Nested case-control and case-cohort studies

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Points to be covered

- Outcome-dependent sampling designs a.k.a. **case-control** studies *vs.* **full cohort** design.
- **Nested case-control** study (NCC): sampling of controls from risk-sets during follow-up of study population.
- **Matching** in selection of control subjects in NCC.
- R tools for NCC: function `ccwc()` in `Epi` for sampling controls, and `clogit()` in `survival` for model fitting.
- **Case-cohort** study (CC): sampling a subcohort from the whole cohort as it is at the start of follow-up.
- R tools for CC model fitting: function `cch()` in `survival`

Example: Smoking and cervix cancer

Study population, measurements, follow-up, and sampling design

- Joint cohort of $N \approx 500\,000$ women from 3 Nordic biobanks.
- Follow-up: From variable entry times since 1970s till 2000.
- For each of 200 cases, 3 controls were sampled; matched for biobank, age (± 2 y), and time of entry (± 2 mo).
- Frozen sera of cases and controls analyzed for cotinine *etc.*

Main result: Adjusted OR = 1.5 (95% CI 1.1 to 2.3) for high (>242.6 ng/ml) *vs.* low (<3.0 ng/ml) cotinine levels.

Simen Kapeu *et al.* (2009) *Am J Epidemiol*

Example: USF1 gene and CVD

Study population, measurements, follow-up, and sampling design

- Two FINRISK cohorts, total $N \approx 14000$ M & F, 25-64 y.
- Baseline health exam, questionnaire & blood specimens at recruitment in the 1990s – Follow-up until the end of 2003.
- Subcohort of 786 subjects sampled.
- 528 incident cases of CVD; 72 of them in the subcohort.
- Frozen blood from cases and subchort members genotyped.

Main result: Female carriers of a high risk haplotype had a
2-fold hazard of getting CVD [95% CI: 1.2 to 3.5]

Komulainen *et al.* (2006) *PLoS Genetics*

Full cohort design & its simple analysis

- **Full cohort design**: Data on exposure variables obtained for all subjects in a large study population.
- Summary data for crude comparison:

	Exposed	Unexposed	Total
Cases	D_1	D_0	D
Non-cases	B_1	B_0	B
Group size at start	N_1	N_0	N
Follow-up times	Y_1	Y_0	Y

- Crude estimation of **hazard ratio** $\rho = \lambda_1/\lambda_0$:
  incidence rate ratio IR, with standard error of log(IR):

$$\widehat{\rho} = \mathsf{IR} = \frac{D_1/Y_1}{D_0/Y_0} \qquad \mathsf{SE}[\log(\mathsf{IR})] = \sqrt{\frac{1}{D_1} + \frac{1}{D_0}}.$$

- More refined analyses: Poisson or Cox regression.

Problems with full cohort design

Obtaining exposure and covariate data

- Slow and expensive in a big cohort.
- Easier with questionnaire and register data,
- Extremely costly and laborious for *e.g.*
  - measurements from biological specimens, like genotyping, antibody assays, *etc.*
  - dietary diaries & other manual records

Can we obtain equally valid estimates of hazard ratios etc. with nearly as good precision by some other strategies?

Yes – we can!

Estimation of hazard ratio

The incidence rate ratio can be expressed:

$$\text{IR} = \frac{D_1/D_0}{Y_1/Y_0} = \frac{\text{cases: exposed / unexposed}}{\text{person-times: exposed / unexposed}}$$

$$= \frac{\textit{exp're odds} \text{ in cases}}{\textit{exp're odds} \text{ in p-times}} = \textbf{exposure odds ratio} \text{ (EOR)}$$

= Exposure distribution in cases *vs.* that in cohort!

Implication for more efficient design:

- *Numerator*: Collect exposure data on all cases.
- *Denominator*: Estimate the ratio of person-times Y_1/Y_0 of the exposure groups in the cohort by **sampling** "control" subjects, on whom exposure is measured.

Case-control designs

General principle: Sampling of subjects from a given study population is *outcome-dependent*.

Data on risk factors are collected separately from

(I) **Case group**: All (or high % of) the D subjects in the study population (total N) encountering the outcome event during the follow-up.

(II) **Control group**:

- Random **sample** (simple or stratified) of C subjects ($C << N$) from the population.
- Eligible controls must be bf risk (alive, under follow-up & free of outcome) at given time(s).

Study population in a case-control study?

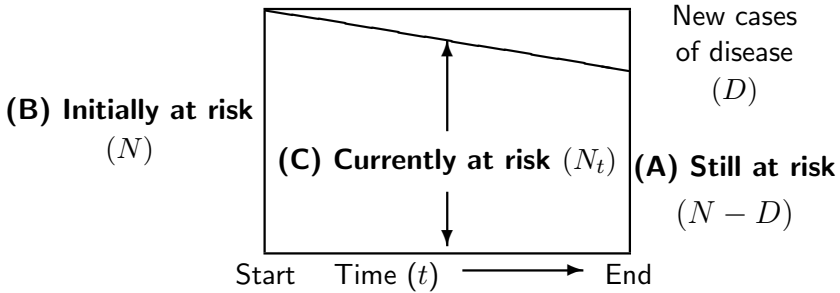
Ideally: The study population comprises subjects who *would be* included as cases, *if they got* the outcome in the study

- *Cohort-based studies*: **cohort** or **closed** population of well-identified subjects under intensive follow-up for outcomes (*e.g.* biobank cohorts).
- *Register-based studies*: **open** or **dynamic** population in a region covered by a disease register.
- *Hospital-based* studies: dynamic **catchment** population of cases – may be hard to identify (*e.g.* hospitals in US).

In general, the role of control subjects is to represent the distribution of person-times by exposure variables in the underlying population from which the cases emerge.

Sampling of controls – alternative frames

Illustrated in a simple longitudinal setting:
Follow-up of a cohort over a fixed risk period & no censoring.



Rodrigues, L. & Kirkwood, B.R. (1990). Case-control designs of common diseases . . . *Int J Epidemiol* **19**: 205-13.

Sampling schemes or designs for controls

(A) Exclusive or **traditional, "case-noncase" sampling**

- Controls chosen from those $N - D$ subjects still at risk (healthy) *at the end* of the risk period (follow-up).

(B) Inclusive sampling or **case-cohort design** (CC)

- The control group – *subcohort* – is a random sample of the cohort (N) *at start*.

(C) Concurrent sampling or **density sampling**

- Controls drawn *during the follow-up*
- **Risk-set** or **time-matched sampling:**
  A set of controls is sampled from the *risk set at each time* t *of diagnosis* of a new case – a.k.a. **nested case-control design** (NCC)

Nested case-control – two meanings

- In some epidemiologic books, the term "nested case-control study" (NCC) covers jointly all variants of sampling: **(A)**, **(B)**, and **(C)**, from a cohort.

  Rothman *et al.* (2008): *Modern Epidemology, 3rd Ed.*
  Dos Santos Silva (1999): *Cancer Epidemiology.* Ch 8-9

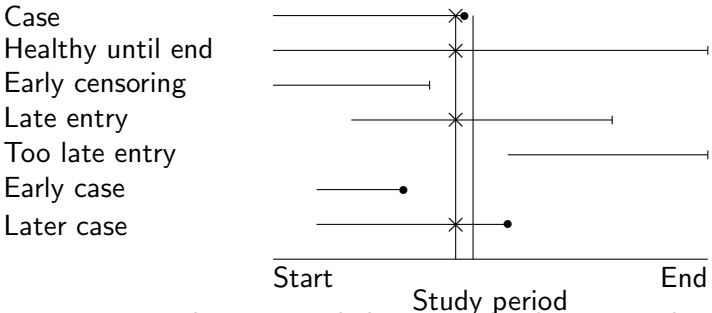
- In biostatistical texts NCC typically refers only to the variant of concurrent or density sampling **(C)**, in which *risk-set* or *time-matched* sampling is employed.

  Borgan & Samuelsen (2003) in *Norsk Epidemiologi*
  Langholz (2005) in *Encyclopedia of Biostatistics.*

- We shall follow the biostatisticians!

NCC: Risk-set sampling with staggered entry

Sampling frame to select controls for a given case:
Members ($\times$) of the **risk set** at t_k, *i.e.* the population at risk at the time of diagnosis t_k of case k.



Sampled risk set contains the case and the control subjects randomly sampled from the non-cases in the risk set at t_k.

Use of different sampling schemes

(A) Exclusive sampling, or "textbook" case-control design

- Almost exclusively(!) used in studies of epidemics.
- (Studies on birth defects with *prevalent* cases.)

(B) Inclusive sampling or case-cohort design

- Good esp. for multiple outcomes, if measurements of risk factors from stored material remain stable.

(C) Concurrent or density sampling (without or with time-matching)

- The only logical design in an open population.
- Most popular in chronic diseases (Knol *et al.* 2008).

Designs **(B)** and **(C)** allow valid estimation of hazard ratios ρ without any "rare disease" assumption.

Case-control studies: Textbooks vs. real life

- Many epi texts focus on the traditional design:
  exclusive sampling of controls, ignoring other designs.
- Claim: "*Odds ratio is the only estimable parameter.*"
- Yet, over 60% of published case-control studies apply **concurrent sampling** or **density sampling** of controls from an **open** or **dynamic** population.
- Thus, the parameter most often estimated is the
  hazard ratio (HR) or **rate ratio** ρ.
- Still, 90% of authors really estimating HR, reported as having estimated an OR (*e.g.* Simen Kapeu *et al.* 2009)

Knol *et al.* (2008). What do case-control studies estimate?
Am J Epidemiol **168**: 1073-81.

Exposure odds ratio – estimate of what?

- Crude summary of case-control data

	exposed	unexposed	total
cases	D_1	D_0	D
controls	C_1	C_0	C

- Depending on study base & sampling strategy, the **exposure odds ratio**

$$\text{EOR} = \frac{D_1/D_0}{C_1/C_0} = \frac{\text{cases: exposed / unexposed}}{\text{controls: exposed / unexposed}}$$

  is a consistent estimator of

  (a) hazard ratio, (b) risk ratio, (c) risk odds ratio,

  (d) prevalence ratio, or (e) prevalence odds ratio

- **NB.** In case-cohort studies with variable follow-up times C_1/C_0 is substituted by $\widehat{Y}_1/\widehat{Y}_0$, from estimated p-years.

Precision and efficiency

With exclusive **(A)** or concurrent **(C)** sampling of controls (unmatched), the estimated variance of log(EOR) is

$$\begin{aligned} \widehat{\text{var}}[\log(\text{EOR})] &= \frac{1}{D_1} + \frac{1}{D_0} + \frac{1}{C_1} + \frac{1}{C_0} \\ &= \text{cohort variance} + \text{sampling variance} \end{aligned}$$

- Depends basically on the numbers of cases, with ≥ 4 controls per case.
- Is not much bigger than $1/D_1 + 1/D_0 =$ variance in a full cohort study with same numbers of cases.

$\Rightarrow$ Usually < 5 controls per case is enough.

$\Rightarrow$ *These designs are very cost-efficient!*

Estimation in concurrent or density sampling

- Assume a simple situation: Prevalence of exposure in the study population stable over time.

$\Rightarrow$ The exposure odds C_1/C_0 among controls
$=$ a consistent estimator of exposure odds Y_1/Y_0 of person-times.

- Therefore, the crude EOR $= (D_1/D_0)/(C_1/C_0)$
$=$ a consistent estimator of hazard ratio $\rho = \lambda_1/\lambda_0$.
- Variance of log(EOR) estimated as above.
- Yet, stability of exposure distribution may be unrealistic, especially in a closed study population or cohort.
- Solution: **Time-matched** sampling of controls from **risk sets**, *i.e.* NCC, & matched EOR to estimate HR.

Prentice & Breslow (1978), Greenland & Thomas (1982).

Matching in case-control studies

- **Stratified sampling** of controls, *e.g.* from the same region, sex, and age group as a given case
- **Frequency matching** or **group matching:** For cases in a specific stratum (*e.g.* same sex and 5-year age-group), a set of controls from a similar subgroup.
- **Individual matching** (1:1 or 1:m matching): For each case, choose 1 or more (rarely > 5) closely similar controls (*e.g.* same sex, age within ± 1 year.
- **NCC**: Sampling from risk-sets implies time-matching at least. Additional matching for other factors possible.
- **CC**: Subcohort selection involves no matching with cases.

Virtues of matching

- Increases *efficiency*, if the matching factors are both
  (i) strong *risk factors* of the disease, and
  (ii) *correlated* with the main exposure.
  – Major reason for matching.
- *Confounding* due to poorly quantified factors (sibship, neighbourhood, *etc.*) may be removed by close matching – only if properly analyzed.
- Biobank studies: Matching for storage time, freeze-thaw cycle & analytic batch improves **comparability of measurements** from frozen specimens
  $\rightarrow$ Match on the time of baseline measurements within the case's risk set.

Warnings for overmatching

Matching a case with a control subject is a different issue than matching an unexposed subject to an exposed one in a cohort study – much trickier!

- Matching on an *intermediate* variable between exposure and outcome.

  $\Rightarrow$ *Bias*!

- Matching on a *surrogate* or *correlate* of exposure, which is not a true risk factor.
  $\Rightarrow$ *Loss of efficiency*.

$\rightarrow$ **Counter-matching:** Choose a control which is not similar to the case w.r.t a correlate of exposure.

$\Rightarrow$ Increases efficiency!

- Requires appropriate weighting in the analysis.

Sampling matched controls for NCC using R

- Suppose key follow-up items are recorded for all subjects in a cohort, in which a NCC study is planned.
- Function `ccwc()` in package `Epi` can be used for risk-set sampling of controls. – Arguments:

`entry` :	Time of entry to follow-up
`exit` :	Time of exit from follow-up
`fail` :	Status on exit (1 for case, 0 for censored)
`origin` :	Origin of analysis time scale (e.g. time of birth)
`controls` :	Number of controls to be selected for each case
`match` :	List of matching factors
`data` :	Cohort data frame containing input variables

- Creates a data frame for a NCC study, containing the desired number of matched controls for each case.

Analysis of matched studies

- Close matching induces a new parameter for each matched case-control set or stratum.

  $\Rightarrow$ **unconditional logistic regression** breaks down.

- Matching on well-defined variables (like age, sex)
  – include these factors as covariates.

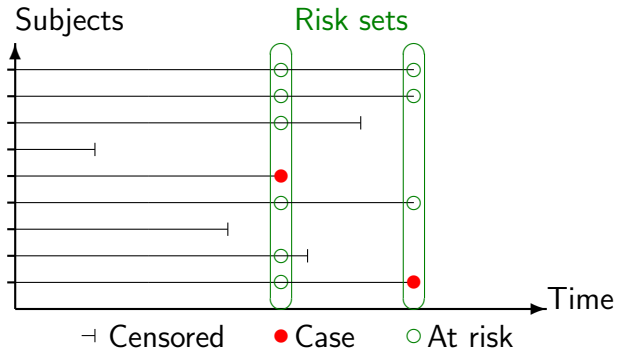
- Matching on "soft" variables (like sibship) can be dealt with **conditional logistic regression**.

- Same method in matched designs **(A)**, exclusive, and **(C)**, concurrent, but interpretation of β_js differs:

  (A) β_j = log of risk odds ratio (ROR),
  (C) β_j = log of hazard ratio (HR).

Full cohort design: Follow-up & risk sets

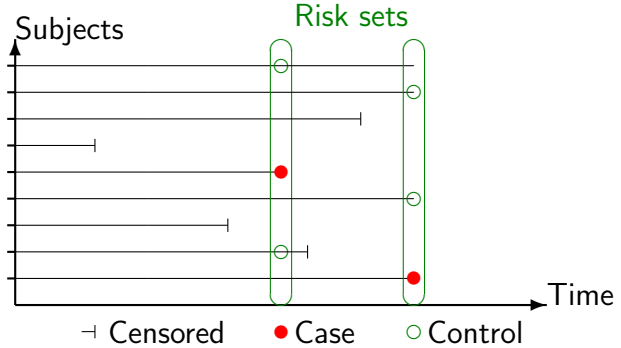
Each member of the cohort provides exposure data for all cases, as long as this member is at risk, *i.e.* (i) alive, (ii) not censored & (iii) free from outcome.



Times of new cases define the **risk-sets**.

Nested case-control (NCC) design

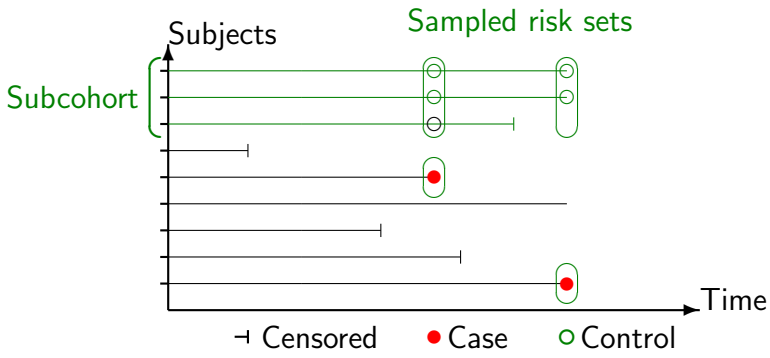
Whenever a new case occurs, a set of controls (here 2/case) are sampled from its risk set.



NB. A control once selected for some case can be selected as a control for another case, and can later on become a case, too.

Case-cohort (CC) design

Subcohort: Sample of the whole cohort randomly selected at the outset.
– Serves as a reference group for all cases.



NB. A subcohort member can become a case, too.

Modelling in NCC and other matched studies

Cox proportional hazards model:

$$\lambda_i(t, x_i; \beta) = \lambda_0(t) \exp(x_{i1}\beta_1 + \cdots + x_{ip}\beta_p),$$

Estimation: partial likelihood $L^P = \prod_k L_k^P$:

$$L_k^P = \exp(\eta_{i_k}) / \sum_{i \in \widetilde{R}(t_k)} \exp(\eta_i),$$

where $\widetilde{R}(t_k) =$ **sampled risk set** at observed event time t_k, containing the case + sampled controls $(t_1 < \cdots < t_D)$

$\Rightarrow$ Fit stratified Cox model, with $\widetilde{R}(t_k)$'s as the strata.

$\Leftrightarrow$ **Conditional logistic regression**
– function `clogit()` in `survival`, wrapper of `coxph()`.

Modelling case-cohort data

Cox's PH model $\lambda_i(t) = \lambda_0(t)\exp(\eta_i)$ again, but ...

- Analysis of survival data relies on the theoretical principle that *you can't know the future*.
- Case-cohort sampling breaks this principle:
  cases are sampled based on what *is known* to be happening to them during follow-up.
- The union of cases and subcohort is a mixture
  1. random sample of the population, and
  2. "high risk" subjects who are *certain* to become cases.

$\Rightarrow$ Ordinary Cox partial likelihood is wrong.

- Overrepresentation of cases must be corrected for, by (I) **weighting**, or (II) **late entry method**.

Correction method I – weighting

The method of **weighted partial likelihood** borrows some basics ideas from survey sampling theory.

- Sampled risk sets
  $\widetilde{R}(t_k) = \{\text{cases}\} \cup \{\text{subcohort members}\}$ at risk at t_k.
- Weights:
  - $w = 1$ for all cases (within and outside the subcohort),
  - $w = N_{\text{non-cases}}/n_{\text{non-cases}}$ = inverse of sampling-fraction f for selecting a non-case to the subcohort.
- Function `coxph()` with option `weights = w` would provide consistent estimation of β parameters.
- However, the SEs must be corrected!
- R solution: Function `cch()` – a wrapper of `coxph()` – in package `survival`, with `method = "LinYing"`.

Comparison of NCC and CC designs

- Statistical efficiency

  Broadly similar in NCC and CC with similar numbers of cases and controls.

- Statistical modelling and valid inference

  Straightforward for both designs with appropriate software,
  now widely available for CC, too

- Analysis of outcome rates on several time scales?

  NCC: Only the time scale used in risk set definition can be the time variable t in the baseline hazard of PH model.

  CC: Different choices for the basic time in PH model possible, because subcohort members are not time-matched to cases.

Comparison of designs (cont'd)

- Missing data

  NCC: With close 1:1 matching, a case-control pair is lost, if either of the two has data missing on key exposure(s).

  CC: Missingness of few data items is less serious.

- Quality and comparability of biological measurements

  NCC: Allows each case and its controls to be matched also for analytic batch, storage time, freeze-thaw cycle, $\rightarrow$ better comparability.

  CC: Measurements for subcohort performed at different times than for cases $\rightarrow$ differential quality & misclassification.

- Possibility for studying many diseases with same controls

  NCC: Complicated, but possible if matching is not too refined.

  CC: Easy, as no subcohort member is "tied" with any case.

Conclusion

- "Case-controlling" is very cost-effective.
- Case-cohort design is useful especially when several outcomes are of interest, given that the measurements on stored materials remain stable during the study.
- Nested case-control design is better suited *e.g.* for studies involving biomarkers that can be infuenced by analytic batch, long-term storage, and freeze-thaw cycles.
- Matching helps in improving effciency and in reducing bias – but only if properly done.
- Handy R tools are available for all designs.