

Distribution of weights

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- larger weights lead to noisier estimates of causal effects
 - ex.: suppose 1 person has a weight of 10,000; then this single person essentially represents 10,000 people
- this one person's outcome data can greatly affect the parameter estimate, \Rightarrow causes large standard error.
 - standard deviation of the statistic's sampling dist. (e.g. \bar{X} as sample mean)

Bootstrapping:

- a method to estimate standard errors as follows:
 1. randomly sample N_{samples} w/ replacement from the original sample
 2. estimate parameters
 3. repeat 1. and 2. many times
 4. the standard deviation of the bootstrap estimates is an estimate of the standard error

→ someone w/ a very large weight will be included in some bootstrap samples, but not others.

↳ whether or not they are included, will have a LARGE impact on the parameter estimates \Rightarrow thus, a lot of variability of the estimator would be due to this one subject with an extreme weight

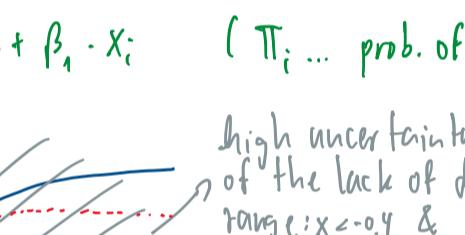
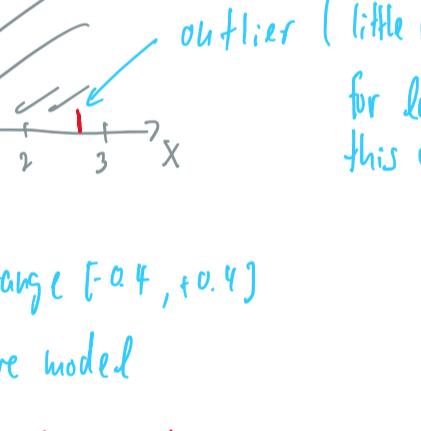
Relationship of large weight with positivity assumption:

- large weight means that the probability of that treatment was very small: $P(T=1|X) \approx 0$

→ thus: large weights indicate near violations of the positivity assumption

- i.e. people w/ certain covariate values are extremely unlikely to get one of the treatments

Checking weights:

- plotting ↗ 1) density plot: 
- 2) order statistics plot: 

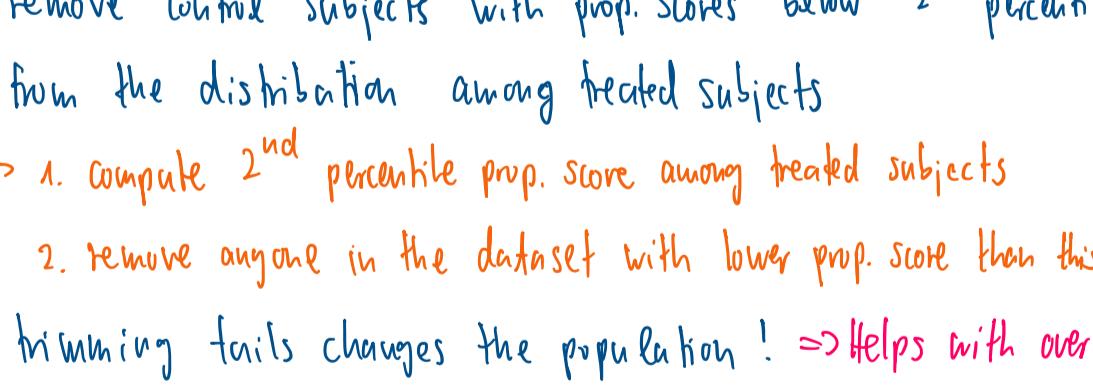
Remedies for large weights:

INVESTIGATIVE STEP: (why are the weights large?)

- 1) identify subjects with large weights
 - ↳ what is unusual about them? their data?
- 2) is there a problem w/ the propensity score model?

Example: propensity score model: logistic regression

$$\text{logit}(T_i) = \beta_0 + \beta_1 \cdot X_i \quad (T_i \dots \text{prob. of treatment})$$



TRIMMING THE TAILS: (getting rid of subjects in your dataset)

- large weights occur at observations (X) in the tails of the propensity score distribution

⇒ trimming the tails can eliminate some extreme values of the propensity score

Common trimming strategy:

- remove treated subjects with prop. scores above 98th percentile from the distribution among controls
 - ↳ 1. compute 98th percentile prop. score value among those in the control group
 - 2. remove anyone in the dataset with higher prop. score than this 98th percentile value.

- remove control subjects with prop. scores below 2nd percentile from the distribution among treated subjects
 - ↳ 1. compute 2nd percentile prop. score among treated subjects
 - 2. remove anyone in the dataset with lower prop. score than this 2nd percentile value.

- trimming tails changes the population! \Rightarrow Helps with overlap!

- trimming tails helps making the positivity assumption more plausible b/c it gets rid of the extremes

WEIGHT TRUNCATION:

- truncating the large weights

Steps:

1. determine a max. allowable weight
 - ↳ could be specific value (e.g. 100)
 - ↳ could be based on percentile (e.g. 99th)

2. if a weight is greater than max. allowable weight,

then we set it to the max. allowable weight

(e.g. max is 100 and weight is 1000, then set weight to 100)

- truncating weights involves a bias-variance-tradeoff b/c we lose more precisely weight each subject

↳ truncation: bias, but smaller variance

no truncation: unbiased, but noisy estimators, i.e. high variance

- truncating: accept some bias and gain less variance of your estimator

- truncating extremely large weights can result in estimators with lower mean-squared-error (MSE).