**Public Training**

CIDA Lab Session: Answer Key

**Input Files**

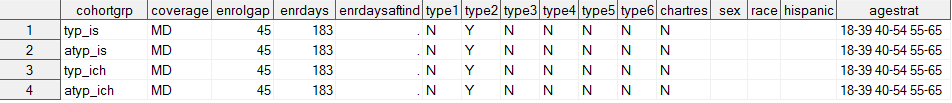
*Monitoring File*





*Cohort File*

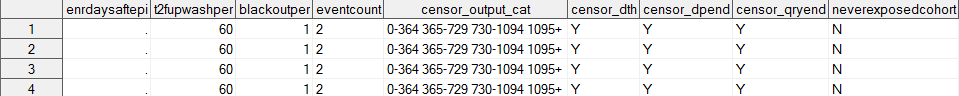




*Type 2 File*

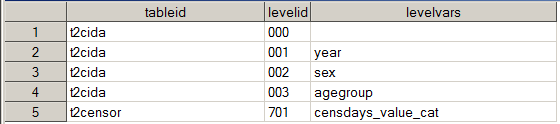






*User-Defined Strata File*

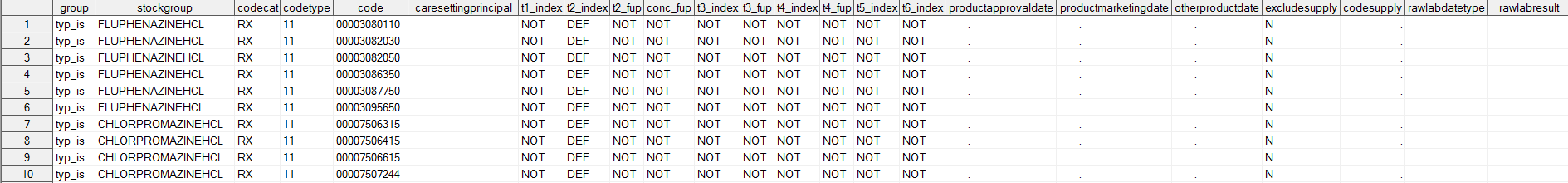




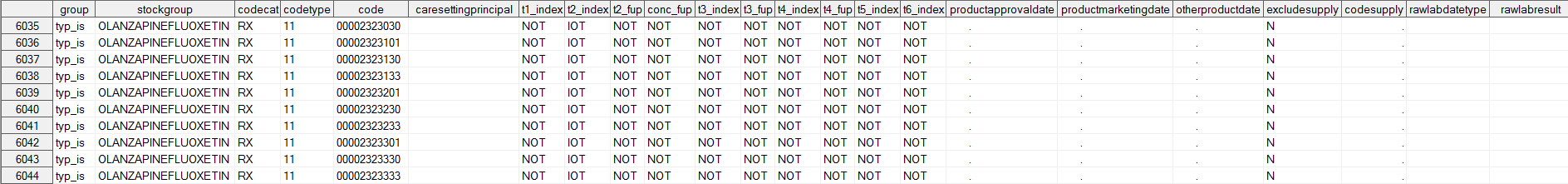
*Cohort Codes File*



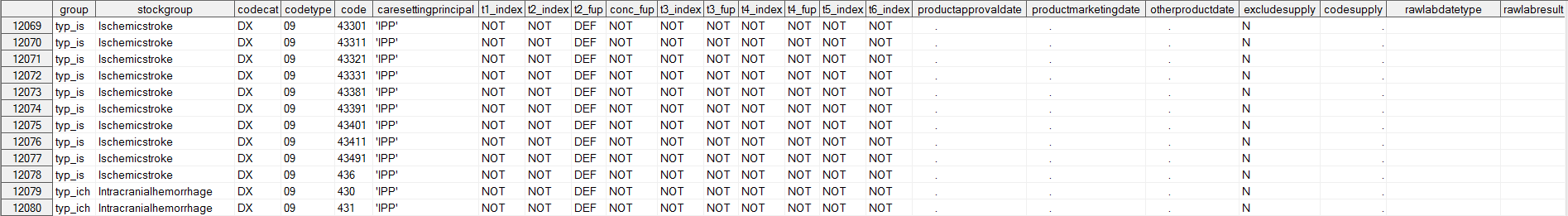
**Exposure index-defining codes**



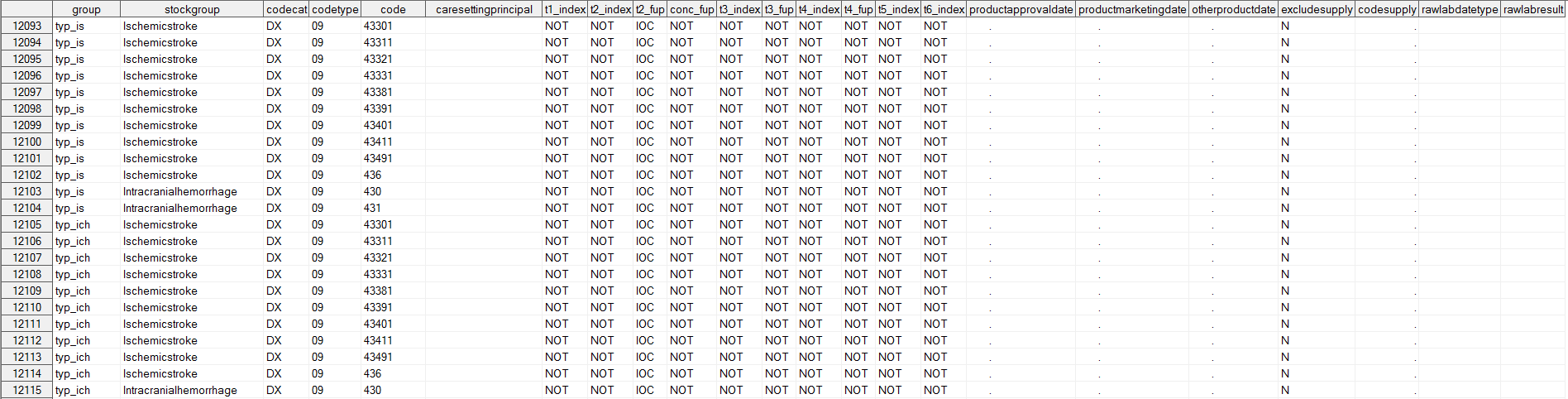
**Exposure incidence-defining codes**



**Outcome-defining codes**

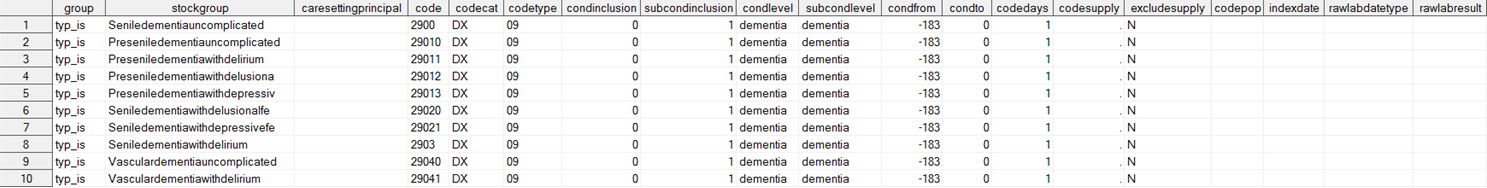


**Outcome incidence-defining codes**



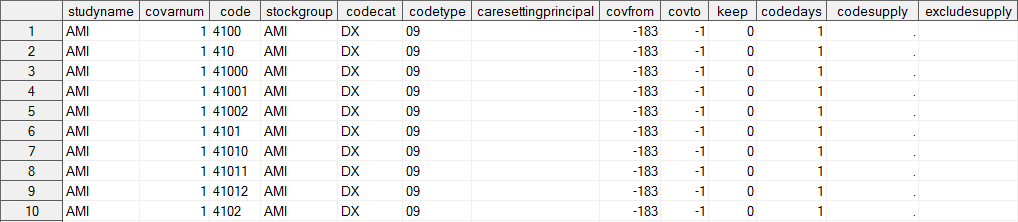
*Inclusion / Exclusion Codes File*





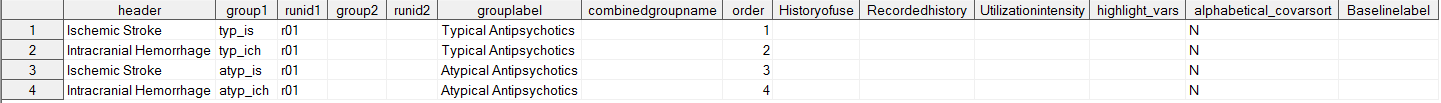
*Covariate Codes File*





*Groups Table File*





*Create Report File*











**Input File SAS Code**

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**1. Create Monitoring File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

**data** out.&wpnum.\_monitoring;

format periodid **8.** startfollowup date9. enddate date9.;

periodid = **1**;

startfollowup =**"01JAN2008"d**; /\* Type the query start date in format "04APR2019"d \*/

enddate = **"31DEC2010"d**; /\* Type the query end date in format "04APR2019"d \*/

**run**;

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**2. Create Cohort File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

%let grouplist = typ\_is typ\_ich atyp\_is atyp\_ich ;

%let groupcount = %sysfunc(Countw(&grouplist));

options mlogic mprint symbolgen;

ods listing close;

**%macro** cohortcreate(cohortlist);

proc datasets lib=work nolist nowarn;

delete cohort;

run;

%let cohortcount = %sysfunc(Countw(&&&cohortlist));

%do a = **1** %to &cohortcount;

%let curr\_name = %scan(&&&cohortlist, &a);

data work.cht;

format cohortgrp $40. coverage $2. enrolgap **8.** enrdays **8.** enrdaysaftind **8.** type1 $1. type2 $1. type3 $1. type4 $1. type5 $1. type6 $1.

chartres $1. sex $3. race $1. hispanic $1. agestrat $100.;

cohortgrp = "&curr\_name";

coverage = 'MD'; /\* Coverage Type Requirement; Valid values: 'MD' 'M' or 'D' for medical and drug, medical only, or drug only\*/

enrolgap = **45**; /\* Enrollment Gap; Numerical \*/

enrdays = **183**; /\* Minimum Pre-Index Enrollment Days; Numerical\*/

type1 = 'N'; /\* Type 1 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

type2 = 'Y'; /\* Type 2 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

type3 = 'N'; /\* Type 3 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

type4 = 'N'; /\* Type 4 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

type5 = 'N'; /\* Type 5 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

type6 = 'N'; /\* Type 6 Cohort Identification Strategy Indicator; Valid values: 'Y' or 'N' \*/

sex = ''; /\* Sex criteria to apply to cohort; Valid values: 'A' 'F' 'M' 'U'; Leave blank if no restrictions \*/

race = ''; /\* Race criteria to apply to cohort; Leave blank if no restrictions \*/

hispanic = ''; /\* Hispanic criteria to apply to cohort; Leave blank if no restrictions \*/

agestrat = '18-39 40-54 55-65';

enrdaysaftind = **.**;

chartres = 'N';

run;

proc append data = work.cht

base = work.cohort force;

run;

%end;

data out.&wpnum.\_cohort;

set work.cohort;

run;

**%mend**;

%***cohortcreate***(grouplist);

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**3. Create Type 2 File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

%let grouplist = typ\_is typ\_ich atyp\_is atyp\_ich ;

%let groupcount = %sysfunc(Countw(&grouplist));

options mlogic mprint symbolgen;

ods listing close;

**%macro** typecreate(typelist);

proc datasets lib=work nolist nowarn;

delete type;

run;

%let typecount = %sysfunc(Countw(&&&typelist));

%do a = **1** %to &typecount;

%let curr\_name = %scan(&&&typelist, &a);

data work.type;

format group $40. t2cohortdef $2. t2washper **8.** ittdays **8.** episodegaptype $1. episodegap **8.** expextper **8.**

minepisdur **8.** maxepisdur **8.** mindaysupp **8.** enrdaysaftepi **8.** t2fupwashper **8.** blackoutper **8.** eventcount **8.**

censor\_output\_cat $30. censor\_dth $1. censor\_dpend $1. censor\_qryend $1. neverexposedcohort $1. ;

group = "&curr\_name";

t2cohortdef = '01'; /\* Allowed Number of Exposure Episodes per Individual; Valid values: '01' '02' '03' for first episode only, all episodes, or all episodes until event\*/

t2washper = **183**; /\* Type 2 Exposure Washout Period; Numerical; Required - enter 0 if not using \*/

ittdays = **.**; /\* Requester-defined Exposure Episode Length; Numerical; Leave blank if creating as-treated episodes \*/

episodegaptype= 'F'; /\* Treatment Episode Gap Type; Valid values: 'F' or 'P' for fixed or percent \*/

episodegap = **30**; /\* Exposure Episode Gap; Numerical; Required - enter 0 if not using \*/

expextper = **30**; /\* Exposure Episode Extension Period; Numerical; Optional \*/

minepisdur = **1**; /\* Minimum Exposure Episode Duration; Numerical; Required - enter 0 if not using \*/

maxepisdur = **.**; /\* Maximum Exposure Episode Duration; Numerical; Optional \*/

mindaysupp = **1**; /\* Minimum Days Supplied; Numerical; Required - enter 0 if not using \*/

t2fupwashper = **60**; /\* Type 2 HOI Washout Period; Numerical; Required - enter 0 if not using \*/

blackoutper = **1**; /\* HOI Blackout Period; Numerical; Required - enter 0 if not using \*/

censor\_dth = 'Y'; /\* Censor Episodes at Evidence of Death; Valid values: 'Y' or 'N'; Required\*/

censor\_dpend = 'Y'; /\* Censor Episodes at Data End Date; Valid values: 'Y' or 'N'; Required\*/

censor\_qryend = 'Y'; /\* Censor Episodes at Query End Date; Valid values: 'Y' or 'N'; Required\*/

censor\_output\_cat = '0-364 365-729 730-1094 1095+';

enrdaysaftepi = **.**;

eventcount = **2**;

neverexposedcohort= 'N';

run;

proc append data = work.type

base = work.type2 force;

run;

%end;

data out.&wpnum.\_type2;

set work.type2;

run;

**%mend**;

%***typecreate***(grouplist);

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**4. Create the Strata Levels File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

**data** out.&wpnum.\_type2strata;

format tableid $20. levelid $3. levelvars $30.;

tableid = "t2cida";

levelid = "000";

levelvars = "";

output;

tableid = "t2cida";

levelid = "001";

levelvars = "year";

output;

tableid = "t2cida";

levelid = "002";

levelvars = "sex";

output;

tableid = "t2cida";

levelid = "003";

levelvars = "agegroup";

output;

tableid = "t2censor";

levelid = "701";

levelvars = "censdays\_value\_cat";

output;

**run**;

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**5. Create Cohort Codes File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname in "&basename./codes";

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

options mlogic mprint symbolgen;

ods listing close;

/\*SPECIFY EXPOSURE INDEX-DEFINING CODES\*/

**%macro** indexcodes (title,group,codes);

data indexcodes&title.;

format group $40. stockgroup $30. codecat $2. codetype $3. code1 $11. code $11. caresettingprincipal $41.

t1\_index $3. t2\_index $3. t2\_fup $3. conc\_fup $3. t3\_index $3. t3\_fup $3. t4\_index $3. t4\_fup $3. t5\_index $3. t6\_index $3.

productapprovaldate Date9. productmarketingdate Date9. otherproductdate Date9. excludesupply $1. codesupply **8.**

rawlabdatetype $3. rawlabresult $30. ;

set in.&codes.;

group = "&group.";

stockgroup = compress (descrip, ', ./\\_-<>=;&[](){}%');

codecat = CodeCat1;

codetype = CodeType1;

code = compress (code1, ".");

caresettingprincipal = " ";

t1\_index = 'NOT';

t2\_index = 'DEF'; /\* When defining index-defining codes for exposure, t2\_index must = 'DEF' \*/

t2\_fup = 'NOT'; /\* When defining exposure, t2\_fup must = 'NOT' \*/

conc\_fup = 'NOT';

t3\_index = 'NOT';

t3\_fup = 'NOT';

t4\_index = 'NOT';

t4\_fup = 'NOT';

t5\_index = 'NOT';

t6\_index = 'NOT';

productapprovaldate = **.**;

productmarketingdate = **.**;

otherproductdate = **.**;

excludesupply = "N";

codesupply = **.** ;

rawlabdatetype = "";

rawlabresult = "";

drop code1 codecat1 codetype1 descrip;

run;

**%mend**;

%***indexcodes*** (**1**,typ\_is, typical\_antipsychotics); /\*Fill in group 1 name and code list to define index exposure \*/

%***indexcodes*** (**2**,typ\_ich, typical\_antipsychotics); /\*Fill in group 2 name and code list to define index exposure \*/

%***indexcodes*** (**3**,atyp\_is, atypical\_antipsychotics); /\*Fill in group 3 name and code list to define index exposure \*/

%***indexcodes*** (**4**,atyp\_ich, atypical\_antipsychotics); /\*Fill in group 4 name and code list to define index exposure \*/

**%macro** exportindexcodes(start,end);

data index;

set %do i=&start. %to &end.;

indexcodes&i.

%end;

;

run;

**%mend**;

%***exportindexcodes*** (**1**,**4**);

/\*SPECIFY EXPOSURE INCIDENCE AND TRUNCATION CODES\*/

**%macro** inc\_trunc\_codes (title,group,codes);

data inc\_trunc\_codes&title.;

format group $40. stockgroup $30. codecat $2. codetype $3. code1 $11. code $11. caresettingprincipal $41.

t1\_index $3. t2\_index $3. t2\_fup $3. conc\_fup $3. t3\_index $3. t3\_fup $3. t4\_index $3. t4\_fup $3. t5\_index $3. t6\_index $3.

productapprovaldate Date9. productmarketingdate Date9. otherproductdate Date9. excludesupply $1. codesupply **8.**

rawlabdatetype $3. rawlabresult $3. ;

set in.&codes.;

group = "&group.";

stockgroup = compress (descrip, ', ./\\_-<>=;&[](){}%');

codecat = CodeCat1;

codetype = CodeType1;

code = compress (code1, ".");

caresettingprincipal = " ";

t1\_index = 'NOT';

t2\_index = 'IOT'; /\* When defining incidence and truncation criteria for exposure, t2\_index should = 'IOT' \*/

t2\_fup = 'NOT'; /\* When defining exposure, t2\_fup must = 'NOT' \*/

conc\_fup = 'NOT';

t3\_index = 'NOT';

t3\_fup = 'NOT';

t4\_index = 'NOT';

t4\_fup = 'NOT';

t5\_index = 'NOT';

t6\_index = 'NOT';

productapprovaldate = **.**;

productmarketingdate = **.**;

otherproductdate = **.**;

excludesupply = "N";

codesupply = **.** ;

rawlabdatetype = "";

rawlabresult = "";

drop code1 codecat1 codetype1 descrip;

run;

**%mend**;

%***inc\_trunc\_codes*** (**1**,typ\_is, atypical\_antipsychotics); /\*Fill in group 1 name and code list to define incidence and truncation criteria \*/

%***inc\_trunc\_codes*** (**2**,typ\_ich, atypical\_antipsychotics); /\*Fill in group 2 name and code list to define incidence and truncation criteria \*/

%***inc\_trunc\_codes*** (**3**,atyp\_is, typical\_antipsychotics); /\*Fill in group 3 name and code list to define incidence and truncation criteria \*/

%***inc\_trunc\_codes*** (**4**,atyp\_ich, typical\_antipsychotics); /\*Fill in group 4 name and code list to define incidence and truncation criteria \*/

**%macro** exportinc\_trunc\_codes(start,end);

data incidence;

set %do i=&start. %to &end.;

inc\_trunc\_codes&i.

%end;

;

run;

**%mend**;

%***exportinc\_trunc\_codes*** (**1**,**4**);

/\*SPECIFY OUTCOME-DEFINING CODES\*/

**%macro** outcomecodes (title,group,codes);

data outcomecodes&title.;

format group $40. stockgroup $30. codecat $2. codetype $3. code1 $11. code $11. caresettingprincipal $41.

t1\_index $3. t2\_index $3. t2\_fup $3. conc\_fup $3. t3\_index $3. t3\_fup $3. t4\_index $3. t4\_fup $3. t5\_index $3. t6\_index $3.

productapprovaldate Date9. productmarketingdate Date9. otherproductdate Date9. excludesupply $1. codesupply **8.**

rawlabdatetype $3. rawlabresult $3. ;

set in.&codes.;

group = "&group.";

stockgroup = compress (descrip, ', ./\\_-<>=;&[](){}%');

codecat = CodeCat1;

codetype = CodeType1;

code = compress (code1, ".");

caresettingprincipal = "'IPP'";

t1\_index = 'NOT';

t2\_index = 'NOT'; /\* When defining outcome, t2\_index must = 'NOT' \*/

t2\_fup = 'DEF'; /\* When defining outcome, t2\_fup must = 'DEF' \*/

conc\_fup = 'NOT';

t3\_index = 'NOT';

t3\_fup = 'NOT';

t4\_index = 'NOT';

t4\_fup = 'NOT';

t5\_index = 'NOT';

t6\_index = 'NOT';

productapprovaldate = **.**;

productmarketingdate = **.**;

otherproductdate = **.**;

excludesupply = "N";

codesupply = **.** ;

rawlabdatetype = "";

rawlabresult = "";

drop code1 codecat1 codetype1 descrip;

run;

**%mend**;

%***outcomecodes*** (**1**,typ\_is, ischemic\_stroke); /\*Fill in group 1 name and code list to define outcome \*/

%***outcomecodes*** (**2**,typ\_ich, intracranial\_hemorrhage); /\*Fill in group 2 name and code list to define outcome \*/

%***outcomecodes*** (**3**,atyp\_is, ischemic\_stroke); /\*Fill in group 3 name and code list to define outcome \*/

%***outcomecodes*** (**4**,atyp\_ich, intracranial\_hemorrhage); /\*Fill in group 4 name and code list to define outcome \*/

**%macro** exportoutcomecodes(start,end);

data outcome;

set %do i=&start. %to &end.;

outcomecodes&i.

%end;

;

run;

**%mend**;

%***exportoutcomecodes*** (**1**,**4**);

/\*SPECIFY OUTCOME INCIDENCE-DEFINING CODES\*/

**%macro** outcomeinccodes (title,group,codes);

data outcomeinccodes&title.;

format group $40. stockgroup $30. codecat $2. codetype $3. code1 $11. code $11. caresettingprincipal $41.

t1\_index $3. t2\_index $3. t2\_fup $3. conc\_fup $3. t3\_index $3. t3\_fup $3. t4\_index $3. t4\_fup $3. t5\_index $3. t6\_index $3.

productapprovaldate Date9. productmarketingdate Date9. otherproductdate Date9. excludesupply $1. codesupply **8.**

rawlabdatetype $3. rawlabresult $3. ;

set in.&codes.;

group = "&group.";

stockgroup = compress (descrip, ', ./\\_-<>=;&[](){}%');

codecat = CodeCat1;

codetype = CodeType1;

code = compress (code1, ".");

caresettingprincipal = " ";

t1\_index = 'NOT';

t2\_index = 'NOT'; /\* When defining outcome incidence, t2\_index must = 'NOT' \*/

t2\_fup = 'IOC'; /\* When defining outcome incidence, t2\_fup must = 'IOC' \*/

conc\_fup = 'NOT';

t3\_index = 'NOT';

t3\_fup = 'NOT';

t4\_index = 'NOT';

t4\_fup = 'NOT';

t5\_index = 'NOT';

t6\_index = 'NOT';

productapprovaldate = **.**;

productmarketingdate = **.**;

otherproductdate = **.**;

excludesupply = "N";

codesupply = **.** ;

rawlabdatetype = "";

rawlabresult = "";

drop code1 codecat1 codetype1 descrip;

run;

**%mend**;

%***outcomeinccodes*** (**1**,typ\_is,intracranial\_hemorrhage); /\*Fill in group 1 name and code list to define outcome incidence\*/

%***outcomeinccodes*** (**2**,typ\_ich,ischemic\_stroke); /\*Fill in group 2 name and code list to define outcome incidence \*/

%***outcomeinccodes*** (**3**,atyp\_is,intracranial\_hemorrhage); /\*Fill in group 3 name and code list to define outcome incidence \*/

%***outcomeinccodes*** (**4**,atyp\_ich,ischemic\_stroke); /\*Fill in group 4 name and code list to define outcome incidence\*/

**%macro** exportoutcomeinccodes(start,end);

data outcomeinc;

set %do i=&start. %to &end.;

outcomeinccodes&i.

%end;

;

run;

**%mend**;

%***exportoutcomeinccodes*** (**1**,**4**);

**data** out.&wpnum.\_cohortcodes;

set index incidence outcome outcomeinc;

**run**;

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**6. Create Inclusion/Exclusion Codes File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname in "&basename./codes";

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

%let grouplist = typ\_is typ\_ich atyp\_is atyp\_ich ;

%let groupcount = %sysfunc(Countw(&grouplist));

options mlogic mprint symbolgen;

ods listing close;

**%macro** exclusioncreate(exclusionlist);

proc datasets lib=work nolist nowarn;

delete exclusion;

run;

%let exclusioncount = %sysfunc(Countw(&&&exclusionlist));

%do a = **1** %to &exclusioncount;

%let curr\_name = %scan(&&&exclusionlist, &a);

data work.excl;

format group $40. stockgroup $30. caresettingprincipal $30. code $11. codecat $2. codetype $3.

condinclusion **8.** subcondinclusion **8.** condlevel $30. subcondlevel $30.

condfrom **8.** condto **8.** codedays **8.** codesupply **8.** excludesupply $1.

codepop $2. indexdate $30. rawlabdatetype $3. rawlabresult $30. ;

set in.dementia;

group = "&curr\_name";

stockgroup = compress (descrip, ", .//\_-<>=;&[]'(){}%");

caresettingprincipal = " ";

code = compress (code1, ' .//\_-()%');

codecat = codecat1;

codetype = codetype1;

condinclusion = **0**; /\* Condition Exclusion Indicator; Numerical; Valid values: 0 or 1 to exclude or include if evidence of condition; Required \*/

condlevel = "dementia"; /\* Name of inclusion/exclusion condition; Required\*/

condfrom = -**183**; /\* Evaluation Period Start; Numerical; Required \*/

condto = **0**; /\* Evaluation Period End; Numerical; Required \*/

codedays = **1**; /\* Indicates number of instances the criteria should be found in evaluation period; Numerical; Required \*/

subcondinclusion = **1**;

subcondlevel = "dementia";

codesupply= **.**;

excludesupply= "N";

codepop="";

indexdate="";

rawlabdatetype = "";

rawlabresult = "";

drop code1 codecat1 codetype1 descrip ;

run;

proc append data = work.excl

base = work.exclusion force;

run;

%end;

data out.&wpnum.\_exclusion;

set work.exclusion;

run;

**%mend**;

%***exclusioncreate***(grouplist);

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**7. Create Covariate File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname in "&basename./codes";

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

**data** out.&wpnum.\_covariates;

format studyname $50. covarnum **8.** code $50. stockgroup $30. codecat $2. codetype $3.

caresettingprincipal $30. covfrom **8.** covto **8.** keep **8.** codedays **8.** codesupply **8.** excludesupply $1.;

set in.covariates;

if studyname = 'AMI' then covarnum=**1**;

if studyname = 'Diabetes' then covarnum=**2**;

if studyname = 'Heart failure' then covarnum=**3**;

if studyname = 'Hypercholesterolemia' then covarnum=**4**;

if studyname = 'Hypertension' then covarnum=**5**;

if studyname = 'Kidney failure' then covarnum=**6**;

if studyname = 'Depression' then covarnum=**7**;

if studyname = 'Anxiety' then covarnum=**8**;

if studyname = 'Bipolar' then covarnum=**9**;

if studyname = 'Schizophrenia/psychotic' then covarnum=**10**;

if studyname = 'Substance abuse' then covarnum=**11**;

if studyname = 'Transient ischemic attack' then covarnum=**12**;

stockgroup = compress (studyname, ", './{};[]\_-()%");

studyname = studyname;

codecat = codecat1;

codetype = codetype1;

code = compress (code1, '.');

caresettingprincipal = " ";

covfrom = -**183**;

covto = -**1**;

keep = **0**;

codedays = **1**;

codesupply = **.**;

excludesupply = "";

drop codecat1 codetype1 code1;

**run**;

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**8. Create Report Files**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

**%macro** groups (title,group,grouplabel,header);

data groups\_table&title.;

format header $60. group1 $30. runid1 $10. group2 $30. runid2 $10. grouplabel $50.

combinedgroupname $50. order **8.** Historyofuse $50. Recordedhistory $50.

Utilizationintensity $50. highlight\_vars $60. alphabetical\_covarsort $1. Baselinelabel $50.;

header = "&header.";

group1 = "&group.";

runid1= 'r01';

group2 = "";

runid2 = "";

grouplabel= "&grouplabel.";

combinedgroupname= "";

order = &title.;

Historyofuse = "";

Recordedhistory = "";

Utilizationintensity = "";

highlight\_vars = "";

alphabetical\_covarsort = 'N';

Baselinelabel = "";

run;

**%mend**;

%***groups*** (**1**,typ\_is, Typical Antipsychotics, Ischemic Stroke);

%***groups*** (**2**,typ\_ich, Typical Antipsychotics, Intracranial Hemorrhage);

%***groups*** (**3**,atyp\_is, Atypical Antipsychotics, Ischemic Stroke);

%***groups*** (**4**,atyp\_ich, Atypical Antipsychotics, Intracranial Hemorrhage);

**%macro** exportgroups(start,end);

data out.groups\_table;

set %do i=&start. %to &end.;

groups\_table&i.

%end;

;

run;

**%mend**;

%***exportgroups***(**1**,**4**);

**data** out.createreport;

format type **1.** requestid $23. groups\_table $30. columns\_table $30. alltypefiles $50.

monitoringfile $30. cohortfile $30. userstrata $30. covariatecodes $30.

customtitle $50. exclude $50. stratify\_by\_level $50.

zipfile $15. agegroupfmt $100. logo $30. output\_baselinetable $1. look\_start **1.** look\_end **1.**

output\_cdf\_km $1. cdf\_title1 $50. km\_title1 $50. km\_title2 $50. cdf\_footnote1 $50. cdf\_footnote2 $50.

km\_footnote1 $50. km\_footnote2 $50. cdf\_xmin **8.** cdf\_xmax **8.** cdf\_xtick **8.** km\_xmin **8.** km\_xmax **8.** km\_xtick **8.**

cdf\_ymin **8.** cdf\_ymax **8.** cdf\_ytick **8.** km\_ymin **8.** km\_ymax **8.** km\_ytick **8.** km\_ep\_xmin **8.** km\_ep\_xmax **8.** km\_ep\_xtick **8.**

km\_ep\_ymin **8.** km\_ep\_ymax **8.** km\_ep\_ytick **8.** censoring\_display $40. cens\_elig $20. cens\_dth $20. cens\_dpend $20. cens\_qryend $20.

cens\_episend $20. cens\_spec $20. cens\_event $20. displayn $1. line\_spacing **8.**;

type=**2**;

requestid= 'public\_mpl1r\_wp001';

groups\_table= 'groups\_table';

columns\_table= '';

alltypefiles='wp001\_type2';

monitoringfile= 'wp001\_monitoring';

cohortfile= 'wp001\_cohort';

userstrata= 'wp001\_type2strata';

covariatecodes = 'wp001\_covariates';

customtitle= 'Typical and Atypical Antipsychotics and Stroke';

exclude= '8';

stratify\_by\_level= '000 001 002 003';

zipfile= '';

agegroupfmt= '';

logo= 'sentinel\_logo.jpg';

output\_baselinetable= 'Y';

look\_start= **1**;

look\_end= **1**;

output\_cdf\_km= 'N';

cdf\_title1= '';

km\_title1='';

km\_title2='';

cdf\_footnote1='';

cdf\_footnote2='';

km\_footnote1='';

km\_footnote2='';

cdf\_xmin=**.**;

cdf\_xmax=**.**;

cdf\_xtick=**.**;

km\_xmin=**.**;

km\_xmax=**.**;

km\_xtick=**.**;

cdf\_ymin=**.**;

cdf\_ymax=**.**;

cdf\_ytick=**.**;

km\_ymin=**.**;

km\_ymax=**.**;

km\_ytick=**.**;

km\_ep\_xmin=**.**;

km\_ep\_xmax=**.**;

km\_ep\_xtick=**.**;

km\_ep\_ymin=**.**;

km\_ep\_ymax=**.**;

km\_ep\_ytick=**.**;

censoring\_display='';

cens\_elig='';

cens\_dth='';

cens\_dpend='';

cens\_qryend='';

cens\_episend='';

cens\_spec='';

cens\_event='';

displayn='N';

line\_spacing= **1.75**;

**run**;

**/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**9. Create Propensity Score Model Comparison File**

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*/**

%let basename = C:/Public\_Training\_Materials/Lab;

libname out "&basename./public\_mpl1r\_wp001\_synpufs\_v01/inputfiles";

%let wpnum = wp001 ;

**%macro** psm (title,comp,control);

data psm&title.;

format comp\_order **8.** comp $40. control $40. caliper best12. ratio $1. class $999. noclass $999.

hdps $1. hdpswinfrom **8.** hdpswinto **8.**;

comp\_order = &title.;

comp = "&comp"; /\* Exposure of Interest; Valid values: typ\_is typ\_ich atyp\_is atyp\_ich; Required \*/

control = "&control"; /\* Comparator of Interest; Valid values: typ\_is typ\_ich atyp\_is atyp\_ich; Required \*/

caliper=**0.050**; /\* Matching Caliper; Numerical; Valid values: Any value between 0-1; Required \*/

ratio='F'; /\* Matching Ratio; Valid values: 'F' or 'V' for fixed 1:1 matching or variable 1:n matching; Required \*/

class="Sex Covar1 Covar2 Covar3 Covar4 Covar5 Covar6 Covar7 Covar8 Covar9 Covar10 Covar11 Covar12";

noclass="Age";

hdps='N';

hdpswinfrom=**.**;

hdpswinto=**.**;

run;

**%mend**;

%***psm*** (**1**,typ\_is, atyp\_is); /\* Fill in group 1 name (exposure) and group 3 name (comparator) \*/

%***psm*** (**2**,typ\_ich,atyp\_ich); /\* Fill in group 2 name (exposure) and group 4 name (comparator) \*/

**%macro** exportpsm(start,end);

data out.&wpnum.\_psm;

set %do i=&start. %to &end.;

psm&i.

%end;

;

run;

**%mend**;

%***exportpsm***(**1**,**2**);