SAS coding examples for case-cohort designs

"Simple" scenario (Table, row 1) All cases selected, selection probability of sub-cohort = x%
Example: O'Brien et al. (2017) Serum Vitamin D and Risk of Breast Cancer within Five Years. *Environ Health Persp*

cc1 = a data set containing the case-cohort data, including the following variables
- subcohort = 1 if in subcohort; 0 if not
- case = 1 if a case; 0 if not
- age_enrollment = age at enrollment
- age_eof = age at end of follow-up (e.g. event time or censoring time)
- exp = exposure of interest
- covar1, covar2, covar3 = covariates of interest (coded as categories)
- ID = identification variable

sampling_rate= number of particants in sub-cohort / number of participants in full eligible cohort

```
*test code;
%LET epsilon=0.01; *or any number smaller than your smallest time
unit;
%LET sampling_rate=0.05; *for the example data set cc1;

*restructure data set so that cases in sub-cohort weighted differently
according to time (will appear as two entries);
DATA ccnew1;
      SET wcc.cc1;
      *cases within subcohort - contribute fully until just before
      diagnosis;
      IF subcohort=1 AND case=1 THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
      wt= 1/&sampling_rate; *inverse probability of sampling weight;
      OUTPUT;
      END;

      *all cases contribute person-time right before event, count as
      event;
      IF case=1 THEN DO;
            start = age_eof - &epsilon;
            stop = age_eof;
            event = 1;
            wt=1;
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time,
      censored;
      ELSE IF subcohort=1 AND case=0 THEN DO;
            start = age_enrollment;
            stop = age_eof;
```

```
            event = 0;
            wt= 1/&sampling_rate;
            *inverse probability of sampling weight;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew1 covs(aggregate);
      CLASS covar1 covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar1 covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;
```

	Full-cohort, n=2,983 cases	**Case-cohort,** n=2,983 cases
HR (95% CI)	1.14 (1.04, 1.19)	1.15 (1.00, 1.33)

Covariate-stratified case-cohort (Table, row 2) All cases selected, Sub-cohort selection probabilities of x_A% (Group A) and x_B% (Group B)
Example: Niehoff et al. (*in review*) Metals and breast cancer risk: a prospective study using toenail biomarkers

cc2 = a data set containing the case-cohort data, including the following variables
subcohort = 1 if in subcohort; 0 if not
case = 1 if a case; 0 if not
age_enrollment = age at enrollment
age_eof = age at end of follow-up (e.g. event time or censoring time)
exp = exposure of interest
covar2, covar3 = covariates of interest (coded as categories)
ID = identification variable
groupA=1 if in group A; 0 if in group B

sampling_rateA= number in sub-cohort from group A / number in full cohort from group A
sampling_rateB= number in sub-cohort from group B / number in full cohort from group B

```
%LET sampling_rateA=0.08; *for the example data set cc2;
%LET sampling_rateB=0.15; *for the example data set cc2;

*restructure data set so that cases in sub-cohort weighted differently
according to time (will appear as two entries);
DATA ccnew2;
      SET wcc.cc2;
      *cases within subcohort - contribute fully until just before
      diagnosis;
      IF subcohort=1 AND case=1 THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
      IF groupA=1 THEN wt= 1/&sampling_rateA;
      ELSE IF groupA=0 THEN wt= 1/&sampling_rateB;
      *inverse probability of sampling weights;
      OUTPUT;
      END;

      *all cases contribute person-time right before event, count as
      event;
      IF case=1 THEN DO;
            start = age_eof - &epsilon;
            stop = age_eof;
            event = 1;
            wt=1;
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time, c
      ensored;
      ELSE IF subcohort=1 AND case=0 THEN DO;
```

```
            start = age_enrollment;
            stop = age_eof;
            event = 0;
      IF groupA=1 THEN wt= 1/&sampling_rateA;
      ELSE IF groupA=0 THEN wt= 1/&sampling_rateB;
      *inverse probability of sampling weights;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew2 covs(aggregate);
      CLASS covar2 covar3;
      MODEL (start,stop)*event(0) = exp groupA covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;


*group-stratified;
PROC PHREG DATA=ccnew2 covs(aggregate);
      WHERE groupA=1;
      CLASS covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;
PROC PHREG DATA=ccnew2 covs(aggregate);
      WHERE groupA=0;
      CLASS covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;
```

	Full-cohort, n=2,983 cases (2,573 Group A, 214 Group B)	**Case-cohort** n=2,983 cases (2,573 Group A, 214 Group B)
Overall, HR (95% CI)	1.14 (1.04, 1.25)	
Groups A and B only	1.12 (1.02, 1.23)	1.09 (0.96, 1.23)
Group A, HR (95% CI)	1.12 (1.01, 1.23)	1.10 (0.97, 1.26)
Group B, HR (95% CI)	1.11 (0.81, 1.50)	1.10 (0.76, 1.59)

Outcome-stratified case-cohort (Table, row 3) 100% of type I cases and y% of type 2 cases selected; sub-cohort selection probability x% for all
Example: Sampling 100% of estrogen receptor-negative breast cancers and 50% of estrogen receptor-positive breast cancers, with the desire to look at subtype-specific and overall exposure-disease associations

cc3 = a data set containing the case-cohort data, including the following variables
subcohort = 1 if in subcohort; 0 if not
case = 1 if a case; 0 if not
age_enrollment = age at enrollment
age_eof = age at end of follow-up (e.g. event time or censoring time)
exp = exposure of interest
covar2, covar3 = covariates of interest (coded as categories)
ID = identification variable
Subtype1=1 if case of disease subtype 1; 0 otherwise
Subtype2=1 if case of disease subtype 2; 0 otherwise

sampling_rate= number of particants in sub-cohort / number of participants in full eligible cohort
sampling_rate_subtype1= number of case of subtype 1 selected / total number of subtype 1 cases
sampling_rate_subtype2= number of case of subtype 2 selected / total number of subtype 2 cases

```
%LET epsilon=0.01; *or any number less than your smallest time unit;
%LET sampling_rate=0.05; *for the example data set cc3;
%LET sampling_rate_subtype1=0.50; *50% of subtype1 selected;
%LET sampling_rate_subtype2=1; *100% of subtype2 selected;

*restructure data set so that cases in sub-cohort weighted differently
according to time (will appear as two entries);
DATA ccnew3;
      SET wcc.cc3;
      *selected cases within subcohort - contribute fully until just
      before diagnosis;
      IF subcohort=1 AND (subtype1=1 | subtype2=1) THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
            wt= 1/&sampling_rate;
            *inverse probability of sampling weight;
      OUTPUT;
      END;

      *cases contribute person-time right before event only if
      selected, contribute based on weights;
      IF (subtype1=1 | subtype2=1) THEN DO;
            start = age_eof - &epsilon;
            stop = age_eof;
            event = 1;
            IF subtype1=1 THEN wt=1/&sampling_rate_subtype1;
                  ELSE IF subtype2=1 THEN wt=1/&sampling_rate_subtype2;
```

```
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time,
      censored;
      ELSE IF subcohort=1 AND subtype1=0 AND subtype2=0 THEN DO;
            start = age_enrollment;
            stop = age_eof;
            event = 0;
            wt= 1/&sampling_rate;
      *inverse probability of sampling weight;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew3 covs(aggregate);
      CLASS covar1 covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar1 covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;

*subtype 1 only;
DATA ccnew3_1;
      SET wcc.cc3;
      *selected cases within subcohort - contribute fully until just
      before diagnosis;
      IF subcohort=1 AND subtype1=1 THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
            wt= 1/&sampling_rate; *inverse probability of sampling
            weight;
      OUTPUT;
      END;

      *cases contribute person-time right before event only if
      selected, contribute based on weights;
      IF subtype1=1 THEN DO;
            start = age_eof - &epsilon;
            stop = age_eof;
            event = 1;
            wt=1/&sampling_rate_subtype1;
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time,
      censored;
      ELSE IF subcohort=1 AND subtype1=0 THEN DO;
            start = age_enrollment;
            stop = age_eof;
```

```
            event = 0;
            wt= 1/&sampling_rate;
            *inverse probability of sampling weight;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew3_1 covs(aggregate);
      CLASS covar1 covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar1 covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;

*subtype 2 only;
DATA ccnew3_2;
      SET wcc.cc3;
      *selected cases within subcohort - contribute fully until just
      before diagnosis;
      IF subcohort=1 AND subtype2=1 THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
            wt= 1/&sampling_rate;
            *inverse probability of sampling weight;
      OUTPUT;
      END;

      *cases contribute person-time right before event only if
      selected, contribute based on weights;
      IF subtype2=1 THEN DO;
            start = age_eof - &epsilon;
            stop = age_eof;
            event = 1;
            wt=1/&sampling_rate_subtype2;
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time,
      censored;
      ELSE IF subcohort=1 AND subtype2=0 THEN DO;
            start = age_enrollment;
            stop = age_eof;
            event = 0;
            wt= 1/&sampling_rate;
      *inverse probability of sampling weight;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew3_2 covs(aggregate);
```

```
      CLASS covar1 covar2 covar3;
      MODEL (start,stop)*event(0) = exp covar1 covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;
```

	Full-cohort n=2,983 cases (2,197 Subtype 1, 393 Subtype 2)	**Case-cohort** n=1,349 cases (956 Subtype 1, 393 Subtype 2)
Overall, HR (95% CI)	1.14 (1.04, 1.25)	
Subtype 1 or 2 only	1.11 (1.01, 1.23)	1.13 (0.96, 1.34)
Subtype 1, HR (95% CI)	1.07 (0.96, 1.20)	1.09 (0.90, 1.31)
Subtype 2, HR (95% CI)	1.33 (1.05, 1.68)	1.35 (1.04, 1.75)

Covariate and outcome-stratified case-cohort (Table, row 4) 100% of type I cases and y% of type 2 cases selected; Sub-cohort selection probabilities of x_A% (Group A) and x_B% (Group B)
NOTE: This assumes that case status and subgroup status are selected independently; if not, weights can be re-calculated for each combination (= a product of the specified weights)
Example: Oversampling for Black women and estrogen receptor-negative breast cancers

cc4 = a data set containing the case-cohort data, including the following variables
- subcohort = 1 if in subcohort; 0 if not
- case = 1 if a case; 0 if not
- age_enrollment = age at enrollment
- age_eof = age at end of follow-up (e.g. event time or censoring time)
- exp = exposure of interest
- covar1, covar2, covar3 = covariates of interest (coded as categories)
- ID = identification variable
- groupA=1 if in group A; 0 if in group B
- Subtype1=1 if case of disease subtype 1; 0 otherwise
- Subtype2=1 if case of disease subtype 2; 0 otherwise

sampling_rateA= number in sub-cohort from group A / number in full cohort from group A
sampling_rateB= number in sub-cohort from group B / number in full cohort from group B
sampling_rate_subtype1= number of case of subtype 1 selected / total number of subtype 1 cases
sampling_rate_subtype2= number of case of subtype 2 selected / total number of subtype 2 cases

```
%LET epsilon=0.01; *or any number less than your smallest time unit;
%LET sampling_rateA=0.08; *for the example data set cc4;
%LET sampling_rateB=0.15; *for the example data set cc4;
%LET sampling_rate_subtype1=0.50; *50% of subtype1 selected;
%LET sampling_rate_subtype2=1; *100% of subtype2 selected;

*restructure data set so that cases in sub-cohort weighted differently
according to time (will appear as two entries);
DATA ccnew4;
      SET wcc.cc4;
      *selected cases within subcohort - contribute fully until just
      before diagnosis;
      IF subcohort=1 AND (subtype1=1 | subtype2=1) THEN DO;
            start = age_enrollment;
            stop= age_eof - &epsilon;
            event = 0; *considered a censored observation;
            IF groupA=1 THEN wt= 1/&sampling_rateA;
                  ELSE IF groupA=0 THEN wt=1/&sampling_rateB;
            *inverse probability of sampling weight;
      OUTPUT;
      END;

      *cases contribute person-time right before event only if
      selected, contribute based on weights;
      IF (subtype1=1 | subtype2=1) THEN DO;
            start = age_eof - &epsilon;
```

```
            stop = age_eof;
            event = 1;
            IF subtype1=1 THEN wt=1/&sampling_rate_subtype1;
                  ELSE IF subtype2=1 THEN wt=1/&sampling_rate_subtype2;
      OUTPUT;
      END;

      *non-cases within subcohort - contribute full person time,
      censored;
      ELSE IF subcohort=1 AND subtype1=0 AND subtype2=0 THEN DO;
            start = age_enrollment;
            stop = age_eof;
            event = 0;
            IF groupA=1 THEN wt= 1/&sampling_rateA;
                  ELSE IF groupA=0 THEN wt=1/&sampling_rateB;
            *inverse probability of sampling weight;
      OUTPUT;
      END;
RUN;

PROC PHREG DATA=ccnew4 covs(aggregate);
      CLASS covar2 covar3;
      MODEL (start,stop)*event(0) = exp groupA covar2 covar3;
      WEIGHT wt;
      ID ID;
      HAZARDRATIO exp;
RUN;

*subtype-specific estimates computed as for example 3;
```

	Full-cohort	**Case-cohort**
All women		
Overall, HR (95% CI)	1.14 (1.04, 1.25)	
Group A or B; Subtype 1 or 2 only	1.09 (0.99, 1.21)	1.05 (0.89, 1.23)
Subtype 1, HR (95% CI)	1.07 (0.96, 1.20)	1.01 (0.84, 1.22)
Subtype 2, HR (95% CI)	1.33 (1.05, 1.68)	1.23 (0.94, 1.60)
Group A		
Overall, HR (95% CI)	1.12 (1.01, 1.23)	
Subtype 1 or 2 only	1.09 (0.98, 1.21)	1.06 (0.89, 1.25)
Subtype 1, HR (95% CI)	1.07 (0.96, 1.20)	1.04 (0.86, 1.25)
Subtype 2, HR (95% CI)	1.18 (0.90, 1.54)	1.15 (0.87, 1.53)
Group B		
Overall, HR (95% CI)	1.11 (0.81, 1.50)	
Subtype 1 or 2 only	1.10 (0.77, 1.58)	0.91 (0.51, 1.62)
Subtype 1, HR (95% CI)	0.92 (0.60, 1.40)	0.68 (0.32, 1.44)
Subtype 2, HR (95% CI)	2.02 (0.99, 4.14)	1.98 (0.88, 4.47)

Case-independent designs (Table, row 5) v% cases and z% of non-cases included in case-cohort sample; want to measure the association between previously measured exposure ("exp") and a second exposure ("exp2"), independent of case status
Example: Lawrence et al. (2020) Association of neighborhood deprivation with epigenetic aging using four clock methodologies. *JAMA Open*

Sampling_rate_cases= number of selected cases / total number of cases
sampling_rate_subcohort= number selected into subcohort / total number in cohort

```
%LET sampling_rate_cases=1; *for the example data set cc5 (all cases);
%LET sampling_rate_subcohort=0.05; *5% of cohort selected into
subcohort;

DATA wcc.cc5;
      SET wcc.cc5;
      IF case=1 THEN wt= 1/&sampling_rate_cases;
            ELSE IF case=0 THEN wt= 1/&sampling_rate_subcohort;
      *create indicator versions of covariates;
      IF covar1=1 THEN covar1_1=1;
            ELSE covar1_1=0;
      IF covar1=2 THEN covar1_2=1;
            ELSE covar1_2=0;
      IF covar1=3 THEN covar1_3=1;
            ELSE covar1_3=0;

      IF covar2=1 THEN covar2_1=1;
            ELSE covar2_1=0;
      IF covar2=2 THEN covar2_2=1;
            ELSE covar2_2=0;
      IF covar2=3 THEN covar2_3=1;
            ELSE covar2_3=0;

      IF covar3=2 THEN covar3_2=1;
            ELSE covar3_2=0;
      IF covar3=3 THEN covar3_3=1;
            ELSE covar3_3=0;
RUN;

PROC REG DATA=wcc.cc5;
      MODEL exp2 = age_enrollment covar1_1 covar1_2 covar1_3 covar2_1
      covar2_2 covar2_3 covar3_2 covar3_3/ SOLUTION CLPARM;
      WEIGHT wt;
RUN;
QUIT;
```

	Full-cohort	**Case-cohort**
β (95% CI)	1.41 (1.28, 1.54)	1.34 (1.21, 1.47)