

## Submission of Pharmacokinetics (PK) Data in a CDISC Compliant Format

Yu Zhu, PPD LLC., Shanghai

### ABSTRACT

The legacy Pharmacokinetic (PK) data are usually produced from different sources with different data format: sample collection on CRF, concentration results from Lab findings, and parameters calculated by pharmacokineticist. This brings a lot challenge when preparing SDTM and ADaM datasets for submission. This paper introduces some of the challenges and solutions associated with mapping the concentration data and the PK parameters data into SDTM (e.g. PC and PP) and subsequent creation of ADaM datasets.

### INTRODUCTION

Since SDTM Implementation Guide (IG) version 3.1.2, the pharmacokinetics domains for pharmacokinetic concentrations (PC) and the resulting pharmacokinetic parameters (PP) were formally included in Findings General Observation Class (Section 6.3). Since then pharmaceutical companies have started to incorporate the generation of these domains into their pharmacokinetics analysis process. This standardization will provide benefits to companies such as improving efficiency and reducing drug discovery time in the long run. But at this moment, it's quite clear to conclude that the process is not straightforward. The common considerations and challenges are as follows:

- Inconsistent data structures or format
- Controlled terminology
- Challenge in relating PC and PP data
- Creation of ADPC and ADPP
- CDISC compliance checking issues

This paper will firstly introduce some basic knowledge about PK and its analysis process, implementation of CDISC standards, then will discuss the considerations and challenges during the mapping process.

### PK INTRODUCTION

Pharmacokinetics is defined as the study of the time course of drug absorption, distribution, metabolism, and excretion (ADME). Clinical pharmacokinetics is the application of pharmacokinetic principles to the safe and effective therapeutic management of drugs in an individual patient.

Primary goals of clinical pharmacokinetics include enhancing efficacy and decreasing toxicity of a patient's drug therapy. The development of strong correlations between drug concentrations and their pharmacologic responses has enabled clinicians to apply pharmacokinetic principles to actual patient situations.

After a drug is administered to study subjects, concentrations of the drug (and often metabolites) in blood and/or urine are analyzed at various time points.

The time-concentration profiles are analyzed for the pharmacokinetic characteristics of the drug and related analytes, resulting in multiple pharmacokinetic parameters for each profile, such as  $C_{max}$ ,  $T_{max}$ , Half-Life, and various AUC values (see Figure 1).

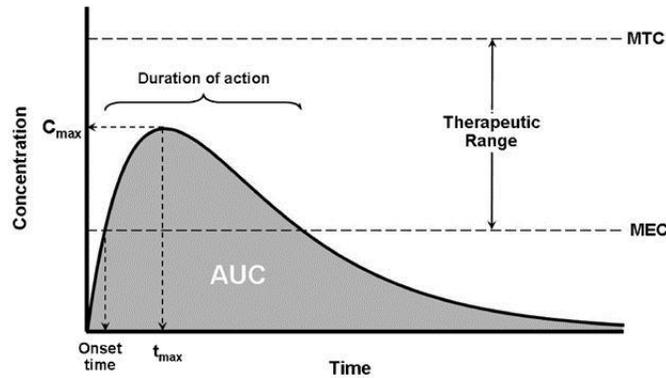


Figure 1. Common PK parameters  $C_{max}$ ,  $T_{max}$ , and AUC for a Time-Concentration Profile for a Drug Following Single-Dose Administration

## SDTM AND ADAM BASICS

The main purpose of creating CDISC SDTM and ADaM compliant data sets is to provide Case Report Tabulation (eCRT) data to a regulatory agency like FDA, EMEA, CFDA, etc. in a standardized format. This standardized data is compatible with available software tools that allow efficient access and correct interpretation of the data submitted.

In the SDTM, observations collected about subjects who participated in a clinical trial are organized into series of domains. Each domain is identified by a two-letter abbreviation and is defined as a collection of variables that share a common topic. The data submitted in a domain can be collected on one or more case report forms (CRFs), and conversely, data collected on one CRF may be submitted in more than one domain. In addition, data can come from sources other than data collection forms or EDC systems. Lab data is generally obtained from an electronic data transfer (eDT) file from a central lab, and PK concentration data are usually provided by a sponsor's or an external bioanalytical group. It is important to recognize that data are placed into domains according to their topic or meaning and not according to their source.

There are three general observation classes where the majority of subject-related data collected during a study are submitted. These classes are as follows:

- **Interventions:** investigational treatments, therapeutic treatments, and surgical procedures administered to the subject or animal. One record per constant dosing/treatment interval.
- **Events:** occurrences or incidents independent of planned study evaluations occurring during the trial (e.g., adverse events) or prior to the trial (e.g., medical history). One record per event.
- **Findings:** observations resulting from planned evaluations (e.g. lab tests, ECGs, microscopic findings). One record per finding result or measurement.
  - **Findings About:** findings about events or interventions are a specialization of the Findings General Observation Class. As such, it shares all qualities and conventions of Findings observations but is specialized by the addition of the --OBJ variable.

In addition to these general domain classes, the SDTM defines several special-purpose domains that do not use the general observation-class models. The Demographics domain describes the essential characteristics that apply to study subjects such as treatment assignment and study start and stop dates. The Supplemental Qualifiers (SUPP--) datasets play an important role in the submission of variables that cannot be mapped into the standard domain variables. The Related Records (RELREC) dataset is used to describe collected relationships between records in two (or more) datasets, such as an Event record and an Intervention record, or a Finding record and an Event record. RELREC is also used to describe relationships between datasets.

ADaM model datasets are based upon CDISC SDTM domains with additional metadata. The underlying principle of these models is to provide clear and unambiguous communication of the content, source, and quality of the datasets submitted in support of the statistical analysis performed by the sponsor.

In most cases, the ADaM datasets (ADxx) contain variables from multiple SDTM domains and contain derived variables for specific analyses. To achieve the principle of clear and unambiguous communication relies on clear ADxx documentation. This documentation provides the link between the general description of the analysis found in the protocol or statistical analysis plan and the source data.

Analysis datasets generated from the analysis dataset creation process must:

- Include a subject-level analysis dataset named ADSL
- Consist of the optimum number of analysis datasets needed to generate the statistical results for a clinical trial with little or no programming or data manipulation
- Must maintain the link with any base SDTM datasets used (i.e. SDTM variables carried into the analysis dataset must keep their attributes)

## CONVERTING PHARMACOKINETIC DATA IN SDTM AND ADAM DATASETS

### GENERAL PROCESS

The clinical pharmacokinetic data are collected and created in various steps. The original sample collection information and primary analysis data are collected from case report form (CRF) and bio-analytical data. Then the derived PK parameters calculated by scientists. For example, in one of the study, the data collected from CRF is stored in dataset named PK. The PK concentration data is provided by vendor as Import data. Usually different drug and metabolites are collected in different datasets, an append step is needed to generate the combined PKCONC. The derived PK parameters data named PATPK contains the calculated parameters in variables like TMAX, CMAX, LAMBDAAZ (half-life).

SDTM PC dataset is created from clinical datasets (e.g. PK), and bioanalytical dataset (e.g. PKCONC) based on SDTM structure. Based on the ADaM structure dataset, SDTM PC dataset and ADaM ADSL (Subject Level Analysis Dataset) are merged to create ADaM ADPC dataset. ADaM ADPC dataset provides information to create PK concentration tables and figures.

PK parameters are usually calculated by PK scientists. The raw PK parameters dataset (e.g. PATPK) is created including all these calculated PK parameter information, and SDTM PP dataset is created based on this dataset. ADaM ADPP dataset is created based ADaM structure dataset and SDTM PP. ADPP dataset is the PK analysis dataset which is used for producing summary tables, statistical tables, and any other PK analysis.

The general process for creating SDTM and ADaM PK-related datasets is summarized in Figure 2.

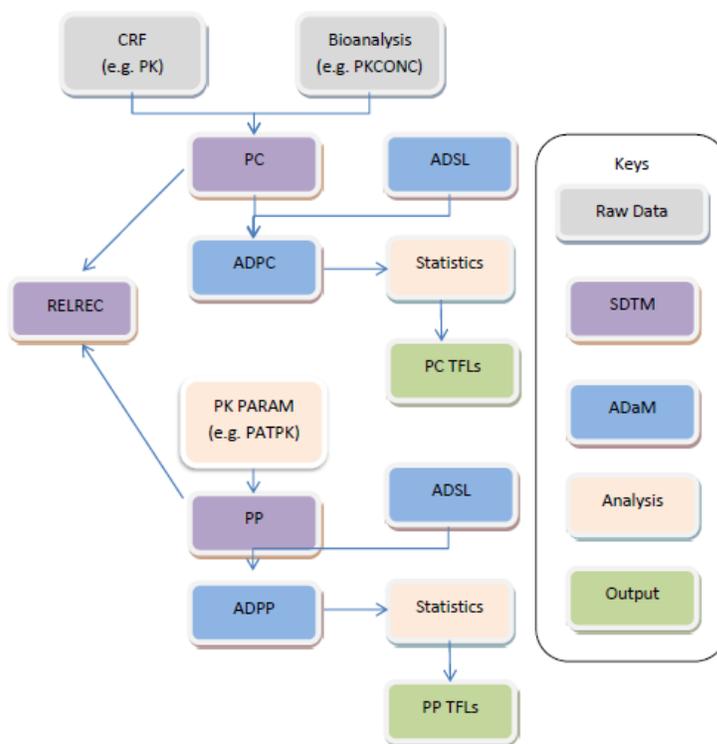


Figure 2. Process map for the creation of SDTM and ADaM PK datasets

There is another way to generate PK parameters dataset directly from ADPC. Using specific software for non-compartmental analysis such as SAS or WinNonlin®, PK parameters are calculated from ADaM ADPC. A derived dataset is created including all these calculated PK parameter information, and SDTM PP dataset is created based on this dataset. The ADaM ADPP dataset is created based ADaM structure dataset and SDTM PP.

The following contents will mainly focus on the first process. Below bullets will discuss in detail about the considerations and challenges..

## SDTM Mapping

In the previous example, the PK parameters are presented in variables in PATPK, which can be called as 'horizontal' way. That means the parameter by time data are collected in new variables rather than adding new observations. In this case, a proper transpose procedure will be needed to convert the data into 'vertical' way. That makes one observation as one subject one test (parameter) one visit one time point. A utility macro %DTT\_transpose is used to achieve this purpose, after the transpose, the variables (LAMBDAZ, TMAX, CMAX, AUCINFO, AUC24) value will be put in PPORRES, the variables name will be keys in PPTESCD, and the variables label will be key labels in PPTEST.

```
%DTT_transpose(import,work,patpk,pp,LAMBDAZ TMAX CMAX AUCINFO AUC24,
PPORRES,PPTESCD,PPTEST,OCBY=,BY=SUBJECT PERIOD ASTYP);
```

When the data structure is transformed, the next step is to convert non-standard variables into SDTM standard ones. Below steps describe a general way to convert variables into different classes of standard variables.

### Step1: Identify the Required Variables

Once the Data Class has been determined, for PC and PP they are FINDINGS. Identifying the required variables is a straightforward look-up of the implementation guide. To start with, STUDYID, DOMAIN, USUBJID, and SEQ are all required within the General Observation Classes. Then using the Domain model definition selects other required variables (for example within FINDINGS --TEST, --TESTCD.).

### Step2: Identify the Expected Variables

Follow same process as step 1, identifying the key expected variable, they are --ORRES, --ORRESU, --STRESC, --STRESN, --STRESU, --DTC. For PC domain, variables PCSPEC, PCNAME, CLLOQ are also expected.

### Step3: Identify the Permissible Variables

For permissible variables, as opposed to identify what all the permissible variables are, instead look at your source data to identify what has been captured, but not yet mapped to a required/expected variable in Step1 & 2 above. This enables you to focus on the permissible variables applicable to your study data. For PC and PP the variable --GROPID is mandatory for the purpose of linkage.

### Step4: Identify the Relationship Variables

There may then be variables that are captured, however do not fit into the required, expected or permissible core set of variables. These remaining variables would be mapped to a related domain (such as CO or SUPP--).

To map the variables from raw data to the describe SDTM standard variables above; a clearly defined mapping spec (figure 3) can help this purpose. The columns on the left side (column InName to InLength) are the variable information from PK raw data. Columns on the right side (column OutName to Role) are SDTM variables. The spec was generated by a macro which took raw data and SDTM IG version input to generate the corresponding columns. Column Flag and Calculation were used for editing the derivation logics. There are 5 types of derivation:

- **Direct:** a variable is copied directly to a domain variable without any changes other than assigning the CDISC standard label. Example: spec line 7, variable STUDYID from PK raw data was copied directly to PC variable.
- **Rename:** only the variable name and label may change but the contents remain the same. Example: spec line 9, variable SUBJECT from PK raw data was renamed to USUBJID in PC.
- **Derivation:** creating a domain variable based on a computation, algorithm, series of logic rules or decoding using one or more variables. Example: spec line 14, 18, PCTESTCD and PCORRES were created based on certain derivation logic specified in column Calculation.
- **Standardize:** mapping reported values to standard units or standard terminology. Example: spec line 19, PCORRESU was derived from PK raw data variable UNITS, but column OutFormat specified PCORRES should follow the Controlled Terminology UNIT.

- **Reformat:** the actual value being represented does not change, only the format in which is stored changes, such as converting a SAS date to an ISO8601 format character string

For those remaining variables would be mapped to a related domain as SUPPPC, the spec has a column Flag to identify. Example: spec line 45-47, these Assay related variables will be mapped to SUPPPC.

Dataset/Table Name	InData	InName	InLabel	InType	InLength	OutName	OutLabel	OutType	OutLen	OutFor	Flag	Calculation	Order	Origin	Core	Role	
1 Dataset/Table Name: PC																	
2 Sort Order: STUDYID, USUBJID, PCGRPID, PCREFID, PC																	
3 Dataset Structure: One record per analyte per planned time point number per time point reference per visit per subject																	
4 Programmers Notes:																	
5																	
6 InData																	
7 PC	STUDYID	StudyIdent	char	39	STUDYID	Study Identifier	Char	39				"PC"	1	CRF	Req	Identifier	
8																	
9 PC	SUBJECT	Subject Ident	char	40	USUBJID	Unique Subject Identifier	Char	40					2	Assigned	Req	Identifier	
10																	
11						PCGRPID	Group ID	Char	20				3	CRF	Req	Identifier	
12																	
13																	
14						PCTESTCD	Pharmacokinetic Test Short	Char	8				5	Derived	Perm	Identifier	
15																	
16																	
17																	
18						PCORPRES	Result or Finding in Original	Char	25				8	Assigned	Req	Topic	
19 PC	UNITS	Units	char	12	PCORPRESU	Original Units	Char	20	CT:UNIT				12	Derived	Exp	Result Qualifier	
45 PC	ASCM	Comment -	char	100	ASCM	Comment - Assay Services	char	100			S		13	CRF	Exp	Variable Qualifier	
46 PC	ASMED	Assay Medi	char	50	ASMED	Assay Medium	char	50			S		999	CRF			
47 PC	ASSOP	Assay Servi	char	50	ASSOP	Assay Services SOP #	char	50			S		999	CRF			

Figure 3. Mapping spec identifying SDTM standard variables derivation from PK raw data

## CONTROLLED TERMINOLOGY

### PK Parameter Tests and Codes

Most of the variables used in the domain models of Version 3.2 of the SDTM have referenced [Controlled Terminology](#) (CT) in that version. Due to complexity of various PK parameters, new CT for these parameters needs to be created. The CT for PK parameter (PTESTCD and PTEST) has been developed, with the most recent version of CT (27 June 2014) containing 278 values. The PK parameter CT team continues to work on adding more required terms and to improve that list. The parameter codes and names are based upon those used widely in the industry and in PK analysis programs such as WinNonlin®.

There are some general rules when creating the PKPARAM CT. For example, many PK parameters can be calculated using the observed or predicted value of the last non-zero concentration. This dependency is expressed in the code using the letter "O" or "P" in the term. For example, the codes AUMCIFP and AUMCIFO refer to the area under the moment curve (AUMC $\infty$ ) values using the observed or predicted last non-zero concentration value.

The term for the normalized PK parameter is indicated by adding the letter "D", "B", "S", or "W", respectively, to the end of the term for the original term. They stand for original value divided by Dose, Body mass index, Surface area, and Weight. Below is an example of AUC parameters over an interval T1 to T2.

CDISC Submission Value	CDISC Synonym(s)	CDISC Definition	NCI Preferred Term
AUCINT	AUC from T1 to T2	The area under the curve (AUC) over the interval from T1 to T2.	Area Under the Curve from T1 to T2
AUCINTB	AUC from T1 to T2 Norm by BMI	The area under the curve (AUC) over the interval from T1 to T2 divided by the body mass index.	AUC from T1 to T2 Normalized by Body Mass Index
AUCINTD	AUC from T1 to T2 Norm by Dose	The area under the curve (AUC) over the interval from T1 to T2 divided by the dose.	AUC from T1 to T2 Normalized by Dose
AUCINTS	AUC from T1 to T2 Norm by SA	The area under the curve (AUC) over the interval from T1 to T2 divided by the surface area.	AUC from T1 to T2 Normalized by Surface Area
AUCINTW	AUC from T1 to T2 Norm by WT	The area under the curve (AUC) over the interval from T1 to T2 divided by the weight.	AUC from T1 to T2 Normalized by Weight

### PK Parameter Units

The CT development team examined the referenced UNIT codelist to determine which terms might be missing, and to develop CT for PK parameters.

The CT development team concluded that a separate list for PK units was needed. As a result, the PKUNIT codelist was created. It contains more than 190 values for PK parameter units. This list, like most CDISC CT lists, is extensible, which means that sponsors can add new terms, as long as they are indeed new terms, and not synonyms of existing terms. For example, the unit of "kg/L" is not in the PKUNIT codelist as CDISC Submission value; however,

one can find a submission value of “g/mL” (i.e., Gram per Milliliter”), which has the “kg/L” as a synonym. Therefore, the value of g/mL would be the value submitted.

## **RELATIONSHIP BETWEEN PC AND PP**

Because each set of parameters is related to a specific set of concentrations (a curve), representing this relationship is critical. It should be noted that the SDTMIG v3.2 states the following:

“It is a requirement that sponsors document the concentrations used to calculate each parameter. For many sponsors, this need is currently met via the analysis metadata. As a result of feedback received from many sponsors on the draft version of this document, sponsors may continue to document the concentrations used to calculate each parameter via the analysis datasets.”

The foundation for relating PK parameters to PK concentration curve, as described in the SDTMIG, is ensuring that two key values are the same in both domains:

- The date of the reference time point (usually a dose), submitted in the variables PCRFTDTC and PPRFTDTC
- The analyte, which is submitted in PCTEST and PPCAT (since PPTTESTCD/PPTTEST variables contain the names of the PK parameters).

### Link information within PC and PP

According to the description above, one can directly link the data through 2 variables in each dataset. For example, sponsor in one of the project requested that “PC and PP can be linked using XXGRPID and PPCAT/PCTEST variable”. The XXGRPID variables were derived according to PP period information:

1. PP.PPGRPID = Period variable in parameter datasets.
2. PC.PCGRPID = as described below.
  - i. Period 1 – Nominal Time from First Dose between 0-24 hours.
  - ii. Period 2
    1. Nominal Time from First Dose between 480 – 672 hours.
    2. Nominal Time from First Dose between 312 – 672 hours

.....

It is apparent that PPGRPID were referred as relative time point. The relationship through XXGRPID and PPCAT/PCTEST should be correct. However it lacks a clear documentation to describe the linking method.

### Link through RELREC

The following section provides a way to document these relationships using the RELREC dataset. The SDTM uses the Related Records (RELREC) dataset for this purpose. This dataset provides one record per related record, group of records, or dataset.

In this method, the PCSEQ and PPSEQ variables are used to identify the records to be related in the respective domains. In this structure, each record in the PP domain (i.e., each PK parameter) is related to the records from the PC domain that were used to calculate its value. Because this method requires the inclusion of each related record in the RELREC dataset, it will result in a relatively large number of records. On the other hand, the implementation of this method is a rather straightforward two-step process for each subject:

- Create a RELREC record for each PP record.
- Go through the list of PC records and create a RELREC record with the same RELID for each record that was used to calculate the PK parameter in the PP record.

**Method D (One to one, using PCSEQ and PPSEQ)**

Row	STUDYID	RDOMAIN	USUBJID	IDVAR	IDVARVAL	RELTYPE	RELID*
1	ABC-123	PC	ABC-123-0001	PCSEQ	1		1
2	ABC-123	PC	ABC-123-0001	PCSEQ	2		1
3	ABC-123	PC	ABC-123-0001	PCSEQ	3		1
4	ABC-123	PC	ABC-123-0001	PCSEQ	4		1
5	ABC-123	PC	ABC-123-0001	PCSEQ	5		1
6	ABC-123	PC	ABC-123-0001	PCSEQ	6		1
7	ABC-123	PC	ABC-123-0001	PCSEQ	7		1
8	ABC-123	PC	ABC-123-0001	PCSEQ	8		1
9	ABC-123	PC	ABC-123-0001	PCSEQ	9		1
10	ABC-123	PC	ABC-123-0001	PCSEQ	10		1
11	ABC-123	PC	ABC-123-0001	PCSEQ	11		1
12	ABC-123	PC	ABC-123-0001	PCSEQ	12		1
13	ABC-123	PP	ABC-123-0001	PPSEQ	1		1
14	ABC-123	PP	ABC-123-0001	PPSEQ	2		1
15	ABC-123	PP	ABC-123-0001	PPSEQ	3		1
16	ABC-123	PP	ABC-123-0001	PPSEQ	4		1
17	ABC-123	PP	ABC-123-0001	PPSEQ	5		1
18	ABC-123	PP	ABC-123-0001	PPSEQ	6		1
19	ABC-123	PP	ABC-123-0001	PPSEQ	7		1

Figure4, RELREC one to one link through –SEQ. PC observations from row 1 to row 12 (RELID=1) are related to PP observation at row 13 (RELID=1) through same –SEQ value.

### ADaM BASICS (ADPC, ADPP Derivation)

CDISC ADaM does not have guidelines for Pharmacokinetics so far. However the ADaM Basic Data Structure (BDS) variables provide sufficient flexibility to support PK analysis. By working according to the ADaM rules, and thus increasing standardization in the datasets, the time to perform PK analysis decreases. In addition, the information from the protocol and SAP, needed for PK analysis, can be integrated in these standardized datasets.

In order to compile ADPC, the PC domain is merged with the Subject-Level Analysis Dataset (ADSL) which contains general subject information (e.g. demographic information), and with treatment information from the exposure dataset (EX/DOSE) is also imported and derived variables are added. Similar to the creation of ADPC, the PP domain is merged with ADSL and derived variables are added to create ADPP.

In the BDS structure, following variables derivation will need to pay attention to:

#### AVISIT, AVISITN

AVISIT and its numeric counterpart AVISITN are derived from the variables VISIT and VISITNUM from the PC domain. All PK concentrations (in ADPC) or all PK parameters (in ADPP) that refer to the same exposure will have the same AVISIT(N) value.

#### ATPT, ATPTN

The planned analysis time points are presented in ATPT and ATPTN. Only for pre-dose values they differ from the PCTPT and PCTPTNUM (variables from the PC domain). The value of PCTPTNUM, which is in general negative for predose samples, is put to zero in ATPTN. If the variable PCTPTNUM contains the planned time points in minutes, it can be converted to e.g. hours in ATPTN. These variables are not present in ADPP.

#### ANLzzFL

Analysis record flags (ANLzzFL) can be used to select a set of records for one or more analyses. The “zz” represents an index for a record selection algorithm, and will be replaced with 01-99. As multiple analysis flags can be assigned, a new variable, analogue to ANLzzFL, is needed to define the different analysis groups: ANLzzFD (Analysis Record Flag zz Description). In ADPC, the main analysis groups are: ‘PK analysis’, ‘Descriptive statistical analysis’ and ‘Steady state analysis’. In ADPP, the main analysis groups are: ‘Inferential statistical analysis’ and ‘Descriptive statistical analysis’. Subjects, time points or PK parameters can be included or excluded from analyses based upon criteria or as specified in the protocol/SAP.

#### AVAL, AVALC

The analysis value is reported in AVAL. In most cases, it is equal to PCSTRESN, the numeric result in standard unit. The character counterpart is reported in AVALC. However, several rules for data handling are described in the protocol and/or SAP. These adjustments can be done in AVAL. For example, values that are below the limit of quantification can be put to zero.

#### CRITy, CRITyFL, CRITyFN

Analysis criteria are evaluated in CRITy. The “y” is used to categorize the different criteria and will be replaced with a single digit: 0-9. Two important criteria in PK analysis are time deviations and quantifiable predose values. If a sample is taken more than 10% too soon, or too late relative to the scheduled time point, the value can be excluded from the

descriptive statistical analysis. In bioequivalence studies, if the predose value is more than 5% of the maximal concentration, the subject will be excluded from the trial. For statistical analysis of PK parameters, the AUC<sub>peo</sub> (AUC percent extrapolated) should be lower than 20% of AUC<sub>ifo</sub> (AUC infinity)

## OpenCDISC VALIDATION CHECK

Once the SDTM mapping and ADaM derivation are completed, how to confirm that these datasets you have produced actually conform to the SDTM/ADaM, and the SDTM/ADaM Implementation Guide? There is a number of ways to validate, but one of the tools most frequently used is the OpenCDISC Validator.

The OpenCDISC validator provides a method for checking conformance and compliance of mappings against the SDTM Implementation Guide.

OpenCDISC breaks down validation checks into the following categories:

- **Consistency:** There are dependencies between certain variables.
- **Controlled Terminology:** Some variables require only specific values based on pre-defined code lists.
- **Format Compliance:** The values of certain variables must follow a specific format, such as the ISO 8601 standard used for dates, time, and periods of time.
- **Referential Integrity:** There are dependencies across domains.
- **Limits:** The values of certain variables must be within specified limits, such as the variable AGE which must be greater than zero.

Below are some common findings in checking PK datasets. Some sample programs are provided, which can help avoid the issues during development.

- **SD1077 – FDA Expected variables not found**

Even though the SDTM IG did not list EPOCH in the recommended variable list, OpenCDISC validation check will still report EPOCH is expected in PC and PP. So please pay attention and derive EPOCH as other finding domain.

- **SD0007 – Inconsistent value for standard unit**

```
proc freq data=sdm.pp;  
  tables pptestcd * ppstresu / noprint out=tests;  
run;
```

- **SD0026 – Missing units on value**

```
data rep;  
  set sdm.pp;  
  if input(pporres, best.) ne . and pporresu eq "  
run;
```

- **SD0036 – Missing character result when original result provided**

```
proc freq data=sdm.pp;  
  tables pptestcd * pporres * ppstresc / list missing;  
  format pporres ppstresc $missf. ;  
run;
```

```
data rep;  
  set sdm.pp;  
  if pporres ne " and ppstresc eq "  
  then output;  
run;
```

- **SD0064 – Invalid subject**

```
proc sql;  
  create table bad_ids as  
  select distinct usubjid  
  from sdm.pp  
  where usubjid not in(select usubjid from sdm.dm);  
quit;
```

## CONCLUSION

PK data is critical in understanding a drug's safety and determining its dosing frequency. Yet the processes for collection and submission of this data result in challenges to its representation in an SDTM format.

This paper introduced 5 aspects of common considerations and challenges in converting PK data into SDTM format and subsequent creation of ADaM, a summary of CDISC Controlled Terminology that has been developed for the PP domain, specifically the PK parameter code and unit variables. Sponsors should be aware that this terminology exists, and, as with all CDISC CT, should have a plan for its implementation.

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## CONTACT INFORMATION

Your comments and questions are valued and encouraged. Contact the author at:

Name: Yu Zhu  
Enterprise: PPD LLC.  
Address: Suit 2009, No.1 Huai Hai Zhong Road  
City, State ZIP: Shanghai, 200021  
Work Phone: +86 21 53834000 ext. 170  
Fax: +86 21 63863808  
E-mail: [yu.zhu@ppdi.com](mailto:yu.zhu@ppdi.com)  
Web: [www.ppdi.com](http://www.ppdi.com)

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