SENTINEL MODULAR PROGRAMS

Inpatient Encounter Querying Tool: Overview of Functionality and Technical Documentation

Prepared by the Sentinel Operations Center
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Sentinel is sponsored by the U.S. Food and Drug Administration (FDA) to monitor the safety of FDA-regulated medical products. Sentinel is one piece of the Sentinel Initiative, a multi-faceted effort by the FDA to develop a national electronic system that complements previously existing methods of safety surveillance. Sentinel Collaborators include Data and Academic Partners that provide access to health care data and ongoing scientific, technical, methodological, and organizational expertise. The Sentinel Coordinating Center is funded by the FDA through the Department of Health and Human Services (HHS) Contract number HHSF223201400030I.

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Modification History

Version	Date	Modification	By
1.0.0	08/01/2018	• Original published version	Sentinel Operations Center
1.0.1	08/01/2018	• Code change for BloodComp variable/no change to documentation	Sentinel Operations Center

I. PROGRAM PACKAGE AND EXECUTION

When implementing modular programs within the Sentinel Distributed Database (SDD), the Sentinel Operations Center (SOC) uses a uniform folder structure to facilitate communications between SOC and Data Partners and to streamline file management. This section describes the program package structure and requirements for package execution.

A. PROGRAM PACKAGE

Each request package distributed by SOC is assigned a unique Request Identifier, and contains several folders to organize program inputs and outputs:

- *sasprograms*: folder contains the master SAS program that must be edited and then executed by the Data Partner.
- *inputfiles*: folder contains input files and lookup tables needed to execute a request. Input files contain parameter values specific to a particular request (*e.g.,* medical product exposures and outcomes of interest). Input files are created for each request by the SOC query fulfillment team; the contents of this folder are not edited by the Data Partner. The folder also contains one subfolder:
    - *macros*: folder contains the macros that comprise the modular program. The contents of this folder are not edited by the Data Partner.
- *msoc*: folder contains output generated by the request that should be sent to SOC.
- *dplocal*: folder contains output generated by the request that should remain with the Data Partner (and may be used to facilitate follow-up queries).

1. Common Components

Prior to executing the request package, a set of SAS programs known as common components must be initialized. In this context, common components refer to a set of SAS programs that provide appropriate site-specific attributes (e.g., Data Partner description variables, Sentinel Common Data Model (SCDM) table names, folder paths, data completeness dates, etc.) to distributed SAS program packages at the time of code execution. More specifically, when an executing SAS program package accesses the file ms_common_components.sas, global macro variable definitions for key site-specific attributes are made available to the calling program. In this context, common components support two important goals: 1) streamline the setup for the distributed SAS program packages, 2) improve the accuracy of results.

Users must specify the location of their common components file path in the master SAS program in the *sasprograms* folder in order for the package to execute. For more information about common components installation, and to download the SAS programs, visit the common components page on the Sentinel website.

2. Master Program Parameters

In the master SAS program, there are several parameters that must be specified. These include the common components include file, project, work plan, and Data Partner identifiers, and a run identifier. Note that all main program parameters specified are fixed for a single execution of the program. **Table 1** contains detailed specifications for master program parameters.

Table 1. Inpatient Encounter Tool Master Program Parameter Specification

Parameter	Field Name	Description
Common Components Include file	MSCC	**Details**: location for user's common components file path. **Defined by**: User programmer **Input type**: Required **Format:** Alphanumeric **Example**: MSCC = //Sentinel/common-components/ms_cc.sas
Patients to Exclude List File Path	PTSTOEXCLUDE	**Details**: optional. Location of user's patients to exclude list. Allows Data Partners to exclude patients from a particular request. The file must contain one variable, PatID, and list all PatID values to exclude from the request. **Defined by**: User programmer **Input type**: Required **Format:** Alphanumeric **Example**: PTSTOEXCLUDE = indata.ptstoexclude
Project Identifier	MSPROJID	**Details**: project identifier for internal SOC identification and tracking. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: MSPROJID=to16_cap
Work Plan Type	MSWPTYPE	**Details**: work plan type for internal SOC identification and tracking. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: MSWPTYPE=mpl2r
Work Plan Identifier	MSWPID	**Details**: work plan identifier for internal SOC identification and tracking. **Note 1:** should follow the format [wp###]. **Note 2:** should be used to uniquely identify a modular program request. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: MSWPID= wp01

Parameter	Field Name	Description
Data Partner Identifier	MSDPID	**Details**: Data Partner identifier for internal SOC identification and tracking. **Note 1:** if a package is not Data Partner specific, MSDPID should equal “nsdp”. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: MSDPID =nsdp
Version Identifier	MSVERID	**Details**: version identifier for internal SOC identification and tracking. Should track each re-distribution of the package (if multiple distributions are required). **Note 1:** should follow the format [v##]. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: MSVERID =v01

II. INPATIENT ENCOUNTER TOOL TECHNICAL DOCUMENTATION

The Inpatient Encounter tool is designed to be executed as a standalone tool. This technical specification document details the lookup tables, program parameters and input files that must be specified to execute the Inpatient Encounter Tool.

A. LOOKUP TABLES, PROGRAM PARAMETERS, AND INPUT FILES

1. Lookup Tables

There are several lookup tables that may be required for the execution of the Inpatient Encounter Tool depending on the nature of the request. These lookup tables are created and maintained by the SOC.

a) Facility Code Lookup Table

The Facility Code file is an optional lookup file used to restrict the extraction of data based on the facility (i.e., hospital or clinic) in which the encounter occurred. The file contains one field, FACILITY_CODE, which the investigator populates with local facility codes represented in the FACILITY_CODE field in the SCDM. If the table is not created, all facilities are queried.

Table 2. FACILITYCODES Specification

Parameter	Field Name	Description
Facility code	FACILITY_CODE	**Details:** Inpatient facility (e.g., hospital, clinic) code identifier from SCDM. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character of site-specific length. **Example:** 0313203132

b) Transcode Type Lookup Table

The trancode type lookup file is optional. It maps clinical transfusion codes to blood components. **Table 3** contains detailed specifications for this file.

Table 3. TRANSCODE_TYPE_LOOKUP Specification

Parameter	Field Name	Description
Analytical Requirement	REQUIREMENT	**Details:** indicates exposure/transfusion conditions, usually in the form of an acronym. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $15 **Example:** RBCS
Code Category	CODECAT	**Details:** indicates the type of health care event represented by the clinical code. Valid value**:** It is always T for Transfusion for this application. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $1 **Example:** T
Code Type	CODETYPE	**Details:** Code type Valid values are: • **IS:** ISBT • **CD:** CODABAR **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $2 **Example:** Required
Transfusion Code Value	CLINCODE	**Details:** indicates transfusion code value. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $15 **Example:** 32457

Parameter	Field Name	Description
Clinical Condition Description	DESCRIPTION	**Details:** Full description of clinical condition. This is for reference only and is not used in the query. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $135 **Example:** RBC-WB

2. Main Program Parameters

There are several main program parameters that must be specified (Table 4). These include a run identifier and the names of all input files. These parameter values should be set in a program called run_programs.sas, located in the *inputfiles* folder. Note that all main program parameters specified are fixed for a single execution of the program. **Table 4** contains detailed specifications for main program parameters.

Table 4. Inpatient Encounter Tool Main Program Parameter Specification

Parameter	Field Name	Description
Run Identifier	RUNID	**Details**: run identifier for internal SOC identification and tracking. Should uniquely identify each execution of a modular program within the same work plan. **Note 1:** should follow the format [r##]. **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: RUNID =r01
Save all SCDM Data Indicator	FREEZEDATA	**Details:** indicates if all SCDM data for patients selected in the cohort(s) of interest will be saved in the *dplocal* folder for further processing. Valid values are: • **Y:** Yes • **N:** No **Defined by:** Request programmer **Input type:** Required **Format:** Alphanumeric **Example**: FREEZEDATA = Y
Monitoring File	MONITORINGFILE	**Details:** name of the SAS dataset defining the time period(s) for each data extraction. **Defined by:** Request programmer **Input type:** Required **Format:** .sas7bdat file format **Example:** MONITORINGFILE=drugname_monitoring

Parameter	Field Name	Description
Cohort File	COHORTFILE	**Details:** name of the SAS dataset defining the cohort identification requirements. **Defined by:** Request programmer **Input type:** Required **Format:** .sas7bdat file format **Example:** COHORTFILE=drugname_cohort
Cohort Codes File	COHORTCODES	**Details:** name of the SAS dataset listing codes used to define the cohort. **Defined by:** Request programmer **Input type:** Required **Format:** .sas7bdat file format **Example:** COHORTCODES=drugname_cohortcodes
Inclusion/ Exclusion Codes File	INCLUSIONCODES	**Details:** name of the SAS dataset listing codes used to define additional cohort inclusion and exclusion criteria. **Defined by:** Request programmer **Input type:** Optional **Format:** .sas7bdat file format **Example:** INCLUSIONCODES=drugname_inclusioncodes
Covariate Codes File	COVARIATECODES	**Details:** name of the SAS dataset listing codes used to define covariates. **Defined by:** Request programmer **Input type:** Optional **Format:** .sas7bdat file format **Example:** INCLUSIONCODES=drugname_covariatecodes
Facility Code Lookup	FACILITYCODES	**Details:** name of the SAS dataset listing codes of facilities used to restrict cohort. **Defined by:** Request programmer **Input type:** Optional **Format:** .sas7bdat file format **Example:** FACILITYCODES=facility_query_summary
Transcode Type Lookup	TRANSCODE_TYPE_LOOKUP	**Details:** name of the SAS dataset listing codes of blood product components. **Defined by:** Request programmer **Input type:** Optional **Format:** .sas7bdat file format **Example:** TRANSCODE_TYPE_LOOKUP=transcode_type_lookup

3. Input Files

The Inpatient Encounter Tool allows requesters to specify multiple scenarios (or, in other words, define multiple cohorts) within a *single execution* of the program. Each cohort is assigned a unique GROUP value in input files to differentiate cohorts.

There are some parameters that are allowed to vary within a single execution of the program, and some that are not. As noted above, main program parameters are fixed for a single execution of the program. In addition, there are several input file parameters that may not vary within a single execution of the program. Where applicable this is noted for each input file described in this section.

a) Cohort File

The Cohort File is required. It is used to define demographic requirements, encounter care setting requirements, and covariate metric definitions. **Table 5** contains detailed specifications for this file.

Table 5. COHORTFILE Specification

Parameter	Field Name	Description
Cohort Name	GROUP	**Details:** standardized name used to differentiate cohorts. **Note 1**: multiple cohorts can be defined within the same Cohort File. In this case all cohorts are queried independently and results are reported separately and labeled using each GROUP name specified. **Note 2:** GROUP is the primary key linking cohorts across input files; GROUP values must match (including case) between the COHORTFILE and other input files. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $30; no special characters (*e.g.,* commas, periods, hyphens, etc.) allowed, and underscores must be used to mark spaces. **Example:** Nes
Sex criteria to apply to cohort	SEX	**Details:** restricts cohort to specified Sex values. Blank will ensure that all Sex values are included in analyses. **Note 1:** valid values will be in single quotes and separated by a space. Valid values are: • **A**: ambiguous • **F**: female • **M**: male • **U**: unknown **Defined by:** Request programmer **Input type:** Optional **Format:** SAS Character $1 **Example:** ’F’ ‘M’ ‘A’ ‘U’
Race criteria to apply to cohort	RACE	**Details:** restricts cohort to only specified Race values. Blank will ensure that all Race values are included in analyses.

Parameter	Field Name	Description
		Note 1: valid values will be in single quotes and separated by a space. Valid values are: • **0**: Unknown • **1**: American indian or Alaska Native • **2**: Asian • **3**: Black or African American • **4**: Native Hawaiian or Other Pacific Islander • **5**: White **Defined by:** Request programmer **Input type:** Optional **Format:** SAS Character $1 **Example**: '3'
Hispanic criteria to apply to cohort	HISPANIC	**Details:** restricts cohort to specified Hispanic values. Blank will ensure that all Hispanic values are included in analyses. **Note 1:** valid values will be in single quotes and separated by a space. Valid values are: • **N**: no • **U**: unknown • **Y**: yes **Defined by:** Request programmer **Input type:** Optional **Format:** SAS Character $1 **Example:** 'N'
Age Groups	AGESTRAT	**Details:** age group categories for reporting. Specifying this parameter will (1) restrict to certain age groups and (2) specify how age groups will be stratified in result tables. Various units of time can be used following ages. Valid values for units of time are: • **D**: days • **W**: weeks • **Q**: quarters • **M**: months • **Y**: years (default value) **Note 1:** lower value is binding. If AGESTRAT=0-5 5-10, then all 5 year olds will be placed in the second age group. If AGESTRAT=0-5 6-10, then all 5 year olds will be placed in the first age group.

Parameter	Field Name	Description
		For example, to have results stratified by 6 month increments for the first two years of life and then by 2 year increments until the age of 6, AGESTRAT = 00M-05M 06M-11M 12M-17M 18M-23M 02Y-03Y 04Y-05Y needs to be entered. **Note 2**: using an open ended age category (e.g., 85+) imposes an age ceiling of 110 years. If age >110 is desired, the final age category ceiling must be specified (e.g., 85-125). **Note 3:** age groups must be mutually exclusive (i.e., non overlapping). **Note 4:** When constructing age categories that only include one age, the lower and upper values are equal. For example, 00M-<01M, 01M-<02M, 02M-<03M, should be specified as 00M-00M 01M-01M 02M-02M. **Defined by:** Request programmer **Input type:** Optional (default value is 00-01 02-04 05-09 10-14 15-18 19-21 22-44 45-64 65-74 75+ in years) **Format:** Char (100) **Example:** AGESTRAT=40-59 60-79 80-99 will produce results with age stratified by 20 year increments for ages 40-99
Encounter Care setting to apply to cohort	CARESETTING	**Details:** restrict cohort to specific encounter type values. Leave it blank if there is no restriction on enctype. Valid values are: • **IP:** Inpatient hospital stay • **IS:** Non-acute institutional stay • **AV:** Ambulatory visits • **ED:** Emergency department **Defined by:** Request programmer **Input type:** Optional **Format:** SAS Character $30 **Example:** ‘IP’ ‘AV’
Truncate encounter at query end date	TRUNCYN	**Details:** indicates whether or not encounters that extend past the end of the query period are truncated at the ENDDATE of the query period. Valid values are: • **Y:** Yes • **N:** No **Defined by:** Request programmer **Input type:** Required **Format:** SAS Character $1 **Example:** TRUNCYN = N

Parameter	Field Name	Description
Medication administration gap	DAYSGAP	**Details:** number of days allowed between RXADATEs for medication administration covariates in the same encounter. **Note 1:** Used to compute metric days_rx_allow_gap. **Note 2:** Leave blank if medication administration covariates are not requested, **Defined by:** Request programmer **Input type:** Optional **Format:** Numeric **Example:** 1
Deduplicate medication administration covariates	CODEFREQ_NODUP	**Details:** Indicates whether or not to deduplicate medication administration covariates that occur on the same date and at the same time. Valid values are: • **Y:** Yes, remove duplicates • **N:** No, do not remove duplicates **Note 1:** Used to compute metric codefreq. **Note 2:** Leave blank if medication administration covariates are not requested. **Defined by:** Request programmer **Input type:** Optional **Format:** SAS Character $1 **Example:** Y

b) Monitoring File

The Monitoring File is required. It specifies the extraction period. **Table 6** contains detailed specifications for this file.

Table 6. MONITORINGFILE Specification

Parameter	Field Name	Description
Time Period Indicator	PERIODID	**Details:** identifier for each STARTFOLLOWUP/ ENDDATE combination. Valid value: It is always 1 for this application. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 1
Query Period Start	STARTFOLLOWUP	**Details:** start date for the query period. **Defined by:** Request programmer **Input type:** Required

Parameter	Field Name	Description
		Format: Numeric (Date9.) **Example:** 01JAN2015
Query Period End	ENDDATE	**Details:** end date for the query period. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric (Date9.) **Example:** 31DEC2015

c) Cohort Codes File

The Cohort Codes File is required. It will include diagnosis codes (specified by ICD-9-CM and ICD-10-CM codes); procedure codes (specified by ICD-9-CM, ICD-10-PCS, HCPCS and or CPT codes); NDCs; ISBT and/or CODABAR to define exposures and events in the final population. It is the primary file for specifying codes used to define exposures and outcomes. NDCs, ICD procedure and diagnosis codes, HCPCS codes, and/or transfusion code values can be used in any combination and can be restricted to specific care settings and diagnosis code positions (*e.g.,* principal discharge diagnoses only). **Table 7** contains detailed specifications for this file.

Table 7. COHORTCODES Specification

Parameter	Field Name	Description
Name of Cohort	GROUP	**Details:** standardized name used to differentiate cohorts. **Note 1**: multiple cohorts can be defined within the same Cohort Codes File. In this case all cohorts are queried independently and results are reported separately and labeled using each GROUP name specified. **Note 2:** GROUP is the primary key linking cohorts across input files; GROUP values must match (including case) between the COHORTCODES file and other input files. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $30; no special characters (*e.g.,* commas, periods, hyphens, etc.) allowed, and underscores must be used to mark spaces. **Example:** Nes
Code Category	CODECAT	**Details:** type of each code category value included in the CODETYPE field (below) of this file. Valid values are: • **DX:** Diagnosis code • **PX:** Procedure code • **IR:** Inpatient pharmacy NDC code • **TR**: Transfusion code **Defined by:** Request programmer **Input type:** Required

Parameter	Field Name	Description
		Format: SAS character $2. **Example:** DX
Code Type	CODETYPE	**Details:** type of each code value included in the CODE field (below) of this file. Valid values are: **If CODECAT = DX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11:** ICD-11-CM • **OT:** Other **If CODECAT = PX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11**: ICD-11-CM • **C4**: CPT-4 (*i.e.,* HCPCS Level I) • **HC**: HCPCS (*i.e.,* HCPCS Level II) • **H3**: HCPCS Level III • **C2**: CPT Category II • **C3**: CPT Category III • **ND**: 11-digit NDC • **RE**: Revenue • **LO**: Local homegrown • **OT**: Other **If CODECAT = TR:** • **IS: ISBT** • **CD: CODABAR** **If CODECAT = IR:** • **09:** 9-digit NDC • **11:** 11-digit NDC **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $3 **Example:** 09
Code	CODE	**Details:** can be NDC, procedure, diagnosis, ISBT and/or CODABAR code of interest. **Note 1:** Codes are matched using exact values (*i.e.,* 3-digit code lookup requires an exact 3-digit code match). Wildcard match (*) functionality is also available for ICD-9 diagnosis codes (*e.g.,* querying “250*0” would be used to find any ICD-9-CM diagnosis codes for diabetes type II, or “250**” to find ICD-9-CM diagnosis codes for all diabetes codes in the range “250.00 - 250.99”).

Parameter	Field Name	Description
		Note 2: For NDCs, either 9 or 11 digit codes can be entered. **Note 3:** remove decimal points in the code value. **Note 4**: CODETYPE/CODECAT must be consistent with the expected format of the CODE value (*e.g.,* the program will not find any valid matches in the data for CODECAT=IR, CODETYPE=11 and a 9-digit NDC value). **Note 5**: Duplicate CODECAT-CODETYPE-CODE-CARESETTING-PRINCIPAL-PADMIT combinations are removed by the algorithm. **Note 6**: 'V' and 'E' ICD-9-CM diagnosis codes must be specified using uppercase 'V' and 'E'. **Defined by:** Request programmer, with support from the SOC as needed **Input type:** Required **Format:** SAS character $11. **Example: (CODECAT=IR; CODETYPE=11):** 12345678911
Care Setting and Diagnosis Position Requirements	CARESETTINGPRINCIPAL	**Details:** defines the care setting and principal diagnosis position requirements for each code. This field uses combination(s) of the SCDM variables care setting (ENCTYPE) and principal discharge diagnosis flag (PDX) to restrict the observance of codes to those in the requested care settings and with the requested diagnosis position. If no restrictions are required (*e.g.,* requester wants all care settings and any value of PDX), leave the field blank. **Note 1:** the wildcard symbol (*) can be used to represent "any" values of either care setting or principal discharge diagnosis flag. For example, CARESETTINGPRINCIPAL = 'IP*' will restrict codes to those observed in the inpatient setting irrespective of the principal diagnosis flag value. CARESETTINGPRINCIPAL = '**P' will restrict diagnosis codes to those in the principal position, irrespective of the care setting. **Note 2:** the principal discharge diagnosis flag is only relevant for diagnosis codes. All other codes should use the * wildcard for the third digit of the CARESETTINGPRINCIPAL value. **Note 3:** CARESETTINGPRINCIPAL is allowed to vary between CODEs within the same GROUP. For example, CARESETTINGPRINCIPAL is allowed to equal 'IPP' for one diagnosis code and 'IPP' 'EDP' for another diagnosis code *in the same GROUP*.

Parameter	Field Name	Description
		Note 4: valid values will be in single quotes and separated by a space. Valid values are: • **IPP:** inpatient hospital stays, principal diagnoses • **IPS:** inpatient hospital stays, secondary diagnoses • **IPX:** inpatient hospital stays, unclassified diagnoses • **ISP:** non-acute institutional stays, principal diagnoses • **ISS:** non-acute institutional stays, secondary diagnoses • **ISX:** non-acute institutional stays, unclassified diagnoses • **ED*:** emergency department encounters • **AV*:** ambulatory visits • **OA*:** other ambulatory visits **Defined by:** Request programmer **Input type:** Optional; Default: blank (*i.e.,* no restrictions) **Format:** SAS character $50. **Example:** 'IPX' 'ED*' '**P'
Code Relevance to Cohort Index Date Definition	INDEX	**Details:** indicates, for each code listed in the file, what role the code will play in defining exposures and covariates. Valid values are: • **DEF**: code should be used to identify encounters with exposures • **NOT**: code should not be used to define cohort index date **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $3. **Example:** DEF
Code Relevance to Cohort HOI Definition	FUP	**Details:** indicates, for each code listed in the file, what role the code will play in defining HOI. Valid values are: • **HOI1:** cohort HOI1 • **HOI2:** cohort HOI2 • **…** • **HOIn:** cohort HOIn • **NOT:** code should not be used/does not identify HOI **Defined by:** Request programmer **Input type:** Required

Parameter	Field Name	Description
		Format: SAS character $4. **Example:** HOI1
Present on Admission Requirement	PADMIT	**Details:** defines the present on admission requirement for each code. If no restrictions are required (*e.g.,* requester wants all any value of PADMIT), leave the field blank. **Note 1:** Only valid for DX codes. Leave blank for other code types. **Note 2:** if requester defines diagnosis as NOT present at admission, PAdmit='N' 'U' or 'X'. **Note 3:** valid values will be in single quotes and separated by a space. Valid values are: • **N:** No • **Y:** Yes • **U:** Unknown/Unable to determine • **X:** Unreported/Not used **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $1. **Example:** if requester defines the diagnosis as NOT present at admission, PAdmit='N' 'U' 'X'

d) Inclusion/Exclusion Codes File

The Inclusion/Exclusion Codes File is optional. It contains the comprehensive set of codes that are used to define additional cohort inclusion/exclusion criteria (*e.g.,* restrict cohort to encounters with no evidence of co-occuring conditions). NDCs, ICD procedure and diagnosis codes, HCPCS codes, and/or transfusion code values can be used in any combination and can be restricted to specific care settings and diagnosis code positions (*e.g.,* principal discharge diagnoses only). **Table 8** contains detailed specifications for this file.

Table 8. INCLUSIONCODES Specification

Parameter	Field Name	Description
Name of Cohort	GROUP	**Details:** standardized name used to differentiate cohorts. **Note 1**: multiple cohorts can be defined within the same Inclusion/Exclusion Codes File. In this case all cohorts are queried independently and results are reported separately and labeled using each GROUP name specified. **Note 2:** GROUP is the primary key linking cohorts across input files; GROUP values must match (including case) between the INCLUSIONCODES file and other input files. **Defined by:** Request programmer

Parameter	Field Name	Description
		Input type: Required **Format:** SAS character $30; no special characters (*e.g.,* commas, periods, hyphens, etc.) allowed, and underscores must be used to mark spaces. **Example:** Insulin
Code Category	CODECAT	**Details:** type of each code category value included in the CODETYPE field (below) of this file. Valid values are: • **DX:** Diagnosis code • **PX:** Procedure code • **IR:** Inpatient pharmacy NDC code • **TR:** Transfusion code **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $2. **Example:** DX
Code Type	CODETYPE	**Details:** type of each code value included in the CODE field (below) of this file. Valid values include: **If CODECAT = DX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11:** ICD-11-CM • **OT:** Other **If CODECAT = PX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11**: ICD-11-CM • **C4**: CPT-4 (*i.e.,* HCPCS Level I) • **HC**: HCPCS (*i.e.,* HCPCS Level II) • **H3**: HCPCS Level III • **C2**: CPT Category II • **C3**: CPT Category III • **ND**: 11-digit NDC • **RE**: Revenue • **LO**: Local homegrown • **OT**: Other **If CODECAT = TR:** • **IS**: ISBT • **CD**: CODABAR **If CODECAT = IR:** • **09**: 9-digit NDC • **11:** 11-digit NDC

Parameter	Field Name	Description
		Defined by: Request programmer **Input type:** Required **Format:** SAS character $3. **Example:** 09
Code	CODE	**Details:** NDC, procedure, diagnosis, ISBT and/or CODABAR code of interest. **Note 1**: Codes are matched using exact values (*i.e.,* 3-digit code lookup requires an exact 3-digit code match). Wildcard match (*) functionality is also available for ICD-9 diagnosis codes (*e.g.,* querying “250*0” would be used to find any ICD-9-CM diagnosis codes for diabetes type II, or “250**” to find ICD-9-CM diagnosis codes for all diabetes codes in the range “250.00 - 250.99”). To get “starts with” codes, the user will have to specify 250, 250*, 250**. **Note 2**: For NDCs, either 9 or 11 digit codes can be entered. **Note 3:** remove decimal points in the code value. **Note 4**: CODETYPE/CODECAT must be consistent with the expected format of the CODE value (*e.g.,* the program will not find any valid matches in the data for CODECAT=IR, CODETYPE=11 and a 9-digit NDC value). **Note 5**: Duplicate CODECAT-CODETYPE-CODE-CARESETTING-PRINCIPAL-PADMIT combinations are removed by the algorithm **Note 6**: ‘V’ and ‘E’ ICD-9-CM diagnosis codes must be specified using uppercase ‘V’ and ‘E’. **Defined by:** Request programmer, with support from the SOC as needed **Input type:** Required **Format:** SAS character $15. **Example: (CODECAT=IR; CODETYPE=11):** 12345678911
Care Setting and Diagnosis Position Requirements	CARESETTINGPRINCIPAL	**Details:** defines the care setting and principal diagnosis position requirements for each code. This field uses combination(s) of the SCDM variables care setting (ENCTYPE) and principal discharge diagnosis flag (PDX) to restrict the observance of codes to those in the requested care settings and with the requested diagnosis position. If no restrictions are required (*e.g.,* requester wants all care settings and any value of PDX), leave the field blank. **Note 1:** the wildcard symbol (*) can be used to represent “any” values of either care setting or principal discharge diagnosis flag. For example, CARESETTINGPRINCIPAL =

Parameter	Field Name	Description
		'IP*' will restrict codes to those observed in the inpatient setting irrespective of the principal diagnosis flag value. CARESETTINGPRINCIPAL = '**P' will restrict diagnosis codes to those in the principal position, irrespective of the care setting. **Note 2:** the principal discharge diagnosis flag is only relevant for diagnosis codes. All other codes should use the * wildcard for the third digit of the CARESETTINGPRINCIPAL value. **Note 3:** CARESETTINGPRINCIPAL is allowed to vary between CODEs within the same GROUP. For example, CARESETTINGPRINCIPAL is allowed to equal 'IPP' for one diagnosis code and 'IPP' 'EDP' for another diagnosis code *in the same GROUP*. **Note 4:** valid values will be in single quotes and separated by a space. Valid values are: • **IPP:** inpatient hospital stays, principal diagnoses • **IPS:** inpatient hospital stays, secondary diagnoses • **IPX:** inpatient hospital stays, unclassified diagnoses • **ISP:** non-acute institutional stays, principal diagnoses • **ISS:** non-acute institutional stays, secondary diagnoses • **ISX:** non-acute institutional stays, unclassified diagnoses • **ED*:** emergency department encounters • **AV*:** ambulatory visits • **OA*:** other ambulatory visits **Defined by:** Request programmer **Input type:** Optional; Default: blank (*i.e.,* no restrictions) **Format:** SAS character $50. **Example:** 'IPX' 'ED*' '**P'
Inclusion/Exclusion indicator	CONDINCLUSION	**Details:** indicates whether each criterion specified (i.e., CONDLEVEL value) is for an inclusion (=1) or exclusion (=0) criterion. Valid values are: • **1:** Inclusion • **0:** Exclusion **Note 1**: within GROUP values, CONDINCLUSION = 0 and CONDINCLUSION = 1 criteria are separated by an "and" operator. For example, in a scenario with 1) CONDLEVEL =

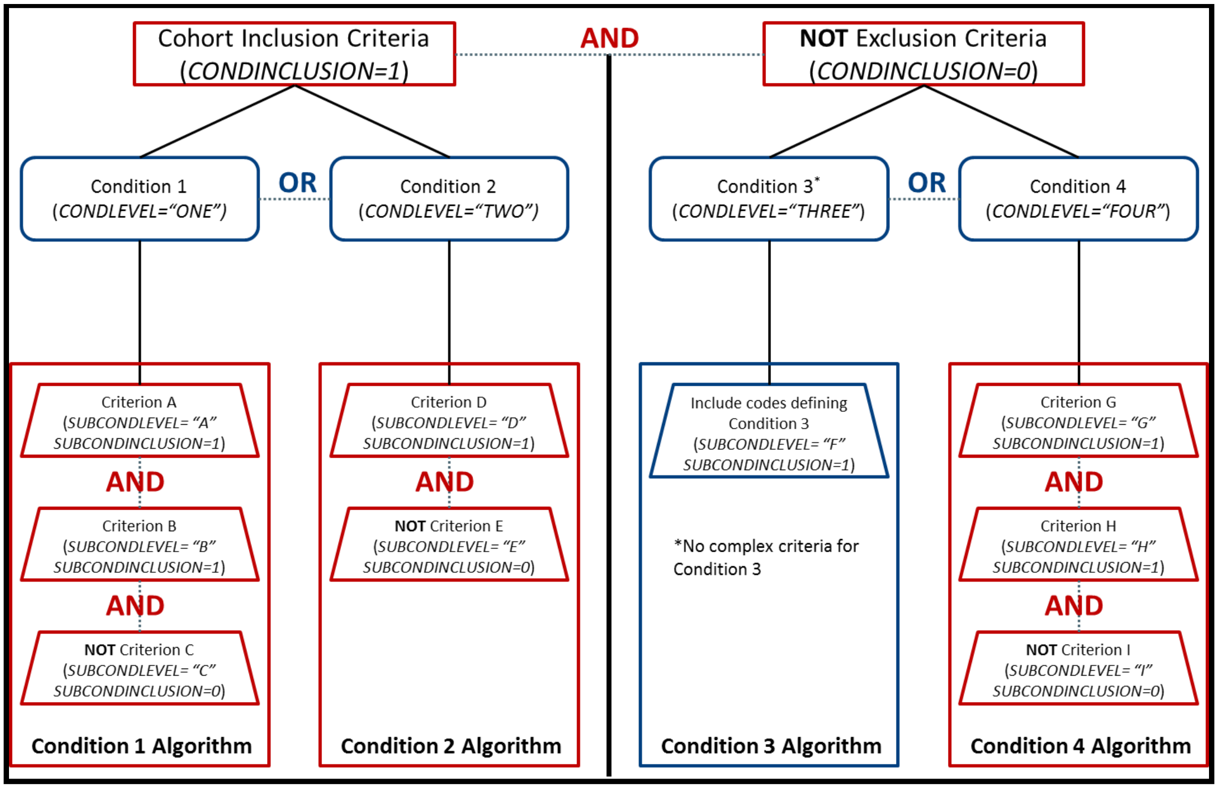
Parameter	Field Name	Description
		"Diabetes" and CONDINCLUSION=1; and 2) CONDLEVEL = "Heart_Failure" and CONDINCLUSION=0, the program will require presence of Diabetes **and** absence of Heart Failure during the encounter for an encounter to be eligible for cohort entry. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 1
Name of inclusion or exclusion condition	CONDLEVEL	**Details:** requester-defined name to represent a unique inclusion or exclusion criterion. **Note 1**: within GROUP and CONDINCLUSION values, CONDLEVEL values indicate criteria separated by an "or" operator. For example, in a scenario with 1) CONDLEVEL = "Diabetes" and CONDINCLUSION=1; and 2) CONDLEVEL = "Heart_Failure" and CONDINCLUSION=1, the program will require presence of Diabetes **or** presence of Heart Failure for an encounter to be eligible for cohort entry. **Defined by:** Request programmer **Input type:** Required **Format: SAS** character $200 **Example:** Diabetes
Name of inclusion or exclusion subcondition	SUBCONDLEVEL	**Details:** requester-defined name to represent unique inclusion or exclusion criteria **within CONDLEVEL values.** Allows requesters to define an individual inclusion/exclusion criterion (e.g., Diabetes) using a complex algorithm (e.g., diagnosis codes **and** antidiabetic medication). **Note 1**: within GROUP, CONDINCLUSION, and CONDLEVEL values, criteria specified with the same SUBCONDLEVEL value are separated by an "and" operator. For example, in a scenario with 1) CONDLEVEL = "Diabetes", CONDINCLUSION=1, SUBCONDLEVEL= "diagnoses" and SUBCONDINCLUSION=1; and 2) CONDLEVEL = "Diabetes", CONDINCLUSION=1, SUBCONDLEVEL= "DiabetesRX" and SUBCONDINCLUSION=1, the program will define Diabetes as presence of a diagnosis code indicative of diabetes **and** an inpatient dispensing of an antidiabetic medication. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $200 **Example:** Diabetes_DX

Parameter	Field Name	Description
Inclusion/Exclusion subcondition indicator	SUBCONDINCLUSION	**Details:** indicates whether each SUBCONDLEVEL criterion is for an inclusion or exclusion criterion. Valid values are: • **1:** Inclusion • **0:** Exclusion **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 1
Present on Admission Requirement	PADMIT	**Details:** defines the present on admission requirement for each code. If no restrictions are required (*e.g.,* requester wants all any value of PADMIT), leave the field blank. **Note 1:** Only valid for DX codes. Leave blank for other code types. **Note 2:** if requester defines diagnosis as NOT present at admission, PAdmit='N' 'U' or 'X'. **Note 3:** valid values will be in single quotes and separated by a space. Valid values are: • **N:** No • **Y:** Yes • **U:** Unknown/Unable to determine • **X:** Unreported/Not used **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $1. **Example:** if requester defines the diagnosis as NOT present at admission, PAdmit='N' 'U' 'X'
Indicates the number of instances for the condition	CODEDAYS	**Details:** sets the number of days during the encounter the SUBCONDLEVEL should be found. **Note**: multiple codes for the same SUBCONDLEVEL identified on the same day will only count once (i.e., count code days not code instances). **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 1 (default)
Inclusion/Exclusion episode gap	GAPDAYS	**Details:** is used with CODEDAYS. If GAPDAYS is set to a non-missing value, the program builds a use episode that starts with the first use date and uses the GAPDAYS

Parameter	Field Name	Description
		criterion. Then it evaluates whether the use episode meets the CODEDAYS criterion. **Example 1**: GAPDAYS=1, CODEDAYS=3, and a patient with RXADATEs on 7/1, 7/3, 7/6, 7/7, and 7/9. The episode considered is 7/1-7/3. It starts with the first RXADATE and has no more than 1 GAPDAY. This episode meets the CODEDAYS criterion being at least 3 days long. Note that the 7/6 – 7/9 episode is not considered, since it is not the first use episode during the encounter. **Example 2**: GAPDAYS=1, CODEDAYS=3, and a patient with RXADATEs on 7/1, 7/2, 7/6, 7/7, and 7/9. The episode considered is 7/1-7/2. It does not meet the CODEDAYS criterion because it is 2 days long. **Example 3**: GAPDAYS=2, CODEDAYS=5, and a patient with RXADATEs on 7/1, 7/4, 7/6, 7/7, and 7/9. The episode considered is 7/1-7/9. It meets the CODEDAYS criterion. **Note 1:** For transfusions, only bridge across TDATE_START. For example, if TDATE_START=7/1 and TDATE_END=7/2, this only counts as 1 codeday. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 1

Specifying the Inclusion/Exclusion Codes File, and understanding the relationships among parameters, can be challenging. **Figure 1** describes file parameters and the interactions between “and” and “or” operators. The fictitious example includes two inclusion criteria and two exclusion criteria. Each inclusion criterion is defined using a complex algorithm (i.e., Condition 1 is defined as Criterion A and Criterion B and not Criterion C); one of the two exclusion criteria is defined using a complex algorithm (i.e., Condition 4 is defined as Criterion G and Criterion H and not Criterion I). If an encounter meets the definition of Condition 4, it is excluded from the cohort.

Figure 1. Relationship Between Parameters Defining Inclusion/Exclusion Criteria



In terms of creating input files, the following two examples demonstrate how input files should be created to ensure different inclusion/exclusion criteria.

Example 1:

Inclusion criteria: Condition A or Condition B
Exclusion criteria: Condition C and Condition D

Group	Stockgroup	CondInclusion	CondLevel	SubcondLevel	Subcondinclusion
Group A	Condition A	1	Cond1	SubCond1	1
Group A	Condition B	1	Cond2	Subcond1	1
Group A	Condition C	0	Cond3	Subcond2	1
Group A	Condition D	0	Cond3	Subcond3	1

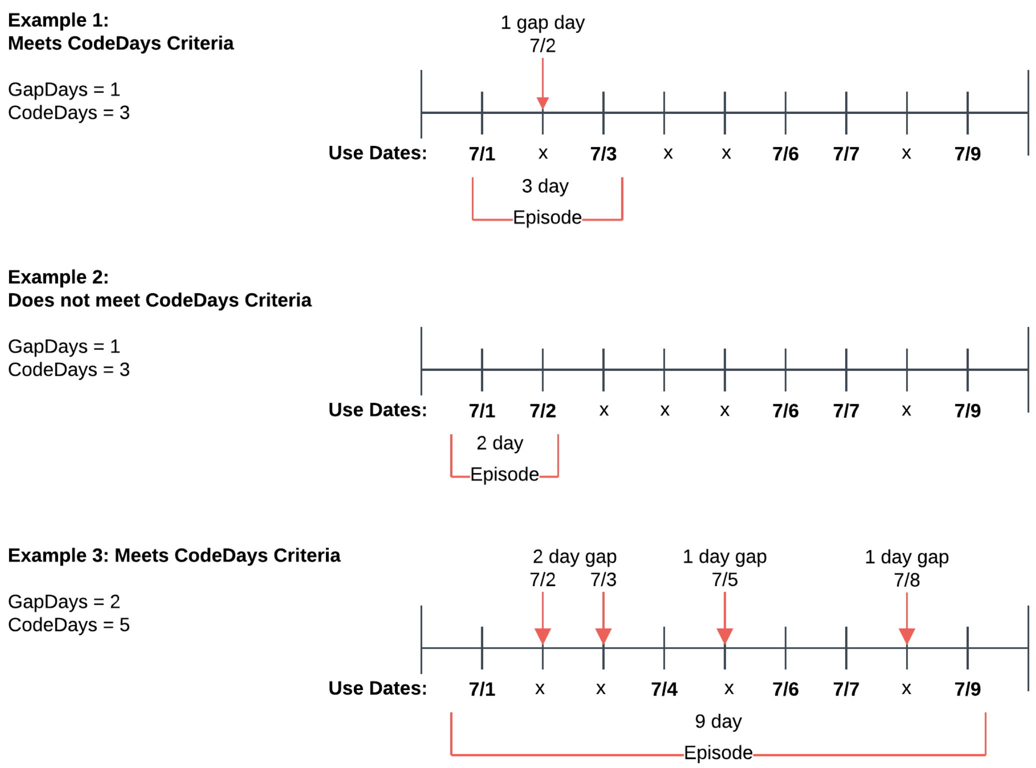
Example 2:

Inclusion criteria: Condition A and not Condition B
Exclusion criteria: (Condition C and Condition D) or (Condition E and Condition F)

Group	Stockgroup	Condinclusion	CondLevel	SubcondLevel	Subcondinclusion
Group A	Condition A	1	Cond1	SubCond1	1
Group A	Condition B	1	Cond1	Subcond2	0
Group A	Condition C	0	Cond3	Subcond3	1
Group A	Condition D	0	Cond3	Subcond4	1
Group A	Condition E	0	Cond4	Subcond5	1
Group A	Condition F	0	Cond4	Subcond6	1

Creating use episodes using the GAPDAYS variable and evaluating whether the criterion represented by the CODEDAYS variable is met is illustrated in Figure 2. Creating and Evaluating Use Episodes***Figure 2**.

Figure 2. Creating and Evaluating Use Episodes*



e) Covariate Codes File

The covariate codes file is optional. It is used to identify comorbidities and medications administered during the same encounter. It can include diagnosis codes, procedure codes, NDCs or ISBTand/or CODABAR codes. Only one Covariate Codes file can be specified per execution of the Inpatient Encounter Tool. Therefore, all cohorts (GROUPs) included in an execution will extract information for the same covariates. **Table 9** contains detailed specifications for this file.

Table 9. COVARIATECODES Specification

Parameter	Field Name	Description
Covariate Name	STUDYNAME	**Details:** unique name for each covariate defined in the file. **Note 1:** STUDYNAME is used as a display name for each covariate in the report. **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $50. **Example:** Comorbidity 1
Numeric Covariate Indicator	COVARNUM	**Details:** a numeric indicator for each covariate specified to identify covariates for further processing and determine the order of covariates in output. **Note 1:** each unique STUDYNAME should have a unique COVARNUM value. **Note 2:** COVARNUM must start at 1 and be incremented by 1 for each additional covariate. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 11
Covariate Type	COVARTYPE	**Details:** used to separate codes for comorbidity from codes for medication administered. Valid values are: • **COMORB:** comorbidity in the same encounter • **MEDADM:** medications administered in the same encounter **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $6. **Example:** COMORB
Code Category	CODECAT	**Details:** type of each code category value included in the CODETYPE field (below) of this file. Valid values are: • **DX:** Diagnosis code

Parameter	Field Name	Description
		• **PX:** Procedure code • **IR:** Inpatient pharmacy NDC code • **TR:** Transfusion code **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $2. **Example:** DX
Code Type	CODETYPE	**Details:** type of each code value included in the CODE field (below) of this file. Valid values are: **If CODECAT = DX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11:** ICD-11-CM • **OT:** Other **If CODECAT = PX:** • **09**: ICD-9-CM • **10**: ICD-10-CM • **11**: ICD-11-CM • **C4**: CPT-4 (*i.e.,* HCPCS Level I) • **HC**: HCPCS (*i.e.,* HCPCS Level II) • **H3**: HCPCS Level III • **C2**: CPT Category II • **C3**: CPT Category III • **ND**: 11-digit NDC • **RE**: Revenue • **LO**: Local homegrown • **OT**: Other **If CODECAT = TR:** • **IS**: ISBT • **CD**: CODABAR **If CODECAT = IR:** • **09**: 9-digit NDC • **11:** 11-digit NDC **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $2. **Example:** 09
Code	CODE	**Details:** NDC, diagnosis, procedure, and/or transfusion code of interest. **Note 1**: Codes are matched using exact values (*i.e.,* 3-digit code lookup requires an exact 3-digit code match).

Parameter	Field Name	Description
		Wildcard match (*) functionality is also available for ICD-9 diagnosis codes (*e.g.,* querying "250*0" would be used to find any ICD-9-CM diagnosis codes for diabetes type II, or "250**" to find ICD-9-CM diagnosis codes for all diabetes codes in the range "250.00 - 250.99"). To get "starts with" codes, the user will have to specify 250, 250*, 250**. **Note 2**: For NDCs, either 9 or 11 digit codes can be entered. **Note 3:** remove decimal points in the code value. **Note 4**: CODETYPE/CODECAT must be consistent with the expected format of the CODE value (*e.g.,* the program will not find any valid matches in the data for CODECAT=IR, CODETYPE=11 and a 9-digit NDC value). **Note 5**: Duplicate CODECAT-CODETYPE-CODE-CARESETTING-PRINCIPAL-PADMIT combinations are removed by the MP algorithm. **Note 6**: 'V' and 'E' ICD-9-CM diagnosis codes must be specified using uppercase 'V' and 'E'. **Note 7**: If CODECAT = CC, this field contains the algorithm for the combination of COVARNUM values, e.g., "1 and (2 or 3)" to describe an algorithm requesting presence of COVARNUM=1 and (COVARNUM=2 or COVARNUM=3). The referenced COVARNUM values to define the combination must be previously defined (i.e., be listed on rows preceding the CODECAT=CC row). Any combination of "and", "or", and "not" may be used in combination with parentheses to define algorithms. Example algorithms (these are all different): • (1 or 9) and not 2 • 1 or 9 and not 2 • Not 2 and 1 or 9 Unless all expressions are of one type (i.e. 1 and 2 and 3), it is highly recommended to use parentheses for algorithm clarity (i.e., bullets 2 and 3 above should be avoided). **Defined by:** Request programmer, with support from the SOC as needed **Input type:** Required **Format:** SAS character $50. **Example1: (CODECAT=IR; CODETYPE=11):** 12345678911

Parameter	Field Name	Description
Care Setting and Principal Diagnosis Indicator	CARESETTINGPRINCIPAL	**Details:** defines the care setting and principal diagnosis position requirements for each code. This field uses combination(s) of the SCDM variables care setting (ENCTYPE) and principal discharge diagnosis flag (PDX) to restrict the observance of codes to those in the requested care settings and with the requested diagnosis position. If no restrictions are required (*e.g.,* requester wants all care settings and any value of PDX), leave the field blank. **Note 1:** the wildcard symbol (*) can be used to represent "any" values of either care setting or principal discharge diagnosis flag. For example, CARESETTINGPRINCIPAL = 'IP*' will restrict codes to those observed in the inpatient setting irrespective of the principal diagnosis flag value. CARESETTINGPRINCIPAL = '**P' will restrict diagnosis codes to those in the principal position, irrespective of the care setting. **Note 2:** the principal discharge diagnosis flag is only relevant for diagnosis codes. All other codes should use the * wildcard for the third digit of the CARESETTINGPRINCIPAL value. **Note 3:** CARESETTINGPRINCIPAL is allowed to vary between CODEs within the same GROUP. For example, CARESETTINGPRINCIPAL is allowed to equal 'IPP' for one diagnosis code and 'IPP' 'EDP' for another diagnosis code *in the same GROUP*. **Note 4:** valid values will be in single quotes and separated by a space. Valid values are: • **IPP:** inpatient hospital stays, principal diagnoses • **IPS:** inpatient hospital stays, secondary diagnoses • **IPX:** inpatient hospital stays, unclassified diagnoses • **ISP:** non-acute institutional stays, principal diagnoses • **ISS:** non-acute institutional stays, secondary diagnoses • **ISX:** non-acute institutional stays, unclassified diagnoses • **ED*:** emergency department encounters • **AV*:** ambulatory visits • **OA*:** other ambulatory visits **Defined by:** Request programmer

Parameter	Field Name	Description
		Input type: Optional; Default: blank (*i.e.,* no restrictions) **Format:** SAS character $50. **Example:** 'IPX' 'ED*' '**P'
Covariate Evaluation Period Start	COVFROM	**Details:** used in combination with COVTO (below). COVFROM defines the start of the evaluation period for each CODE value specified, expressed in terms of "days from Index Date". **Note 1:** Because all covariates are evaluated within the same encounter, the value should be set to 0. **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** 0
Covariate Evaluation Period End	COVTO	**Details:** used in combination with COVFROM (above). COVTO defines the end of the evaluation period for each CODE value specified, expressed in terms of "days from Index Date". **Note 1**: individual CODE values within the same GROUP are allowed to have different evaluation periods and therefore have different COVTO values. **Note 2:** : when COVTO = missing, the program considers a covariate met if the member has the code in their entire encounter. It is recommended to always set COVTO = . **Defined by:** Request programmer **Input type:** Required **Format:** Numeric **Example:** .
Present on Admission Requirement	PADMIT	**Details:** defines the present on admission requirement for each code. If no restrictions are required (*e.g.,* requester wants all any value of PADMIT), leave the field blank. **Note 1:** Only valid for DX codes. Leave blank for other code types. **Note 2:** if requester defines diagnosis as NOT present at admission, PAdmit='N' 'U' or 'X'. **Note 3:** valid values will be in single quotes and separated by a space. Valid values are: • **N:** No • **Y:** Yes

Parameter	Field Name	Description
		• **U:** Unknown/Unable to determine • **X:** Unreported/Not used **Defined by:** Request programmer **Input type:** Required **Format:** SAS character $1. **Example:** if requester defines the diagnosis as NOT present at admission, PAdmit='N' 'U' 'X'

B. PROGRAMMING STEPS

Once the input files, lookup files, and main program parameters described above are set, the Inpatient Encounter Tool can be run.

Below is a high-level view of program execution:

1. Import input files
2. Extract the records from the diagnosis, procedure, inpatient pharmacy, and inpatient transfusion tables that match records in the input files
3. Extract all encounters that fall within the query period

Begin scenario loop

4. Extract scenario-specific records from the diagnosis, procedure, inpatient pharmacy, and inpatient transfusion records extracted above
5. Restrict encounters based on demographic, care setting, and facility criteria and retain claims that occur during valid encounters
6. Group records by Point of View (POV), which is the tool's way of describing how the record is used:
    - POV 1: Records that define exposure
    - POV 3: Records that define encounter inclusion/exclusion criteria
    - POV 5: Records that define HOIs
7. Create a master list of encounters with a POV 1 record and designate encounters that meet the POV 3 criterion
8. Evaluate the occurrence of Health Outcomes of Interest (HOIs)
9. Finalize the master encounter list and determine encounter characteristics:
    - Calculate length of stay
    - If exposure is defined using transfusion codes, determine blood components and count total number of transfusions during the encounter
10. Compute attrition information
11. Compute eligible encounters

End scenario loop

12. Extract covariates and compute covariate metrics
13. Aggregate and output MSOC tables

C. OUTPUT

Please note in the output tables below, the parameters presented in bold are stratifiers.

1. MSOC Folder

The Inpatient Encounter Tool generates output to the MSOC. All output tables for all types of analyses are described below.

a) [*RUNID*] _descstat.sas7bdat

This is an aggregate data set which contains the number of encounters in the cohort, HOIs, eligible encounters, eligible members, eligible facitilies, length of stay metrics, and mean age. All metrics are reported overall, and count metrics are stratified by age group, sex, year, race, Hispanic, encounter setting, discharge disposition, blood component, and number of transfusions. **Table 10** contains detailed specifications for this file.

Table 10. [RUNID] _descstat Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **000:** overall • **001:** year • **002:** sex • **003:** age group • **110:** race • **114:** Hispanic origin • **200:** encounter setting • **205:** discharge disposition • **210:** number of transfusion units • **215:** blood compondent • **220:** age • **225:** length of stay **Format:** SAS character $3
SEX	Sex. Valid values are those in the SCDM. **Format:** SAS character $1
AGEGROUP	Age group. Categories are requester-defined. **Format:** Varying SAS character
AGE	Indicates whether to interpret the value of Count_Enc as mean age or standard deviation of age.

Variable	Description
	Valid values are: - **Mean_age**: Mean age - **Std_age:** Standard deviation of age **Format:** SAS character $7
RACE	Race. Valid values are those in the SCDM. **Format:** SAS character $1
HISPANIC	A person of Cuban, Mexican, Puerto Rican, South or Central American, or other Spanish culture or origin, regardless of race. Valid values are those in the SCDM. **Format:** SAS character $1
YEAR	Year of admission. **Format:** Numeric (YYYY)
ENCTYPE	Encounter type. If the care setting of the encounter is inpatient (IP) or non-acute institutional stay (IS), ENCTYPE = IP. Valid values are: - **IP:** Inpatient - **ED:** Emergency department - **AV:** AV **Format:** SAS character $2
DISCHARGE_DISPOSITION	Discharge disposition. Valid values are: **A:** Discharged Alive **E:** Expired **U:** Missing; Unknown **Format:** SAS character $1
TRANS_UNIT	Total units transfused within one encounter. **Format:** Numeric
BLOODCOMP	Blood components included in transfusion. Valid values are: If RBC_Any = 1 but Plate_Any, Plasma_Any, and Other_Blood do not = 1 - **RBCs** If Plasma_Any = 1 but Plate_Any, RBCs_Any, and Other_Blood do not = 1 - **Plasma** If Plate_Any = 1 but RBC_Any, Plasma_Any, and Other_Blood do not = 1 - **Platlets** If Plate_Any and Plasma_Any = 1 but RBC_Any and Other_Blood do not = 1 - **Platelets and Plasma** If RBC_Any and Plasma_Any = 1 but Plate_Any and Other_Blood do not = 1 - **RBCs and Plasma** If RBC_Any and Plate_Any = 1 but Plasma_Any and Other_Blood do not= 1

Variable	Description
	• **RBCs and Platelets** If RBC_Any, Plasma_Any, and Plate_Any = 1 but Other_Blood does not = 1 • **RBCs and Plasma and Platelets** If Other_bld = 1 • **Other** **Format:** SAS character $65
LOS	Length of stay metrics. Valid values are: • **Los_min:** Minimum length of stay • **Los_p1:** Length of stay at the 1st percentile • **Los_p5:** Length of stay at the 5th percentile • **Los_25:** Length of stay at the 25th percentile • **Los_md:** Median length of stay • **Los_mean:** Mean length of stay • **Los_75:** Length of stay at the 75th percentile • **Los_95:** Length of stay at the 95th percentile • **Los_99:** Length of stay at the 99th percentile • **Los_max:** Maximum length of stay **Format:** SAS character $8
COUNT_ENC	Number of encounters. **Note 1:** For levels 220 and 225 (Age and LOS), this field contains age and LOS metrics). **Format:** Numeric
COUNT_EVENT*N*	Number of encounters with an event of interest. Count_Event1-Count_EventN correspond to HOI1-HOIN (as coded in the field FUP in the COHORTCODES table), unless LEVEL= 200 or 225, in which case this field contains age or LOS metrics, respectively). **Format:** Numeric
DENNUMENC	Number of encounters that meet all cohort demographic, inclusion, and exclusion criteria. **Format:** Numeric
DENNUMPT	Number of patients with at least 1 encounter that meets all cohort demographic, inclusion, and exclusion criteria. **Format:** Numeric
DENNUMFAC	Number of facilities with at least 1 encounter that meets all cohort demographic, inclusion, and exclusion criteria. **Format:** Numeric

b) [*RUNID*]_descstat_covariates.sas7bdat

This is an aggregate data set which contains counts of encounters with exposures by covariates. The data set will be saved under MSOC and send back to SOC. **Table 11** contains detailed specifications for this file.

Table 11. [RUNID]_descstat_covariates Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **000:** Covarnum • **305:** Covarnum*Days_rx_allow_gap • **310:** Covarnum*Days_rx_nogap • **315:** Covarnum*CodeFreq **Format:** SAS character $3
STUDYNAME	Unique name for each covariate defined in the file. **Format:** SAS character $50
COVARTYPE	Indicates covariate type. Valid values are: • COMORB: Comorbidity • MEDADM: Medication administered **Format:** SAS character $6
COVARNUM	A numeric indicator that is correspondent to studyname. **Format:** Numeric
DAYS_RX_ALLOW_GAP	Number of a days during the encounter with the covariate, including requester defined gap. **Note 1:** Only computed for MEDADM covariates. **Format:** Numeric
DAYS_RX_NO_GAP	Number of days during the encounter with the covariate of interest. **Note 1:** Only computed for MEDADM covariates. **Format:** Numeric
CODEFREQ	Number of covariate codes during the encounter. **Note 1:** Only copmuted for MEDADM covariates. **Format:** Numeric
COUNT_ENC	Number of encounters in the cohort with the covariate of interest. **Format:** Numeric

Variable	Description
COUNT_EVENTN	Number of encounters with an event of interest. Count_Event1-Count_EventN correspond to HOI1-HOIN (as noted in field FUP in the table COHORTCODES), unless LEVEL (in this table) = 200 or 225, in which case this field contains age or LOS metrics, respectively). **Format:** Numeric

c) [*RUNID*]_ipharm_summary.sas7bdat

This is an aggregate dataset that contains counts of encounters for each NDC used to define cohort index, stratified by RxRoute, RxDose, and RXUOM. This dataset is not produced if cohort is not defined using inpatient NDCs. **Table 12** contains detailed specifications for this file.

Table 12. [RUNID]_ ipharm_summary Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $50
NDC	National Drug Code. **Format:** SAS character $11
RXROUTE	Medication route. **Format:** SAS character $10
RXDOSE	Dosage of medication **Format:** Numeric
RXUOM	Dose unit of medication **Format:** SAS character $10
COUNT	Number of encounters **Format:** Numeric

d) [*RUNID*]_attrition.sas7bdat

This table is created to include the number encounters excluded and remaining at each cohort creation criterion application during the query execution. **Table 13** contains detailed specifications for this file.

Table 13. [RUNID] _attrition Output

Variable	Description
GROUP	Cohort name. **Format:** SAS character $30
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **1:** Encounters during the query period • **2:** Encounters restricted by facilities during the query period • **3:** Encounters restricted by encounter type • **4:** Encounters restricted by age group • **5:** Encounters restricted by specified sex • **6:** Encounters restricted by specified ethnicity • **7:** Encounters restricted by specified race • **8:** Encounters restricted by additional inclusion/exclusion criteria • **9:** Encounters with exposure of interested during the query period **Format:** Numeric
DESCR	Criterion description. **Format:** SAS character $500
REMAININGENC	Number of Encounters remaining after previous exclusion criterion. **Format:** Numeric
REMAINFAC	Number of Facilities remaining after previous exclusion criterion. **Format:** Numeric
REMAINPTS	Number of Patients remaining after previous exclusion criterion. **Format:** Numeric
EXCLUDEDENC	Number of Encounters excluded by the exclusion criterion. **Format:** Numeric
EXCLUDEDFAC	Number of facilities that are excluded . **Format:** Numeric
EXCLUDEDPTS	Number of Patients that are excluded. **Format:** Numeric

e) [*RUNID*]_signature.sas7bdat

This table contains metadata associated with the request, including request identifiers, program identifiers, database version, and run time metrics. **Table 14** contains detailed specifications for this file.

Table 14. [RUNID]_signature Output

Variable	Description
VAR	Metric name. **Format:** SAS character $15
VALUE	Metric value. **Format:** SAS character $200

2. DPLOCAL Folder

a) [*RUNID*]_all_encounter.sas7bdat

This table contains one record per encounter for every cohort (GROUP) specified in the Inpatient Encounter Tool execution. Encounters in this table meet facility code and demographic criteria, but do not necessarily meet inclusion/exclusion conditions. **Table 15** contains detailed specifications for this file.

Table 15. [RUNID] _all_encounter Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
PATID	Arbitrary person-level identifier. Used to link across files. Must be between 5 and 25 characters in length. **Format:** Varying SAS character
ENCOUNTERID	Encounter-level identifier. Used to link across files. **Format:** Varying SAS character
ADATE	Encounter start date. **Format:** Numeric (MMDDYY10.)
DDATE	Encounter end date. **Format:** Numeric (MMDDYY10.)
DISCHARGE_DISPOSITION	Patient status at discharge time. **Format:** SAS character $1
ENCTYPE	Encounter Type. **Format:** SAS character $2
FACILITY_CODE	Local facility code which indicates hospital or clinic. **Format:** Varying SAS character
BIRTH_DATE	Birth Date. **Format:** Numeric (MMDDYY10.)
AGE	Age at encounter ADATE in years. Age=(ADATE-Birth_date)/365.25. **Format:** Numeric

Variable	Description
AGEGROUP	AgeGroup at encounter ADate. **Format:** Varying SAS character
SEX	Sex. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
RACE	Race. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
HISPANIC	A person of Cuban, Mexican, Puerto Rican, South or Central American, or other Spanish culture or origin, regardless of race. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
EVENT*1*-EVENT*N*	Indicator if HOI*N* occurred occurred during the encounter. **Format:** Numeric
EXCL	Indicator if the encounter meets inclusion and exclusion criteria. **Format:** Numeric
LOS	Length of stay. If ENCTYPE ='IP' or 'IS' then LOS=DDATE-ADATE+1. LOS is missing for other encounter types. **Format:** Numeric
PLATE_ANY	If the cohort is defined using transfusion codes and the transfusion type lookup table is provided, this indicates whether a transfusion that defines an exposure has Requirement = 'PLATE'. **Format:** Numeric
RBC_ANY	If the cohort is defined using transfusion codes and the transfusion type lookup table is provided, this indicates whether a transfusion that defines an exposure has Requirement = 'RBCS'. **Format:** Numeric
PLASMA_ANY	If the cohort is defined using transfusion codes and the transfusion type lookup table is provided, this indicates whether a transfusion that defines an exposure has Requirement = 'PLATE'. **Format:** Numeric
OTHER_BLD	If the cohort is defined using transfusion codes and the transfusion type lookup table is provided, this indicates whether a transfusion that defines an exposure has Requirement = 'CRYO' or 'OTHER'. **Format:** Numeric
BLOODCOMP	Blood components included in transfusion. Valid values are: If RBC_Any = 1 but Plate_Any, Plasma_Any, and Other_Blood do not = 1 • **RBCs** If Plasma_Any = 1 but Plate_Any, RBCs_Any, and Other_Blood do not = 1 • **Plasma** If Plate_Any = 1 but RBC_Any, Plasma_Any, and Other_Blood do not = 1

Variable	Description
	• **Platelets** If Plate_Any and Plasma_Any = 1 but RBC_Any and Other_Blood do not = 1 • **Platelets and Plasma** If RBC_Any and Plasma_Any = 1 but Plate_Any and Other_Blood do not = 1 • **RBCs and Plasma** If RBC_Any and Plate_Any = 1 but Plasma_Any and Other_Blood do not= 1 • **RBCs and Platelets** If RBC_Any, Plasma_Any, and Plate_Any = 1 but Other_Blood does not = 1 • **RBCs and Plasma and Platelets** If Other_bld = 1 • **Other** **Format:** SAS character $65
TRANS_UNIT	Count of all transfusions that occur during the encounter, regardless of whether the transfusion code is defined as an exposure. **Format:** Numeric

b) [*RUNID*]_all_covariates.sas7bdat

This table contains one record per encounter and covariate for every cohort defined in Inpatient Encounter Tool execution. Encounters in this table meet facility code and demographic criteria, but do not necessarily meet inclusion/exclusion conditions. **Table 16** contains detailed specifications for this file.

Table 16. [RUNID] _all_covariates Output

Variable	Description
PATID	Arbitrary person-level identifier. Used to link across files. **Format:** Varying SAS character (varies)
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
COVARTYPE	Covariate type. Valid values are: • **COMORB:** Comorbidity • **MEDADM:** Medication administered **Format:** SAS character $6
ENCOUNTERID	Encounter-level identifier. Used to link across files. **Format:** Varying SAS character
STUDYNAME	Unique name for each covariate. **Format:** SAS character $50
COVARNUM	Numeric indicator for each covariate. **Format:** Numeric

Variable	Description
DAYS_RX_ALLOW_GAP	Number of days during the encounter in which the covariate occurs, including days in a requester defined gap. **Note 1:** Only calculated for covartype=MEDADM. **Note 2:** Days_Rx_Aloow_Gap will be the same as Days_Rx_No_Gap when DAYSGAP=0. For example: Patid NDC Encounterid Rxadate 001 1000 1001 01/01/2017 001 1000 1001 01/02/2017 001 1000 1001 01/05/2017 If user defined DAYSGAP=2, then Days_Rx_Allow_Gap=01/01/2017-01/05/2017=5 If user defined DAYSGAP=1 then Dx_Rx_Allow_Gap=3. **Format:** Numeric
DAYS_RX_NOGAP	Number of days of medications administered during the same encounter. This variable does not allow gaps between RxaDate. **Note 1:** Only calculated for COVARTYPE=MEDADM. **Format:** Numeric
CODEFREQ	Number of time a medication is administered during the encounter. For example: If Drug A is administered on: 1/1/2013 at 8:00 am; 1/1/2013 at 9:00 am; and 1/2/2013 at 8:00 am, then Codefreq=3. **Format:** Numeric

c) [*RUNID*]_denomcounts

This table contains denominators by demographic factors. **Table 17** contains detailed specifications for this file.

Table 17. [RUNID] _denomcounts Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **000:** overall • **001:** year • **002:** sex • **003:** age grup • **110:** race • **114:** Hispanic • **200:** encounter setting • **205:** discharge disposition **Format:** SAS character $3
SEX	Sex. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
AGEGROUP	Age Groups. Categories are requester-defined. **Format:** SAS character $6
RACE	Race. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
HISPANIC	A person of Cuban, Mexican, Puerto Rican, South or Central American, or other Spanish culture or origin, regardless of race. Valid values are those in the SCDM. **Format:** SAS character $1
YEAR	Year of admission. **Format:** Numeric (YYYY)
ENCTYPE	Encounter type. Valid values are: • **IP:** Inpatient • **ED:** Emergency Department • **AV**: Ambulatory visit **Format:** SAS character $2
DISCHARGE_DISPOSITION	Discharge disposition.

Variable	Description
	Valid value are: • **A:** Discharged Alive • **E:** Expired • **U:** Missing; Unknown **Format:** SAS character $1
DENUMENC	Number of encounters for the cohort. **Format:** Numeric
DENUMPT	Number of patients for the cohort. **Format:** Numeric
DENUMFAC	Number of facilities for the cohort**.** **Format:** Numeric

d) [*RUNID*]_numcounts

This table contains numerators by demographic factors. **Table 18** contains detailed specifications for this file.

Table 18. [RUNID] _numcounts Output

Variable	Description
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **000:** overall • **001**: year • **002**: sex • **003:** age grup • **110:** race • **114:** Hispanic • **200:** encounter setting • **205:** discharge disposition • **210:** number of transfusion units • **215:** blood compondent • **220:** Age • **225:** Length of Stay **Format:** SAS character $3
SEX	Sex. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
AGEGROUP	Age Groups. Categories are requester-defined. **Format:** SAS character $6

Variable	Description
AGEGROUPSORT	Sorting order for age groups. **Format:** Numeric
RACE	Race. Valid values are those in the SCDM Demographic table. **Format:** SAS character $1
YEAR	Year of admission. **Format:** Numeric (YYYY)
HISPANIC	A person of Cuban, Mexican, Puerto Rican, South or Central American, or other Spanish culture or origin, regardless of race. Valid values are those in the SCDM. **Format:** SAS character $1
ENCTYPE	Encounter type. Valid values are: • **IP:** Inpatient • **ED:** Emergency Department • **AV:** Ambulatory visit **Format:** SAS character $2
DISCHARGE_DISPOSITION	Discharge disposition. Valid value are: • **A:** Discharged Alive • **E:** Expired • **U:** Missing; Unknown **Format:** SAS character $1
TRANS_UNIT	Total units transfused within one encounter. **Format:** Numeric
BLOODCOMP	Blood components included in transfusion. Valid values are: If RBC_Any = 1 but Plate_Any, Plasma_Any, and Other_Blood do not = 1 • **RBCs** If Plasma_Any = 1 but Plate_Any, RBCs_Any, and Other_Blood do not = 1 • **Plasma** If Plate_Any = 1 but RBC_Any, Plasma_Any, and Other_Blood do not = 1 • **Platlets** If Plate_Any and Plasma_Any = 1 but RBC_Any and Other_Blood do not = 1 • **Platelets and Plasma** If RBC_Any and Plasma_Any = 1 but Plate_Any and Other_Blood do not = 1 • **RBCs and Plasma** If RBC_Any and Plate_Any = 1 but Plasma_Any and Other_Blood do not= 1 • **RBCs and Platelets** If RBC_Any, Plasma_Any, and Plate_Any = 1 but Other_Blood does not = 1 • **RBCs and Plasma and Platelets**

Variable	Description
	If Other_bld = 1 - **Other** **Format:** SAS character $65
AGE	**Details:** Indicates whether to interpret the value of Count_Enc as mean age or standard deviation of age. Valid values are: - **Mean_age**: Mean age - **Std_age:** Standard deviation of age **Format:** SAS character $7
LOS	**Details:** Indicates whether to interpret the value of Count_Enc as length of stay metrics. - **Los_min:** Minimum length of stay - **Los_p1:** Length of stay at the 1st percentile - **Los_p5:** Length of stay at the 5th percentile - **Los_25:** Length of stay at the 25th percentile - **Los_md:** Median length of stay - **Los_mean:** Mean length of stay - **Los_75:** Length of stay at the 75th percentile - **Los_95:** Length of stay at the 95th percentile - **Los_99:** Length of stay at the 99th percentile - **Los_max:** Maximum length of stay **Format:** SAS character $8
COUNT_ENC	Number of encounters. **Format:** Numeric

e) [*RUNID*]_numcovarcounts

This table contains numerators by covariates. **Table 19** contains detailed specifications for this file.

Table 19. [RUNID] _numcovarcounts Output

Variable	Description
GROUP	Standardized name used to differentiate cohorts. **Format:** SAS character $30
LEVEL	Each unique combination of strata (*i.e.,* variables bolded in the Variable column) receives a unique level value that remains consistent across requests. This allows for simpler development of reusable report generation tools. Valid values are: • **000:** Covarnum • **305:** Covarnum*Days_rx_allow_gap • **310:** Covarnum*Days_rx_nogap • **315:** Covarnum*CodeFreq **Format:** SAS character $3
Studyname	Unique name for each covariate defined in the file. **Format:** SAS character $50
Covarnum	Numeric indicator that corresponds to STUDYNAME. **Format:** Numeric
Covartype	Indicates covariate type. Valid values: • COMORB: Comorbidity • MEDADM: Medication administered **Format:** SAS character $6
Days_rx_allow_gap	Number of days gap allowed for medications administered during the same encounter. **Format:** Numeric
Days_rx_nogap	Number of days of medications administered during the same encounter with no gap. **Format:** Numeric
Codefreq	Frequency of comorbidities presented during the same encounter. **Format:** Numeric
Count_enc	Number of encounters. **Format:** Numeric