



lmt: An R Package for Non-Parametric Causal Effects Based on Modified Treatment Policies

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Abstract

The majority of causal inference methods consider treatment effects based on counterfactual outcomes where exposure is deterministically established. When exposure is continuous, deterministic treatment effects may be irrelevant and impossible to bring about. As a solution, modified treatment policies offer a non-parametric alternative to deterministic treatment effects that allow for the study of feasible interventions and offer a safeguard against positivity violations. The **lmt** package implements the estimators of [Diaz, Williams, Hoffman, and Schenck \(2020\)](#) for estimating causal effects based on non-parametric modified treatment policies in R. The provided methods can be applied to both point-treatment and longitudinal settings, and can account for time-varying exposure, covariates, and right censoring. Additionally, two of the provided estimators can incorporate flexible data-adaptive algorithms for estimation while maintaining valid statistical inference.

Keywords: causal inference, non-parametric, modified treatment policies, R.

1. Introduction

Most modern causal inference methods consider the effects of a exposure on a population mean outcome under interventions that set the treatment value deterministically. For example, the average treatment effect (ATE) considers the hypothetical difference in a population mean outcome if a dichotomous exposure was applied to all observations versus if it was applied to none. In the case of a categorical or continuous exposure, it is unlikely any policy could bring this about. Furthermore, the estimation of causal effects requires the so called positivity assumption which states that all observations have a greater than zero chance of experiencing the exposure levels ([Rosenbaum and Rubin 1983](#)). This assumption is often violated when evaluating the effects of deterministic interventions and is usually exacerbated with longitudinal data.

First introduced by Haneuse and Rotnitzky (2013), and building off work by Muñoz and van der Laan (2012), modified treatment policies (MTPs) are stochastic treatment regimes that can be formulated to avoid violations of the positivity assumption. Diaz *et al.* (2020) later extended MTPs to the longitudinal setting with time-varying treatment, covariates, and right-censoring of the outcome.

The package **lmt** implements four methods for estimating the effects of MTPs. Two of these estimators, a targeted minimum-loss based estimator (Laan and Rose 2011; Laan and Rubin 2006) and a sequentially doubly-robust estimator (Buckley and James 1979; Fan and Gijbels 1994; van der Laan and Dudoit 2003; Rotnitzky, Faraggi, and Schisterman 2006; Rubin and Laan 2006; Kennedy, Ma, McHugh, and Small 2017), are multiply-robust. In addition to MTPs, the package naturally allows for estimation of the ATE, causal risk ratio, and causal odds ratio and can thus be used for a variety of causal inference problems. In this article we describe how **lmt** can be used for estimating the causal effects of MTPs and both static and dynamic deterministic treatment effects. The package may be download from CRAN at cran.r-project.org/package=lmt.

2. Notation and modified treatment policies

2.1. Data structure

In this article, we will use the notation of Diaz *et al.* (2020) with slight modification. Let i be the index of an observation from a data set with n total units and t be the index of time for a total time of τ . The observed data for observation Z_i may be denoted as

$$Z_i = (W, L_1, A_1, L_2, A_2, \dots, L_\tau, A_\tau, Y_{\tau+1}) \quad (1)$$

where W denotes baseline covariates, L_t denotes time-varying covariates, A_t denotes a vector of exposure variables and Y denotes an outcome at the end of study follow-up. We observe n i.i.d. copies of Z with distribution P . We use $A_t = a_t$ to denote a realization of a random variable. If right-censoring exists, A_t can be adapted so that $A_t = (A_{1,t}, A_{2,t})$ where $A_{1,t}$ equals one if an observation is still in the study at time t and zero otherwise, and $A_{2,t}$ denotes the exposure at time t . We use an overbar to indicate the history of a variable up until time t . We then use $H_t = (\bar{L}_t, \bar{A}_{t-1})$ to denote the history of all variables up until just before A_t .

2.2. Modified treatment policies

We will use the potential outcomes framework to define the causal effect of interest using our established data structure. We consider a hypothetical policy where \bar{A} is set to a regime d defined as $A_t^d = d_t(A_t, H_t^d)$, where $H_t^d = (\bar{L}_t, \bar{A}_t^d - 1)$, for a set of user-given regimes $d_t : t \in \{1, \dots, \tau\}$. The defining characteristic that makes regime d_t a modified treatment policy is that it depends on the *natural value* of \bar{A}_t and \bar{L}_t .

Formally, consider a longitudinal study with loss-to-follow-up. Let $A_t = (A_{1,t}, A_{2,t})$ where $A_{1,t}$ equals one if an observation is still in the study at time t and zero otherwise, and $A_{2,t}$ denote a continuous exposure at time t that can be changed through some intervention. A

modified treatment policy that decreases A_t is then

$$d_t(a_t, h_t) = \begin{cases} (1, a_{2,t} - \delta_t) & \text{if } a_{2,t} > u_t(h_t) + \delta_t \\ (1, a_{2,t}) & \text{if } a_{2,t} \leq u_t(h_t) + \delta_t \end{cases} \quad (2)$$

where $0 < \delta_t < u_t(h_t)$ is a user-defined value and A_t is supported in the data. Notice that the hypothetical exposure after intervention, A_t^d depends on the actually observed exposure, A_t . This is in contrast to a deterministic intervention where A_t^d would be set to some arbitrary value with probability one. If right-censoring did not exist in the data, the MTP d would simplify to removing $A_{1,t}$ from the MTP definition. In analogue to [Diaz et al. \(2020\)](#), in this article we will focus on estimating the the causal effect of MTP d on outcome Y , using `lmtp`, through the causal parameter

$$\theta = E\{Y(A^d)\}, \quad (3)$$

where $Y(A^d)$ is the potential outcome in a world, contrary to fact, where \bar{A} was modified according to the MTP d . When Y is continuous, θ is the mean population value of Y under MTP d ; when Y is dichotomous, θ is the population proportion of event Y under MTP d . Similarly, when Y is a survival outcome, θ is defined as the cumulative incidence of Y under MTP d .

2.3. Identification

Causal interpretation of θ requires identifying an expression of θ as a function of the data generating distribution P using only the observed data Z . A full review of these identification assumptions is outside the scope of this article. Briefly, the following standard assumptions must hold

Assumption 1 (Consistency) $\bar{A} = \bar{a} \implies Y = Y(\bar{a})$ for all $\bar{a} \in \text{supp } \bar{A}$

Assumption 2 (Exchangeability) If $(a_t, h_t) \in \text{supp}\{A_t, H_t\}$ then $(d(a_t, h_t), h_t) \in \text{supp}\{A_t, H_t\}$ for $t \in \{1, \dots, \tau\}$

Assumption 3 (Positivity) $A_t \perp\!\!\!\perp Y(\bar{a})|H_t$ for all $\bar{a} \in \text{supp } \bar{A}$ and $t \in \{1, \dots, \tau\}$

The consistency assumption states that the potential outcome for an observation under their observed exposure is the value of the outcome that we did actually observe. Assumption 2, the exchangeability assumption, is often also referred to as the no-unmeasured confounding assumption; it is satisfied if all common causes of the exposure and outcome are measured and adjusted for. Of particular importance to this article is the positivity assumption which states that the distribution of the exposure under the MTP is supported in the data. Concretely, in a study with a continuous exposure and loss-to-follow-up, the positivity assumption states that if an observation with covariate history h_t and exposure a_t who was not lost-to-follow-up at time t exists then there is also an observation with covariate history h_t who was not lost-to-follow-up at time t but whose exposure was observed as $d(a_t, h_t)$ that also exists.

The strength of MTPs is that they may be formulated to avoid violations of the positivity assumption, which is often an issue when working with continuous exposures.

3. Estimating modified treatment policy effects

3.1. Estimation methods

The **lmtp** package implements four estimation methods: a targeted minimum-loss based estimator (TMLE), a sequentially doubly-robust estimator (SDR), an estimator based on the parametric G-formula, and an inverse probability weighted (IPW) estimator. We will only describe the use of the TMLE, **lmtp_tmle**, and SDR, **lmtp_sdr**, estimators as their use is strongly suggested over the others.

Discuss the difference between TMLE and SDR estimators and when one may have an advantage over the other. All examples in this article will use both the TMLE and SDR estimators.

3.2. Required data structure

Data is passed to **lmtp** estimators through the **data** argument, and should be in wide format with one column per variable per time point under study (i.e., there should be one column for every variable in Z). These columns do not have to be in any specific order and the data set may contain variables that won't be used in estimation. The names of treatment variables, censoring variables, baseline covariates, and time-varying covariates are specified using the **trt**, **cens**, **baseline**, and **time_vary** arguments respectively. The **trt**, **cens**, and **baseline** arguments accept character vectors and the **trt** and **cens** arguments should be ordered according to the time-ordering of the data generating mechanism. The **time_vary** argument accepts an unnamed list ordered according to the time-ordering of the model with each index containing the name of the time-varying covariates for the given time. The outcome variable is specified through the **outcome** argument.

The provided estimators can work with dichotomous, continuous, or survival outcomes. In the case of a dichotomous or continuous outcome, only a single variable name should be passed to the **outcome** argument. For survival outcomes, a vector containing the names of the intermediate outcome and final outcome variables ordered according to time should be passed to the **outcome** argument. Dichotomous and survival outcomes should be coded using zero's and one's where one indicates the occurrence of an event and zero otherwise. The **outcome_type** argument should be set to "continuous" for continuous outcomes and "binomial" for dichotomous and survival outcomes. If missingness is present in the outcome variable, the **cens** argument must be provided. Censoring indicators should be coded using zero's and one's where one indicates an observation is observed at the next time and zero indicates loss-to-follow-up. Once an observation's censoring status is switched to zero it cannot change back to one. Missing data before an observation is lost-to-follow-up is not allowed.

The **k** argument controls a Markov assumption of the data. With **k = Inf**, the entire history H_t will be used for estimation at time t while **k = 0** will restrict the set of variables in H_t used for estimation to time-varying covariates at time $t - 1$. Baseline confounders are always included in estimation. The **create_node_list** function may be used to inspect how variables

will be used for estimation. It is specified with the same `trt`, `baseline`, `time_vary`, and `k` arguments as **lmtp** estimators and is used internally to create a “node list” that encodes which variables should be used at each time point of estimation. For example, consider a study with the observed data structure

$$Z = (W_1, W_2, L_{1,1}, L_{1,2}, A_1, L_{2,1}, L_{2,2}, A_2, Y_3) \quad (4)$$

We can translate this data structure to R with

```
R> baseline <- c("W_1", "W_2")
R> trt <- c("A_1", "A_2")
R> time_vary <- list(c("L_11", "L_12"),
R+                  c("L_21", "L_22"))
R> create_node_list(trt = trt, baseline = baseline,
R+                  time_vary = time_vary, tau = 2)

$trt
$trt[[1]]
[1] "W_1" "W_2" "L_11" "L_12" "A_1"

$trt[[2]]
[1] "W_1" "W_2" "L_11" "L_12" "L_21" "L_22" "A_1" "A_2"

$outcome
$outcome[[1]]
[1] "W_1" "W_2" "L_11" "L_12" "A_1"

$outcome[[2]]
[1] "W_1" "W_2" "L_11" "L_12" "A_1" "L_21" "L_22" "A_2"
```

A list of lists is returned with the names of the variables in H_t to be used for estimation of the outcome regression and the propensity at every time t . Notice that variables A_1 and A_2 are included for their own estimation. The **lmtp** package recasts the density ratio nuisance parameter estimation into a classification problem based on a $2n$ observations augmented data set where an indicator variable Λ is used as a pseudo outcome (Cheng and Chu 2004; Qin 1998). In the augmented data set, the data structure at time t is redefined as

$$(H_{\lambda,i,t}, A_{\lambda,i,t}, \Lambda_{\lambda,i} : \lambda = 0, 1; i = 1, \dots, n) \quad (5)$$

where $\Lambda_{\lambda,i} = \lambda_i$ indexes the duplicate values. For all duplicated observations $i \in \{1, \dots, 2n\}$, $H_{\lambda,i,t}$ is the same. While, for $i \in \{1, \dots, n\}$ duplicated observations $A_{0,i,t}$ are the observed exposure values and $A_{1,i,t}$ for $i \in \{n+1, \dots, 2n\}$ are the exposure values under the MTP d , A_t^d .

3.3. Coding modified treatment policies

Treatment policies are specified using the `shift` argument, which takes a user-defined function that returns a vector of exposure values according the policy of interest. Shift functions should take two arguments, the first for specifying a data set and the second for specifying the current exposure variable. For example, a possible MTP may increase exposure by 2 units if the natural exposure value was below 5 units and do nothing otherwise. A shift function for this MTP would look like

```
R> function(data, trt) {
R+   (data[[trt]] < 5)*(data[[trt]] + 2) + (data[[trt]] >= 5)*data[[trt]]
R+ }
```

This framework is flexible and allows for specifying complex treatment regimes that can also depend on time and covariates. In the case of a binary exposure, two shift functions are installed with the package: `static_binary_on` which sets $A_{i,t} = 1$, and `static_binary_off` which sets $A_{i,t} = 0$.

3.4. The estimation engine

An attractive property of multiply-robust estimators is that they can incorporate flexible machine-learning algorithms for the estimation of nuisance parameters while remaining \sqrt{n} -consistent. The super learner algorithm is an ensemble learner that incorporates a set of candidate models through a weighted convex-combination based on cross-validation (Laan, Polley, and Hubbard 2007). Asymptotically, this weighted combination of models, called the meta-learner, will outperform any single one of its components.

Access to the super learner is provided by the `sl3` package (Coyle, Hejazi, Malenica, and Sofrygin 2020). Analysts must create `sl3` learner stacks which are then included in `lmtmp_tmle` and `lmtmp_sdr` calls with the `lrmrs_trt` and `lrmrs_outcome` arguments. The outcome variable type should guide users on selecting the appropriate candidate learners for use with the `lrmrs_outcome` argument. Regardless of whether an exposure is continuous, dichotomous, or categorical, the exposure mechanism is estimated using classification, users should thus only include candidate learners capable of binary classification with the `lrmrs_trt` argument.

Candidate learners that rely on cross-validation for the tuning of hyper-parameters should support grouped data if used with `lrmrs_trt`. Because estimation of the treatment mechanism relies on the augmented $2n$ duplicated data set, duplicated observations must be put into the same fold during sample-splitting.

User's may install `sl3` from <https://github.com/tlverse/sl3>. Because `sl3` is not available for installation from a standard repository, it is not required to use `lmtmp`. Instead, the `lrmrs_trt` and `lrmrs_outcomes` arguments can be set equal to `NULL` and nuisance parameters will be estimated using a generalized linear model (GLM) with the `glm` function from the `stats` package.

3.5. Additional arguments

Cross-fitting is used with all methods (Zheng and van der Laan 2011; Chernozhukov, Chetverikov, Demirer, Duflo, Hansen, Newey, and Robins 2018), and the number of folds can be set with the `folds` argument; the minimum number of allowed folds is two. If data has a hierarchical structure, the `id` argument is used to indicate the name of a variable in the data set indicating

unique groups. These identifiers will be used for generation of cross-validation folds and will be accounted for in standard error calculations.

3.6. Contrasts

In addition to the MTP effect, researchers may be interested in a comparison of the MTP effect and the outcome under the observed exposures, or other treatment policies. This is the role of the `lmtptest` function. Users may specify any number of objects returned by calls to `lmtptest` or `lmtptest` to be compared to a single a reference value or a single reference MTP, specified using the `ref` argument. Depending on the outcome type, contrasts may be either additive (`type = "additive"`), an odds ratio (`type = "or"`), or the relative risk (`type = "rr"`)

3.7. Examples

Example 1: Longitudinal MTP with no loss-to-follow-up

We have simulated data on $n = 5000$ observations over a 5-month period. Each observation has a continuous exposure (`A_1`, `A_2`, `A_3`, `A_4`) and covariate (`L_1`, `L_2`, `L_3`, `L_4`) recorded at months one through four and a dichotomous outcome (`Y`) at month five. We assume no loss-to-follow-up and no Markov property. This data set is installed with the package and is stored in the object `sim_t4`.

For this example, we are interested in the effect of a longitudinal MTP where at each month an observation's exposure decreases by one only if their observed exposure wouldn't be less than one if modified. Our data structure has no baseline confounders and we will use only GLMs for estimation so the only objects we must specify are the treatment variables, the time-varying covariates, the outcome variable, and the MTP shift function.

```
R> trt <- c("A_1", "A_2", "A_3", "A_4")
R> time_vary <- list(c("L_1"), c("L_2"), c("L_3"), c("L_4"))
R> y <- "Y"
R> shift <- function(data, trt) {
R+   (data[[trt]] - 1) * (data[[trt]] - 1 >= 1) +
R+   data[[trt]] * (data[[trt]] - 1 < 1)
R+ }
R> lmtptest(sim_t4, trt, y, time_vary = time_vary, shift = shift)
```

```
LMTP Estimator: TMLE
  Trt. Policy: (shift)
```

```
Population intervention effect
  Estimate: 0.2646
  Std. error: 0.019
  95% CI: (0.2274, 0.3019)
```

```
R> lmtptest(sim_t4, trt, y, time_vary = time_vary, shift = shift)
```

```
LMTP Estimator: SDR
  Trt. Policy: (shift)
```

```
Population intervention effect
  Estimate: 0.2608
  Std. error: 0.021
  95% CI: (0.2196, 0.3019)
```

Example 2: Longitudinal MTP, right-censoring, and the super learner

For this example, we have a simulated dataset of $n = 1000$ observations. Data was simulated for three time points with a continuous time-varying exposure at times $t \in \{1, 2\}$ (A1, A2), a dichotomous time-varying covariate at times $t \in \{1, 2\}$ (L1, L2), and a dichotomous outcome (Y) at time $t = 3$. Loss-to-follow-up is present after time $t = 1$ so the data set contains censoring indicators (C1, C2). This data is installed with the package and is stored in the object `sim_cens`.

Suppose we are interested in the additive effect of an MTP where exposure is increased by 0.5 at every time point for all observations. Instead of using a linear model, we will estimate the outcome regression and treatment mechanism using a super learner composed of a GLM, a random forest (Wright and Ziegler 2017), and multivariate adaptive regression splines (Milborrow 2019).

```
R> trt <- c("A1", "A2")
R> cen <- c("C1", "C2")
R> time_vary <- list(c("L1"), c("L2"))
R> y <- "Y"
R> mtp <- function(data, trt) {
R+   data[[trt]] + 0.5
R+ }
R> lnrns <- make_learner_stack(Lnrn_glm,
R+                           Lnrn_ranger,
R+                           Lnrn_earth)
R> tml <- lmtp_tmle(sim_cens, trt, y, time_vary = time_vary,
R+                  cens = cen, shift = mtp, learners_trt = lnrns,
R+                  learners_outcome = lnrns, folds = 3)
R> print(tml)
```

```
LMTP Estimator: TMLE
  Trt. Policy: (mtp)
```

```
Population intervention effect
  Estimate: 0.9011
  Std. error: 0.0094
  95% CI: (0.8826, 0.9196)
```

```
R> sdr <- lmtp_sdr(sim_cens, trt, y, time_vary = time_vary,
R+                  cens = cen, shift = mtp, learners_trt = lnrns,
```



```
R>               learners_outcome = lnrns, folds = 3)
R> print(sdr)
```

```
LMTTP Estimator: SDR
  Trt. Policy: (mtp)
```

```
Population intervention effect
  Estimate: 0.8995
  Std. error: 0.0095
  95% CI: (0.881, 0.918)
```

If loss-to-follow-up exists, we can estimate the population mean outcome under the observed exposures by specifying `shift = NULL`. This estimate can then be used as the reference value for calculating the additive effect of the MTP compared to the observed exposures.

```
R> tml_obs <- lmtpp_tmle(sim_cens, trt, y, time_vary = time_vary,
R+               cens = cen, shift = NULL, learners_trt = lnrns,
R+               learners_outcome = lnrns, folds = 3)
R> lmtpp_contrast(tml, ref = tml_obs)
```

```
LMTTP Contrast: additive
Null hypothesis: theta == 0
```

	theta	shift	ref	std.error	conf.low	conf.high	p.value
1	0.104	0.901	0.797	0.00607	0.0918	0.116	<0.001

```
R> sdr_obs <- lmtpp_sdr(sim_cens, trt, y, time_vary = time_vary,
R+               cens = cen, shift = NULL, learners_trt = lnrns,
R+               learners_outcome = lnrns, folds = 3)
R> lmtpp_contrast(sdr, ref = sdr_obs)
```

```
LMTTP Contrast: additive
Null hypothesis: theta == 0
```

	theta	shift	ref	std.error	conf.low	conf.high	p.value
1	0.0998	0.899	0.8	0.00612	0.0878	0.112	<0.001

Example 3: Survival analysis and deterministic effects

The **lmtpp** package may also be used to estimate deterministic causal effects, such as the causal relative risk. Suppose we have data on $n = 2000$ observations with a time-invariant binary exposure followed for a period of seven days. We wish to estimate the causal relative risk of experiencing an event by day seven. This data is installed with the package and is stored in the object `sim_point_surv`.

```

R> trt <- "trt"
R> baseline <- c("W1", "W2")
R> cens <- paste0("C.", 0:5)
R> y <- paste0("Y.", 1:6)
R> tml1 <- lmtm_tml(sim_point_surv, trt, y, baseline, cens = cens,
R+               learners_trt = lnrns, learners_outcome = lnrns,
R+               shift = static_binary_on, folds = 3)
R> tml0 <- lmtm_tml(sim_point_surv, trt, y, baseline, cens = cens,
R+               learners_trt = lnrns, learners_outcome = lnrns,
R+               shift = static_binary_off, folds = 3)
R> lmtm_contrast(tml1, ref = tml0, type = "rr")

```

LMT Contrast: relative risk
Null hypothesis: $\theta == 1$

	theta	shift	ref	std.error	conf.low	conf.high	p.value
1	1.22	0.812	0.665	0.0341	1.14	1.31	<0.001

```

R> sdr1 <- lmtm_sdr(sim_point_surv, trt, y, baseline, cens = cens,
R+               learners_trt = lnrns, learners_outcome = lnrns,
R+               shift = static_binary_on, folds = 3)
R> sdr0 <- lmtm_sdr(sim_point_surv, trt, y, baseline, cens = cens,
R+               learners_trt = lnrns, learners_outcome = lnrns,
R+               shift = static_binary_off, folds = 3)
R> lmtm_contrast(sdr1, ref = sdr0, type = "rr")

```

LMT Contrast: relative risk
Null hypothesis: $\theta == 1$

	theta	shift	ref	std.error	conf.low	conf.high	p.value
1	1.21	0.809	0.667	0.0338	1.14	1.3	<0.001

3.8. Extra features

Computation time can rapidly increase with many time points and when using the super learner. As a solution, **lmt** can utilize parallel processing provided by the **future** package (Bengtsson 2020a). In addition, **lmt** is compatible with the **progressr** package (Bengtsson 2020b) for producing progress bars by wrapping estimator calls in **with_progress**. For users familiar with the **broom** package (Robinson and Hayes 2020), **lmt** contains a **tidy** method.

4. Reference Manual

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