

The « CDISC Stupidario » (the CDISC Nonsense)

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ABSTRACT

In the last 5-10 years I have been exposed to several studies requiring the use of the CDISC standards, either as programmer study lead or as CDISC SME (Subject Matter Expert) reviewing both internal (Cytel) or external packages (delivered by Pharma or other CROs), where I also regularly provide answers to questions/doubts.

With this presentation I would like to go through the main CDISC “Nonsense” from my experience. This can range from “nonsense” questions to a complete misunderstanding of the CDISC Ig(s); some of this “nonsense” has also emerged from the CDISC packages I have reviewed including CDISC documentation such as the reviewer guide.

The main focus of the presentation will be the SDTM and ADaM standards.

INTRODUCTION

In my professional career I have been exposed to several studies requiring the use of CDISC standards either as programmer study lead or as a CDISC SME reviewing CDISC packages. In this capacity, I have seen several define.xml and reviewer guides that demonstrate how differently individual users and companies approach the same mapping issue in SDTM or the same analysis “modelling” in ADaM. I’ve also observed wide variations in the level of details provided for example in a reviewer’s guide, or a computational algorithm used to describe a derivation in an ADaM define.xml.

MY TOP 10 (OR MORE) CDISC “STUPIDARIO”

In the eighties in Italy the term “Stupidario”¹ became the object of a book where the author, a medical doctor, collected some real cases of medical nonsense (figure 1). Since then the term has been commonly used to reference a collection of situations in which people demonstrated their “stupidity” on one particular topic, while considering themselves an expert on the same.



Figure 1: An exaple of “Stupidario Medico”: << Madame you can safely go home: that virus was on computer storing all diagnoses >>

¹ Literally translated from Italian into “Directory of sentences and sayings worthy of quotation for their stupidity” (or “collection of nonsense”)

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In the next pages I would like to share my top-10 favorite CDISC “Stupidario” (in random order).

1. TOO LAZY TO CORRECT ISSUES (SDTM AND ADAM)

Very often people pay different “attention” to details, perhaps (incorrectly) thinking they do not matter. If for example you created an SDTM dataset and for one variable you assigned the wrong label (not as per the SDTM Ig) or you did not assign a label at all and this has been detected from the Pinnacle21 validation outcome, why not correct the issue in the dataset instead of leaving the issue as it is and justifying it in the study data reviewer guide [1] as a “Programmatic Error”?

DEFINE	Define.xml/CDISC dataset Description mismatch	Warning	4	LB, IE, QS, FA dataset label is incorrect on xpt files (programmed in). Define.xml matches dataset labels.
QS	Variable is in wrong order within domain	Warning	2	QSCAT and QSSCAT are incorrectly placed.
QS	FDA Expected variable EPOCH not found	Warning	1	Variable not used.

Figure 2: Clinical Study Data Reviewer Conformance Section with by “bad” justifications of errors and warnings

We see increasingly, either from the mock-up/test submissions we do for the FDA, or that our clients do with their CROs, that agency concerns about such details is increasing. For example, issues such as variables in define.xml that should have a controlled terminology assigned and they have not; improper use of variables in ADaM: incomplete reviewer’s guide documentation such as not providing a rationale for all warnings and errors P21 reported during the validation of your package, are all the subject of FDA concerns and it is recommended to correct these issues.

You may think these are minor issues because they do not ultimately impact any result. However, you are risking your credibility with the FDA reviewer, who may conclude that your package is not of good quality. Further, if you don’t address those issues on-time, you might receive a request from the FDA to correct them when you think you are done and your package is ready to be delivered. Fixing, for example, an SDTM dataset could have a “cascade” effect as you might also need to re-run other datasets or even re-generate the ADaMs (and outputs as well).

2. WHERE IS MY TRACEABILITY (ADAM)

One of our sponsors requested to review a CDISC ADaM package developed internally by their Biostatistics team. The focus was especially on ADaM where the sponsor did not have that much experience.

In my Issues log containing all issues or recommendations I gave to the sponsor to help them being conformant and traceable enough, I was concerned about the way one of their ADaM datasets supporting the analysis of ECG data was built. The sponsor team derived the mean of the three ECG measurements (triplicates); up to here nothing wrong – this was correctly derived in the ADaM. However, I recommended keeping also the three original records from which the derived parameter was created. The answer from the sponsor was a bit “unsympathetic”: “*The original records were not retained in ADEG because they are in SDTM.EG*”. Here my French colleagues might say “*ca va sans dire*”(it goes without saying). Although there is no ‘obligations’ from the ADaM Ig [2] to keep all records from SDTM when creating ADaM datasets, it is a good attitude to keep these records when these records are the source of records (parameters) derived in ADaM.

Among the four fundamental ADaM principles, traceability is in my opinion (but not only my opinion) the most important. From the ADaM Ig traceability is defined as follows:

“The property that enables the understanding of the data’s lineage and/or the relationship between an element and its predecessor(s). Traceability facilitates transparency, which is an essential component in building confidence in a result or conclusion. Ultimately, traceability in ADaM permits the understanding of the relationship between the analysis results, the ADaM datasets, the SDTM datasets, and the data collection instrument. Traceability is built by clearly establishing the path between an element and its immediate predecessor. The full path is traced by going from one element to its predecessors, then on to their predecessors, and so on, back to the SDTM datasets, and ultimately to the data collection instrument”.

Traceability in ADaM Ig is continuously “stressed” making this principle key for a good ADaM dataset. One aspect stressed in the ADaM Ig is the transparency that you provide by making your ADaM fully traceable:

“Retaining in one dataset all of the observed and derived rows for the analysis parameter provides the clearest traceability in the most flexible manner within the standard BDS. The resulting dataset also provides the most flexibility for testing the robustness of an analysis”

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So unless, you end-up with a huge ADaM dataset, keep original source records in your dataset: this will be beneficial for the traceability of your ADaM derived variables and ultimately it will be transparent for the reviewer which records have been used (and eventually which records have been not used or not analysed).

3. MY PARAM SHOULD BE ENOUGH AND THE CONCEPT OF ANALYSIS-READY (ADAM)

Again, while trying to assist our sponsors and advising them, I was questioning the presence of a variable AVALU in most of their BDS-type ADaM datasets since I did not understand the need and their answer was *"We need it to store the unit of PARAM"*. This is what I call a "decorative variable" since PARAM should already contain this information; from ADaM Ig *"PARAM must include all descriptive and qualifying information relevant to the analysis purpose of the parameter"* (ADaM Ig 1.1 Section 3.3.4) e.g. unit PARAM="Weight (kg)".

The other common "mistake", although not really a conformance issue, is to create PARAM by concatenating for example all SDTM findings qualifiers of the –TEST variable, for example for ECG "Systolic Blood Pressure (mmHg), Sitting Position". This is not really needed unless you are doing an ECG analysis based on the subject position. Again this is clear from the ADaM Ig section 3.3.4: *"PARAM must include all descriptive and qualifying information relevant to the analysis purpose of the parameter"*, this means, in few words, that in most of the cases concatenating the parameter name and its unit should be enough (this is what usually goes into the statistical output).

This satisfies one of the ADaM fundamental principles that require your ADaM dataset to be "analysis-ready". This concept was, and still is, the subject of some misunderstanding. Is it often (mis-)understood as "one-proc-away" meaning that we cannot make for example any merge with any other datasets prior to call for example the SAS Statistical procedure, but the requirement of being analysis-ready "simply" refers to a *particular data point/result on a table*, and any given statistical table might use multiple analysis datasets and multiple statistical procedures.

4. "SUPERFLUO" SUBMISSION (ADAM)

How many analysis ADaM datasets do I need to create given the fact my study SDTM has 22 subject datasets?

There is of course no answer without knowing the details of the statistical analysis to be performed. ADaM, as opposed to SDTM, is analysis-driven, meaning that you do not need to create an ADaM dataset for laboratory data if your Statistical Analysis Plan does not plan for any aggregate analysis on laboratory data (e.g. you might create listings directly from your SDTM if you don't need any major derivation) and very likely you will not need an ADIE ADaM dataset. *ADIE what? An ADaM dataset for violated Inclusion and Exclusion Criteria*. This is really not needed!

These are some of recommendations we give on this topic during the CDISC ADaM training:

What analysis datasets are required for a submission?

ADaM ADSL dataset is required. FDA expects additional ADaM datasets to support primary and secondary analysis. From the FDA Technical Conformance Guidance: *"Sponsors should submit ADaM dataset to support key efficacy and safety analysis and the primary and secondary endpoints of a trial ... should be provided as well"*.

Should there be an ADaM dataset for every SDTM domain?

No. There is no requirement that every SDTM domain has a corresponding analysis dataset. ADaM datasets are needed to support the Statistical Analysis Plan, and they are not simply created as a mechanistic duplication of SDTM data.

5. SDTM CONTROLLED TERMINOLGY (CT) DO NOT NEED TO PARALLEL THE SDTM IG VERSION (SDTM)

CDISC SDTM Ig version does not need to parallel the CDISC CT version

One of our sponsors appointed a CRO specialized in Phase I studies. The CRO had a consolidated standardized system end-to-end from data collection to SDTM production to ADaM and TLFs¹ generation. However, the entire CRO 'system' was based on the SDTM Ig 3.1.3 and CDISC Controlled Terminology from more or less the same era of the SDTM Ig 3.1.3 (2013). We didn't want to ask the CRO to update their system for the sponsor study; this was also not worth it given the fact for the type of study, phase I studies, the differences between SDTM Ig 3.1.3 and 3.2 were minimal. Nevertheless we asked the CRO to at least update the controlled terminology to a more recent version to avoid any major differences when data will be eventually pooled with other studies. The CRO answer was as follows: *"This is XXX Inc. standard, the development of SDTM IG 3.1.3 has been done in 2013"*. The CRO misinterpretation here is to think that the version of the SDTM Ig had to "parallel" the CDISC CT version, but there are actually no requirements to have Ig and CDISC CT from the same period and therefore the CRO, despite working with SDTM Ig 3.1.3, could have implemented a more recent version of the CDISC CT e.g. one of the 2018 CDISC CT.

¹ TLF = Tables Listings and Figures

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Apply Standard CDISC CT whenever you can

Very often people just stick to the SDTM Ig or think that a supplemental qualifier is just a “trash bin” where we can put items we don’t know where else to put. The fact that we stored something in supplemental qualifier dataset does not mean you don’t have to be accurate as much as in the parent domain when migrating data from legacy datasets. For example terminology such as YN or ISO formats, such as the as one for date, should be applied whenever it is applicable. Some examples:

- Is your Supplemental Qualifier a date? ISO format should be applied and therefore original date should be converted to the YYYY-MM-DD ISO format (assuming here it is only containing the date part)
- Does your Supplemental Qualifier have only Yes/No results? Then convert “Yes” to “Y” and “No” to “N”
- Does your result for a specific parameter in a finding dataset have only Yes/No results? Then convert “Yes” to “Y” and “No” to “N”. Similarly for Negative/Positive

Make use of subset CT in your define.xml

Often I have seen define.xml with poor metadata handling. One example is to simply include the entire CDISC CT even if some items of the CDISC CT do not apply at all to that specific variable. The following are just some recommendations on how to properly document CDISC CT in define.xml:

- There are terminologies with broad scope e.g. UNIT has unit applicable to laboratory data, to medication units, etc. In define.xml you can have subset of units e.g. LBUNIT, CMUNIT, etc. where only applicable units are listed in each subset
- Only terms that occurred or CRF pre-printed terms should be reported in the CT definition in the define.xml e.g. if from the CRF 5 races are expected but you had only WHITE subjects, all 5 expected races should be part of the CT
- Do not include in the CT definition all terms if all are not applicable e.g. do not include all terms from the UNIT CDISC CT (>500 terms)
- If a subset of CT is defined in define.xml, you still need to reference “Codelist Code” and “Code” as per CDISC CT. For example, if you define a CT CMUNIT being a CT subset of the standard CT UNIT, the “Codelist Code” and “Code” of the term coming from the CT UNIT should be referenced in your define.xml

Standard terminology for SDTM domain names

Not all domains names are described in the latest SDTM Ig, but they are referenced in the latest CDISC CT version. The CDISC CT contains the list of “reserved” standard domain names up to the date the CDISC CT was released, like any other standard terminology (see figure 3).

Code	Codelist Code	Codelist Extensible (Yes/No)	Codelist Name	CDISC Submission Value	CDISC Synonym(s)	CDISC Definition	NCI Preferred Term
C66734		Yes	SDTM Domain Abbreviation	DOMAIN	SDTM Domain Abbreviation	A unique 2-character domain code used in the regulatory submission process. The domain abbreviation is used consistently throughout the submission, i.e. in the dataset name, as the value of the domain variable within the dataset, and as a prefix for most variable names in the dataset. (CDISC Glossary)	CDISC SDTM Submission Domain Abbreviation Terminology
C49563	C66734		SDTM Domain Abbreviation	AD	Analysis Dataset	A two-letter prefix used to denote ADaM-compliant analysis datasets used for statistical analysis and reporting by the sponsor. These are submitted in addition to the data tabulation datasets.	Analysis Dataset Domain
C49662	C66734		SDTM Domain Abbreviation	AE	Adverse Events	An events domain that contains data describing untoward medical occurrences in a patient or subjects that are administered a pharmaceutical product and which may not necessarily have a causal relationship with the treatment.	Adverse Event Domain
C117755	C66734		SDTM Domain Abbreviation	AG	Procedure Agents	An interventions domain that contains the agents administered to the subject as part of a procedure or assessment, as opposed to drugs, medications and therapies administered with therapeutic intent.	Procedure Agents Domain
C147168	C66734		SDTM Domain Abbreviation	APAE	Associated Persons Adverse Events	The adverse events domain for those persons associated with the study itself, a particular study subject, or a device used in the study.	Associated Persons Adverse Events Domain
C147169	C66734		SDTM Domain Abbreviation	APBS	Associated Persons Biospecimen	The biospecimen domain for those persons associated with the study itself, a particular study subject, or a device used in the study.	Associated Persons Biospecimen Domain
C147170	C66734		SDTM Domain Abbreviation	APDD	Associated Persons Death Details	The death details domain for those persons associated with the study itself, a particular study subject, or a device used in the study.	Associated Persons Death Details Domain
C132354	C66734		SDTM Domain Abbreviation	APDM	Associated Persons Demographics	The demographics domain for those persons associated with the study itself, a particular study subject, or a device used in the study.	Associated Persons Demographics Domain

Figure 3: CDISC CT Study Domain Abbreviation

Please do not change the “case” of a standard dictionary

Whenever data are coded with an external dictionary such as MedDRA, original “case” should be kept e.g. do not uppercase. If you are the “receiver” of the data from data management made them aware of the issue.

Column E (CDISC Submission Value) is the one to be ‘used’ in the dataset

Once again here my French colleagues might say “ca va sans dire” but column E from the CDISC CT excel file (see figure 4) is the one to be used in the submitted SDTM dataset. Column F, CDISC Synonym(s), can be not used. Column F is there to facilitate the conversion to the appropriate CDISC term (CDISC Submission Value).

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For example from figure 4 the CDISC Submission Value for the unit is '10¹²/L' as in column E, while the column F values are there to facilitate the unit conversion in case your data contains similar terms e.g. 1/pL, 10⁶/mm³, 10⁶/uL, T/L, TI/L and Tera/L, are same as 10¹²/L, so in your SDTM dataset you will need to use this term and not the one in column F.

D	E	F
Codelist Name	CDISC Submission Value	CDISC Synonym(s)
Unit	10 ¹² /L	1/pL; 10 ⁶ /mm ³ ; 10 ⁶ /uL; T/L; TI/L; Tera/L

Figure 4: CDISC CT Submission Value vs CDISC Synonyms

6. ACRF CLARIFICATION (SDTM)

As of today there is no industry standard on how the SDTM Annotated CRF (aCRF) should be created, but the CDISC "Metadata Submission Guideline (MSG) for SDTM IG" is a valid document sponsors and CROs should refer to with regards to aCRFs, in particular section 4 "Guideline for Annotating and Bookmarking and CRFs" [3].

The aCRF is a critical document since it visually describes the content of your SDTM datasets; however again from the packages I have reviewed, very often basic rules are not followed.

Domain Name Annotation

From the CDISC MSG "Each domain that is represented on a CRF page should have its own annotation on the left side of the CRF page with the 2 letter domain code and domain name (e.g. IE = Inclusion/Exclusion)". Figure 5 provides a wrong interpretation of such a statement (left) and a correct interpretation (right).

Domain = VS Domain = DM Screening Visit 1 (Day -90) [V1] Demographics [DM]	VS = Vital signs DM = Demographics Screening Visit 1 (Day -90) [V1] Demographics [DM]
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Figure 5: Wrong vs Correct Domain Name Annotation

Requirements for Bookmarking and Table of Contents (TOCs)

From the CDISC MSG "Annotated CRFs included in the eCTD should be bookmarked 2 ways (dual bookmarking): bookmarks by time-points, often analogous to planned visits in the study, and bookmarks by CRF topics or forms. SDTM domains do not necessarily have a 1-to-1 relationship with CRF topics or forms, nor is the reverse true. For example, in the annotated CRF, both DM and SC are collected on the Demography panel, while SC data are collected from the Enrolment Form and the Demography pages".

Figure 6 is an example of an incorrect interpretation of this statement (left) and a correct interpretation (right). In the first example under "Domain" the sponsor has simply used the name of the original legacy data domain, while they should have used the name of the CRF form (the data being collected). In the second example 'By domains', instead of bookmarking the name of the applicable visits for the Clinical Events domains, they bookmarked the CRF page number, which of course does not make sense.

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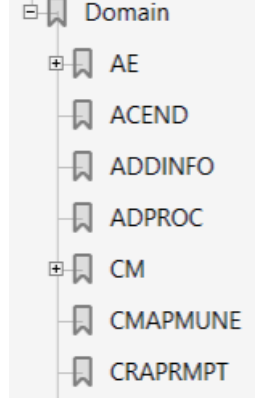
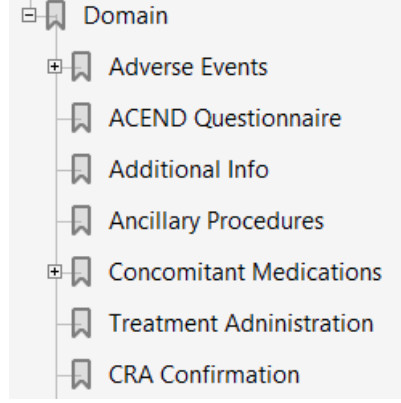
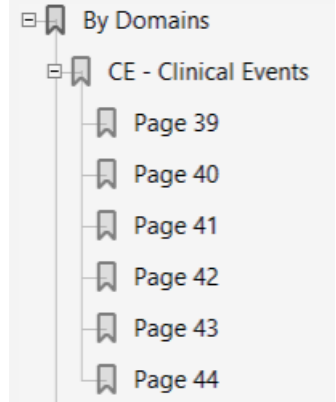
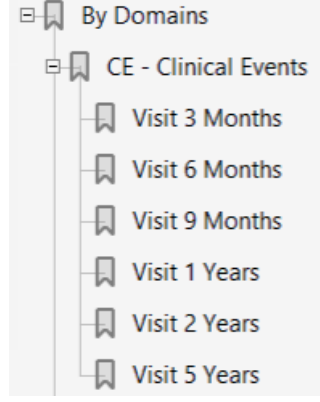
 Domain - AE - ACEND - ADDINFO - ADPROC - CM - CMAPMUNE - CRAPRMPT	 Domain - Adverse Events - ACEND Questionnaire - Additional Info - Ancillary Procedures - Concomitant Medications - Treatment Administration - CRA Confirmation
 By Domains - CE - Clinical Events - Page 39 - Page 40 - Page 41 - Page 42 - Page 43 - Page 44	 By Domains - CE - Clinical Events - Visit 3 Months - Visit 6 Months - Visit 9 Months - Visit 1 Years - Visit 2 Years - Visit 5 Years

Figure 6: Wrong vs Correct SDTM aCRF Bookmarking

7. WHAT STANDARDS IS CDISC FOR? (SDTM AND ADAM)

One day my biostat friend, not yet fully familiar with the CDISC standards, sent me an email requesting some help to prepare her SAP mock-up tables:

My Biostatistics friend: *Angelo can you please let me know what is the CDISC standard for representing summary of demographics in output table?*

My answer (the Good Answer): *CDISC is only for data standards. There are no industry standard output templates yet. PhUSE initiative has released some white paper with some recommendation [4]; however the examples provided in these white papers do not represent yet an industry standard and companies are still free to follow their own standard when developing statistical outputs (tables, listings and figures). Once again this has nothing to do with CDISC or at least as of today.*

8. IMPLEMENTATION GUIDANCE VS AGENCY REQUIREMENTS PLUS CDISC IS NOT THE ONLY STANDARD TO CONSIDER (SDTM AND ADAM)

Regardless of whether or not you are working on a submission project, if you apply CDISC standards you should also be aware of the additional Health Authorities (HA) requirements, either FDA or PMDA, with regards to data standards submission. These two agencies have developed a strong process to help the sponsors submitting data in the most standardized way. As such, the two agencies have developed an ad-hoc guidance [5] where they clarify some aspects of the standards that leave the sponsor some space for interpretation or give one or two implementation options. Awareness of HA data submission requirements should be a must in the curriculum of modern Statistical Programmers (but similarly for Biostatisticians)!

This unfortunately, is often not the case, notably for the following aspects:

- eCTD structure: where do our datasets go?
- naming conventions and limitations of filename lengths
- do I need to submit my SAS programs, and if yes, do they need to be executable?

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- different requirements between FDA and PMDA with regards to naming conventions for reviewer guides
- recommendations for ADaM datasets creation

As mentioned above the HA might also have specific requirements when implementing for example SDTM. In some cases the requirement simply provides the HA recommended approach when, for example, SDTM gives more than one implementation option; take for example the handling of the term OTHER where the FDA does not recommend *“to map a collected value to OTHER when there is a controlled term available to match the collected value – even when the terminology allows for Sponsor expansion”*, while the SDTM Ig gives at least three options from which the CRO could choose.

In some circumstances, the HA guidance “contradicts” the standard e.g. SDTM. This is the case for subjects who are randomized to treatment but not treated (in DM). While the SDTM Ig (v3.2) recommends assigning ACTARMCD= NOTTRT, the FDA Study Data Technical Conformance Guidance requires ACTARMCD is left blank.

Last but not least, people often ignore that the data standards requirements, as it meant by HA such as the FDA, it is not just about CDISC. The eCTD previously mentioned, the medical dictionaries and controlled terminology previously discussed are other standards to consider, as well as the requirements for PDF files [6] or any other standard mentioned for example in the FDA standards catalog [7].

9. ABOUT CREATING PROPER DOCUMENTATION OF YOUR CDISC PACKAGE (SDTM AND ADAM)

Alternatives to define.xml when describing complex algorithms (ADaM)

Proper documentation is of vital importance and could be a success factor for your submission. Do not cut corners! Try to imagine that you are the "recipient" of such packages and check, for example, if the explanation of a derivation in the `define.xml` is clear enough. Do not hesitate to find alternative ways if you identify that `define.xml` is not the most "appropriate" tool to describe a complex derivation. Question yourself if you need more than 1000 characters to describe your derivation, whether you might instead describe your complex algorithm in a separate document (e.g. a PDF document that you hyperlink in the `define.xml`)¹.

See for example figure 7. This is from a define.xml of a successful FDA ISS/ISE submission, where the studies had several endpoints related to different quality of life (QoL) aspects. QoL analysis often requires combining answers to several QoL questions into one summary score, by using complex algorithms requiring several steps and transformations e.g. normalizing the answer.

ADaM-IG 1.0 Analysis Data reviewer's Guide Rescue Medications Consumption Derivation SF-12 Composite Score Derivation Algorithm Link to additional external PDF files	AVAL PARAMCD = "SF1202PC" (SF-12 Mental Health Composite Score)	float	8	Derived: Baseline (eqs Q5BFL eq "Y") SF-12 Mental Health Composite Score Derivation Algorithm SF-12 Composite Score Derivation Algorithm Page 1
	AVAL PARAMCD = "SF1202PC" (SF-12 Physical Composite Score)	float	8	Derived: Baseline (eqs Q5BFL eq "Y") SF-12 Physical Health Composite Score Derivation Algorithm SF-12 Composite Score Derivation Algorithm Page 2

Figure 7: An ADaM define.xml referencing an external PDF file containing description of a complex algorithm

Make sure your reviewer guide has relevant details (SDTM and ADaM)

The reviewer guide (RG) has become a key document in data submission. This is the document that will drive the reviewer once he/she will receive the data package. For this reason you should not hesitate in repeating details that might already be mentioned in other documents since the “redundancy” of information reported in the RG is done on purpose. Often the RGs in the CDISC package I have reviewed contained either too many un-useful details or they were inversely lacking of important details. Some examples:

- One of the standard sections of the Study Data RG (SDRG), the SDTM reviewer guide, has a standard section where all supplemental qualifiers are described for each domain included in the SDTM package. The standard template developed by PhUSE expects to report all QNAM and the associated description (QLABEL). It could be worthwhile to provide also a rationale in a separate column with the reason why the variable was not reported elsewhere, either in the parent domain or in another domain. The example in figure 8 is from the CM section; we added supplemental qualifiers containing WHO-DD medical coding and provided the reason why they were not reported in the parent CM domain.

¹ Note that while you might get an error from P21 while validating your define.xml, this is not an issue anymore when you submit to the FDA so in your define fields you can now have longer than 1000 characters (<https://www.pinnacle21.com/forum/dd0086-maximum-length-1000-characters-data-attributes>)

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- On the contrary some other SDRGs were abusive with details with some data-management folks thinking the SDRG is a data management report. You can of course provide relevant details concerning the quality of the data, but this should be limited to important items.

QNAM	Description	Reason
ATC1	Who Drug ATC1 name	WHO-DD coding. Does not fit into any of the CM Domain variables, therefore required to put into SUPP
ATC1CD	Who Drug ATC1 code	WHO-DD coding. Does not fit into any of the CM Domain

Figure 8: An SDRG containing details and rationale of information stored in the Supplemental Qualifier

- The conformance section of the RG should be not a simple list of issues detected by the validator tool - a clear rationale justifying the unresolved issues should be provided. "Resolvable" issues should really be addressed so they are no longer issues (refer to "Stupidario" #1). Figure 9 shows some examples of bad or insufficient rationale

Rationale provided in the cSDRG	What is wrong with the justification?
Issue: "NULL value in AEDECOD variable marked as Required" Explanation: "Terms were not coded in the database"	Incomplete coding might be the object of a rejection to PMDA and major concern of the FDA. You need a strong rationale and therefore the explanation should have provided the reason why the term was not coded
Issue: "Missing FADY variable, when FADTC variable is present" Explanation: "Variable not used"	Although -DY variable is permissible and sponsor could omit it, the FDA Study Technical Conformance Guide requires -DY variable to be included when -DTC is included in the data. Simply saying "Variable not used" does not matter!
Issue (AE): "Permissible variable with missing value for all Records" Explanation: "No data has been collected"	This is about seriousness criteria. It would have been better to clearly specify in the explanation for which variables this issue concern and probably either say that no serious AE with that specific criteria did occur (and in that in case you can also omit the criteria variable) or mention to the reviewer that the study CRF was not collecting such a detail (if that was the case)
Issue: "Invalid value for --TEST variable" Explanation: "Many instances of --TEST >40 characters. --TEST values are directly assigned from the labels taken from the Case Report Form to have clear understanding of the test code and therefore text was not changed."	This is a wrong implementation! FCTEST should have been abbreviated and full text specified in the SDRG
Issue: "NULL value in SEX variable marked as Required" Explanation: "Data Issue: Sex is collected in the raw data"	Does it mean the sex was collected but for some subject the information was not available in the original data?
Issue: "Inconsistent value for Standard Units" Explanation: "Data Issue: We have not been able to convert these to standard units"	More details about laboratory parameter and unit concerned should have been mentioned

Figure 9: Providing a good rationale to unresolved issues

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10. OPPTS I FORGOT TO VALIDATE MY SDTM/ADAM VS DEFINE.XML (SDTM AND ADAM)

Regardless of the tool you are using in your company (e.g. Pinnacle21 Community), conformance of your datasets to the CDISC standards should be continuously assessed and you should not wait the end of your project before validating your CDISC package; this includes not only the datasets but also their metadata (define.xml), i.e. don't forget to validate the define.xml alone - issues may come out that don't when you validate with the data - and of course datasets need to be validated against their metadata.

Moreover, for ADaM datasets the validation should also include the SDTM datasets DM, EX and AE for which some cross-checks between ADaM and SDTM are also performed e.g. a subject in ADSL should exist in SDTM DM.

Having an eye on conformance issues during the development of your SDTM or ADaM dataset is crucial; delaying the check of conformance might result in later detection of issues in the data and its structure requiring corrections and therefore potentially impacting your timelines.

BONUS. IF SDTM IS SUBMITTED AN ADSL MUST ALSO BE SUBMITTED UHMMMM (ADAM)

While I was finalizing my paper a sponsor came to with a comment related to the CDISC package we did deliver for their submission:

"Our CDISC expert says that if we submit SDTM FDA wants us to also submit an ADSL regardless if ADaM was created or not in support of the Individual Clinical Study Report"

The source and responsible of this possible misunderstanding is the FDA itself; however it was not an issue for many of the submission we did at Cytel. The FDA Study Data Technical Conformance Guidance has the following sentence:

"All submissions containing standard analysis data should contain an ADSL file for each study"

The sentence is clearly saying that the requirement apply to only studies for which we submitted an ADaM package; for example in many submission, for some legacy studies, we do submit only the migrated SDTM because these studies contributed to the ISS only (Integrated Summary of Safety). However unfortunately the way this requirement was "formulated" in the FDA Technical Rejection Criteria for Study Data [8] could be the cause of such misunderstanding:

"DM dataset and define.xml must be submitted in module 4, sections 4.2.3.1, 4.2.3.2, 4.2.3.4. DM dataset, ADSL dataset, define.xml must be submitted in module 5, sections"

We hope FDA will clarify or rephrase the sentence in future version of the Technical Rejection Criteria document.

Of course it would not make sense to submit an ADSL if the data were not analysed using ADaM standards and if the study data were submitted in SDTM format for the only purpose of being integrated for example in a pooled ADaM for supporting an ISS.

CONCLUSION

One of my wife's favourite TV-shows is 'Quattro Ristoranti' (Four Restaurants). In each episode of the show, 4 restaurants of the same style are assessed and the one getting the best evaluation wins the prize. One of the first things the TV presenter Alessandro Borghese, a famous Italian chef, does while visiting the restaurant is to assess (of course!) the kitchen and how much the kitchen and its tools are cleaned. This assessment could have a big impact on the final outcome regardless of the quality of the food served in the restaurant the state of the kitchen and its cleanliness influences Borghese's faith in the chef's work.

This is exactly what could happen in a data submission to health authorities such as the FDA: the efficacy and safety of your drug are of course what matter, but lack of traceability, or poor or insufficient documentation might trigger questions and concerns from the reviewer. While this might not impact the overall final outcome of your submission, approval could be delayed if the reviewer starts questioning what you have done by requesting changes, or new deliverables to clarify the aspects that were not sufficiently clear in your original submission.

When working with CROs it is important that sponsors clearly define what they expect as deliverables from the CRO, not only which files are to be included in the CDISC package but also any position they might have on a particular aspect of the standard that give more than one option. Such requirements can be either specified in a sponsor implementation guidance (complex) or in a simple checklist that could be used during review that could also be provided to the CRO so that the CRO is aware of the additional checks the sponsor will go through once the package is delivered.

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As mentioned at the beginning, the packages I have reviewed demonstrated how differently individual "users" and companies have approached the same mapping issue in SDTM or the same analysis "modelling" in ADaM; hopefully this will be reduced in future, hopefully as soon as the industry, eventually with the HA, will address all standard "nuances" and agree on a common interpretation [9].

REFERENCES

- [1] PhUSE Study Data Reviewer Guide (SDRG) and Analysis Data Reviewer Guide (ADRG) template
<https://www.phuse.eu/css-deliverables>
- [2] CDISC ADaM Implementation Guidance v1.1
<https://www.cdisc.org/standards/foundational/adam>
- [3] Metadata Submission Guideline (MSG) for SDTMIG
<https://www.cdisc.org/standards/foundational/sdtmig>
- [4] PhUSE Standard Analyses & Code Sharing – White Papers
<https://www.phuse.eu/white-papers>
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<https://www.fda.gov/ForIndustry/DataStandards/StudyDataStandards/ucm2005545.htm#guides>
- [6] Portable Document Format (PDF) Technical Specifications Document
<https://www.fda.gov/downloads/Drugs/UCM163565.pdf>
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- [8] FDA Technical Rejection Criteria for Study Data
<https://www.fda.gov/downloads/Drugs/DevelopmentApprovalProcess/FormsSubmissionRequirements/ElectronicSubmissions/UCM523539.pdf>
- [9] SDTM ADaM Implementation FAQ
https://www.phusewiki.org/wiki/index.php?title=SDTM_ADaM_Implementation_FAQ

RECOMMENDED READING

About Traceability

- Traceability: Plan Ahead for Future Needs – S. Minjoe, T. Petrowitsch – PhUSE RG06 [2014]
- Traceability and Data Flow PhUSE-CSS WG
http://www.phusewiki.org/wiki/index.php?title=Traceability_and_Data_Flow
- Summary of Traceability References PhUSE-CSS Wiki Page
http://www.phusewiki.org/wiki/index.php?title=Summary_of_Traceability_References
- « Lost » in Traceability, from SDTM to ADaM finally Analysis Results Metadata – A. Tinazzi – CDISC EU Interchange [2016]

About Data Submission and Proper Documentation

- An FDA Submission Experience Using the CDISC Standards – A. Tinazzi, C. Marchand – PhUSE RG04 [2016]
- How to Prepare High-quality Metadata for Submission – V. Debbeti – PhUSE US Connect SI12 [2018]

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