Package ‘bpbounds’

January 21, 2020

Title  Nonparametric Bounds for the Average Causal Effect Due to Balke and Pearl and Extensions

Version  0.1.4

Description  Implementation of the nonparametric bounds for the average causal effect under an instrumental variable model by Balke and Pearl (Bounds on Treatment Effects from Studies with Imperfect Compliance, JASA, 1997, 92, 439, 1171-1176). The package can calculate bounds for a binary outcome, a binary treatment/phenotype, and an instrument with either 2 or 3 categories. The package implements bounds for situations where these 3 variables are measured in the same dataset (trivariate data) or where the outcome and instrument are measured in one study and the treatment/phenotype and instrument are measured in another study (bivariate data).

Depends  R (>= 3.5.0)

Imports  methods

License  GPL-3

Encoding  UTF-8

LazyData  true

Suggests  dplyr, testthat, knitr, rmarkdown, tidyr, shiny

VignetteBuilder  knitr

RoxygenNote  7.0.2

URL  https://github.com/remlapmot/bpbounds

BugReports  https://github.com/remlapmot/bpbounds/issues

NeedsCompilation  no

Author  Tom Palmer [aut, cre] (https://orcid.org/0000-0003-4655-4511), Roland Ramsahai [aut] (https://orcid.org/0000-0002-7349-1977), Vanessa Didelez [aut] (https://orcid.org/0000-0001-8587-7706), Nuala Sheehan [aut] (https://orcid.org/0000-0001-9094-2605)

Maintainer  Tom Palmer <remlapmot@hotmail.com>

Repository  CRAN

Date/Publication  2020-01-21 11:10:03 UTC
Description

This package implements the nonparametric bounds for the average causal effect defined by Balke and Pearl, Bounds on Treatment Effects from Studies with Imperfect Compliance, JASA, 1997; and some extensions.

Details

The functions implement bounds for the situation where each of the outcome, treatment/phenotype, and instrumental variable are binary; and additionally for when the instrument has 3 categories (e.g. a single genotype under an additive model in a Mendelian randomization study).

The package implements bounds for when the three variables are measured in the same study (trivariate data) and when the outcome and instrument are measured in one study and the treatment/phenotype and instrument in another sample (bivariate/two sample data).

Usage

bpbounds(p, t = NULL, fmt = "trivariate")
Arguments

- **p**: Object of class "table" containing either cell counts or conditional probabilities. For trivariate data these are for the phenotype/treatment-outcome association given Z, i.e. \( P(X, Y | Z) \).
  
  Cell counts could be generated from `xtabs(~ x + y + z, data = data)` and then conditional probabilities obtained by calling `prop.table(..., margins = 3)` on your object from `xtabs()`.

  If you only know the conditional probabilities you can enter these, e.g. for the Balke and Pearl Vitamin A example:

  ```r
  cp = c(.0064, 0, .9936, 0, .0028, .001, .1972, .799)
  tabp = as.table(array(cp,
                         dim = c(2, 2, 2),
                         dimnames = list(x = c(0, 1),
                                         y = c(0, 1),
                                         z = c(0, 1))
                        )
  )
  ```

  And then call `bpbounds()` using this object. For bivariate data this object contains cell conditional probabilities for the outcome-instrument (Y|Z) association.

- **t**: Specified for bivariate data. Object with treatment/phenotype-instrument cell counts or conditional probabilities, i.e. \( (X|Z) \).

- **fmt**: A character string which should be either "bivariate" (i.e. \( X, Z \) in one dataset and \( Y, Z \) in another dataset) or "trivariate" (\( X, Y, Z \) in the same dataset).

Value

List with the following elements:

- **fmt**: whether the data is bivariate or trivariate
- **nzcats**: 2 or 3, the no. instrument categories
- **inequality**: Logical, indicating whether the IV inequality is satisfied
- **bplb**: Lower bound of ACE
- **bpub**: Upper bound of ACE
- **bplower**: Vector of lower bound probabilities
- **bpupper**: Vector of upper bound probabilities
- **p11low**: Lower bound of \( P(Y=1|do(X=1)) \)
- **p11upp**: Upper bound of \( P(Y=1|do(X=1)) \)
- **p10low**: Lower bound of \( P(Y=1|do(X=0)) \)
- **p10upp**: Upper bound of \( P(Y=1|do(X=0)) \)
- **p11lower**: Vector of probabilities for lower bound of \( P(Y=1|do(X=1)) \)
p11upper Vector of probabilities for upper bound of P(Y=1|do(X=1))
p10lower Vector of probabilities for lower bound of P(Y=1|do(X=0))
p10upper Vector of probabilities for upper bound of P(Y=1|do(X=0))
crrlb Lower bound of CRR
crrub Upper bound of CRR
monoinequality Logical, indicating whether the monotonicity inequality is satisfied
monobplb Lower bound of ACE assuming monotonicity
monobpub Upper bound of ACE assuming monotonicity
monobplower Vector of probabilities for lower bound of ACE assuming monotonicity
monobpupper Vector of probabilities for upper bound of ACE assuming monotonicity
monop11low Lower bound of P(Y=1|do(X=1)) assuming monotonicity
monop11upp Upper bound of P(Y=1|do(X=1)) assuming monotonicity
monop10low Lower bound of P(Y=1|do(X=0)) assuming monotonicity
monop10upp Upper bound of P(Y=1|do(X=0)) assuming monotonicity
monop11lower Vector for corresponding bound above
monop11upper Vector for corresponding bound above
monop10lower Vector for corresponding bound above
monop10upper Vector for corresponding bound above
monocrrlb Lower bound of CRR assuming monotonicity
monocrub Upper bound of CRR assuming monotonicity

Examples

# Vitamin A example, using cell counts

```r
tab1dat <- data.frame(
  z = c(0, 0, 1, 1, 1, 1, 0, 0),
  x = c(0, 0, 0, 0, 1, 1, 1, 1),
  y = c(0, 1, 0, 1, 0, 1, 0, 1),
  freq = c(74, 11514, 34, 2385, 12, 9663, 0, 0)
)
tab1inddat = uncount(tab1dat, freq)
xt = xtabs(~ x + y + z, data = tab1inddat)
p = prop.table(xt, margin = 3)
bpres = bpbounds(p)
sbpres = summary(bpres)
print(sbpres)
```
# Vitamin A example, using conditional probabilities

```r
require(bpbounds)
cp = c(.0064, 0, .9936, 0, .0028, .001, .1972, .799)
tabp = as.table(array(
cp,
dim = c(2, 2, 2),
dimnames = list(
x = c(0, 1),
y = c(0, 1),
z = c(0, 1)
)
))
bpbounds(tabp)
```

---

**runExample**

Run Shiny App demonstrating the package

**Description**

Run Shiny App demonstrating the package

**Usage**

```r
runExample(...)```

**Arguments**

`...` passed to `shiny::runApp()`, e.g. `port`, `launch.browser`

**Examples**

```r
if (interactive()) {
  bpbounds::runExample()
}
```
Index

bpbounds, 2
bpbounds-package, 2
runExample, 5