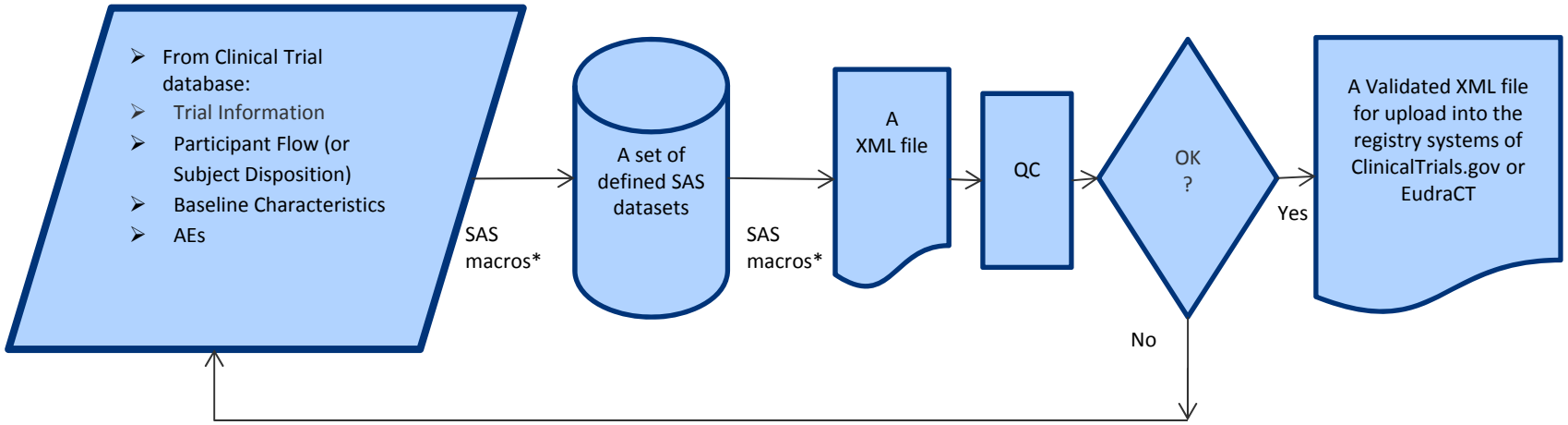
Automation Method

Both ClinicalTrials.gov and EudraCT

- Required Result can be extracted from Clinical Trial Database
  - **Trial Information**
  - **Participant Flow (or Subject Disposition)**
    - Total number of subjects completed / non-completed
    - Reason of discontinuations
  - **Baseline Characteristics**
    - Age, Gender, and other baseline characteristics
  - **Adverse Events**
    - Serious adverse events
    - Frequent adverse events (Non-serious adverse events with max. 5% threshold)

Automation Method

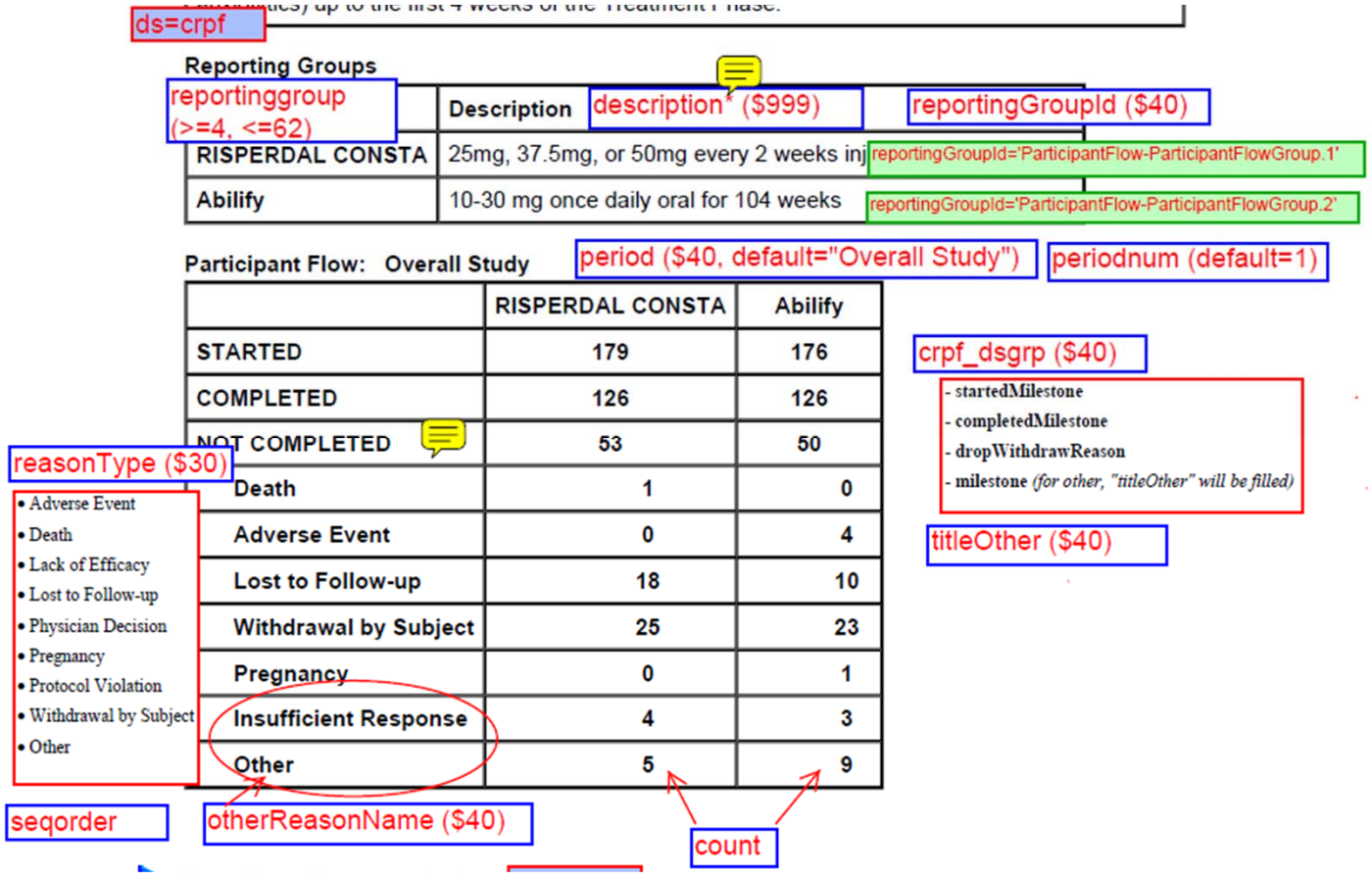
Data Flow of Automation Process



*SAS macros are developed in two sets of macros: one set is based on the requirement of ClinicalTrials.gov; the other set is based on the requirement of EudraCT.

Automation Method

Defined SAS datasets based on result posting requirements: Participant Flow



Automation Method

Defined SAS datasets based on result posting requirements: Participant Flow

Variable name	Variable length	Additional comments
PERIOD	$40	Discrete stages of a clinical trial during which numbers of participants at specific significant events or points of time are reported. If only one period, use “Overall Study”.
PERIODNUM		Sorting order for PERIOD
REPORTINGGROUP	$62	Title of treatment arm. Minimum length is 4
REPORTINGGROUPID	$40	Code for REPORTINGGROUP. It contains value of: “ParticipantFlow-ParticipantFlowGroup.x” with x numerical code from 1-number of reporting groups
TOTAL		Total number of subjects in REPORTINGGROUP in a given period.
REASONTYPE	$30	Withdrawal reason. It contains the value of standard reasons that is defined by clinicaltrials.gov. The values are: Adverse Event Death Lack of Efficacy Lost to Follow-up Physician Decision Pregnancy Protocol Violation Withdrawal by Subject Other
OTHERREASONNAME	$40	Only available for non-standard reason when REASONTYPE=”Other”.
COUNT		Number of subjects with withdrawal reason per REPORTINGGROUP in a given period.
CRPF_DSGRP	$40	Working variable for SAS to XML process. Values are: startedMilestone completedMilestone dropwithdrawreason
SEQORDER		Display sequence order in output

Automation Method

Calling SAS Macros to Create Defined SAS Datasets: Participant Flow

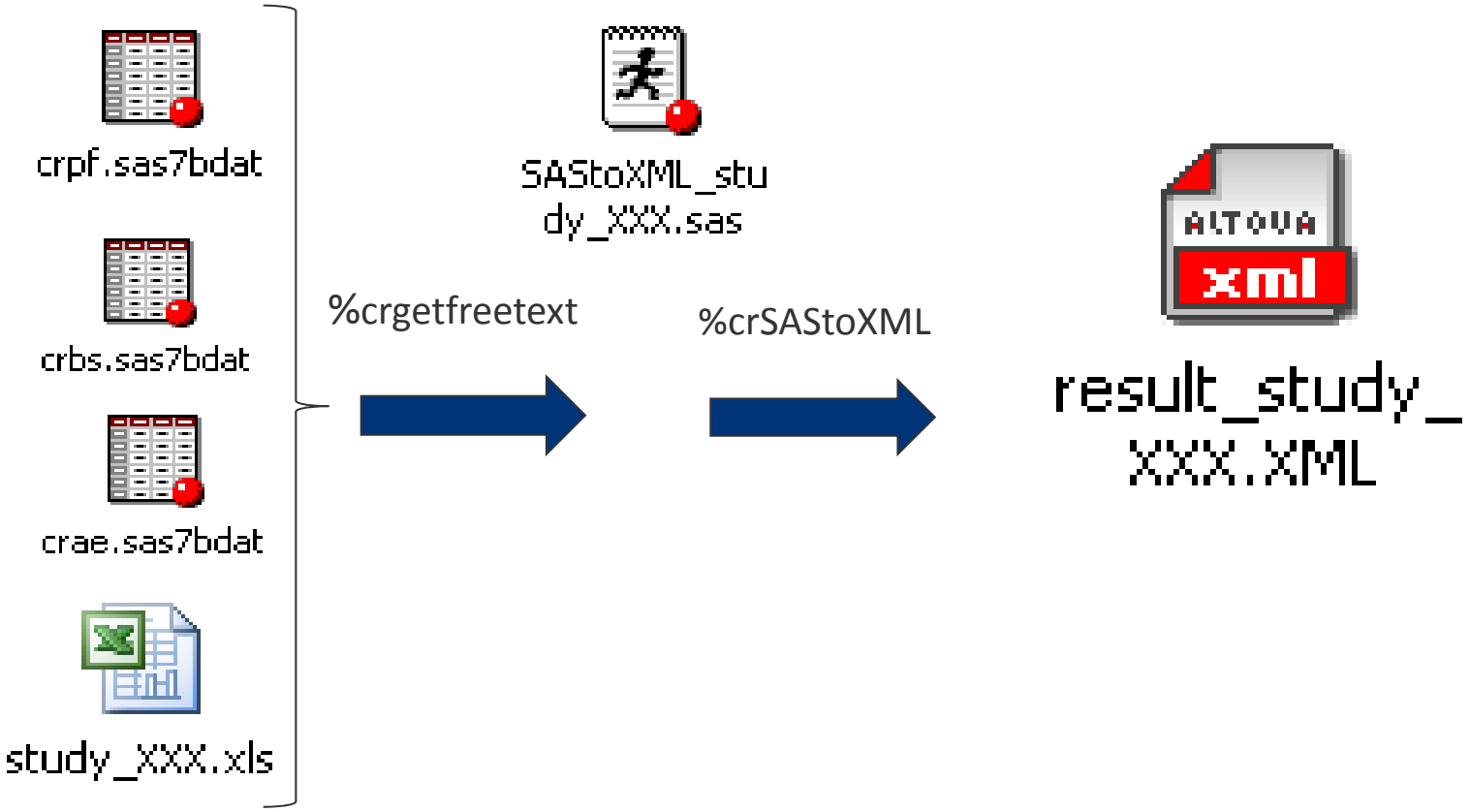
```
/* input left side of format per study, please do not change the right side
of format that is highlighted in yellow !!! */
     value $withdrf
     'ADVERSE EVENT'       = 'Adverse Event'
     'DEATH'               = 'Death'
     'LACK OF EFFICACY'    = 'Lack of Efficacy'
     'LOST TO FOLLOW-UP'   = 'Lost to Follow-up'
     'PHYSICIAN DECISION'  = 'Physician Decision'
     'PREGNANCY'           = 'Pregnancy'
     'OTHER: EXCLUSION #9' = 'Protocol Violation'
     'SUBJECT CHOICE'      = 'Withdrawal by Subject'
      OTHER                = 'Other'
     ;
    run;
```

```
data crds;
  set a_in.adds;
  length xreasons $40 xstart $3;
  where saffl = 'Y'and dscat='DISPOSITION EVENT' and DSSCAT='TRIAL';
  xstart='YES';
  if dsdecod='COMPLETED' then xcomp='YES';
  else do;
    xcomp='NO';
    if compress(dsdecod) in (' ') then dedecod='OTHER';
    xreasons=dsdecod;
    xorder=input(dsdecod, wdordf.);
    /* to display in mixed-case */
    if xorder >90 then do;
       %crfcase(vars=xreasons, case=mixed);
    end;
  end;
run;
```

```
%crpf(indsn   =crds,      /* input data, one record per subject per
                             participant flow period */
      outlib  =a_out,     /* libname for output datasets */
      subj    =usubjid,   /* input var. for unique subject ID */
      arm     =trt01p,    /* arm/treatment group variable */
      armf    =$armf.,    /* format for treatment group */
      armordf =armordf., /* format for display order of treatment group */
      arm_n   =3,         /* number of arms */
      prdnum  =1,         /* input var.for period (num.),default: &period=1 */
      period  =periodf., /* format for period var.,default:1=Overall study */
      started =xstart,    /* input var. for start population: YES/NO */
      comp    =xcomp,     /* input var. for completed population: YES/NO */
      withdraw=xreasons, /* input var. for withdraw reasons */
      withdrf =$withdrf.,/* format for withdraw variable */
      wdordv  =xorder     /* input var. of display order for withdraw reasons *
      );
run;
```

Automation Method

SAS program (2 macro calls) to combine defined SAS datasets and Excel file into single XML file



Automation Method

SAS Macros to Create a Required XML File from Defined SAS Datasets

```
*=== combine prepared files with free text ============;
 %crgetfreetext(excelfile1          = &ipath\freetextfields_Study123.xls, /*an input free-text file */
                outfile             = &opath\CRissues.xls, /*an output list of issues found in XML file */
                baselineds          = a_in.crbs, /* input defined SAS dataset of Baseline meas. */
                participantflowds = a_in.crpf, /* input defined SAS dataset of Participant flow */
                aeds                = a_in.crae, /*input defined SAS dataset of AE */
                );
*=== Join all Sections ============================;
 %crSAStoXML;
```

Automation Method

SAS to XML:
Programs consists of repeated calls to the SECTION macro

```
*=== Participant Flow ==========================================================================;
*--- Flow Groups sub-section ----------------------------------------------------------------;
data participantFlowGroups;
     set &&lib..participantFlowGroups;
     rename reportingGroupId=flowGroup;
run;
```

```
%section(dset  =participantFlowGroups,
         txtb  ="<participantFlowGroups>",
         vars  =flowGroup description title,
         idvar =flowGroup,
         order =flowGroup);

*--- Create sub-sections ignoring period ----------------------------------------------------;
%section(dset  =&lib..StartedMilestone,out=StartedMilestone,
         txtb  ="<startedMilestone><milestoneAchievements>",
         txt   ="<milestoneAchievement>",
         byvars=period title_prd,
         vars  =reportingGroupId comment subjectsAchieve,
         order =reportingGroupId);

%section(dset  =&lib..CompletedMilestone,out=completedMilestone,
         txtb  ="<completedMilestone><milestoneAchievements>",
         txt   ="<milestoneAchievement>",
         byvars=period title_prd,
         vars  =reportingGroupId comment subjectsAchieve,
         order =reportingGroupId);
```

Automation Method

Automated Verification Tool:

- ✓ validate the XML file against the required schema
- ✓ build-in stylesheet to view XML easily

```
<?xml version="1.0" ?>
- <my:study_collection
    xmlns:my="http://clinicaltrials.gov/rrs"
    xmlns:xsi="http://www.w3.org/2001/XMLSchema-
    instance"
    xsi:schemaLocation="http://clinicaltrials.gov/rrs
    clinical_study_limited.xsd">
  - <clinical_study>
    - <id_info>
        <org_name>JNJ</org_name>
        <org_study_id>CR011074</org_study_id>
      </id_info>
    - <result>
      - <baseline>
        - <baselineMeasures>
          - <baselineMeasure>
              <dispersionType>Standard
                Deviation</dispersionType>
            - <measureCategories>
              - <measureCategory>
                - <reportedValues>
                  - <reportedValue>
```

(Without stylesheet)

Summary of Results for Study CR011074

Only for internal purpose to facilitate the validation of the content of the xml file

Participant Flow

Recruitment Details

Key information relevant to the recruitment process for the overall study, such as dates of the recruitment period and locations
The recruitment period for this out-patient, multicenter study occurred between 14 November 2006 and 25 July 2008.

Pre-Assignment Details

Significant events and approaches for the overall study following participant enrollment, but prior to group assignment
The study consisted of a screening period (duration up to 14 days), a washout period (duration 3 to 7 days), and an open label active treatment phase with titration and maintenance (total duration of 52 weeks).

(With stylesheet)