Pseudocode

Algorithm 1 simMultiStageRAR

Input: $n1$, n, $c1$, num_stage

Stage 1: Identify subgroups

$X_1, T_1, Y_1 \leftarrow$ enroll data for stage 1

thres $\leftarrow$ IdentifyGroup($n1$, X_1, T_1, Y_1), which is the rules that define the subgroups

$S_1 \leftarrow$ GenS($thres$, X_1, m) ,map the data into the identified subgroups using the estimated threshold

$e_{1.hat} \leftarrow$ Estimated propensity scores

tau_1, $sd_{1.t}$, $sd_{1.c} \leftarrow$ Estimate subgroup ATEs and standard errors for Y in treatment and control

Store initial values: $tau_{old} \leftarrow tau_1$, $sd_{old.t} \leftarrow sd_{1.t}$, $sd_{old.c} \leftarrow sd_{1.c}$, $S_{old} \leftarrow S_1$, $n_{old} \leftarrow n1$, $T_{old} \leftarrow T_1$, $X_{old} \leftarrow X_1$, $Y_{old} \leftarrow Y_1$, $e_{1.hat.old} \leftarrow e_{1.hat}$

Stage 2 to (num_stage+1): confirm subgroups

for $i = 1$ **to** num_stage **do**

- $X_i \leftarrow$ enroll more data for the new experiment stage
- $S_i \leftarrow GenS(thres, X_i, m)$ before experiment, classify the sample into subgroups using the rules given by stage 1
- $S_{new}, n_{new} \leftarrow$ Combine the new data with old data
- $e_{opt} \leftarrow SubAlloc(tau_{old}, sd_{old.t}, sd_{old.c}, c1, S_{new}, n_{new}, m)$
- $e_{calibrated} \leftarrow$ adjust optimal treatment allocation for combined data
- $T_i \leftarrow$ Assign treatments based on $e_{calibrated}$
- $Y_i \leftarrow$ GenY(n, X_i, T_i)
- Combine the new data with the old one, and update S_{old}, X_{old}, Y_{old}, T_{old}
- tau_{old}, $sd_{old.t}$, $sd_{old.c} \leftarrow$ estimate subgroup ATE and standard errors for Y based on the combined data

end for

$tau_{opt} \leftarrow tau_{old}$ Calculate final tau

return tau_1, tau_{opt}, m, $thres$

Algorithm 2 IdentifyGroup: TSMCD Algorithm

1: **Input**: n, X,T, Y
2: Y is the outcome and (X,T) is the covariate
3: **for** $\ell = 1$ **to** 20 **do**

4: **Step 1: Splitting stage**
5: Set $m = \lfloor 0.1\ell\sqrt{n^*} \rfloor$ and $q_n = \left\lfloor \frac{n^*}{m} \right\rfloor - 1$, where n^* is the number of events;
6: Split the data sequence into $q_n + 1$ segments $\mathcal{I}_j, j = 1, \ldots, q_n + 1$;
7: Estimate $\hat{\theta} = \left(\left(\hat{\theta}_1 \right)^\top, \ldots, \left(\hat{\theta}_{q_n+1} \right)^\top \right)^\top$ by minizing a penalized loss function;
8: Compute the index sets $\hat{\mathcal{A}}^* \equiv \left\{ \hat{k}_1, \ldots, \hat{k}_{\hat{s}} \right\}$, where $\hat{k}_1 < \hat{k}_2 < \ldots < \hat{k}_{\hat{s}}$ and $\hat{s} = \sharp\hat{\mathcal{A}}^*$ that indicating which segment includes the threshold;

9: **Step 2: Refining stage**
10: **if** $\hat{s} = 0$ **then**
11: Go to step 13;
12: **else if** $\hat{s} > 0$ **then**
13: Estimate the threshold a_j in $\left(\tilde{Z}_{\left(n^* - \left(q_n - \hat{k}_j + 3\right) m\right)}, \tilde{Z}_{\left(n^* - \left(q_n - \hat{k}_j + 1\right) m\right)} \right]$
14: **end if**
15: Estimate the coefficient of the subgroup defined by the threshold, $\theta^* = \left((\beta_1^*)^\top, (\mathbf{d}_1^*)^\top, \ldots, (\mathbf{d}_\mathbf{s}^*)^\top \right)^\top$ by minimizing a penalized loss function;
16: Return the set of estimated thresholds $\hat{\mathcal{M}}_\ell = \{\hat{a}_{1,\ell}, \ldots, \hat{a}_{\hat{s}_\ell,\ell}\}$ from step 11 and the estimator of the coefficient $\hat{\theta}_\ell^*$ from step 13, and compute $BIC_{\hat{\mathcal{M}}_\ell}$

17: **end for**
18: Choose $\hat{\ell}$ that minimizes $BIC_{\hat{\mathcal{M}}_\ell}$ and obtain the final estimators $\hat{\mathcal{M}}_{\text{opt}} = \hat{\mathcal{M}}_{\hat{\ell}}$ and $\hat{\theta}^*_{\text{opt}} = \hat{\theta}^*_{\hat{\ell}}$.
19: obtain subgroup treatment effect τ based on the estimated coefficient $\hat{\theta}^*_{\hat{\ell}}$, and the threshold that define the subgroup, $thres \leftarrow \hat{\mathcal{M}}_{\text{opt}}$
20: **Return:** τ, $thres$