



Making Your Studies AI-Ready: From Analysis to Regulatory Review



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Code Traceability

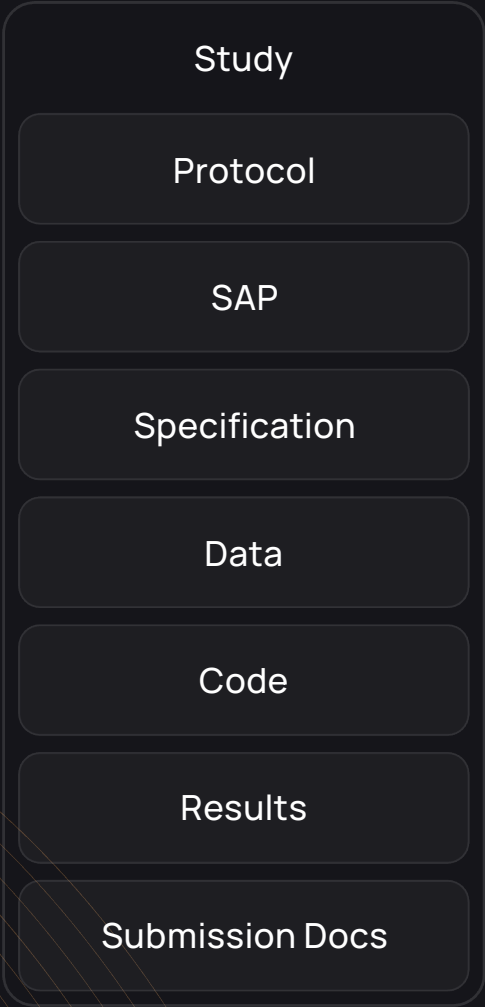
Connects your specifications, data, code, results (TLFs), and submission documentation

Code Traceability

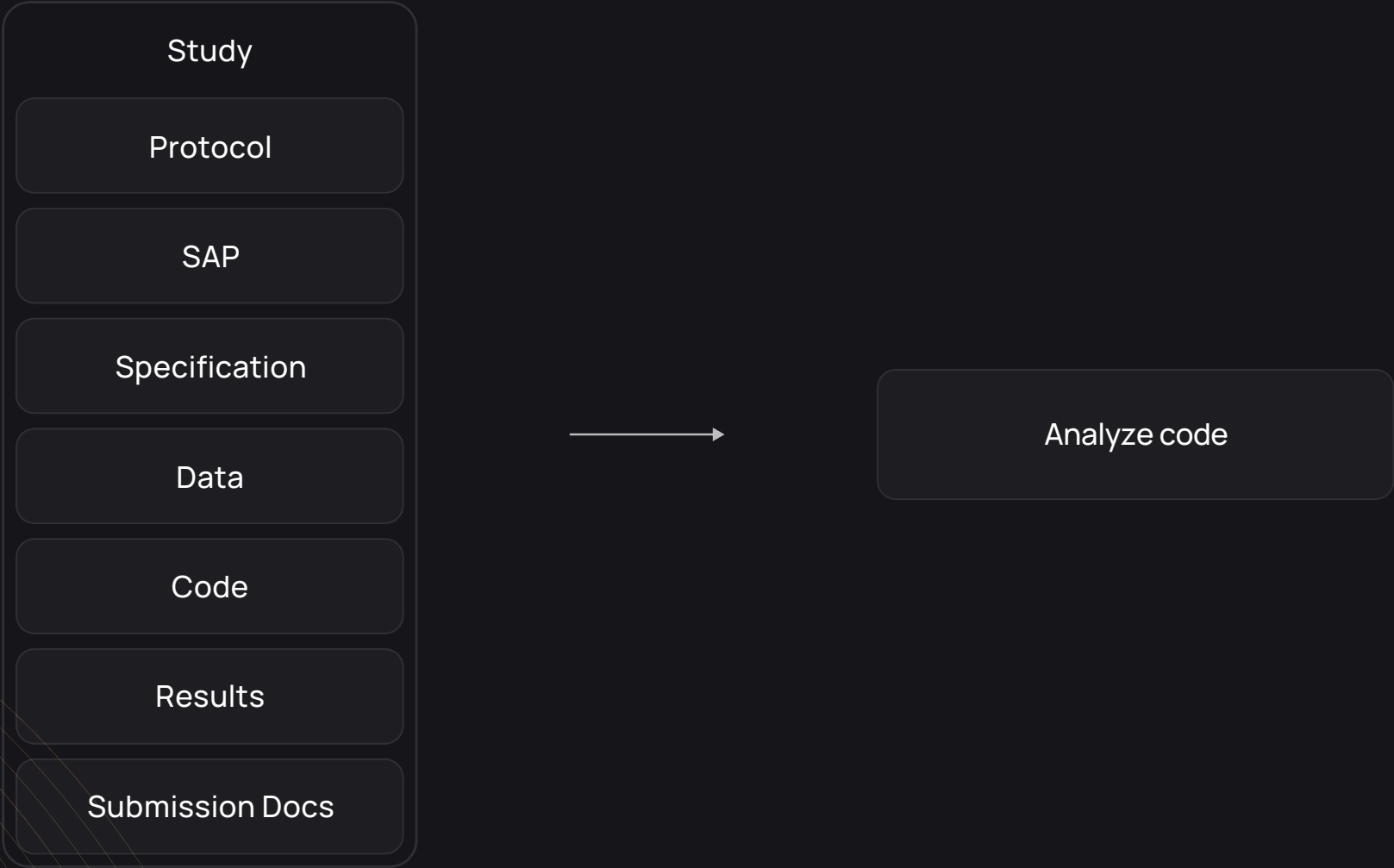
Connects your specifications, data, code, results (TLFs), and submission documentation

Independent of CDISC standards, language (R or SAS), and SCEs

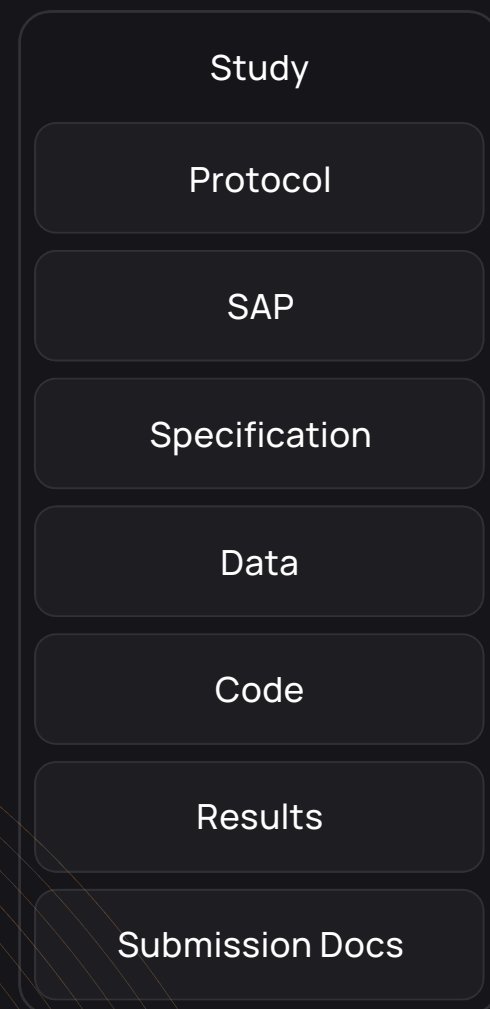
Building Traceability: From Code to Graph



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Building Traceability: From Code to Graph



Analyze code



The **source of truth** of a clinical trial is its **code**

Variable Traceability: SDTM.DM.AGE in a demo study

AGE is a simple concept, but can be derived in different ways

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dob	firstdose
1974-02-05	2010-03-28
...	...
...	...
...	...
...	...

Variable Traceability: SDTM.DM.AGE in a demo study

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```
age.sas
...
firstdose=min(firstdose,startdt,enddt);
age=intck('year',dob,firstdose,'c');
```


Variable Traceability: SDTM.DM.AGE in a demo study

AGE is a simple concept, but can be derived in different ways

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```
age.sas
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firstdose=min(firstdose,startdt,enddt);
age=intck('year',dob,firstdose,'c');
```



age
36
...
...
...
...

How is **AGE** derived and what data does it depend on?

 macros	 source	 sdtm	 adam	 tlf
 %derive_baseline.sas	 demographic.sas	 dm.sas	 adae.sas	 t14_1_1.sas
 %dtc2dt.sas	 dosing.sas	 ae.sas	 adef.sas	 t14_2_1.sas
 %derive_age.sas	 labs.sas	 cm.sas	 adsl.sas	 t14_3_1.sas
 %flag_last.sas	 adverse.sas	 ex.sas	 adef.sas	 l162_1.sas
 %km_plot.sas	 exposure.sas	 lb.sas	 adtte.sas	 l16_2_2.sas
 %visit_window.sas	 vital_signs.sas	 vs.sas	 advs.sas	 f14_2_1.sas
 +14 more	 +18 more	 +30 more	 +16 more	 +174 more

dm.sas

```
proc sort data=source.dosing(keep=subject startdt enddt) out=dosing;
by subject startdt;
run;

data dose_sum;
set dose_raw;
by subject;

retain firstdose lastdose;

if first.subject then do;
firstdose=.;
lastdose=.;
end;

firstdose=min(firstdose,startdt,enddt);
lastdose=max(lastdose,startdt,enddt);

if last.subject;
run;

proc sort data=source.demographic out=demographic;
by subject;
run;

data demog_dose;
merge demographic dosing;
by subject;
run;

options missing=' ';

data sdtm.dm;
set EMPTY_DM demog_dose(rename=(race=_race));

studyid='XYZ123';
domain='DM';
usubjid=left(uniqueid);
subjid=put(subject,3.);
rfstdtc=put(firstdose,yymmdd10.);
rfendtc=put(lastdose,yymmdd10.);
rfxstdtc=put(firstdose,yymmdd10.);
rfxendtc=put(lastdose,yymmdd10.);
rficdte=put(icdate,yymmdd10.);
rfpendtc=put(lastdoc,yymmdd10.);
dthfl='N';
siteid=substr(subjid,1,1) || "00";
brthdte=put(dob,yymmdd10.);
age=intck('year', dob, firstdose, 'c');
if age ne . then ageu='YEARS';
sex=put(gender,sex_demographic_gender.);
race=put(_race,race_demographic_race.);
armcd=put(trt,armcd_demographic_trt.);
arm=put(trt,arm_demographic_trt.);
actarmcd=put(trt,armcd_demographic_trt.);
actarm=put(trt,arm_demographic_trt.);
country="USA";
run;
```

dm.sas

```
proc sort data=source.dosing(keep=subject startdt enddt) out=dosing;
by subject startdt;
run;

data dose_sum;
set dose_raw;
by subject;

retain firstdose lastdose;

if first.subject then do;
firstdose=.;
lastdose=.;
end;

firstdose=min(firstdose,startdt,enddt);
lastdose=max(lastdose,startdt,enddt);

if last.subject;
run;

proc sort data=source.demographic out=demographic;
by subject;
run;

data demog_dose;
merge demographic dosing;
by subject;
run;

options missing=' ';

data sdm.dm;
set EMPTY_DM demog_dose(rename={race=_race});

studyid='XYZ123';
domain='DM';
usubjid=left(uniqueid);
subjid=put(subject,3.);
rfstdtc=put(firstdose,ymmddl0.);
rfendtc=put(lastdose,ymmddl0.);
rfxstdtc=put(firstdose,ymmddl0.);
rfxendtc=put(lastdose,ymmddl0.);
rficdte=put(icdate,ymmddl0.);
rfpendtc=put(lastdoc,ymmddl0.);
dthfl='N';
siteid=substr(subjid,1,1) || "00";

age=intck('year', dob, firstdose, 'c');

sex=put(gender,sex_demographic_gender.);
race=put(_race,race_demographic_race.);
armcd=put(trt,armcd_demographic_trt.);
arm=put(trt,arm_demographic_trt.);
actarmcd=put(trt,armcd_demographic_trt.);
actarm=put(trt,arm_demographic_trt.);
country="USA";
run;
```


How is AGE derived and what data does it depend on?

macros	source	sdtm	adam	tlf
 %derive_baseline.sas	 demographic.sas	 dm.sas	 adae.sas	 t14_1_1.sas
 %dtc2dt.sas	 dosing.sas	 ae.sas	 adef.sas	 t14_2_1.sas
 %derive_age.sas	 labs.sas	 cm.sas	 adsl.sas	 t14_3_1.sas
 %flag_last.sas	 adverse.sas	 ex.sas	 adef.sas	 l162_1.sas
 %km_plot.sas	 exposure.sas	 lb.sas	 adtte.sas	 l16_2_2.sas
 %visit_window.sas	 vital_signs.sas	 vs.sas	 advs.sas	 f14_2_1.sas
 +14 more	 +18 more	 +30 more	 +16 more	 +174 more

```
demographics.sas

proc format;
value trt 1="Active" 0="Placebo";
value gender 1="Male" 2="Female";
value race 1="White" 2="Black" 3="Other";
run;

data source.demographic;
set raw.demographic;
label subject="Subject Number" trt="Treatment" gender="Gender"
race="Race"
orace="Other Race Specify" dob="Date of Birth" uniqueid=
"Company Wide Subject ID" randdt="Randomization Date" icdate=
"Informed Consent Date" lastdoc="Last date of contact";
input subject 1-3 trt 5 gender 7 race 9 orace $ 11-20 +1 dob
mmddyy10. +1
randdt mmddyy10. +1 icdate mmddyy10. +1 lastdoc mmddyy10.;
uniqueid='UNI' || put(subject,3.);
format dob randdt icdate lastdoc mmddyy10.;
run;

data _null_;
rc = filename('xptdir', "&xptdir");
if fexist('xptdir') = 0 then rc = dcreate("xpt",
"/mnt/viya-share/homes/demo-study/data/xpt");
run;

libname xpt_demo xport "&xptdir./demographic.xpt";
data xpt_demo.demograp;
set source.demographic;
run;
libname xpt_demo clear;
```

```
dosing.sas

* dosing.sas;
data source.dosing;
label subject="Subject Number" startdt="Dosing start date" enddt=
"Dosing end date" ddose="Daily dose taken (pills)" uniqueid=
"Company Wide Subject ID" startmm="Month of Start Dose" startdd=
"Day of Start Dose" startyy="Year of Start Dose" endmm=
"Month of End Dose" enddd="Day of End Dose" endyy=
"Year of End Dose";
input subject 1-3 startmm 5-6 startdd 8-9 startyy 11-14 endmm 16-17
enddd
19-20 endyy 22-25 ddose 27;
uniqueid='UNI' || put(subject,3.);
startdt=mdy(startmm, startdd , startyy);
enddt=mdy(endmm, enddd, endyy);
format startdt enddt mmddyy10.;
datalines;
;
run;
```

```
dm.sas

proc sort data=source.dosing(keep=subject startdt enddt) out=dosing;
by subject startdt;
run;

data dose_sum;
set dose_raw;
by subject;

retain firstdose lastdose;

if first.subject then do;
firstdose=.;
lastdose=.;
end;

firstdose=min(firstdose,startdt,enddt);
lastdose=max(lastdose,startdt,enddt);

if last.subject;
run;

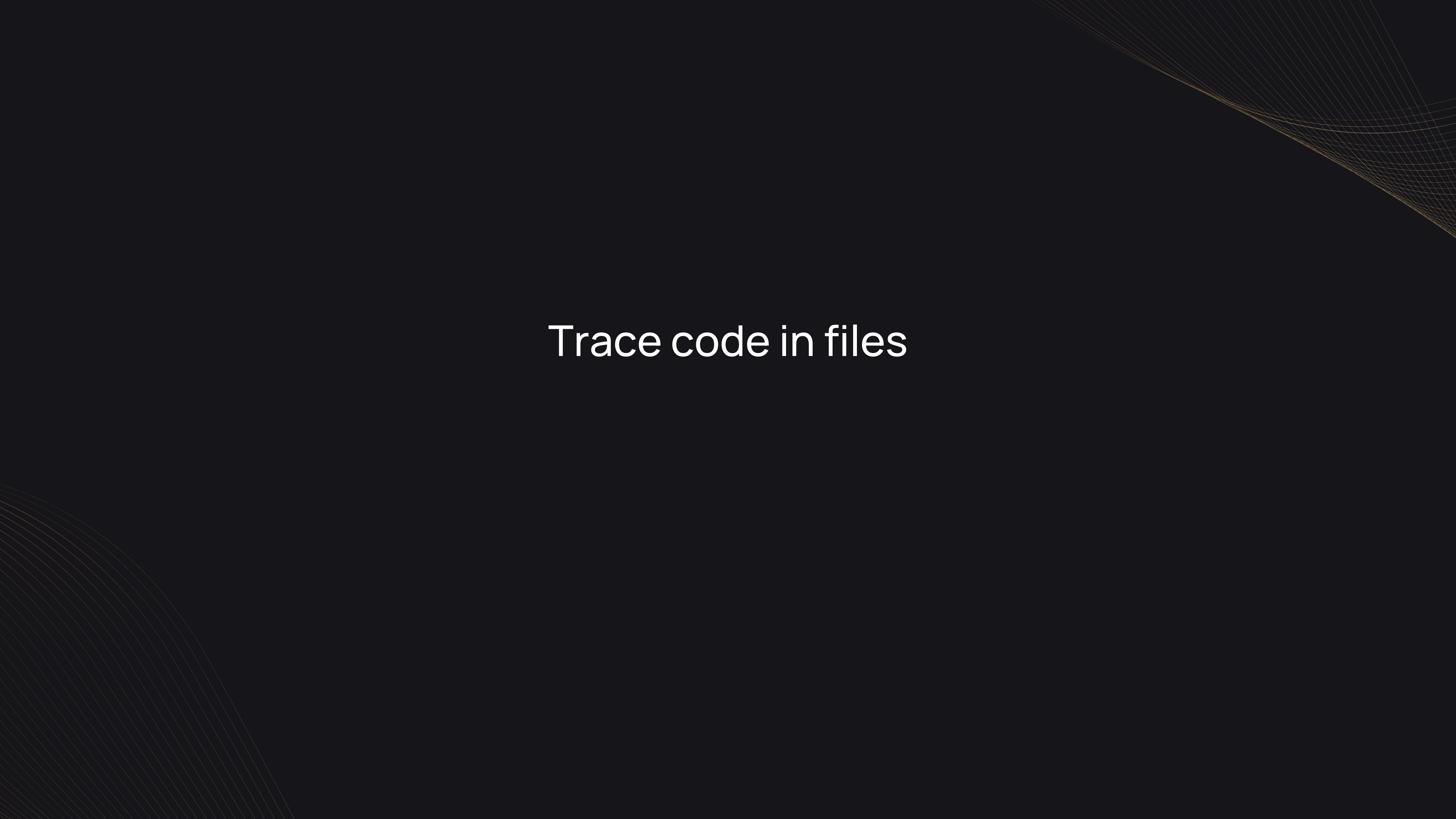
proc sort data=source.demographic out=demographic;
by subject;
run;

data demog_dose;
merge demographic dosing;
by subject;
run;

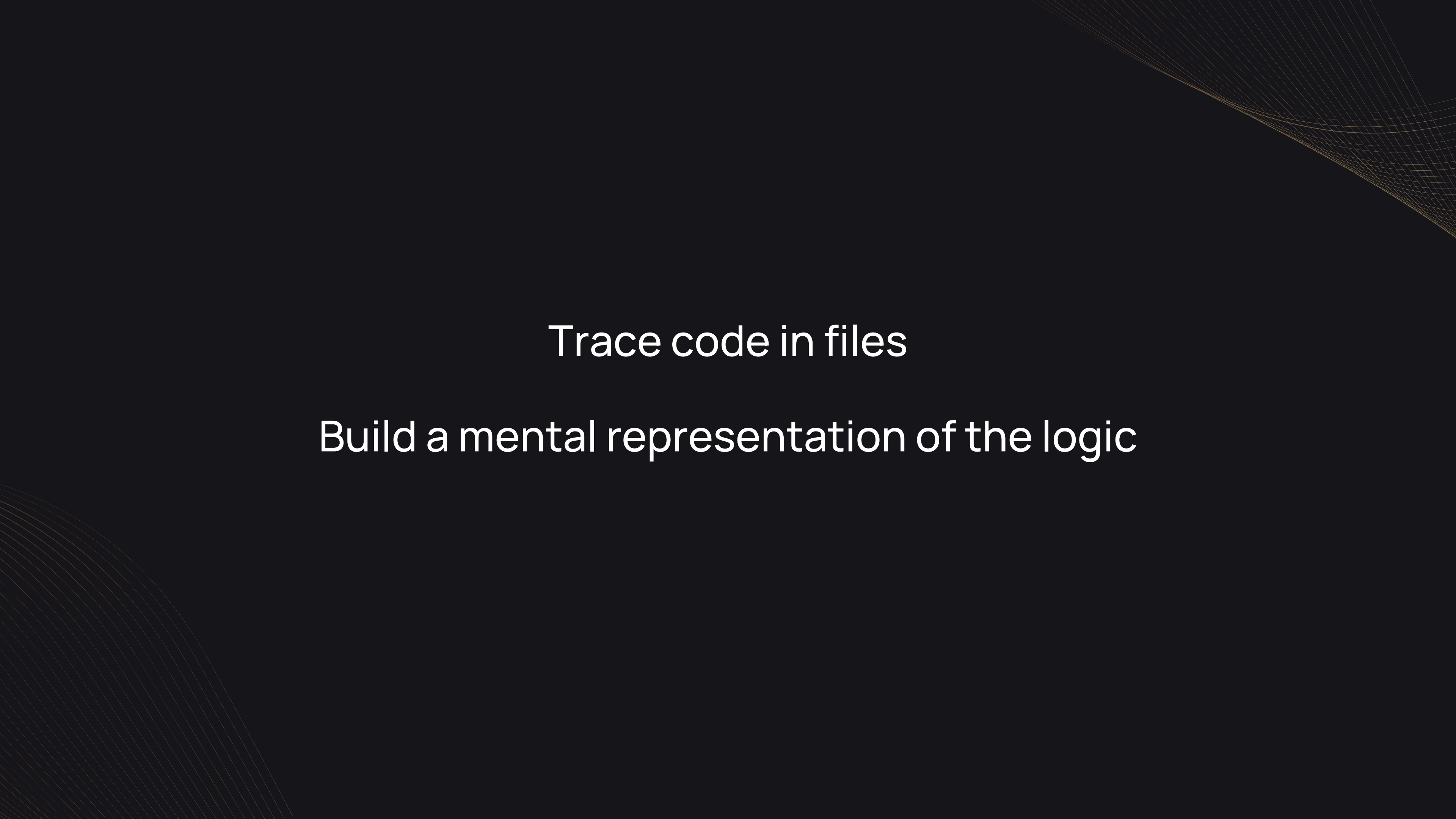
options missing=' ';

data sdtm.dm;
set EMPTY_DM demog_dose(rename=(race=_race));

studyid='XYZ123';
domain='DM';
usubjid=left(uniqueid);
subjid=put(subject,3.);
rfstdtc=put(firstdose,ymmdd10.);
rfendtc=put(lastdose,ymmdd10.);
rfxstdtc=put(firstdose,ymmdd10.);
rfxendtc=put(lastdose,ymmdd10.);
rficdtc=put(icdate,ymmdd10.);
rfpendtc=put(lastdoc,ymmdd10.);
dthfl='N';
siteid=substr(subjid,1,1) || "00";
brthdte=put(dob,ymmdd10.);
age=intck('year', dob, firstdose, 'c');
if age ne . then ageu='YEARS';
sex=put(gender,sex_demographic_gender.);
race=put(_race,race_demographic_race.);
armcd=put(trt,armcd_demographic_trt.);
arm=put(trt,arm_demographic_trt.);
actarmcd=put(trt,armcd_demographic_trt.);
actarm=put(trt,arm_demographic_trt.);
country="USA";
run;
```

Trace code in files



Trace code in files

Build a mental representation of the logic

What variables does **AGE** depend on?

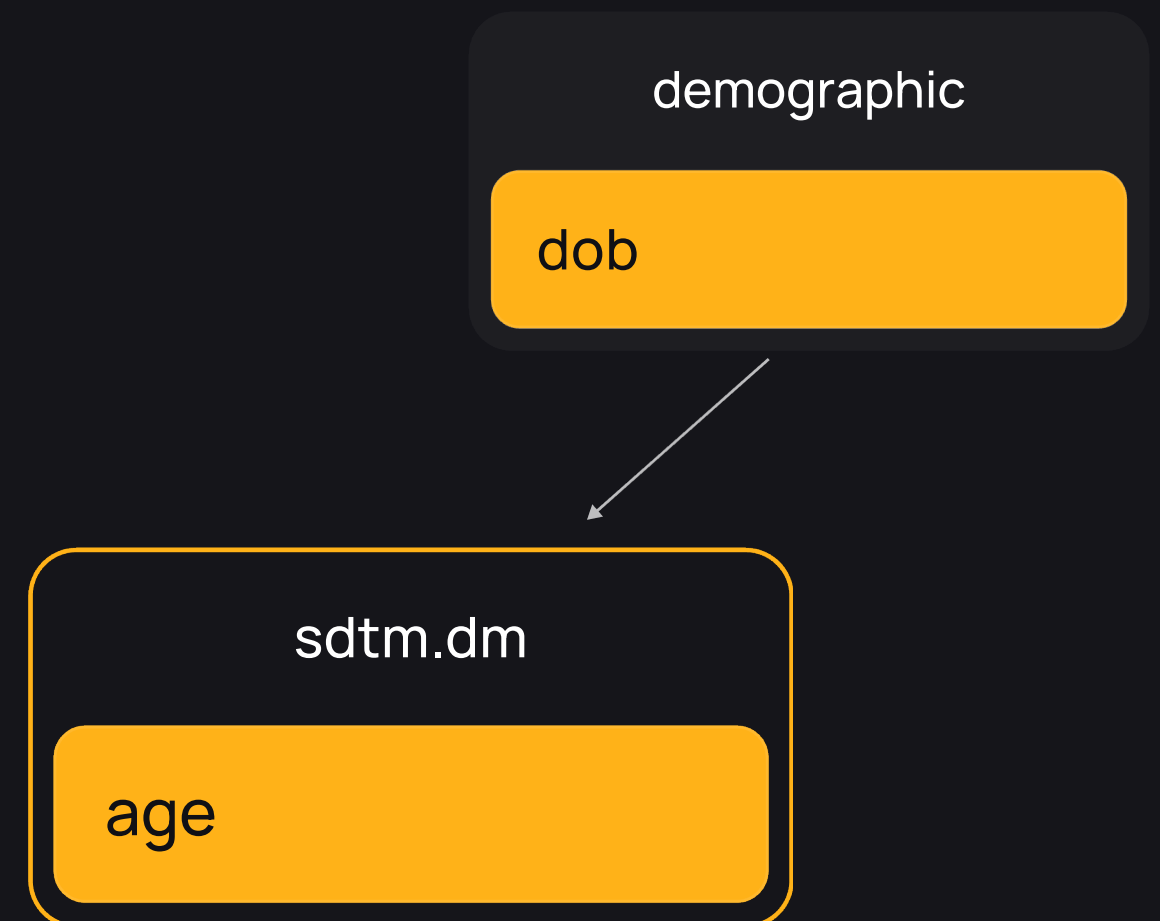
```
data sdtm.dm;  
age=intck('year',dob,firstdose,'c');
```

sdtm.dm

age

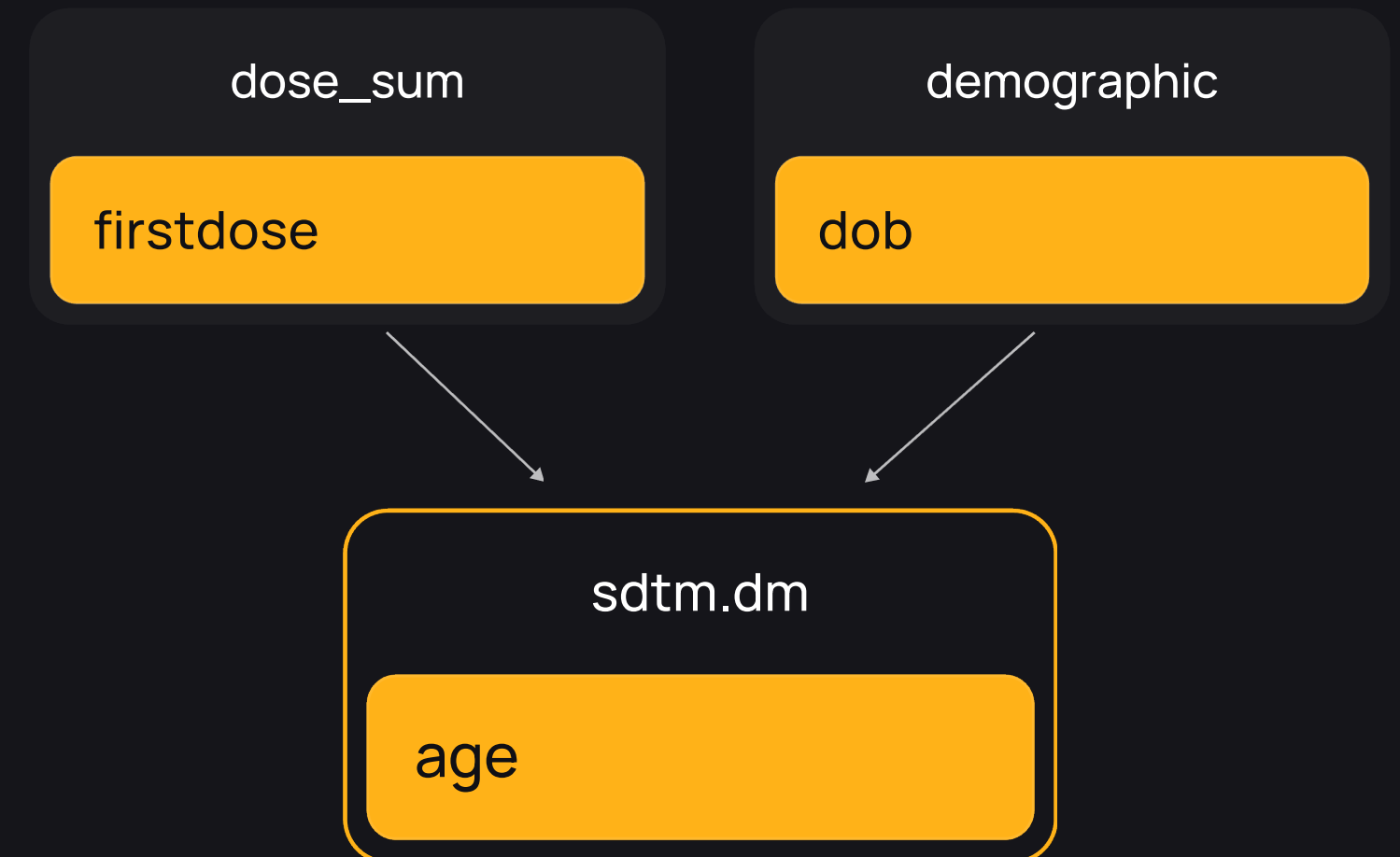
What variables does **AGE** depend on?

```
data demographic;  
set raw_demographics;  
  
data sdtm.dm;  
set demographic dose_sum;  
age=intck('year', dob, firstdose, 'c');
```



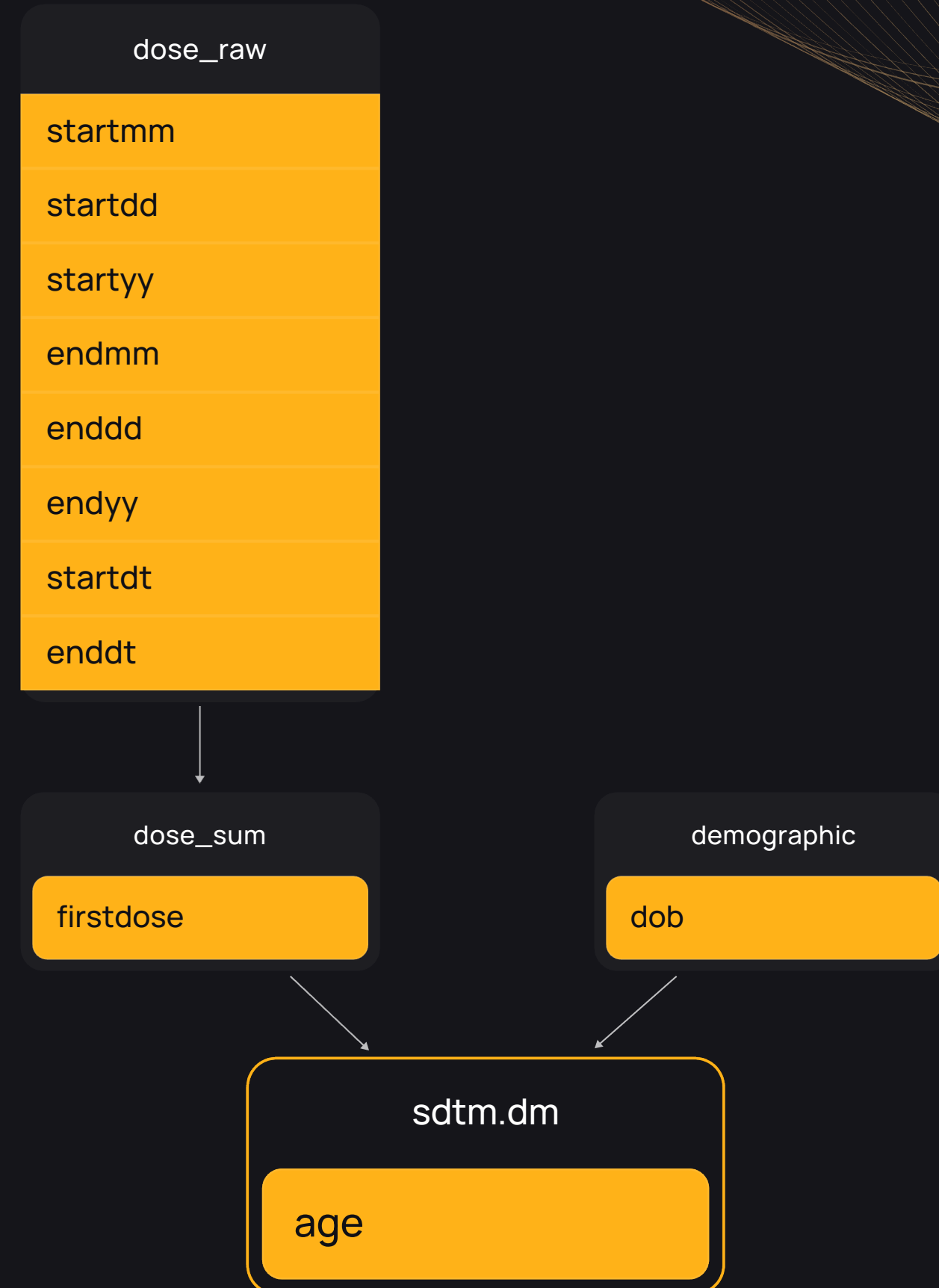
What variables does **AGE** depend on?

```
data dose_sum;  
if first.subject then do;  
firstdose=.;  
firstdose=min(firstdose, startdt, enddt);  
  
data demographic;  
set raw_demographics;  
  
data sdtm.dm;  
set demographic dose_sum;  
age=intck('year', dob, firstdose, 'c');
```



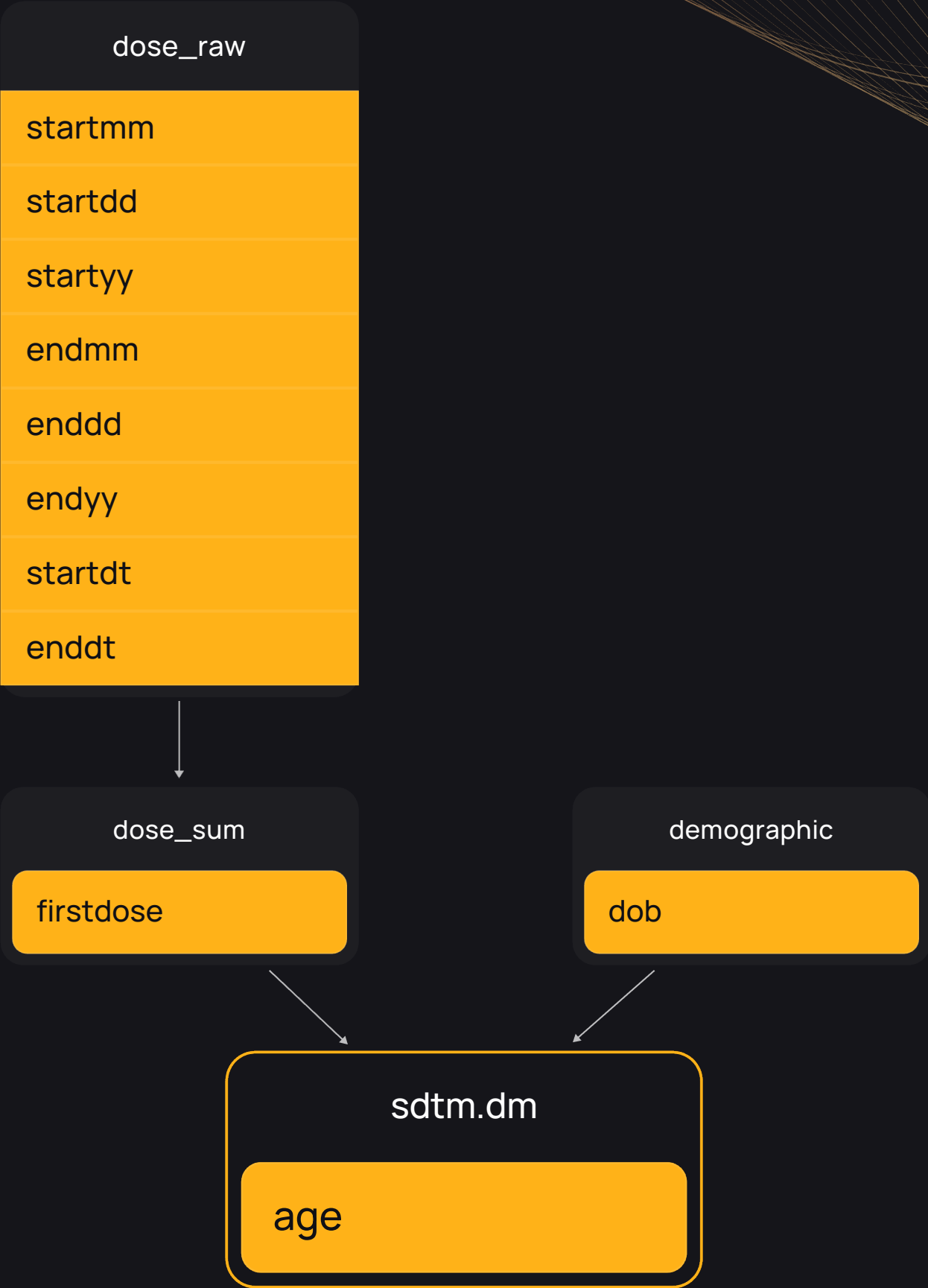
What variables does **AGE** depend on?

```
data dose_raw;  
startdt=mdy(startmm, startdd , startyy);  
enddt=mdy(endmm, enddd, endyy);  
run;  
  
data dose_sum;  
if first.subject then do;  
firstdose=.;  
firstdose=min(firstdose,startdt,enddt);  
run;  
  
data demographic;  
set raw_demographics;  
run;  
  
data sdtm.dm;  
set demographic dose_sum;  
age=intck('year', dob, firstdose, 'c');
```



What variables does AGE depend on?

Dataset	Variable
dose_raw	startmm
dose_raw	startdd
dose_raw	startyy
dose_raw	endmm
dose_raw	enddd
dose_raw	endyy
dose_raw	startdt
dose_raw	enddt
dose_raw	firstdose
demographic	dob



What is **age**?

dob	firstdose
1974-02-05	2010-03-28
...	...
...	...
...	...
...	...



```
age.sas
...
firstdose=min(firstdose,startdt,enddt);
age=intck('year',dob,firstdose,'c');
```



age
36
...
...
...
...

Perfect transparency, trust and confidence in submissions

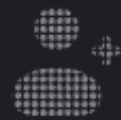
Handle more studies, faster, with fewer resources at higher quality

Lower cost

From planning to regulatory review



Planning



Onboarding



Programming



Validation



Submission

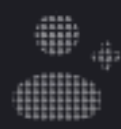


Regulatory review

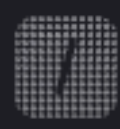
Validation, submission & regulatory review



Planning



Onboarding



Programming



Validation



Submission



Regulatory review

Automate **validation** of study analyses



Planning



Onboarding



Programming



Validation



Submission



Regulatory review

Automate **validation** of study analyses

1. Validating that code matches specs

Automate **validation** of study analyses

1. Validating that code matches specs
2. Validating that data is correct

Automate **validation** of study analyses

1. Validating that code matches specs
2. Validating that data is correct
3. Validating outputs

Automate **validation** of study analyses

1. Validating that code matches specs
2. Validating that data is correct
3. Validating outputs

Automated by 95%+

Dataset	Variable	Label	Status	Type
ADAE	EXFDT	Date of First Exposure to Treatment	✓	Trace
ADAE	AESTDT	Adverse Event Start Date	✓	AI
ADAE	AEENDY	Analysis Relative Day of Adverse Event End	!	Trace
ADAE	ASTDT	Analysis Start Date	✓	AI

Validating that `code` matches specs

1. Constants

Validating that `code` matches specs

1. Constants
2. Mappings

Validating that `code` matches specs

1. Constants
2. Mappings
3. Standard macros

Validating that **code** matches specs

1. Constants
2. Mappings
3. Standard macros
4. Study-specific derivations

Validating that **code** matches specs

1. Constants
2. Mappings
3. Standard macros
4. Study-specific derivations

Goal is to fully automate validation of SDTM and ADaM analyses

Validating that **data** is correct

1. CDISC CORE

Validating that **data** is correct

1. CDISC CORE
2. Missing values

Validating that **data** is correct

1. CDISC CORE
2. Missing values
3. Outliers

Validating that **data** is correct

1. CDISC CORE
2. Missing values
3. Outliers
4. Codelist mismatches

Validating outputs

Tracing from output to raw data

Automate **submission** documentation



Planning



Onboarding



Programming



Validation



Submission



Regulatory review

Submission documentation is a bottleneck

Reviewer's Guides and Define-XMLs are time-consuming and error-prone to produce

- Documentation is often inconsistent with the actual analysis and data
- Documentation is started after analyses are completed, delaying submission readiness

Inconsistencies confuse regulators, slow review, and delay time-to-market

Verisian AI to generate submission documentation

Bayer applied Verisian to build full study traceability and automate submission documentation

- Documentation was generated from the code that was actually run, not the specifications
- Guaranteed consistency between code, data, results, and documentation
- Powered by deterministic, fully reproducible graph theory

"The Verisian AI infrastructure is enabling Bayer to take big steps towards delivering our data caterer vision, where 80% of the busywork is automated by trustworthy and evidence-based AI."

Sascha Ahrweiler, VP, Head Statistical Programming & Analysis - Strategy & Operations

What **Verisian AI** delivered to Bayer

On a non-CDISC clinical trial for a NMPA Full Approval Submission:

- Complete ADaM-level Define-XML generated, 90-95% at submission quality
- Crucial Reviewer's Guide sections generated at submission quality
- Generated in minutes

“While the computational methods for complicated efficacy endpoint variables are not perfect and require a review, overall about 90-95% are good enough to submit as-is. The important sections in the ADRG that needed an update from the last NMPA submission, mainly those concerned with explaining dataset lineage and summarizing their inputs, content, and ultimate use, were generated at submission quality as well.”

“Given the short timeframe and low resource availability, this would not have been possible without Verisian.”

Cornelia Fulgenzi, Compound Lead, Bayer

Augmented submissions

Faster approvals



Planning



Onboarding



Programming



Validation



Submission



Regulatory review

Make your studies AI-ready in **one day**



Verisian

AI-ready information
infrastructure for clinical trials

Statisticians

Clinicians

Data managers

Medical writers

Statistical programmers

...

↻ File transfer

Data, TLFs, Code,
SAP, specs



Your systems



SCE



Storage



...

Across any **operating model**



In-house teams



CRO outsourcing

...and your entire study team



Perfect transparency, trust and confidence in submissions

Perfect transparency, trust and confidence in submissions

Handle more studies, faster, with fewer resources at higher quality

Perfect transparency, trust and confidence in submissions

Handle more studies, faster, with fewer resources at higher quality

Lower cost