

Standardizing FDA Data to Improve Success in Pediatric Drug Development

Case Study: Harmonizing Hypertensive Pediatric Data across Sponsors using SAS® and the CDISC Model

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ABSTRACT

The United States Food and Drug Administration (FDA) have accumulated the largest number of regulatory submissions of pediatric clinical trial data in the world. In line with the Critical Opportunities list initiated by the FDA in 2006, topic 6, opportunity 72 describes the development of a pediatrics database with a key goal of converting existing electronic datasets from pediatric studies to a standardized format so that the data can be imported into a data repository that can be queried. In order to facilitate analysis of data across various pediatric trials, the FDA needed the data transformed into a uniform standard structure. The FDA and SAS Institute initiated a pilot project to implement a standardized data repository of pediatric hypertensive data that can be queried, analyzed and reported on to promote the analysis of data across pediatric studies. The Clinical Data Standards Consortium (CDISC) Study Data Tabulation Model (SDTM V3.1.1) was selected as the standard for this data repository. This paper describes the methodologies, technologies and processes used to transform and harmonize the legacy pediatric data into the CDISC SDTM model.

INTRODUCTION

In recent years, the number of pediatric clinical drug trials submitted to the FDA has increased substantially. The data from these studies have provided new information regarding safety, efficacy, dosing and unique risks of drugs in pediatric patients. SAS Institute and the FDA collaborated on a pilot project to analyze antihypertensive pediatric trial data submitted to the FDA. To facilitate the analysis across multiple studies from various sponsors, the data was transformed into the CDISC SDTM standard structure. The purpose of this paper is to document the methodologies, technologies and processes used to transform and harmonize pediatric antihypertensive legacy clinical data into CDISC SDTM model.

PROJECT OVERVIEW

The main goal of this project was to improve the success rate of pediatric clinical trials by optimizing the design and efficiency of future pediatric studies based on lessons learned from the retrospective analysis of relevant pediatric clinical trial data submitted to the FDA. In addition, the project objectives included the following:

- Test methodologies for data transformation of legacy data into CDISC compliant SDTM datasets and accompanying metadata.
- Create a repository of standardized clinical trial data from studies submitted to the FDA in response to Pediatric Written Requests (PWRs).
- Identify and prioritize research questions and develop hypotheses
- Analyze data and develop recommendations for future pediatric clinical trials

This paper discusses the first two objectives listed above. A number of antihypertensive pediatric trials have been conducted and submitted to the Agency with a majority of these trials failing to demonstrate efficacy in pediatric patients. All of the submissions were in electronic format, but none of the data from the trials are CDISC compliant. The FDA provided data from these trials as raw source data for the project.

SAS Institute supplied the technology to transform, load, and store the data. In addition, SAS provided team members to develop and execute the processes for transforming the data into the SDTM model. The FDA project members supplied all the data and documentation to SAS, and provided access to reviewers who were familiar with the submissions in order to answer questions. In addition, the FDA team provided input surrounding issues with mapping to the SDTM model.

In the beginning of the project the project team agreed it would be very resource intensive to attempt to convert all

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possible data domains. As a result, the FDA members identified the domains they considered a priority for integrated analysis. These domains included:

- DM – Demographics
- EX – Exposure (Dosing)
- AE – Adverse Events
- VS – Vital Signs
- PC – Pharmacokinetic Concentrations
- SC – Subject Characteristics

PROCESS OVERVIEW

For this project, the SAS team developed a standard process for organizing, standardizing, analyzing, transforming, and validating the clinical trial data. A SAS® Drug Development repository was created to organize and control access to the clinical data. The SAS Drug Development repository provided secure and compliant internet access (HTTPS) to all project members which facilitated easy collaboration between team members. SAS® Data Integration Server and SAS® Data Integration Studio were used to transform and standardize the data. Several different SAS tools including base SAS, the SAS® Drug Development Data Explorer, and the SAS® Drug Development Data Definition Explorer were used to map and validate the transformed data. The following process was followed for each of the studies:

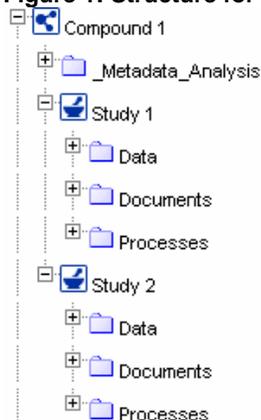
- A standard hierarchy structure was created in the SAS Drug Development repository to organize the data and documentation.
- A mapping matrix was created for each domain to describe the variables and algorithms to convert the raw data to the SDTM data model.
- Data transformation processes were developed in Data Integration Studio to transform the submission data into the SDTM data model.
- Validation was performed on the resulting SDTM data sets.
- A single set of SDTM tables was created aggregating all the study data within each domain.
- Cross-study validation was performed to standardize data values across studies.

The following sections provide details of each step in the process and how the tools were utilized.

DATA ORGANIZATION

The clinical data used in this project consisted of 29 clinical trials within thirteen compounds from eight sponsors. To organize and store the data, a standardized hierarchy was built within SAS Drug Development and SAS Data Integration Studio. This standardized hierarchy streamlined the setup of each of the studies and provided a consistent interface for the project team. In SAS Drug Development a structure was created for each compound including a folder for each study and a folder containing the results of the metadata analysis across studies. Within each study, separate folders were created for documentation, raw data and SDTM data. Figure 1 displays a sample of the compound/study hierarchy.

Figure 1: Structure for Studies within a Compound in SAS Drug Development



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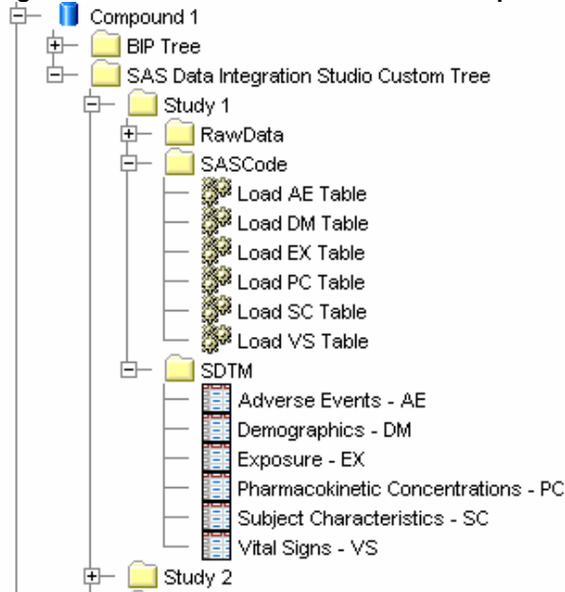
An additional hierarchy was built in SAS Drug Development to contain the aggregated data across all studies as shown in Figure 2. This hierarchy contained documentation and processes that applied to the aggregated data.

Figure 2: All Studies Structure in SAS Drug Development



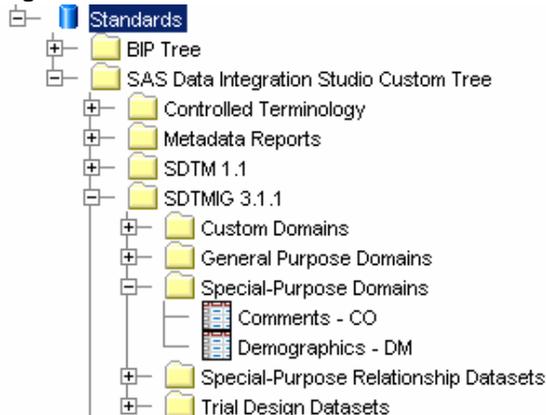
In SAS Data Integration Server, a metadata repository was created for each compound. Similar to the structure in SAS Drug Development, each of the compound repositories contained a folder referencing the metadata for the Raw Data, SAS Code and resulting SDTM tables (see Figure 3). All data was physically stored in the SAS Drug Development repository and simply referenced by the SAS code in SAS Data Integration Studio using the SAS® WebDAV libname engine.

Figure 3: Structure for Studies within a Compound in Data Integration Studio



A standards repository was also created which defines the physical structure, metadata, and business rules for creating SDTM domains as well as controlled terminology tables. Figure 4 shows an example of the organizational hierarchy within SAS Data Integration Studio.

Figure 4: Structure for CDISC Standards in Data Integration Studio



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DATA STANDARDIZATION

In clinical trials, coded values are often used to collect responses on the Case Report Form. One of the challenges of working with study data collected from multiple sponsors is reconciling the differences in response values. The CDISC Controlled Terminology team, in cooperation with the U.S. National Cancer Institute Enterprise Vocabulary Services, is in the process of developing standardized responses for SDTM variables. To date, the SDTM Package-1 contains 30 production code lists (examples include adverse event severity and accepted dose forms) with more than 700 controlled terms. SDTM Package-2A is currently undergoing public review and SDTM Package-2B is under development.⁴ The SAS team created a dictionary to collect a centralized list of all terminology used across the studies and mapped the raw values to the proposed SDTM controlled terminology.

Production SDTM code lists were used for fourteen variables within the Adverse Events, Demographics, Exposure, and Vital Signs domains:

Adverse Events

AEACN - Action Taken with Study Treatment
 AEOUT - Outcome of Adverse Event
 AEREL – Causality
 AESEV - Severity/Intensity

Demographics

AGEU – Age Units
 COUNTRY – Country
 SEX –Sex

Exposure

EXDOSFRM - Dose Form
 EXROUTE - Route of Administration

Subject Characteristics

SCORRESU - Original Units
 SCSTRESU - Standard Units

Vital Signs

VSORRESU - Original Units
 VSSTRESU - Standard Units
 VSTESTCD - Vital Signs Test Short Name

Values for other domain columns (e.g. RACE, ARM, ARMCD, SCTESTCD) were standardized across studies based on feedback from the FDA team. The dictionary was created as a SAS data set and stored within SAS Drug Development. The dictionary contained a key structure to facilitate mapping each raw value to a standardized value based on the compound, study, and domain. The dictionary served two purposes. First, the dictionary provides a single table used while developing processes to transform the data. Using the SAS Data Integration Studio Look-up transformation, the SAS team referenced the dictionary to apply the data standardization to the raw data during the transformation process. Therefore, when a controlled terminology value was modified, the change only had to be made in the dictionary, and all of the transformation processes referenced this table. Second, the dictionary provided a central location to allow the FDA to explore and review the different coding terminology used across the studies. Figure 5 shows a sample of the dictionary table.

Figure 5: Sample Controlled Terminology Dictionary

SDTM Variable Name	Original Rawdata Mapped Value	Standardized SDTM Mapped Value
AEACN	Interrupt Study Drug	DRUG INTERRUPTED
AEACN	Discontinue Study Drug	DRUG WITHDRAWN
AEACN	Increase Study Drug	DOSE INCREASED
AEACN	Decrease Study Drug	DOSE REDUCED
AEACN	None	DOSE NOT CHANGED
AEREL	Not Related	DEFINITELY NOT
AEREL	Unlikely	PROBABLY NOT
AEREL	Possible	POSSIBLY
AEREL	Probable/Likely	PROBABLY
AEREL	Certain	DEFINITE
SEX	Male	M
SEX	Female	F
EXDOSFRM	INFUSION	INFUSION
EXROUTE	IV	IV
VSTESTCD	SYSBP	SYSBP
VSTESTCD	DIABP	DIABP
VSTESTCD	HR	HR

METADATA ANALYSIS

The next step in the process was to review the accompanying study documentation to gain an understanding of the study. Most of the studies included a Data Definition Document (define.pdf), an annotated Case Report Form, and the study report. From this information, the SAS team created a detailed mapping matrix for each domain within a study for a given compound. Due to the variability in the data across sponsors and the learning curve for the study designs and data structures, creating the mapping matrix was a time consuming process. Frequent discussions between the SAS team and FDA reviewers familiar with the data were required to resolve questions and issues about the data and how the study was conducted.

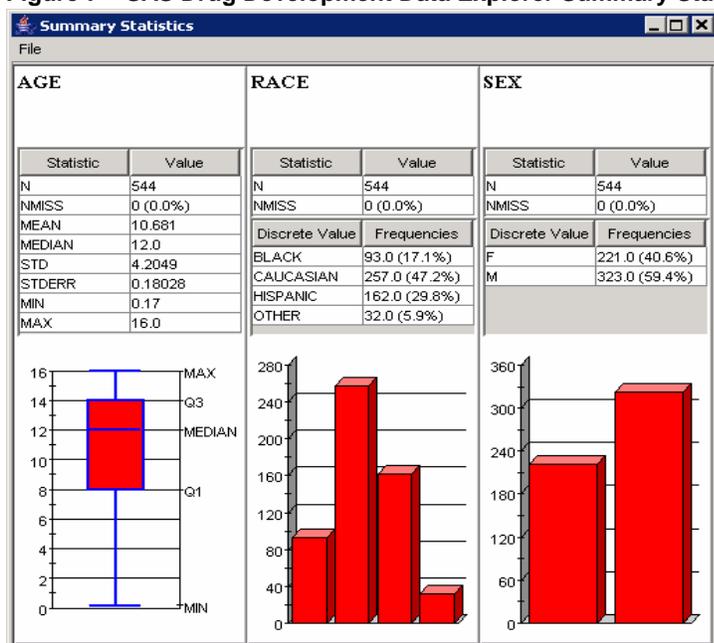
In addition to the study documentation, the team used several SAS tools to aid in the metadata analysis. The primary tool utilized was the SAS Drug Development Data Definition Explorer (see Figure 6). This tool is designed specifically for metadata exploration and allowed the team members to run reports comparing the metadata across tables to determine differences in the raw metadata across the studies. For example, in the report below for the AGE variable, the two studies being compared have different values for the format, informat and label. Further investigation is required to determine if age was measured in years for both studies and if age was in reference to a baseline date.

Figure 6 – SAS Drug Development Data Definition Explorer

	Library Name	Column Name	Column Status	Column Notes	Column Label	Column Length	Column Format	Column Informat
1	DDE1	age	Problem		Age in Years at Baseline	8.0	BEST12.	F12.
2	DDE2	age	Problem	Differences: label; format; informat	age	8.0		
6	DDE1	HEIGHT	Problem		Height in Centimeters	8.0	BEST12.	F12.
7	DDE2	HEIGHT	Problem	Differences: label; format; informat	HEIGHT	8.0		

Another tool which was useful in exploring the data is the SAS Drug Development Data Explorer. This tool aided the metadata analysis by providing a list of possible values (i.e. code lists) for each of the variables. The Summary Statistics report in Figure 7 shows an example of a report generated by the Data Explorer. At a glance, this report shows that the age of participants ranged from 0.17 to 16 years, there were four race groups who participated, and 40.6% of the participants were female.

Figure 7 – SAS Drug Development Data Explorer Summary Statistics



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The metadata analysis resulted in a set of domain mapping matrices for each study. The mapping matrix for a given domain contained:

- A list of the SDTM variables
- A table name and column name of the raw data variable
- Any conversions which may be required (i.e. changing SAS date variables to character variables in ISO 8601⁵ format)
- Any derivations required to define the SDTM variable
- Comments for additional explanation

Figure 8 shows a sample of a mapping matrix for Vital Signs. The matrix maps raw data from the VITALS table to the VS SDTM domain. The mappings for the SDTM variables fell into one of five categories: simple mapping, reformat variable, simple derivation, complex derivations, and dictionary lookups (i.e. code lists). Examples of each of these categories in the mapping matrix below are:

- Simple one-to-one mappings - STUDY →STUDIYID and VNUM→VISITNUM
- Simple expression – USUBJID = “COMPOUND1” + STUDY+CENTER+PATID
- Reformatting variables - VSDTC = PUT(VISITDT,IS8601DA.)
- Complex derivations for inclusion/exclusion criteria – VSORRES, the value for SOUND should be retained until the next non-missing value is encountered.
- Dictionary lookups - for Korotkoff Sound vital sign VSPOS is derived by performing a dictionary lookup on the raw variable MEASURE.

Figure 8 -Sample Mapping Matrix for Vital Signs SDTM Domain

Mapping Matrix
Compound: Compound 1
Study: 101
SDTM Domain: VS (Vital Signs)

SDTM Variable Name	Source Column (Raw Data Set)			
	PULSE (VITALS)	SOUND (VITALS)	BASE_PUL (VITALS)	CHG_PUL (VITALS)
STUDIYID	STUDY	▶	▶	▶
DOMAIN	“VS”	▶	▶	▶
USUBJID	“COMPOUND1” + STUDY+CENTER+PATID	▶	▶	▶
VSSEQ	See algorithm below	▶	▶	▶
VSTESTCD	“HR”	“KSOUND”	“BASE_HR”	“CHG_HR”
VSTEST	“HEART RATE”	“KOROTKOFF SOUND”	“BASELINE HEART RATE”	“CHANGE FROM BASELINE HEART RATE”
VSPOS	“SITTING”	MEASURE (dictionary lookup)	“SITTING”	“SITTING”
VSORRES	PULSE	SOUND		
VSSTRESC	PULSE case when PULSE>. then put(PULSE,8.) else “ “ end	SOUND (dictionary lookup)	BASE_PUL case when BASE_PUL>. then put(BASE_PUL,8.) else “ “ end	CHG_PUL case when CHG_PUL>. then put(CHG_PUL,8.) else “ “ end
VSSTRESN	PULSE	SOUND	BASE_PUL	CHG_PUL
VSSTRESU	“BEATS/MIN”		“BEATS/MIN”	“BEATS/MIN”
VSLOC		BP_LOC (dictionary lookup)		
VSBLFL	“Y”		“Y”	
VSDRVFL			“Y”	“Y”
VISIT	VISIT	▶	▶	▶
VISITNUM	VNUM	▶	▶	▶
VSDTC	PUT(VISITDT,IS8601DA.)	▶	▶	▶
VSDY	VISDAY	▶	▶	▶

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General Notes:

- ▶ Same as previous column
- Blank cells in table set to null/blank/missing
- SDTM variables not listed have null values.

Record inclusion/exclusion criteria:

- All columns: Exclude record if column value is missing
- BASE_PUL: Keep records only where baseflag=1

Column algorithms:

- VSORRES: Retain non-missing value of SOUND until next non-missing value
- VSSEQ: Generate a sequence number to ensure each record has a unique value within a USUBJID.

Dictionary look-up values:

MEASURE:	SOUND:	BP_LOC:
1='SITTING'	1='KOROTKOFF IV'	1='RIGHT ARM'
2='STANDING'	2='KOROTKOFF V'	2='LEFT ARM'
3='SUPINE'		3='LEG'

The mapping matrix above demonstrates the complexity of some of the domain mappings that were necessary to transform the data. This is one of the reasons the process of understanding the data was the most time consuming part of the project.

DATA TRANSFORMATION

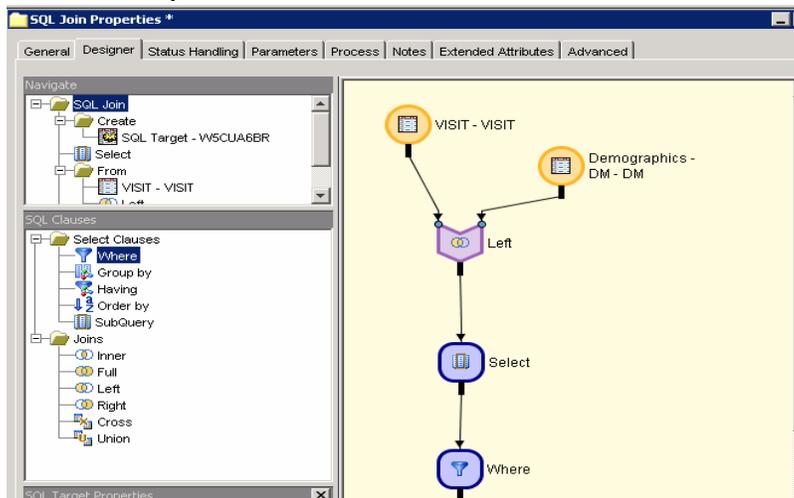
Using the mapping matrix as a guideline, the SAS team used SAS Data Integration Studio to transform the data. SAS Data Integration Studio is a visual design tool for building, implementing and managing data integration processes. This tool provided a multi-user environment for the programmers to build metadata driven transformation processes. Using this tool, the SAS team created consistent, validated, transformation processes for each of the domains in the studies. For some of the compounds, the data transformation process from study to study was almost identical. In these cases, the process from the first study could be copied and simple modifications made (e.g. change the name of the raw data table, modify variable mappings). In other cases, a completely new process needed to be defined for each study.

The SAS Data Integration Server was set up with a separate repository for each of the compounds and a clinical data standards repository containing the metadata for the SDTM domains. For each study, the programmer would login to the appropriate compound repository and import the metadata for the raw data tables. The raw data and the resulting SDTM domains were stored in the SAS Drug Development repository.

The SAS team designed each process to transform the raw data into the SDTM domains. SAS Data Integration Studio provides a variety of data transformations. Below is a summary of the transformations used most frequently in the project:

- SQL Join – The first step in the process often required joining two or more raw data sets. This transformation allows the transformation programmer to define how to join tables (e.g. inner, outer), to define which variables to retain, and to define subsetting where clauses. Figure 9 shows the properties window for the SQL Join transformation.

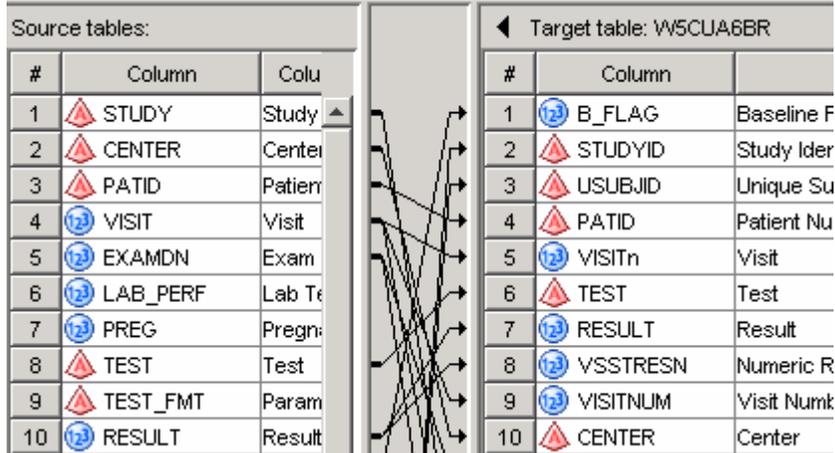
Figure 9 - SQL Join Properties



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- Extract – This transformation allows the transformation programmer to subset the data from the raw data (rows and columns) as well as define simple derivations.
- Table Loader – This transformation allows the transformation programmer to map raw data columns to the SDTM domains, to define derivations, and to load the data into the target SDTM domains. Figure 10 displays the mapping of the raw columns to the target columns.

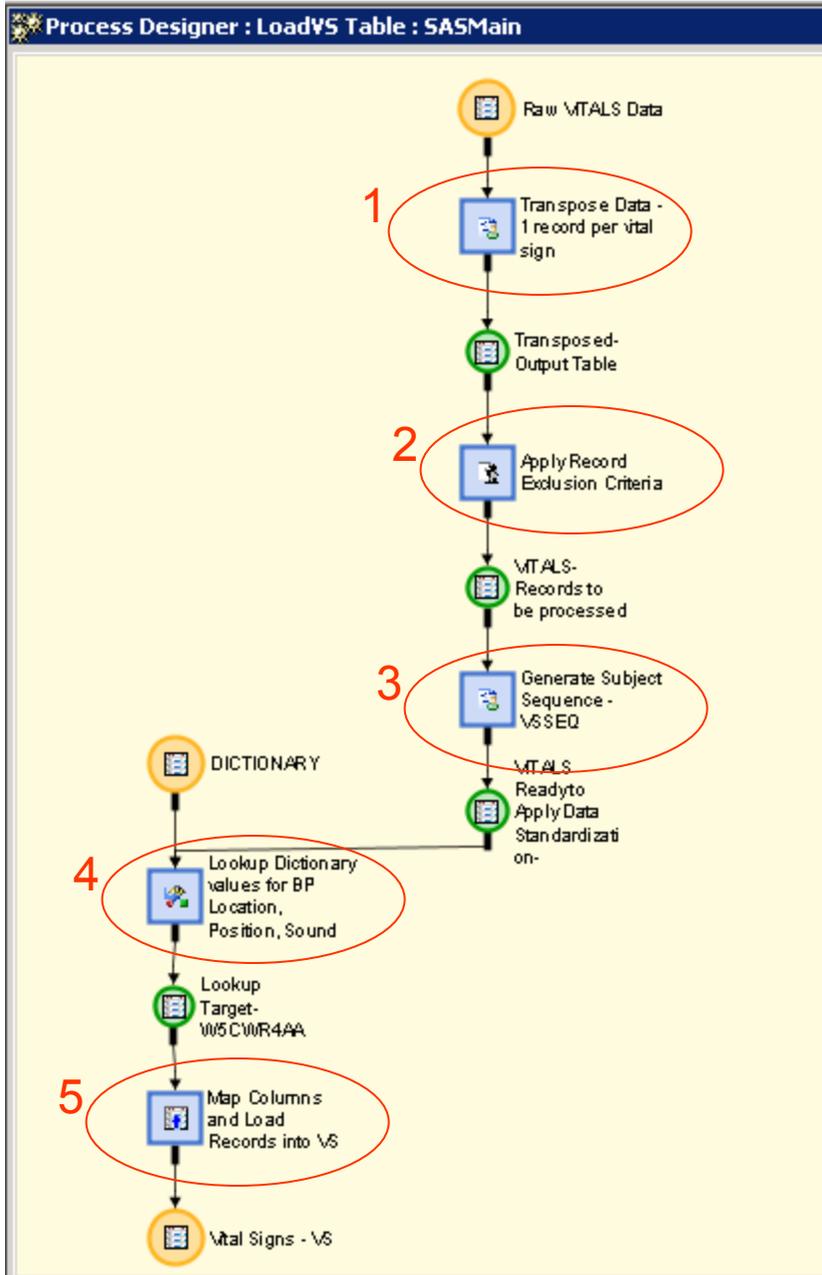
Figure 10 - Data Loader Mapping Properties



- Lookup – This transformation allows the transformation programmer to use the dictionary to 'look up' and replace raw data responses with standardized terminology.
- Transpose – This transformation allows the transformation programmer to alter the structure of the data to meet the SDTM specification. Several of the SDTM domains (e.g. VS, SC) require one record per measure. Most of the raw data contained a single record per patient visit, with multiple measurements.
- Sequence Generator – This custom transformation was developed specifically for SDTM transformations. Based on a unique key structure, this transformation creates the sequence variable (i.e. AESEQ, VSSEQ) needed in some of the domains.
- User Written Code – This transformation allows the transformation programmer to implement an algorithm that could not be applied with one of the standard transformations. For example, extracting the first and last record for a patient.

Figure 11 displays a sample process flow transforming raw data into the SDTM Vital Signs domain.

Figure 11 – Sample Transformation Process for Vital Signs Domain



In the Data Integration Studio process flow above, the VITALS data set contains all of the vital signs recorded during each visit (one column per vital sign). The following steps were followed to transform the data into the SDTM standard for VS.

1. Transpose the data to create data with one record per measure per visit.
2. Execute user-written code to apply the exclusion/inclusion criteria (i.e. exclude any missing vital signs; include baseline vital sign for first visit only).
3. Create a sequence number given to ensure uniqueness within a dataset for a subject (VSSEQ).
4. Use the Lookup transformation to apply the controlled terminology for the vital sign test codes, VSTESTCD.
5. Map the raw data columns to the SDTM VS standard columns and load the records into the SDTM VS table.

In addition to creating SDTM domains for each study, the FDA also requested a process to aggregate the data from all of the studies into a single table for each SDTM domain.

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DATA VALIDATION

The final step in the process was to ensure the transformation process mapped the raw data to the SDTM domains correctly. The SAS team developed a process for validating each domain. A checklist was defined for each domain requiring that all outstanding data integrity and data quality issues be resolved before the domain for that study was declared production. The validation steps included:

- Reviewer analyzed each compound/domain combination using the validation checklist
- Reviewer uploaded the completed checklist into SAS Drug Development and notified the transformation programmer responsible for this study/domain
- Transformation programmer reviewed validation report and updated the transformation process flows as necessary
- Transformation programmer updated the validation report with code changes made and uploaded the completed validation report into the SAS Drug Development hierarchy
- Transformation programmer verified the changes again, and marked the domain complete. If the changes were significant, the transformation programmer could request the reviewer to inspect the domain again.

To verify the results, the validation reviewer used the SAS Drug Development Data Explorer and ad-hoc programming in base SAS. Examples of validation checks performed included verifying:

- the record count against the raw data
- the inclusion/exclusion criteria have been applied
- the controlled terminology have been applied
- the dates and numeric variables were formatted correctly

In addition, aggregated data for each domain was validated using a similar checklist. This validation identified issues such as missing data from study to study and discrepancies in the values across studies.

MODEL AND DATA LIMITATIONS

During the process of analyzing the data and metadata, there were a number of gaps identified in mapping to the SDTM standard. Some of these issues involved limitations in the model specification while other issues involved limitations in the raw data available. This section presents examples of issues identified while working with the SDTM model and “real world” data.

Model Limitations:

The study design for a number of these studies was somewhat complex, involving multiple phases, dose escalation, and crossover studies. The Trial Arm codes and descriptions (ARM, ARMCD) varied widely across compounds. Since the scope of this project did not include implementing the Trial Design domains, the team had to determine how to consistently describe treatments across compounds within the Demographics and Exposure domains. These complex treatments had to be described in a single field (ARM) within the Demographics domain.

The structure of the Vital Signs SDTM specification is very different from how the raw data was collected for all of the studies. The SDTM specification is a normalized vertical structure with one record per measurement. Currently, most sponsors are collecting data with a single record per time-point (i.e. visit) with a column for each measurement. While the structure defined by CDISC might ultimately be better for analysis and regulatory review, the large differences in structure caused the mapping definition and transformation processes to be quite complex in some studies.

There is ambiguity around the SDTM model technical specifications for each variable. For example, with the exception of a few cases, there are no rules about column length or what case character variable should have. If the SDTM variable values were clearly specified, then combining data across sponsors would be more rapid. Also, standardized controlled terminology definitions would reduce the need for re-mapping data values (e.g. PK Test names).

Finally, the SDTM standards were written to support the submission of a single compound and study. To accommodate data from multiple compounds and studies, the model may require changes. A subset of the data from this project is being used in the CDISC FDA Integrated Safety Data Pilot. This pilot will help identify issues with using the SDTM model to collect data for integrated reports such as an Integrated Summary of Safety.

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Data Limitations:

The SDTM specification defines a key set of variables for each domain. In addition, it defines variables that are required, expected and permitted. In the case of legacy data, there were many examples in which the data was just not available to populate the required fields. In the case of keys variables, in some instances the team had to 'break' the SDTM rules and either remove keys or include additional keys to ensure uniqueness. In some other cases the team had to remove the required constraints (i.e. not null) on some variables to allow the data tables to be created.

There was a significant amount of work done to deal with dates across domains. The SDTM specification indicates all dates should be converted to an ISO format and stored as a character variable. The studies in this project varied a great deal as to how the dates were collected. The dates were collected as SAS numeric dates, character dates, partial dates, and parts of the date fields in separate variables. The team had to define specific algorithms for converting the dates to the necessary ISO formats.

CONCLUSION

Overall the project was successful at meeting the following goals:

- Building a standardized database of pediatric hypertension data for use in cross-trial analysis.
- Gaining experience with the CDISC SDTM model.
- Developing a repeatable process for transforming legacy data into the SDTM domains.
- Utilizing SAS tools and solutions to organize, transform, and validate the data repository.
- Providing feedback on the CDISC SDTM model.

This project demonstrates the value of standardizing data for cross study analysis. Public health has a great need for assessing safety across studies, compounds and pharmacologic classes, especially to detect drug interactions. Mapping multiple sponsors' legacy data to SDTM will facilitate good review practice, safety analysis and reporting, as well as provide insight into the patient populations to improve future clinical trial designs.

REFERENCES

1. <http://www.fda.gov/oc/initiatives/criticalpath/opportunities06.html>
2. http://www.fda.gov/oc/initiatives/criticalpath/reports/opp_list.pdf
3. <http://www.cdisc.org/standards>
4. <http://www.cdisc.org/standards/terminology/index.html>
5. <http://www.iso.org/iso/en/prods-services/popstds/datesandtime.html>

TERMINOLOGY

The following terms are used throughout this document.

CDISC - Clinical Data Interchange Standards Consortium (CDISC) is a non-profit organization, whose mission is "to develop and support global, platform-independent data standards that enable information system interoperability to improve medical research and related areas of healthcare".

SAS Data Integration Server – This tool provides organizations with a flexible, reliable and complete solution for meeting all data integration needs. It supports many data integration initiatives including: data warehousing/data marts, data cleansing and enrichment, data migration and data consolidation, and data synchronization.

SAS Data Integration Studio – This application provides a graphical user development environment for designing data integration processes.

SAS Drug Development – This solution provides a controlled and compliant platform for developing, executing and managing the transformation, analysis and submission of clinical research data. SAS Drug Development supports business processes such as data transformations, statistical programming and regulatory compliance, as well as CDISC standards, 21 CFR Part 11 compliance and data exploration across trials.

SDTM – CDISC Study Data Tabulation Model

FDA – United States Food and Drug Administration

Transform - Convert data from a raw data format into a target data format

Standardize – Transform values to standardize terminology across studies

Domain – A specific collection of data within one of the CDISC models (ex. AE – Adverse Events)

WebDAV - Web-Based Distributed Authoring and Versioning

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