

# Research Design

Practice Session 6

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# Today

- Presentation by group 1: propensity score matching
- Demonstration & team work:
  - Genetic matching
  - Exact matching
  - Matching with calipers

# At the end of this session, you can...

- ... conduct genetic matching and use the output for data analysis
- ... perform exact matching
- ... perform matching with calipers

# Group 1: Propensity Score Matching

# Strategies: Matching: Steps

1. Select distance measure
  - Exact matching (same covariates values)
  - One-dimensional summary measure (e.g. Propensity-score, Mahalanobis)
  - Caliper: "One strategy to avoid poor matches is to impose a caliper and only to select a match if it is within the caliper." (Stuart 2010, 10)
    - Describes bandwidth that matches are allowed to have (e.g., accept someone aged between 40 and 44 for someone aged 42)
2. Matching method (see Savje et al. 2016, 5, Fig. 1)
  - Nearest neighbor matching (1:1 or k:1 nearest neighbor, optimal matching, replacement)
  - Subclassification, full matching and weighting
3. Assessing balance
  - Compare covariate distribution between treatment and control
  - In practice: one-dimensional measures (std. difference in means, variance ratio etc)
  - Repeat prior steps until balance is good
4. Analysis of outcome based on matched sample (estimate regression)

# Teamwork: Tasks (slide 1/2)

1. Using the code on caliper matching above, find the approximate distance/caliper value at which we achieve "perfect" balance with respect to age AND education. Spend max. five minutes on this task.
2. Perform exact and caliper matching using all of the following variables simultaneously (in one single matching procedure): age, education, black, hispanic, married, nodegree. For each variable, choose the appropriate type of matching/distance (make sure that not more than treated 40 individuals will be excluded by matching). Note the help page on ?Match and check the information on "caliper": "The exact option takes precedence over the caliper option". However, there's a "workaround" to solve this problem! (You find hints at the end of this file.)

# Teamwork: Tasks (slide 2/2)

3. Bonus task, if you still have time: Take the following matching results data we created above: "matching.NSW.cal". Create a table/matrix/data frame that shows the index numbers of the individuals matched to each other, as well as how much weight is given to each matched observation (hint: check the structure of matching.NSW.cal). Make sure to understand how the weights are chosen.

# Summary / Take-home messages

- Genetic matching: `OBJECT <- GenMatch(X = cbind(COVARIATES), Tr = TREATMENT)`.
  - To estimate ATT, add: `Y = OUTCOME`. Then: `summary(OBJECT)`
- Exact matching: add: `exact = TRUE`.
- Caliper matching: add: `caliper = DISTANCE/SD`
- Also possible to give different instructions for different variables:
  - `exact = c(TRUE, FALSE...)`
  - `caliper = c(0.5, 1.3...)`



# To do until next week

- Check ILIAS on/after Friday evening for next week's text (again, focus on methods)
- If you have any questions on the code or want to share your solutions/want to get feedback, write to me: [fgerdon@mail.uni-mannheim.de](mailto:fgerdon@mail.uni-mannheim.de)
  - Solutions will be uploaded on Monday