# Longitudinal trimmed and smooth trimmed effects with flip and S-flip interventions

**Alec McClean** and Iván Díaz

New York University Grossman School of Medicine

# Trimming with single timepoint data

$\{(X_i, A_i, Y_i)\}_{i=1}^n \overset{iid}{\sim} \mathcal{P}$ with $X_i$ covariates, $A_i \in \{0, 1\}$ binary treatment and $Y_i \in \mathbb{R}$ outcome.
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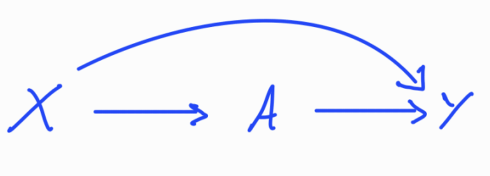


**Positivity violations**: $\pi(X) = \mathbb{P}(A = 1 \mid X) \approx 0$ or $\approx 1$.
$\mathbb{E}\{Y(a)\}$ not identified ($\pi = 0$) or hard-to-estimate ($\pi \approx 0$)

**Trimming:** Change population to satisfy positivity

$$\mathbb{E}\Big[\big\{Y(1) - Y(0)\big\}\mathbb{1}\{\varepsilon < \pi(X) < 1 - \varepsilon\}\Big] \text{ for } \varepsilon \in [0, 0.5)$$

(related to cond. trimming: $\mathbb{E}\{f(Z) \mid \mathcal{E}\} = \mathbb{E}\{f(Z)\mathbb{1}(\mathcal{E})\}/\mathbb{P}(\mathcal{E})$)

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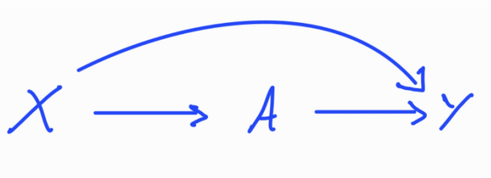


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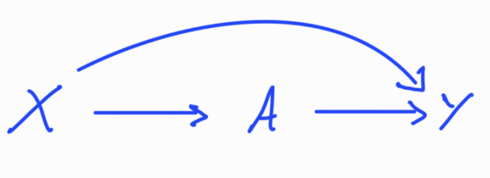


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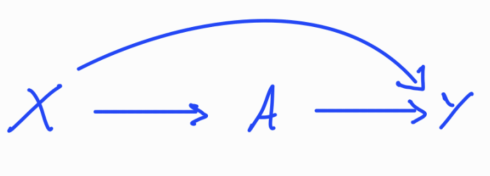


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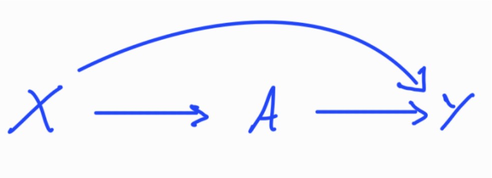


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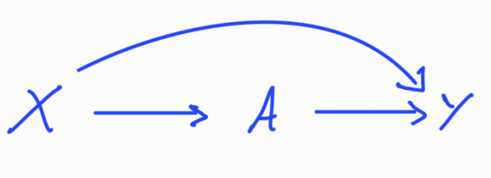


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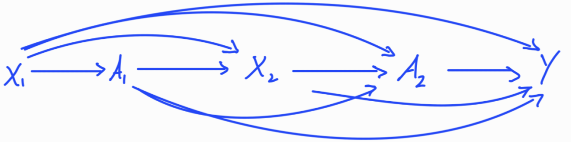
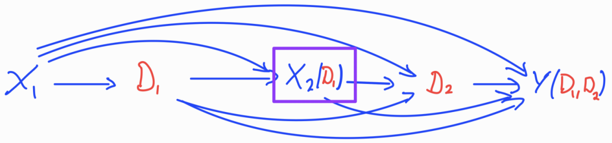



Can we trim on propensity scores in the second timepoint?
(where we often have positivity violations!)

Traditional answer: no




*...the [post-treatment] covariates responsible for positivity violations may themselves be affected by past treatment. Trimming... amounts to conditioning on post-treatment covariates and can thus introduce new bias.* *[Petersen et al., 2012, Section 4.3]* (also, see, e.g., Jensen et al. [2024, Section 6.3])

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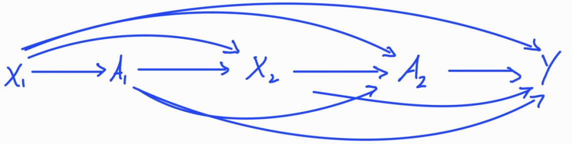


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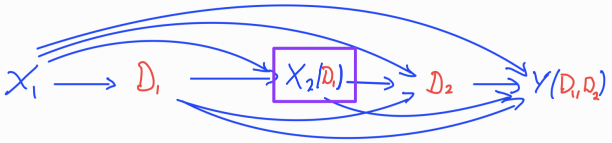


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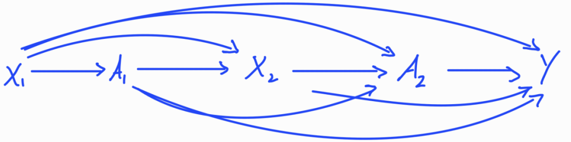


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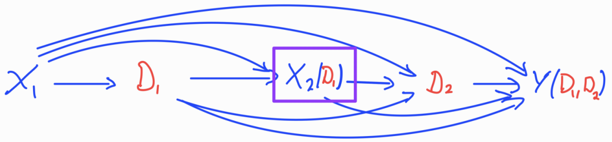


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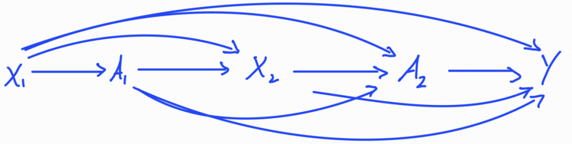

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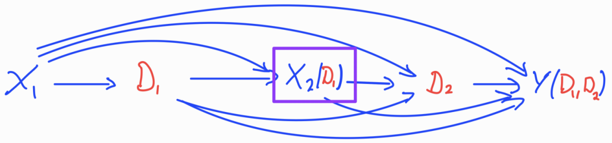

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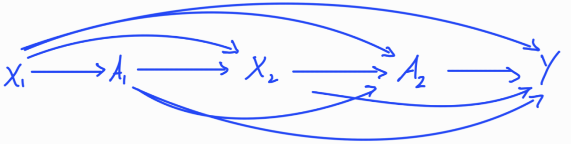


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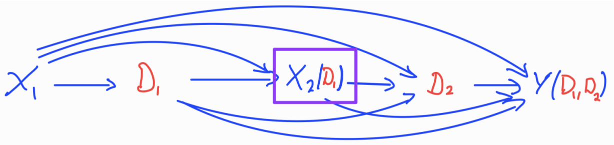


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# Trimming is a dynamic "flip" intervention

**Dynamic stochastic interventions:**
$D = d(A, X)$ adapts so $\mathbb{E}\{Y(D)\}$ IDable and estimable

- Modified treatment policies [Díaz et al., 2023]
- Incremental propensity score interventions [Kennedy, 2019]

Proposition

*Let* $\mathbb{1}(X) \equiv \mathbb{1}\{\varepsilon < \pi(X) < 1 - \varepsilon\}$ *and*

$$D(a) = \begin{cases} A & \text{if } A = a \\ \mathbb{1}(X)a + \{1 - \mathbb{1}(X)\}A & \text{if } A \neq a. \end{cases}$$

*Then, if* $\{Y(1), Y(0)\} \perp\!\!\!\perp A \mid X$,

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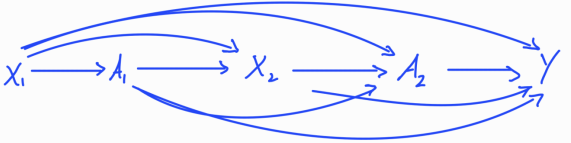
# Longitudinal setup

# Longitudinal data

$\{Z_i\}_{i=1}^n \overset{iid}{\sim} \mathbb{P} \in \mathcal{P}$ where $Z = (X_1, A_1, X_2, A_2, \ldots, X_T, A_T, Y)$




$X_t \in \mathbb{R}^d$: time-varying covariates
$A_t \in \{0, 1\}$: time-varying binary treatment
$Y \in \mathbb{R}$: ultimate outcome of interest

History of $O_t$ at $t$: $\overline{O}_t = (O_1, \ldots, O_t)$
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$H_t = (\overline{X}_t, \overline{A}_{t-1})$: covariate and treatment history at $t$

**NPSEM assumption:** there are $\{f_{X,t}, f_{A,t}\}_{t=1}^T$ and $f_Y$ such that

$$X_t = f_{X,t}(A_{t-1}, H_{t-1}, U_{X,t}),$$
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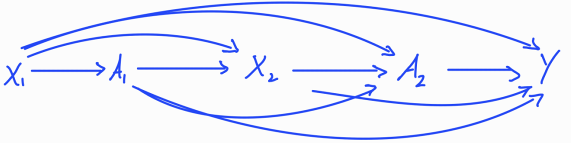


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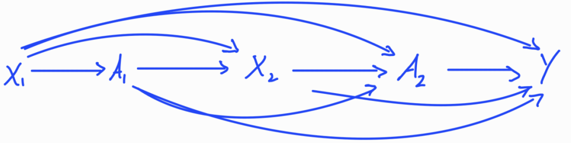


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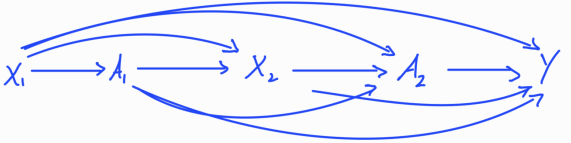


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# Causal assumptions

NPSEM embeds **consistency**

We will avoid **positivity** by trimming/flipping
(e.g. $\exists\, \delta > 0$ s.t. $\mathbb{P}\{\delta < \mathbb{P}(A_t = 1 \mid H_t) < 1 - \delta\} = 1$.)

**Sequential randomization:**

1. **Standard:** $U_{A,t} \perp\!\!\!\perp (\underline{U}_{X,t+1}, U_Y) \mid H_t$ for all $t \leq T$
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**Standard** SR: common causes of $A_t$ and future covariates and outcome measured. Typical in literature.

**Strong** SR: common causes $A_t$ and future covariates and outcome **and treatments** measured. Allows for ID when intervention depends on natural value of treatment.

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1. **Standard:** $U_{A,t} \perp\!\!\!\perp (\underline{U}_{X,t+1}, U_Y) \mid H_t$ for all $t \leq T$
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# Counterfactual variables under $\overline{D}_{t-1}$

$\overline{D}_{t-1}$ generates **counterfactual variables at time $t$**:

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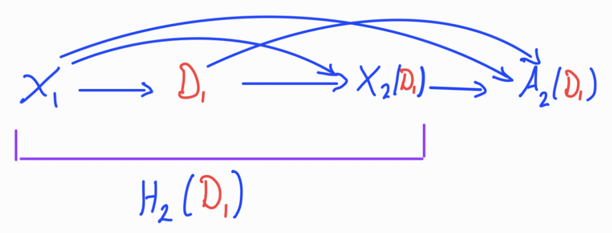

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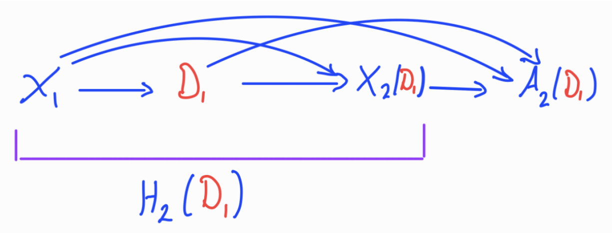

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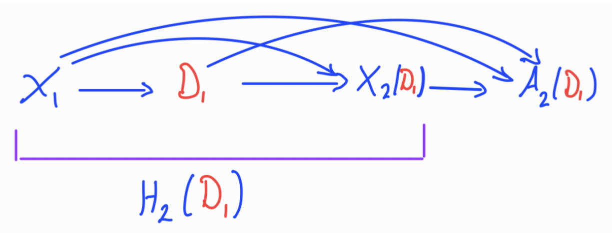
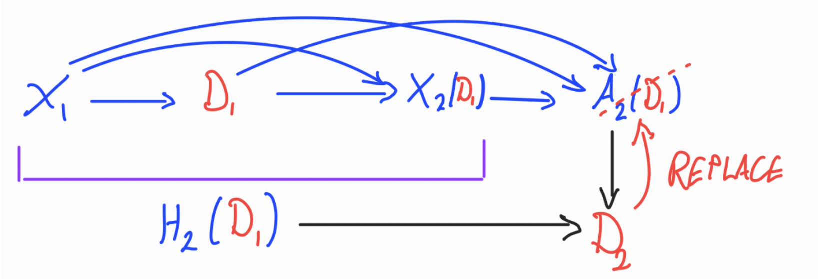


# Intervention $D_t$ and potential outcomes $\overline{D}_T$

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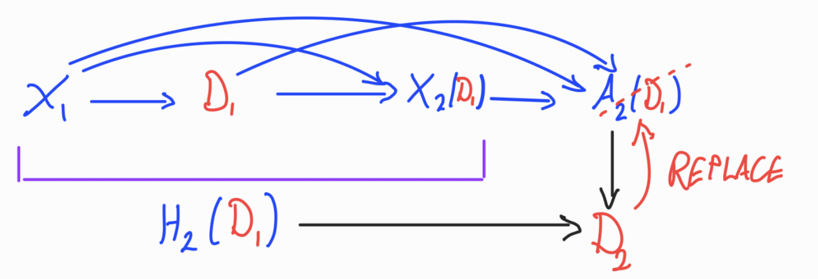


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# Longitudinal trimming with flip interventions

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**Flip intervention** at time $t$ targeting $a_t$ is

$$\boxed{D_t(a_t) = \begin{cases} A_t(\overline{D}_{t-1}), & \text{if } A_t(\overline{D}_{t-1}) = a_t, \\ I_t^c a_t + \left(1 - I_t^c\right) A_t(\overline{D}_{t-1}), & \text{otherwise,} \end{cases}}$$

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Let $I_t(a_t; h_t) = \mathbb{1}\{\mathbb{P}(A_t = a_t \mid h_t) > \varepsilon\}$. Suppose

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Not necessarily true that $\mathbb{E}\{Y(\overline{D}_T) - Y(\overline{D}'_T)\}$ isolates

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# Smooth trimming with S-flip interventions

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Everything we've done so far can be generalized to smooth trimming!

**Why:** flip effects inherit $\widehat{\pi}$ convergence rate

ML estimator $\implies$ slower-than-$\sqrt{n}$ convergence

Smooth trimmed effects: $\sqrt{n}$-convergence w/ ML estimators

**How:** replace $\mathbb{1}(\cdot)$ by $S(\cdot)$: $\mathbb{E}\Big[\{Y(1) - Y(0)\}S(X)\Big]$

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1. $\mathbb{1}(x > 0) \to$ $s(x; k) = 1 - \exp(-kx)$
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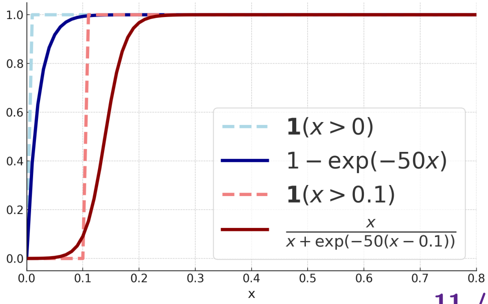

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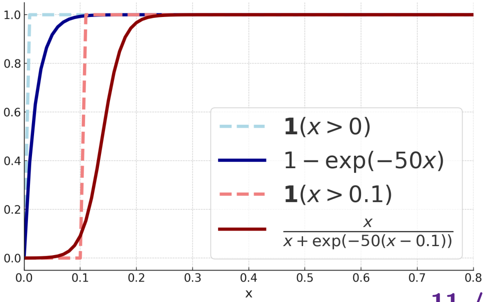

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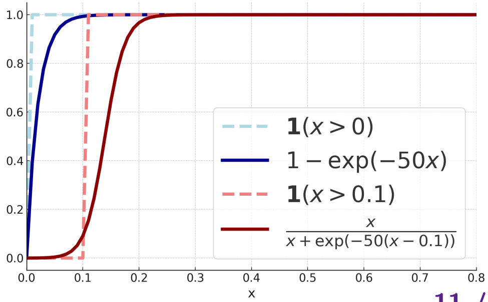

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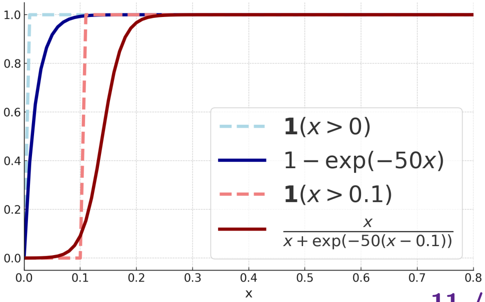

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$$D_t(a_t) = \begin{cases} A_t(\overline{D}_{t-1}), & \text{if } A_t(\overline{D}_{t-1}) = a_t, \\ \mathbb{1}(V_t > S_t^c)a_t + \mathbb{1}(V_t \leq S_t^c)A_t(\overline{D}_{t-1}), & \text{otherwise,} \end{cases}$$

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$s(x) = 1 - \exp(-50x)$ approximates $\mathbb{1}(x > 0)$ :
$s(0) = 0, s(0.01) = 0.39, s(0.1) = 0.99$

# Smooth-flip (S-flip) interventions

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# Theorem: S-flip effect identification

Let $S_t(a_t; h_t) = s\{\mathbb{P}(A_t = a_t \mid h_t), \varepsilon, k\}$. Suppose

- $\overline{D}_T = \{D_1(a_1), D_2(a_2), \ldots, D_T(a_T)\}$ are **S-flip interventions**,
- $s(0) = 0$, and
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Then,

$$\mathbb{E}\{Y(\overline{D}_T)\} = \sum_{\overline{b}_T \in \{0,1\}^T} \mathbb{E}\left\{\mathbb{E}(Y \mid \overline{A}_T = \overline{b}_T,\ \overline{X}_T) \prod_{t=1}^{T} Q_t(b_t \mid \overline{b}_{t-1}, \overline{X}_t)\right\},$$

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# Estimation

(in two slides)

# Estimation of S-flip effects

S-flip effects are pathwise differentiable $\implies$ **efficient influence function** (EIF)-based estimators

We derive the new EIF (plug-in plus weighted residuals)

Inspires two one-step estimators:

1. Multiply robust-style
2. Sequentially doubly robust-style (debias pseudo-outcome in multiply robust-style estimator)

We derive bias bounds, which imply weak convergence for S-flip estimator under nonparametric conditions on nuisance functions

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# Bias bounds

Two new results for multiply robust-style estimator:

1. Observe that bias is **minimum** of two errors
   Díaz et al. [2023] & Kennedy [2019]: unroll into future and past
   $\rightarrow$ Hence, $2(T+1)$ multiply robust-style bound
2. Tighten bias bound from IPSI-style result [Kennedy, 2019]

Sequentially DR-style result is **first-of-its-kind** where $Q_t$ depends on unknown propensity score

**Theorem, informal:** Let $\psi$ denote S-flip effect, $\pi_t$ prop. score at $t$, $\widetilde{m}_t$ denote seq. reg. at $t$ with estimated pseudo-outcome. Then,

$$\boxed{\left|\mathbb{E}\left(\widehat{\psi}_{sdr} - \psi\right)\right| \lesssim \sum_{t=1}^{T} \|\widehat{\pi}_t - \pi_t\| \Big( \|\widehat{m}_t - \widetilde{m}_t\| + \|\widehat{\pi}_t - \pi_t\| \Big).}$$

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# Thank you!

Recap:

- $T = 1$:
  trimming $\equiv$ flip interventions
  smooth trimming $\equiv$ S-flip ints
- $T > 1$: not so simple.
  Flip/S-flip ints avoid positivity asmp and cross-world / future-dependence
- Efficient estimation of S-flip effects: (1) multiply robust and (2) sequentially doubly robust

Ongoing work:

- Data analysis (administrative censoring and censoring by death)

hadera01@nyu.edu

*Prelim draft:*

alecmcclean.github.io/files/LSTTEs-short.pdf

Iván Díaz, Nicholas Williams, Katherine L Hoffman, and Edward J Schenck. Nonparametric causal effects based on longitudinal modified treatment policies. *Journal of the American Statistical Association*, 118(542):846–857, 2023.

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Maya L Petersen, Kristin E Porter, Susan Gruber, Yue Wang, and Mark J Van Der Laan. Diagnosing and responding to violations in the positivity assumption. *Statistical methods in medical research*, 21(1):31–54, 2012.

# Additional remarks

1. Robustness to positivity violations $\implies$ **S-flips are alternative to IPSIs that target a specific regime**
2. **Relax dependence on natural value of treatment:**

$$D_t(a_t) = \mathbb{1}\left[V_t \leq \mathbb{1}(a_t = 1)I_t^c + (1 - I_t^c)\mathbb{P}\{A_t(\overline{D}_{t-1}) = 1 \mid H_t(\overline{D}_{t-1})\}\right]$$

   - Can avoid practical issues — we may not observe natural value of treatment
   - Identification only requires standard sequential randomization
3. Flip interventions inspired by **maximally coupled policies** Levis et al. [2024]