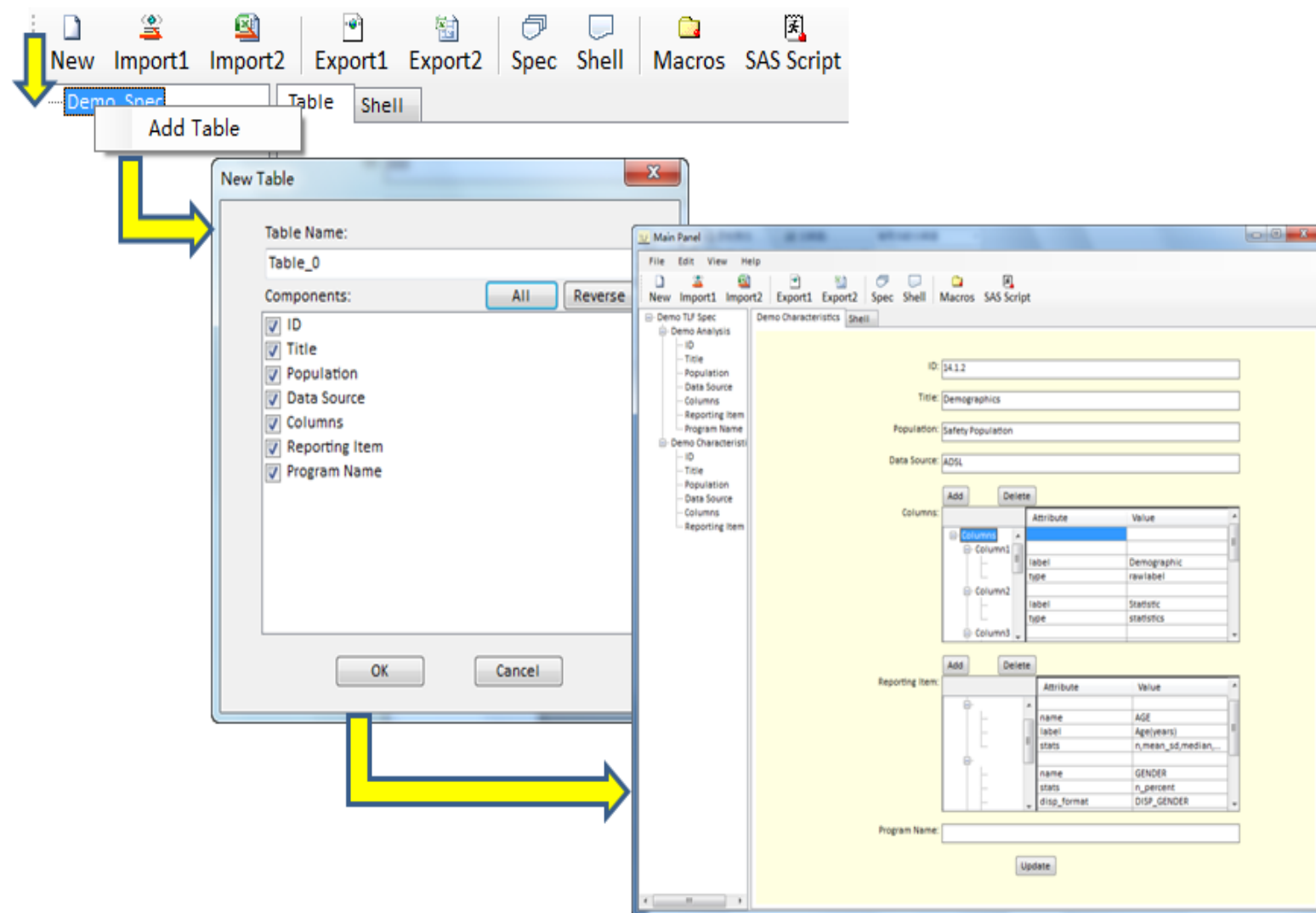
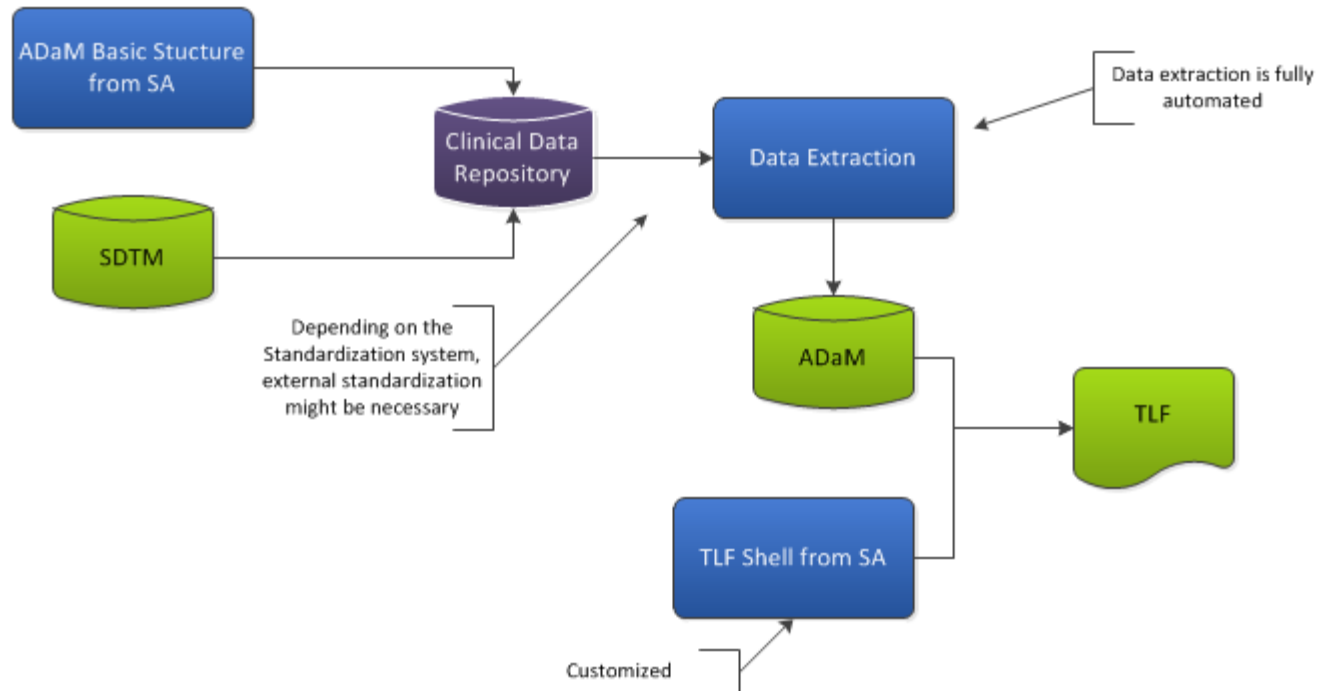


Table 14.1.2			
Demographics			
Safety Population			
Demographic	GROUP A	GROUP B	GROUP C
Age (years)			
n	xxx	xxx	xxx
Mean (Sd)	xx.x (xx.x)	xx.x (xx.x)	xx.x (xx.x)
Min, Max	xx, xx	xx, xx	xx, xx
Median	xx	xx	xx
Gender			
Female	xx(x.xx)	xx(x.xx)	xx(x.xx)
Male	xx(x.xx)	xx(x.xx)	xx(x.xx)
Race			
American Indian or A	xx(x.xx)	xx(x.xx)	xx(x.xx)
Black	xx(x.xx)	xx(x.xx)	xx(x.xx)
White	xx(x.xx)	xx(x.xx)	xx(x.xx)
Asian	xx(x.xx)	xx(x.xx)	xx(x.xx)
Native Hawaiian or o	xx(x.xx)	xx(x.xx)	xx(x.xx)

AUTOMATED ADaM & TLF CREATION

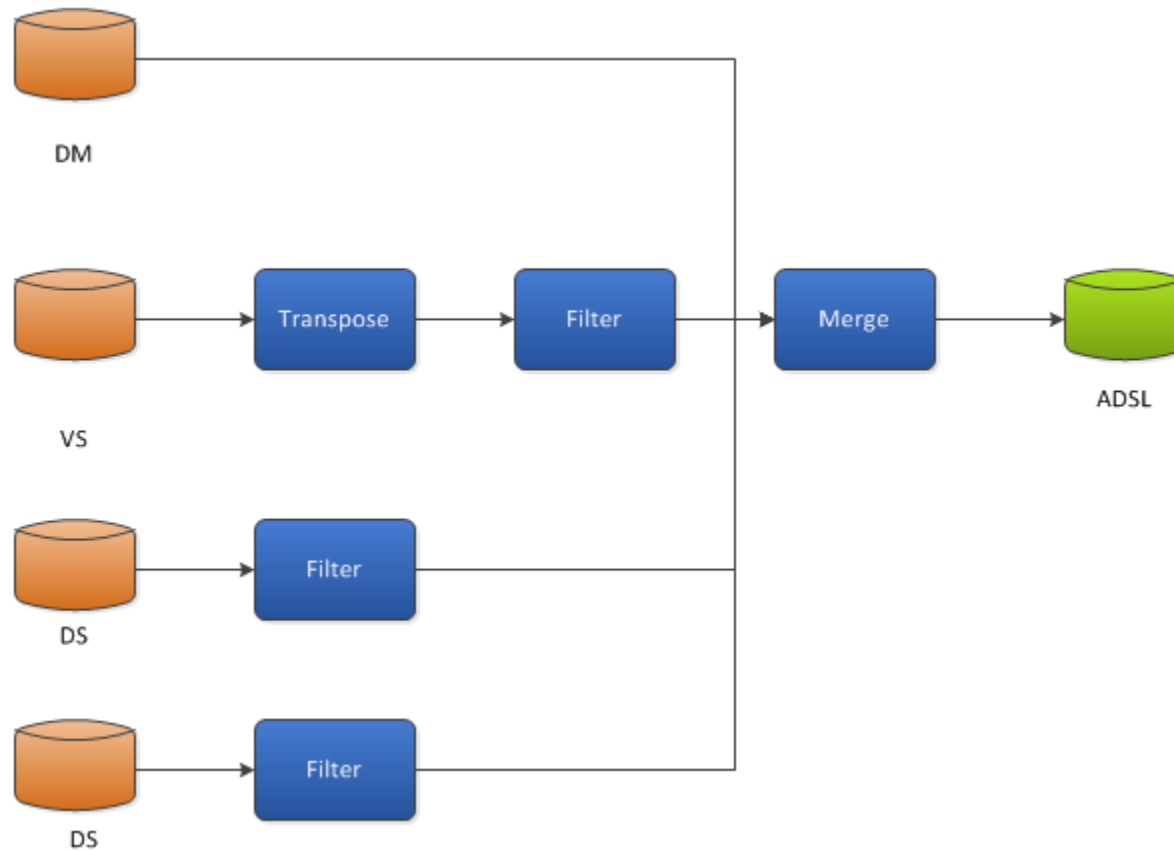
Study Architect-ADaM-TLF



After the clinical data repository which contains rule template as the SDTM repository in page 14-16, ADaM datasets are generated finally.

- **ADaM structure is generated to support TLF creation**
 - Analysis parameter variables
 - Analysis group variables
 - Analysis population variables
 - Analysis visit windowing variables
 - Analysis flag variables
 - Analysis enabling variables
- **Traceability to SDTM is established through ADaM templates**
 - Derivations
 - Macros – with metadata wrapper
- **Traceability to data collection is established through SDTM templates**

- ADSL



- **ADaM data obtained from Combining SA ADaM Structure and Repository**
 - Create different templates firstly. Templates are grouped by dataset.
 - Import SA ADaM structure.
 - Select one or more template for one dataset by turns.
 - Deal with prompts during template reference.
 - Process variables and dataset without definition in template.
 - Generate ADaM data finally.

IMPORT SDTM DATA

RBV-101 X

Properties Source(s) Target(s)/Data-flow-diagram(s) Ldm-operation(s) Term(s) Format(s) Output(s)&Report(s)

If the source data structure is empty:

Upload & Import metadata

Or else:

Re-import data structure(SAS)

Edit Delete Add

Entity Name	Entity Label	Description
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DATA STRUCTURE FROM SA

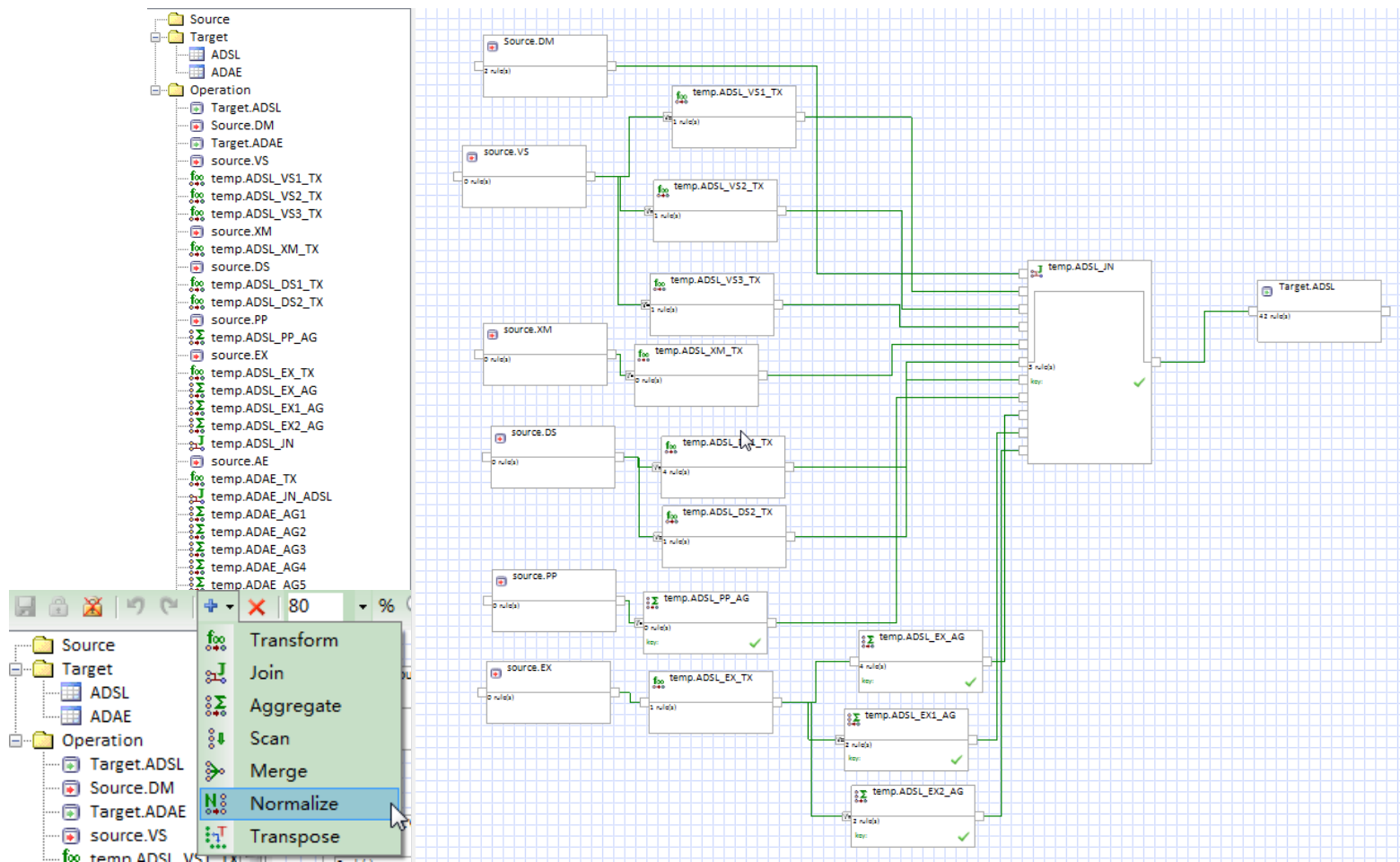
Ldm-entity (ADSL) - Panther Adam

Properties Element(s) Extend Value

	Name	Label	Data Type	Length
▶	STUDYID	Study Identifier	Char	25
	USUBJID	Unique Subject Identifier	Char	20
	SUBJID	Subject Identifier for the Study	Char	10
	SITEID	Site Identifier	Char	4
	AGE	Age	Num	8
	AGEU	Age Units	Char	20
	SEX	Sex	Char	2
	SEXN	Sex (Numeric)	Num	8
	RACE	Race	Char	50
	RACEN	Race (Numeric)	Num	8
	ETHNIC	Ethnicity	Char	50
	ETHNICN	Ethnicity, Numeric	Num	8
	WEIGHTBL	Baseline Weight (kg)	Num	8
	HEIGHTBL	Baseline Height (cm)	Num	8
	BMIBL	Baseline BMI (kg/m^2)	Num	8
	TRTFL	Subject Treated Population Flag	Char	1

OK Cancel

DATA FLOW DIAGRAM



CONVERSION RULE

Rule Definer - Panther Adam

Entity:

	Element	Label	Data Type	Length	Rule Text	Operation
0	STUDYID	Study Identifier	char	25	DM.STUDYID	Target.ADSL
1	USUBJID	Unique Subject Identifier	char	20	DM.USUBJID	Target.ADSL
2	SUBJID	Subject Identifier for the Study	char	10	DM.SUBJID	Target.ADSL
3	SITEID	Site Identifier	char	4	DM.SITEID	Target.ADSL
4	AGE	Age	num	8	DM.AGE	Target.ADSL
5	AGEU	Age Units	char	20	DM.AGEU	Target.ADSL
6	SEX	Sex	char	2	DM.SEX	Target.ADSL
7	SEXN	Sex (Numeric)	num	8	if ADSL.SEX == "M" then 1else if ADSL.SEX == "F" th...	Target.ADSL
8	RACE	Race	char	50	DM.RACE	Target.ADSL
9	RACEN	Race (Numeric)	num	8	if ADSL.RACE == "WHITE" then 1else if ADSL.RACE =...	Target.ADSL
10	ETHNIC	Ethnicity	char	50	DM.ETHNIC	Target.ADSL
11	ETHNICN	Ethnicity, Numeric	num	8	if ADSL.ETHNIC == "HISPANIC OR LATINO" then 1els...	Target.ADSL
12	WEIGHTBL	Baseline Weight (kg)	num	8	ADSL_VS1_TX.WEIGHT	Target.ADSL

1 DM.STUDYID

OK Cancel

Table 14.1.2+
Demographics+
Safety Population+

Demographic+	Statistic+	KD025+ (N=8)+	Total+ (N=8)+
Age (years)+	N+	8+	8+
	Mean (SD)+	31.0 (8.88)+	31.0 (8.88)+
	Median+	29.5+	29.5+
	Min, Max+	19.0, 46.0+	19.0, 46.0+
Gender+			
Male+	n (%)+	7 (87.50%)+	7 (87.50%)+
Female+	n (%)+	1 (12.50%)+	1 (12.50%)+
Race+			
American Indian or Alaska Native+	n (%)+	0 (0.00%)+	0 (0.00%)+
Asian+	n (%)+	0 (0.00%)+	0 (0.00%)+
Black+	n (%)+	4 (50.00%)+	4 (50.00%)+
Native Hawaiian or other Pacific Islander+	n (%)+	0 (0.00%)+	0 (0.00%)+
White+	n (%)+	4 (50.00%)+	4 (50.00%)+
Other+	n (%)+	0 (0.00%)+	0 (0.00%)+
Ethnicity+			
Hispanic or Latino+	n (%)+	1 (12.50%)+	1 (12.50%)+
Not Hispanic or Latino+	n (%)+	7 (87.50%)+	7 (87.50%)+
Weight (kg)+	N+	8+	8+
	Mean (SD)+	78.8 (12.84)+	78.8 (12.84)+
	Median+	80.6+	80.6+
	Min, Max+	58.2, 96.4+	58.2, 96.4+