

Package ‘ccmm’

October 12, 2022

Type Package

Title Compositional Mediation Model

Version 1.0

Date 2017-08-27

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Description Estimate the direct and indirect (mediation) effects of treatment on the outcome when intermediate variables (mediators) are compositional and high-dimensional. Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies. (AOAS: In revision).

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Imports MASS

NeedsCompilation no

Repository CRAN

Date/Publication 2017-08-28 18:17:55 UTC

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Description

Estimate the direct and indirect (mediation) effects of treatment on the outcome when intermediate variables (mediators) are compositional and high-dimensional.

Author(s)

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References

Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies. (AOAS: In revision)

Examples

```
## Not run:
# Load test data
data(ccmm_test_data);
head(ccmm_test_data);
outcome <- ccmm_test_data[,1];
treatment <- ccmm_test_data[,2];
mediators <- as.matrix(ccmm_test_data[,3:22]);
covariates <- as.matrix(ccmm_test_data[,23:24]);

# Run CCMM
rslt.ccmm <- ccmm(outcome, mediators, treatment, covariates);

# Sensitivity analysis
rslt.sa <- ccmm.sa(outcome, mediators, treatment, covariates);
plot(rslt.sa, type="l", xlab=expression(rho), ylab="TIDE")
abline(h=rslt.ccmm$TIDE, lty=2)
abline(h=0, lty=3)
cisa <- tide.ci.zero.rho(outcome, mediators, treatment, covariates)
csqs <- quantile(cisa, c(0.025, 0.975))
segments(0, csqs[1], 0, csqs[2])

## End(Not run)
```

ccmm*Causal Compositional Mediation Model*

Description

Estimate the direct and indirect (mediation) effects of treatment on the outcome when intermediate variables (mediators) are compositional and high-dimensional.

Usage

```
ccmm(y, M, tr, x = NULL, w = NULL, method.est.cov = "bootstrap", n.boot = 2000,
sig.level = 0.05, tol = 1e-06, max.iter = 5000)
```

Arguments

y	Vector of continuous outcomes
M	Matrix of compositional data
tr	Vector of continuous or binary treatments
x	Matrix of covariates
w	Vector of weights on samples
method.est.cov	One of two options ("bootstrap", "normal") to estimate the variance of indirect effects
n.boot	Number of bootstrap samples
sig.level	Significance level to estimate bootstrap confidence intervals for direct and indirect effects of treatment
tol	Error tolerance
max.iter	Maximum number of iteration in a debias procedure

Value

If method.est.cov is "bootstrap",

DE	Direct effect of treatment on an outcome
DE.CI	Bootstrap confidence interval for the direct effect
TIDE	Total indirect effect of treatment on an outcome
TIDE.CI	Bootstrap confidence interval for the indirect effect
IDEs	Component-wise indirect effects of treatment on an outcome
IDE.CIs	Bootstrap confidence intervals for the component-wise indirect effects

If method.est.cov is "normal",

DE	Direct effect of treatment on an outcome
Var.DE	Variance of the direct effect

TIDE	Total indirect effect of treatment on an outcome
Var.TIDE	Variance of the indirect effect
IDEs	Component-wise indirect effects of treatment on an outcome
Var.IDEs	Variances of the component-wise indirect effects

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References

Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies (AOAS: In revision)

Examples

```
# Load test data
data(ccmm_test_data);
outcome <- ccmm_test_data[,1];
treatment <- ccmm_test_data[,2];
mediators <- as.matrix(ccmm_test_data[,3:22]);
covariates <- as.matrix(ccmm_test_data[,23:24]);

# Run CCMM
rslt.ccmm <- ccmm(outcome, mediators, treatment, covariates);
```

ccmm.sa

Sensitivity analysis

Description

Estimated total indirect effects (TIDE) given correlation coefficients (rho)

Usage

```
ccmm.sa(y, M, tr, x = NULL, w = NULL, stp = 0.01)
```

Arguments

y	Vector of continuous outcomes
M	Matrix of compositional data
tr	Vector of continuous or binary treatments
x	Matrix of covariates
w	Vector of weights on samples
stp	Increment of the correlation coefficient

Value

Matrix of rho and TIDE

Author(s)

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References

Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies (AOAS: In revision)

Examples

```
# Load test data
data(ccmm_test_data);
outcome <- ccmm_test_data[,1];
treatment <- ccmm_test_data[,2];
mediators <- as.matrix(ccmm_test_data[,3:22]);
covariates <- as.matrix(ccmm_test_data[,23:24]);

rslt.sa <- ccmm.sa(outcome, mediators, treatment, covariates);
```

ccmm.sensitivity *Sensitivity analysis*

Description

Estimate the total indirect effect (TIDE) given a correlation coefficient

Usage

```
ccmm.sensitivity(rh, y, M, tr, x = NULL, w = NULL)
```

Arguments

rh	Correlation coefficient
y	Vector of continuous outcomes
M	Matrix of compositional data
tr	Vector of continuous or binary treatments
x	Matrix of covariates
w	Vector of weights on samples

Value

Estimated TIDE given a correlation coefficient

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References

Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies (AOAS: In revision)

Examples

```
# Load test data
data(ccmm_test_data);
outcome <- ccmm_test_data[,1];
treatment <- ccmm_test_data[,2];
mediators <- as.matrix(ccmm_test_data[,3:22]);
covariates <- as.matrix(ccmm_test_data[,23:24]);

ccmm.sensitivity(rh=0, outcome, mediators, treatment, covariates);
```

ccmm_test_data *Test Data*

Description

Contains artificial 200 samples with a continuous outcome variable y, a continuous treatment tr, 20 compositional mediators M and 2 covariates X. The true direct and indirect effects of treatment on the outcome both are 1.00. The true component-wise indirect effects (M1-M20) are 0.693, -0.425, 0.135, -0.057, -0.268, 0.970, -0.843, 0.805, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000, 0.000.

Usage

```
data(ccmm_test_data)
```

tide.ci.zero.rho *Bootstrap samples of TIDE with zero correlation*

Description

Generate bootstrap samples of the total indirect effect (TIDE) when the correlation coefficient is zero

Usage

```
tide.ci.zero.rho(y, M, tr, x = NULL, w = NULL, n.boot=2000)
```

Arguments

y	Vector of continuous outcomes
M	Matrix of compositional data
tr	Vector of continuous or binary treatments
x	Matrix of covariates
w	Vector of weights on samples
n.boot	Number of bootstrap samples

Value

bootstrap samples of TIDE

Author(s)

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References

Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies (AOAS: In revision)

Examples

```
# Load test data
data(ccmm_test_data);
outcome <- ccmm_test_data[,1];
treatment <- ccmm_test_data[,2];
mediators <- as.matrix(ccmm_test_data[,3:22]);
covariates <- as.matrix(ccmm_test_data[,23:24]);

cisa <- tide.ci.zero.rho(outcome, mediators, treatment, covariates, n.boot=200)
```

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