Program 13.2 Treatment Weights Calculation

\*\*\* Compute the treatment part of the IPTW weights;

\*\*\* Numerator part, including baseline covariates and time-dependent intercept;

proc genmod data=infile rorder=formatted order=formatted;

class ETH SEX REGION VITDFLAG GLU BLVAC CDAYSINHOSP BLHYPERTENSN

BLHXADEQUACY bldosequartile lag1dosequartile lag2dosequartile lag3dosequartile lag4dosequartile

lag1HYPERTENSION lag1HXADEQUACY lag1VASCULAR;

model dosequartile = ETH SEX REGION VITDFLAG GLU BLVAC

CDAYSINHOSP BLHYPERTENSN BLHXADEQUACY AGE BMI HEMODIALYRS NOCHGDOSES NOHLDDOSES PERLESS11 BLHGB BLIRON BLALB BLFER BLSAT BLPTH bldosequartile lag1dosequartile lag2dosequartile lag3dosequartile lag4dosequartile

hmthno hmthno1 hmthno2 hmthno3

/ dist=multinomial link=clogit;

output out=preds pred=pred;

run;

proc sort data=preds;

by patient biweekno dosequartile \_order\_;

run;

proc transpose data=preds out=predst(keep=patient theta1 theta2 theta3

theta4 biweekno dosequartile) prefix=theta;

by patient biweekno dosequartile;

id \_order\_;

var pred;

run;

data model1;

set predst;

prob1=theta1;

prob2=theta2-theta1;

prob3=theta3-theta2;

prob4=theta4-theta3;

prob5=1-theta4;

if dosequartile=1 then treat\_top=prob1;

else if dosequartile=2 then treat\_top=prob2;

else if dosequartile=3 then treat\_top=prob3;

else if dosequartile=4 then treat\_top=prob4;

else if dosequartile=5 then treat\_top=prob5;

keep patient biweekno dosequartile treat\_top;

run;

\*\*\* Denominator part, including baseline covariates, time-dependent intercept, and also any time-dependent covariates;

proc genmod data=infile rorder=formatted order=formatted;

class ETH SEX REGION VITDFLAG GLU BLVAC CDAYSINHOSP BLHYPERTENSN

BLHXADEQUACY bldosequartile lag1dosequartile lag2dosequartile lag3dosequartile lag4dosequartile

lag1HYPERTENSION lag1HXADEQUACY lag1VASCULAR;

model dosequartile = ETH SEX REGION VITDFLAG GLU BLVAC

CDAYSINHOSP BLHYPERTENSN BLHXADEQUACY AGE BMI HEMODIALYRS NOCHGDOSES NOHLDDOSES PERLESS11 BLHGB BLIRON BLALB BLFER BLSAT BLPTH bldosequartile lag1dosequartile lag2dosequartile lag3dosequartile lag4dosequartile

lag1hb lag2hb lag3hb lag4hb

lag1HYPERTENSION lag1HXADEQUACY lag1VASCULAR lag1NHSPDNUM lag1hospitaldays lag1iron lag1sat lag1alb lag1fer

lag1hbdose0 lag1hbdose1 lag1hbdose2 lag1hbdose3 lag1hbdose4 hmthno hmthno1 hmthno2 hmthno3

/ dist=multinomial link=clogit;

output out=preds pred=pred;

run;

proc sort data=preds;

by patient biweekno dosequartile \_order\_;

run;

proc transpose data=preds out=predst(keep=patient theta1 theta2 theta3

theta4 biweekno dosequartile) prefix=theta;

by patient biweekno dosequartile;

id \_order\_;

var pred;

run;

data model2;

set predst;

prob1=theta1;

prob2=theta2-theta1;

prob3=theta3-theta2;

prob4=theta4-theta3;

prob5=1-theta4;

if dosequartile=1 then treat\_bottom=prob1;

else if dosequartile=2 then treat\_bottom=prob2;

else if dosequartile=3 then treat\_bottom=prob3;

else if dosequartile=4 then treat\_bottom=prob4;

else if dosequartile=5 then treat\_bottom=prob5;

keep patient biweekno dosequartile treat\_top;

run;

data trtmodels;

merge model1 (keep=patient biweekno treat\_top)

model2 (keep=patient biweekno treat\_bottom)

by patient biweekno;

if nmiss(treat\_top, treat\_bottom)>0 then treat\_sw=1;

if nmiss(treat\_top, treat\_bottom)=0 then

treat\_sw=treat\_top/treat\_bottom;

run;