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tmleLite RELEASE 1.0-2

Fixed a bug in calculating counterfactual outcomes when there is missingness in the data.

The new build is under R.10.2.1, and help files are currently not working in the Windows environment. Help for the tmle function is included in this document, until the problem is fixed tmle {tmleLite}

Targeted Maximum Likelihood Estimation of Additive Treatment Effect (Lite)

Description

Carries out a simplified version of targeted maximum likelihood estimation of marginal additive treatment effect of a binary point treatment on an outcome. This parameter is defined as $E(E(Y|A=1,W) - E(Y|A=0,W))$, where `Y` is a continuous or binary outcome variable, `A` is a binary treatment variable, ($A=1$ for treatment, $A=0$ for control), and `W` is a matrix or dataframe of baseline covariates. The `tmle` function is minimally called with arguments `(Y,A,W)`. Missingness in the outcome is accounted for in the estimation procedure, if optional missingness indicator `Delta` is supplied.

Usage

```
tmle(Y, A, W, Delta = rep(1, length(Y)), id = 1:length(Y),
Q = NULL, g_A = NULL, g_M = NULL, wts = rep(1, length(Y)),
DSAargs = NULL, family = "gaussian", epsilon = NULL)
```

Arguments

`...`	
`Y`	continuous or binary outcome variable
`A`	binary treatment indicator, `1` - treatment, `0` - control
`W`	vector, matrix, or dataframe containing baseline covariates
`Delta`	indicator of missing outcome or treatment assignment. `1` - observed, `0` - missing
`id`	id identifying repeated measures
`Q`	$E(Y \mid A,W)$, the `Q` portion of the likelihood, specified in one of three ways: `NULL` specifies `DSA` estimation of $E(Y \mid A=a, W)$, with `A` forced into the model (default). matrix of values, one row per observation, three columns: $E(Y \mid A=a,W)$, $E(Y \mid A=1,W)$, $E(Y \mid A=0,W)$. formula for estimation of $E(Y \mid A, W)$, suitable for call to `glm`
`g_A`	binary treatment mechanism, specified in one of three ways: `NULL` defaults to `DSA` estimation of $P(A=1 \mid W)$ vector of values $P(A=1 \mid W)$, one entry per observation formula for estimation of $P(A=1,W)$, suitable for call to `glm`
`g_M`	missingness mechanism, specified in one of three ways: `NULL` defaults to `DSA` estimation of $P(Delta=1 \mid W)$ vector of values $P(Delta=1 \mid W)$, one entry per observation formula for estimation of $P(Delta=1,W)$, suitable for call to `glm`
`wts`	optional weights on observations. Defaults to unweighted
`DSAargs`	optional settings for `DSA` estimation. See `DSA` help files for further information. Default settings are: `maxsumofpow = 2, maxorderint = 2, maxsize=15, vfold = 5, nsplits=1, Dmove=FALSE, Smove=FALSE.`
`family`	family specification for working regression models, generally ‘gaussian’ for continuous outcomes (default), ‘binomial’ for binary outcomes.
`epsilon`	advanced option. Ordinarily this argument should not be specified, but can optionally be set to 0 to circumvent the targeting step

Value

`psi`	additive treatment effect estimate
`var`	variance of estimate, based on the influence curve
`pvalue`	two-sided p-value
`CI`	95% confidence interval
`epsilon`	MLE for coefficient used in targeting step
`Q`	initial estimate of `Q` portion of the likelihood. `Q$coefficients` are the coefficients for the model for `Q` selected by `DSA` or specified by the user. `Q$Q` is an `nx3` matrix, where `n` is the number of observations. Columns contain targeted predicted values for `Q(A,W),Q(1,W),Q(0,W)`, respectively. `Q$type` is method for estimating `Q`, `NULL`- user supplied, ‘DSA’, or ‘glm’
`g_A`	treatment mechanism estimate. A list with two items: `g_A$coefficients` the coefficients for the model for `g_A` selected by `DSA` or specified by the user. `g_A$g1W` contains values of $P(A=1 \mid W)$ for each observation
`g_M`	missingness mechanism estimate. A list with two items: `g_M$coefficients` the coefficients for the model for `g_M` selected by `DSA` or specified by the user. `g_M$g1W` contains values of $P(Delta=1 \mid A,W)$ for each observation

`Qcounterfactual`	targeted estimate of counterfactual outcomes `Q(1,W),Q(0,W)`

Author(s)

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References

1. Mark J. van der Laan and Daniel Rubin (2006), "Targeted Maximum Likelihood Learning". *The International Journal of Biostatistics*, 2(1). http://www.bepress.com/ijb/vol2/iss1/11/

2. Susan Gruber and Mark J. van der Laan (2009), "Targeted Maximum Likelihood Estimation: A Gentle Introduction". *U.C. Berkeley Division of Biostatistics Working Paper Series*. Working Paper 252. http://www.bepress.com/ucbbiostat/paper252

3. Mark J. van der Laan, Sherri Rose, Susan Gruber editors, (2009) "Readings in Targeted Maximum Likelihood Estimation" . *U.C. Berkeley Division of Biostatistics Working Paper Series*. Working Paper xxx. http://www.bepress.com/ucbbiostat

4. Sandra E. Sinisi and Mark J. van der Laan, (2004). "Loss-Based Cross-Validated Deletion/Substitution/Addition Algorithms in Estimation". *U.C. Berkeley Division of Biostatistics Working Paper Series*. Working Paper 143. http://www.bepress.com/ucbbiostat/paper143

See Also

`summary.tmle`, `estimate_Q`, `estimate_g`, `DSA`

Examples

```
library(tmleLite)

# generate data
  n <- 500
  W <- matrix(rnorm(n*3), ncol=3)
  A <- rbinom(n,1, 1/(1+exp(-(.1*W[,1] - .1*W[,2] + .5*W[,3]))))
  Y <- A + 2*W[,1] + W[,3] + W[,2]^2 + rnorm(n)
  colnames(W) <- paste("W",1:3, sep="")

# Example 1. Simplest function invocation
# DSA called to estimate Q, g_A.
# Because Delta is not supplied, all outcomes are known to be measured.
#
  result1 <- tmle(Y,A,W)
  summary(result1)

# Example 2: Binary outcome
# DSA called to estimate Q
# known treatment mechanism, g_A, is user supplied
#
  A.ex2 <- rbinom(n,1,.5)
  Y.ex2 <- A.ex2 + 2*W[,1] + W[,3] + W[,2]^2 + rnorm(n)
  result2 <- tmle(Y=Y.ex2,A=A.ex2,W, g_A =rep(.5, length(Y)))
  summary(result2)

# Example 3:
# User-supplied (misspecified) model for Q,
# DSA called to estimate g_A, g_M
# approx. 20% missing, MAR

  Delta <- rbinom(n, 1, 1/(1+exp(-(1.7-1*W[,1]))))
```

```
  result3 <- tmle(Y,A,W, Delta=Delta, Q=Y~A+W1+W2+W3)
  summary(result3)
```

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