Analysing data after matching

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- assumption: (1) we have matched the data
  (2) we have checked for covariate balance btw. groups

⇒ goal: outcome analysis with matched and balanced data

Analysis of outcomes in data after successful matching:

- test for treatment effect (e.g. hypothesis testing)
- estimate the treatment effect and its confidence interval
⇒ always we need to take the matching into account

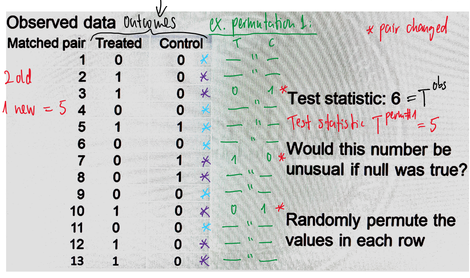
Randomization tests: (a.k.a.: **permutation tests** or exact tests)

- idea:
  (1) compute test statistic from observed data T^{obs}
  (2) assume null-hypothesis (H_0) of no treatment effect is true
  (3) randomly **permute treatment assignment** within pairs and re-compute test-statistic T^{perm}
  (4) repeat step (3) many times and see how unusual the observed test statistic from step (1) is (relative to the test statistics computed on the permuted data)

⇒ if H_0 is true, then T^{obs} should be consistent with the test statistics T^{perm}, that we computed in step (3)

Example:

- 13 matched pairs w/ (binary outcome)
- we Test statistic T.. # of events in the treated group (or in (i.e. # of outcomes in the treated group)



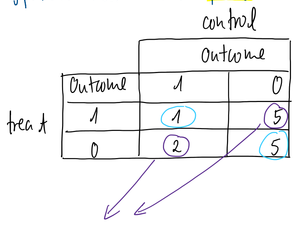
T^0 = 2dd + 1 new = 5

* concordant pairs bc same outcome in both treatment of the pair
* discordant pairs bc different outcomes

↳ permute discordant pairs bc this changes the outcome of the treatment (e.g. matched pair #2 goes from (1,0) → (0,1))
↳ permute pairs based on Bernoulli random variable (meaning that NOT ALL discordant pairs should be permuted!!)

McNemar test: (for testing null hypothesis using a randomization test w/ matched (paired) binomial data)

- hypothesis test used for paired binomial (n=1) / bernoulli data



concordant pairs
discordant pairs
↓
contain the information whether or not there is a treatment effect (i.e. comparing these 5 vs. 2 pairs)

if there is no treatment effect, we would expect these numbers to be close/similar on average (in the long run of running the permutation simulation above)

Randomization tests: (aka permutation tests!) SBP
- the basic idea also works with continuous data (e.g. Systolic blood pressure)
- any other test statistics (e.g. difference in sample means $\bar{X}$)
⇒ **randomly permute treatment labels** and re-compute test statistic T^{perm}, and compare it to T^{obs}! (in matched pairs)

P-value: proportion of times, that we see a statistic as extreme or more extreme as the observed statistic.

→ for paired continuous data we can use the paired t-test instead

Other outcome models:

- Conditional logistic regression: · for matched binary outcome data
- stratified Cox model: · for time-to-event (survival) outcome data
  · Baseline hazard stratified on matched sets using the "match-ID" variable for performing the actual stratification
- Generalized estimating equations (GEE):
  · cluster data on "match-ID" variable
  · useful for binary outcome data
  · can estimate: (i) causal risk ratio (when log-link fct. used)
    (ii) causal odds ratio } depends on the link fct.
    (iii) causal risk difference (when identity-link fct. used)