



Apply Next-Generation Tools in Real Study

OAK Garden, SDTMv Automation
Admiral, ADaM creation

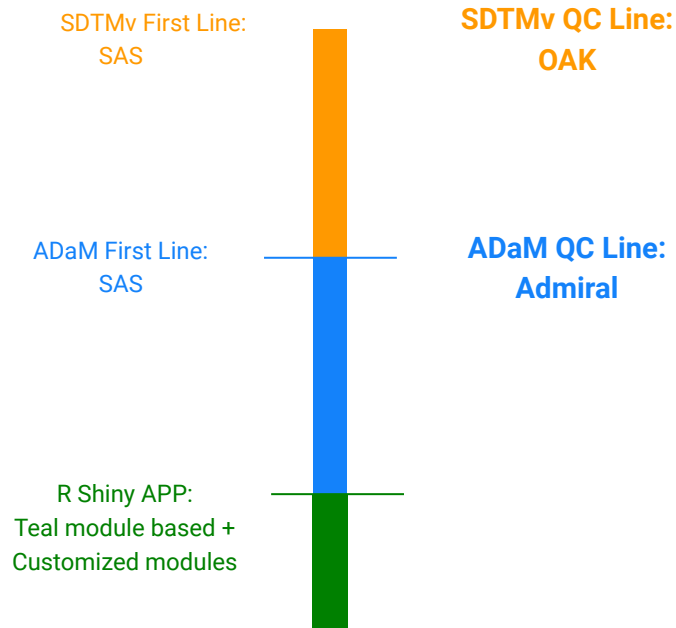
Jia Liu
Analytical Data Scientist from Roche

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- Workflow Design
- Next-Generation Tools Explore
 - OAK
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Workflow Design

Phase I on-going study towards chronic HBV infection.



The QC comparison for SDTMv domains and ADaMs was performed with home-made R scripts

Standard QC process were not totally available at the study setup stage. To solve the problem, we developed R scripts to do QC by comparing ordered datasets (R package used here: *arsenal*)

R Environment Settings:

R version: 4.1.3

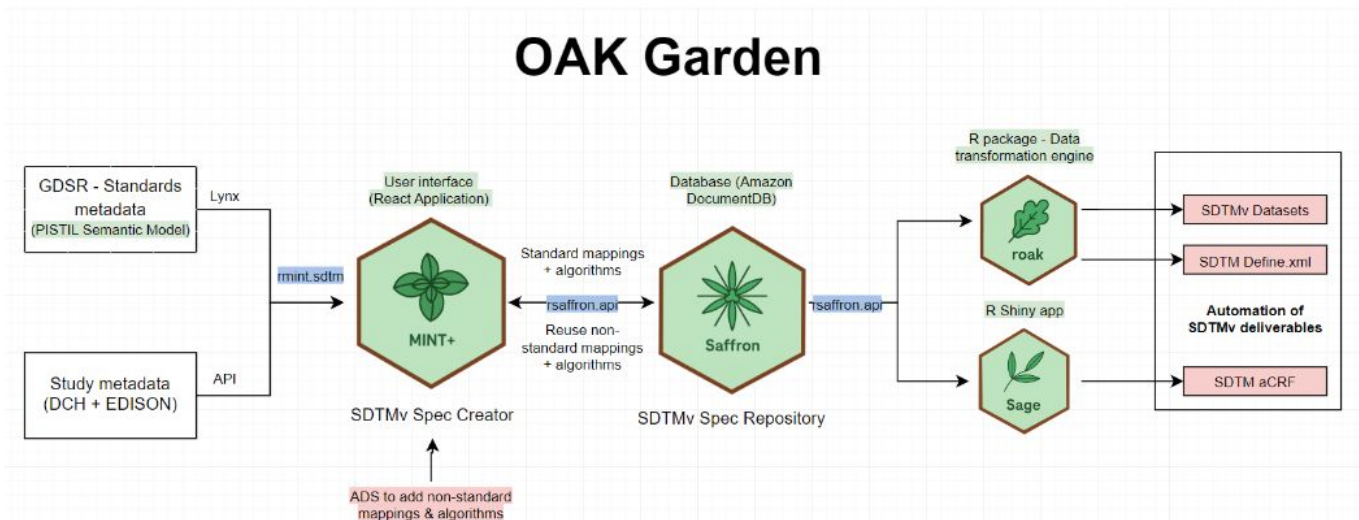
roak package version: 3.0.5

admiral package version: 0.10.1

OAK Applied in Real Data

OAK Garden SDTMv Automation

33 SDTMv domains in the study.

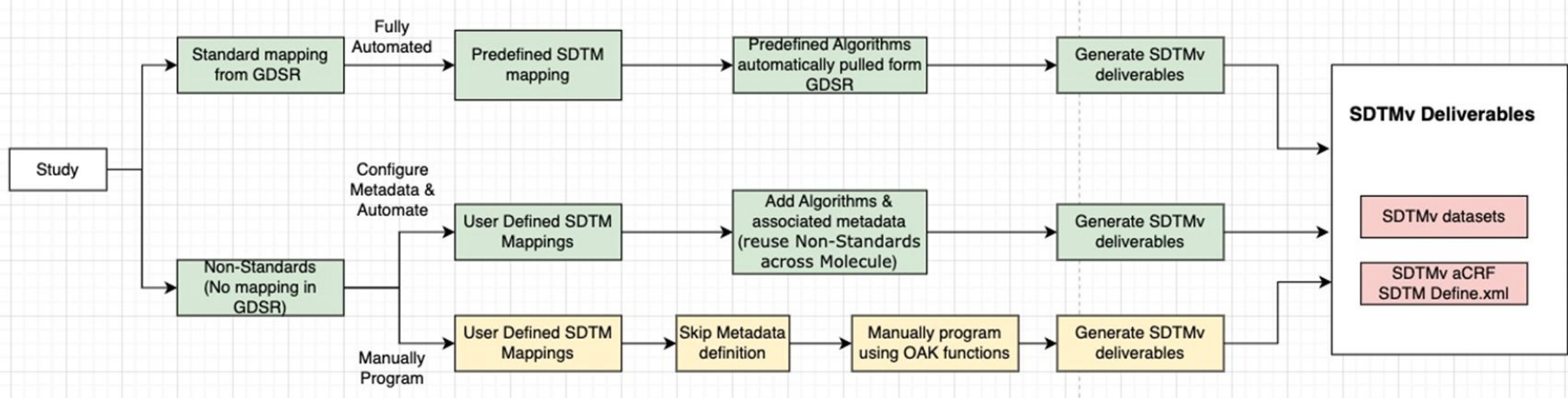


Non-standard SDTM mappings

- Configure custom SDTMv Mappings by adding algorithms & associated metadata in MINT+.
- Manually program the SDTMv Mappings.

Standard SDTM mappings: automatically generated based on standards from GDSR and should not be overridden.

OAK Garden - Study SDTMv setup



Automation of Standards – Closely linked to GDSR, standards are automated out of the box. Based on the studies started after 2019, a study uses **82% (median) Data-standards**.

Flexibility to Automate Non-Standards – Driven by the programmers, MINT+ UI & Saffron enables storing and reusing the Non-standard SDTM mappings & Algorithms across studies.

Manual Programming – Enable to program Non-Standards for complex scenarios in R or in SAS.

From the user side, MINT+ and ROAK are the main tools you directly face to produce SDTMv domains.

Create SDTMv specification

1. Use **MINT+** to **create the study SDTMv spec**, that is, Study SDTMv mappings metadata.
2. Add **Non-Standards SDTMv mappings** and associated metadata for the supported Algorithms.

Create SDTMv domain

3. Install **roak** package
4. Prepare and load **study configuration files**.
5. **Load the SDTMv spec** including controlled terminology created in step 2 from **Saffron**
6. Load **study raw metadata**
7. Load **GDSR metadata**
8. Create **SDTMv domains** for standards & automated Non-standards in the study using **roak**
e.g. `create_domain("DM", study_sdtmv_metadata, study_cont_terms)`
9. Program **complex Non-Standards & SDTMv variables** not supported by roak.

A closer look at MINT+



1 Study ID & Analysis 2 Other parameters 3 Summary

STUDY ID B [REDACTED]
 ANALYSIS LABEL Primary
Analysis details EDIT
 STATUS DRAFT
 GDSR VERSION 2022-Dec.v1: ChicoMendes
 CRF MIG [REDACTED] 28JUL2023_EW
 NON-CRFS [REDACTED]_LAB1_2.0_PUBLISHED,
 [REDACTED]_PKC1_1.0_APPROVED,
 [REDACTED]_IXRS1_1.0_PUBLISHED

Study Information ⓘ

Theme Number: 7 [REDACTED]
 Theme Molecule: H [REDACTED]
 Roche Number: R [REDACTED]
 Therapeutic Area: ID - INFECTIOUS DISEASES & VIROLOGY
 Study Indication: Hepatitis B virus infection
 Study Phase: Phase [REDACTED]
 Accountable Roche Party: p [REDACTED]

MINT+ Home

BACK GO TO SUMMARY CANCEL

Analysis Configuration

Target Domain
 AE

EDIT DERIVED VARIABLES

F.A.I.R Dashboard

SDTM Spec View

Non Standards

Discrepancies

Data Tabulation

Domain	Variable	Label	Type	Length	Controlled Terminology Code	Roche Core	Origin	Source	Annotation Texts
AE	STUDYID	Study Identifier	Char	8		Required Variable	Protocol		Unique identifier for a study.
AE	DOMAIN	Domain Abbreviation	Char	2	C66734	Required Variable	CRF	[AE]	AE = 'Adverse Events'
AE	DOMAIN	Domain Abbreviation	Char	2	C66734	Required Variable	CRF	[SAE]	AE = 'Adverse Events'
AE	USUBJID	Unique Subject Identifier	Char	50		Required Variable	Derived		Set to USUBJID in SDTM.DM domain. Set to Subject for the first trial the subject participated in involving SDTM IG 3.1.2, p29: "Unique subject identifier must be the same across all trials in the submission. This means that the same person who participates in multiple clinical trials (with the same USUBJID value in all trials." Practical guidance: ensure we are aligned with the latest regulatory guidance on study design which anticipates enrolling subjects in multiple studies for the same indication, we must add a CRF

A closer look at MINT+



- Analysis Configuration
- F.A.I.R. Dashboard
- SDTM Spec View
- ★ Non Standards
- ! Discrepancies
- Data Tabulation

Dataset: PKC1 CANCEL EDIT

Raw Source Model	Raw Dataset	Raw Dataset Label	Raw Variable	Raw Variable Label	Study Sites	Annotation Texts	Target SDTM Domain
Non-CRF DC	PKC1	PKC1			TRUE		
Non-CRF DC	PKC1	PKC1	STUDYID	Study Identifier	TRUE		
Non-CRF DC	PKC1	PKC1	PKCNAM	Vendor Name	TRUE		
Non-CRF DC	PKC1	PKC1	PATNUM	Unique Subject Identifier	TRUE		

Annotation definition

1 Text & Algorithm 2 Parameters 3 Summary

CANCEL

Annotation text: TEST_COMP
Mapping algorithm: 09_IF_THEN_ELSE

CONDITION LEFT	CONDITION OPERATOR	CONDITION RIGHT
<input checked="" type="radio"/> Raw variable Dataset: PKC1 Variable: PKCSTAT	Operator: Is checked	<input type="radio"/> Raw variable Dataset: PKC1 Variable: _____
<input type="radio"/> SDTMv variable Dataset: test2 Variable: test2		<input checked="" type="radio"/> SDTMv variable SDTM Domain: _____ SDTM Variable: _____
		<input type="radio"/> Text Value: _____

ACTION IF TRUE

Sub-Mapping Algorithm
02_ASSIGN_CT ▾

Additional entity sub-algorithms:
 15_MULTIPLE_RESPONSES 15A_SPLIT_TO_SUPPQAL

SUB-MAPPING ALGORITHM OPTIONS

SDTM Domain
PC ▾

SDTM Variable
CHECK1 ▲

Create CHECK1 | CUSTOM

SDTM Codelist Code
▾

Non-Standard Derivation in MINT+



Annotation definition

1 Text & Algorithm — 2 Parameters — 3 Summary

FINISH

Annotation added!

Parameter	Value
Annotation Text	TEST_COMP
Annotation Ordinal	1
Entity Ordinal	1
Mapping Algorithm	09_IF_THEN_ELSE
CONDITION LEFT	
Condition Left Type	Non-CRF Column
CONDITION OPERATOR	
Condition Operator	Checked
SUB-ALGORITHM	
Entity Sub-algorithm	02_ASSIGN_CT
Target SDTM Domain	PC
Target SDTM Variable	CHECK1
CUSTOM VARIABLE LABEL: TEST CHECK PKCSTAT	
Target SDTM Variable Role	Grouping Qualifier
Target SDTM Variable CodeList Code	C100120

Analysis Configuration Target Domain: PC [EDIT DERIVED VARIABLES](#)

FALR Dashboard

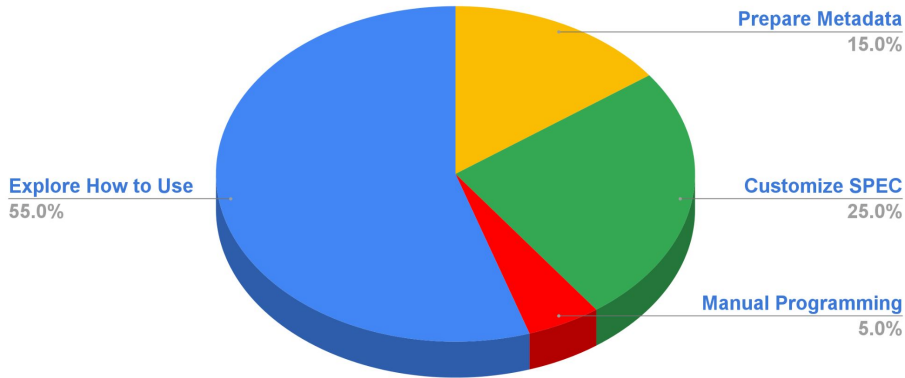
Domain	Variable	Label	Tv...	Le...	Control term code for	Roche Core	Origin	Source	Annotation Texts
PC	CHECK1	TEST check PKCSTAT						[PKC1.PKCSTAT]	TEST_COMP

SDTM SpecView

- Non Standards
- Discrepancies
- Data Tabulation

It takes some time to pick up and get used to, but does reduce programming effort significantly.

Time Spent (%)



The tool request fewer programming skills than the traditional approach. Exclude the non-standard programming part, manual programming is not requested. To define study-specific derivation rules, users could specify them in MINT+ UI.

More resources may focus on metadata setup and SPEC design.

Admiral Applied in Real Data

Revolution ADaM creation across the industry by bringing companies together
to develop one harmonized solution

Modular set-up focused on providing a simple to adopt toolkit that enables users to produce readable and easily constructible ADaM programs

STREAM

```
pre_processing()
```



```
create_ADaM(  
  dataset_name = name,  
  param_01 = ,  
  param_02 = ,  
  param_99 =  
)
```



```
post_processing()
```

Admiral

Input %>%

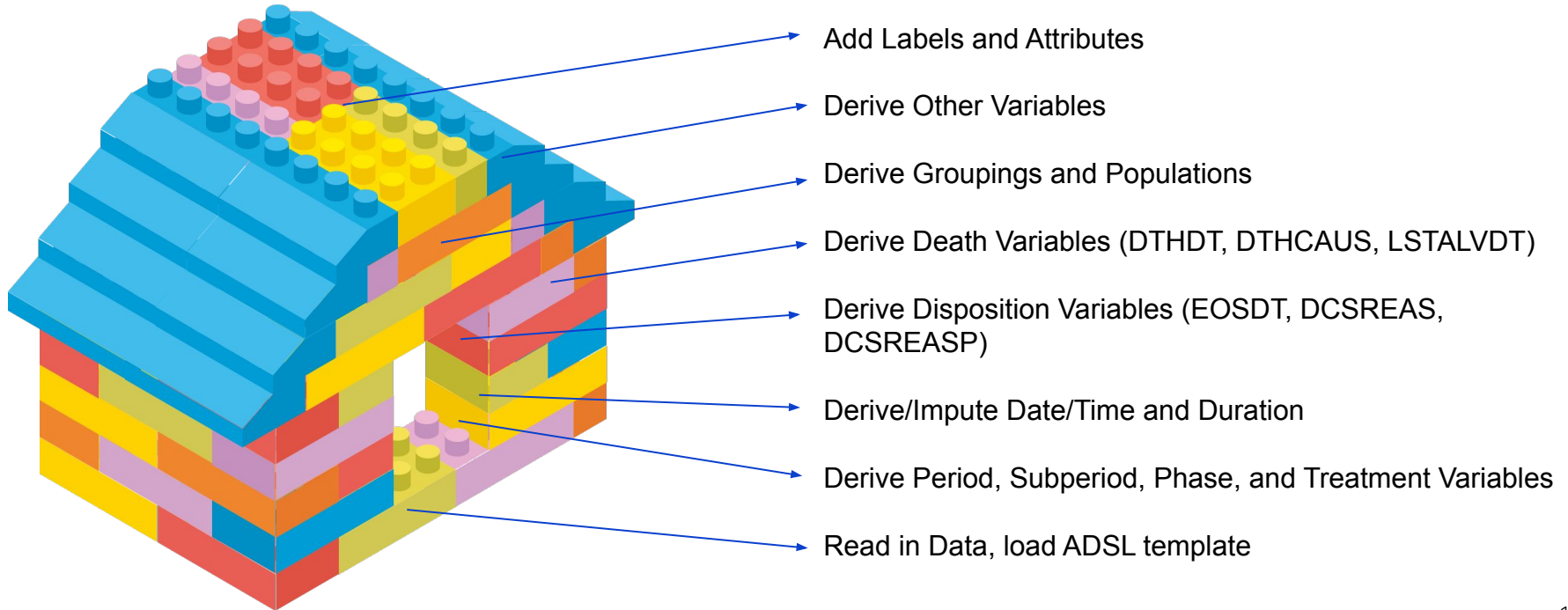
```
admiral_function_a() %>%  
project_function_x() %>%  
admiral_function_b() %>%  
study_function_y() %>%  
admiral_function_c()
```

...

Programming Flow Example: ADSL



Modular set-up focused on providing a simple to adopt toolkit that enables users to produce readable and easily constructible ADaM programs

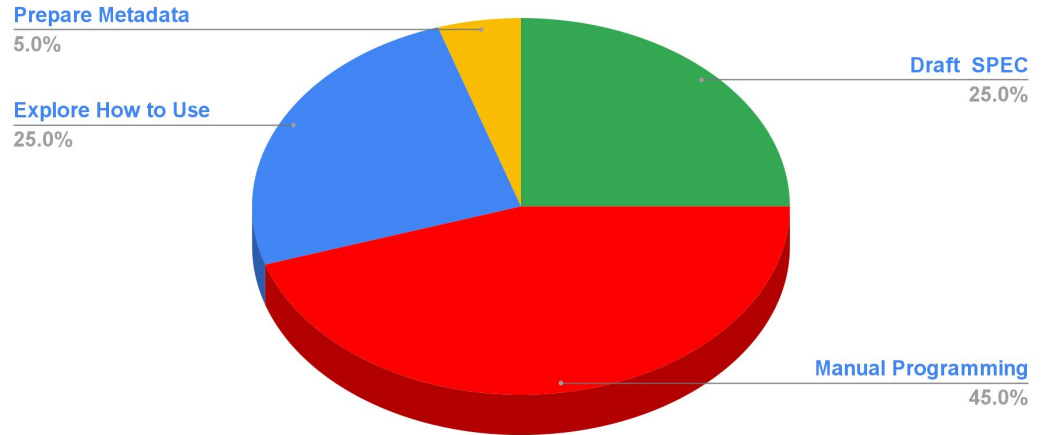


For R programmers, the tool is user-friendly and easy to pick up.

The tool is flexible and operable. Through the detachable blocks (composed of admiral functions, project/study level shared functions, self-made functions, etc.), it can effectively assist users to customize ADaMs.

Like playing with **LEGO**, the user can clearly see the structure of datasets. According to user needs, flexibly customize the derivation rules of variables

Time Spent (%)



Questions & Answers

References

Admiral

<https://pharmaverse.github.io/admiral/cran-release/index.html>

OAK

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

<https://wiki.cdisc.org/display/oakgarden/General+outline>

It is still at initial stage to make oak open source and you can find more information at <https://wiki.cdisc.org/display/oakgarden/General+outline>.

Please note that is not just lift and shift, it is going to be a major overhaul, mostly to be EDC agnostic.

Doing now what patients need next