Package ‘scqe’

May 14, 2021

Title Stability Controlled Quasi-Experimentation
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Description Functions to implement the stability controlled quasi-experiment (SCQE) approach to study the effects of newly adopted treatments that were not assigned at random. This package contains tools to help users avoid making statistical assumptions that rely on infeasible assumptions. Methods developed in Hazlett (2019) <doi:10.1002/sim.8717>.
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The scqe package contains several functions for statistical analysis that factor in confounding variables and their impact on estimates (Hazlett, 2019).

Details

The main function in the package is `scqe`, which computes scqe estimates and confidence intervals for one or two cohorts with summary or full data given.

package dependencies

AER ggplot2

References


Delta optimization method for `scqe` 1 cohort, summary statistics

The print method provides the critical values presented in the summary method for scqe objects.
Usage

```r
delta.optim.scqe(
  Y_T0,
  untreated,
  Y_untreated,
  treated,
  Y_treated,
  obj,
  specified = NULL,
  alpha = 0.05,
  ...
)
```

Arguments

- `Y_T0`  
  Number of untreated individuals.

- `untreated`  
  Outcome for untreated individuals.

- `Y_untreated`  
  Number of treated individuals.

- `treated`  
  Outcome for treated individuals.

- `Y_treated`  
  scqe object.

- `specified`  
  Specified optional arguments.

- `alpha`  
  Numeric alpha for confidence intervals (default alpha = 0.05).

- `...`  
  Extra optional arguments.

Value

Optimal delta.

---

delta.optim.scqe.1cfull

*Delta optimization method for scqe 1 cohort, full data*

Description

The print method provides the critical values presented in the summary method for scqe objects.

Usage

```r
delta.optim.scqe.1cfull(
  treatment,
  outcome,
  delta,
  obj,
  ...)
```
Arguments

- **treatment**: Binary or continuous vector corresponding (usually) to 0,1 (no treatment or treatment) for each observation.
- **outcome**: Continuous vector representing the outcome for each observation.
- **delta**: Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).
- **obj**: scqe object.
- **specified**: Specified optional arguments.
- **alpha**: Numeric alpha for confidence intervals (default alpha=.05).
- **...**: Extra optional arguments.

Value

Optimal delta.

**delta.optim.scqe2**  
*Delta optimization method for scqe 2 cohort, full data*

Description

The print method provides the critical values presented in the summary method for scqe objects.

Usage

```r
delta.optim.scqe2(
  post, 
  treatment, 
  outcome, 
  delta, 
  obj, 
  alpha = 0.05, 
  specified = NULL, 
  ... 
)
```
delta_optim_SCQE_2C

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>post</td>
<td>Binary vector corresponding to T=0,1 for each observation.</td>
</tr>
<tr>
<td>treatment</td>
<td>Binary or continuous vector corresponding (usually) to 0,1.</td>
</tr>
<tr>
<td>outcome</td>
<td>Continuous vector representing the outcome for each observation.</td>
</tr>
<tr>
<td>delta</td>
<td>Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).</td>
</tr>
<tr>
<td>obj</td>
<td>scqe object.</td>
</tr>
<tr>
<td>alpha</td>
<td>Numeric alpha for confidence intervals (default alpha=.05).</td>
</tr>
<tr>
<td>specified</td>
<td>Specified optional arguments.</td>
</tr>
<tr>
<td>...</td>
<td>Extra optional arguments.</td>
</tr>
</tbody>
</table>

Value

Optimal delta.

delta_optim_SCQE_2C  Delta optimization method for scqe 2 cohort, summary statistics

Description

The print method provides the critical values presented in the summary method for scqe objects.

Usage

delta_optim_SCQE_2C(
  delta,
  untr_pre,
  untr_post,
  tr_post,
  tr_pre,
  Y_tr_post,
  Y_untr_post,
  Y_tr_pre,
  Y_untr_pre,
  obj,
  specified = NULL,
  alpha = 0.05,
  ...
)
Arguments

**delta**  
Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).

**untr_pre**  
Integer number of untreated patients in the first cohort if applicable (summary statistics input) (T=0).

**untr_post**  
Integer number of untreated patients in the second cohort if applicable (summary statistics input) (T=1).

**tr_post**  
Integer number of treated patients in the second cohort if applicable (summary statistics input) (T=1).

**tr_pre**  
Integer number of treated patients in the first cohort if applicable (summary statistics input) (T=0).

**Y_tr_post**  
Outcome for patients who received treatment at time T=1 (summary statistics input).

**Y_untr_post**  
Outcome for patients who did not receive treatment at time T=1 (summary statistics input).

**Y_tr_pre**  
Outcome for patients who did receive treatment at time T=0 (summary statistics input).

**Y_untr_pre**  
Outcome for patients who did not receive treatment at time T=0 (summary statistics input).

**obj**  
sqe object.

**specified**  
Specified optional arguments.

**alpha**  
Numeric alpha for confidence intervals (default alpha = 0.05).

**...**  
Extra optional arguments.

Value

Optimal delta.

---

**plot.scqe**  
Plot method for scqe

Description

The print method provides a plot of the estimates and confidence intervals for the scqe estimates for the range of values of delta provided by the user.

Usage

```r
## S3 method for class 'scqe'
plot(x, xlab, ylab, ...)
```
Arguments

- `x`: an object of class `scqe`
- `xlab`: Optional character label for x axis.
- `ylab`: Optional character label for y axis.
- `...`: Extra optional arguments

Value

Plot of estimates and confidence intervals.

Examples

```r
set.seed(1234)
post <- c(rep(0, 100), rep(1, 100))
tx <- c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y <- rbinom(n = 200, prob = 0.1 + 0.02 * post - 0.05 * tx, size = 1)

# Two cohorts, full data
scqe.2cohort.full <- scqe(post = post, treatment = tx, outcome = y,
                           delta = seq(from = -0.1, to = 0.1, by = 0.05))
plot(scqe.2cohort.full)
```

Description

Main `scqe` function. Computes `scqe` estimates and corresponding confidence intervals.

Usage

```r
scqe(
  post,
  treatment,
  outcome,
  min_outcome,
  max_outcome,
  delta,
  min_delta,
  max_delta,
  cohort,
  untr_pre,
  untr_post,
  tr_post,
  tr_pre,
  Y_tr_post,
)```
Arguments

post: Binary vector corresponding to T = 0, 1 for each observation.
treatment: Binary or continuous vector corresponding (usually) to [0,1] (no treatment or treatment) for each observation.
outcome: Continuous vector representing the outcome for each observation.
min_outcome: Minimum value for the outcome. Optional, not used if outcome is supplied.
max_outcome: Maximum value for the outcome. Optional, not used if outcome is supplied.
delta: Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).
min_delta: Minimum delta. Optional, not used if delta is supplied.
max_delta: Maximum delta. Optional, not used if delta is supplied.
cohort: Numeric, 1 or 2 depending on cohort membership.
untr_pre: Integer number of untreated patients in the first cohort if applicable (summary statistics input) (T=0).
untr_post: Integer number of untreated patients in the second cohort if applicable (summary statistics input) (T=1).
tr_post: Integer number of treated patients in the second cohort if applicable (summary statistics input) (T=1).
tr_pre: Integer number of treated patients in the first cohort if applicable (summary statistics input) (T=0).
Y_tr_post: Outcome for patients who received treatment at time T=1 (summary statistics input).
Y_untr_post: Outcome for patients who did not receive treatment at time T=1 (summary statistics input).
Y_tr_pre: Outcome for patients who did receive treatment at time T=0 (summary statistics input).
Y_untr_pre: Outcome for patients who did not receive treatment at time T=0 (summary statistics input).
untr: Integer number of untreated patients (summary statistics input).
tr: Integer number of treated patients (summary statistics input).
Y_tr: Outcome for treated patients (summary statistics input).
Y_untr  Outcome for untreated patients (summary statistics input).
alpha  Numeric alpha for confidence interval (default is alpha = 0.05).
...  Extra optional arguments.

Value

scqe object, results table

References


Examples

```r
set.seed(1234)
post = c(rep(0,100), rep(1,100))
tx = c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y = rbinom(n = 200, prob = 0.1 + .02 * post - 0.05 * tx, size = 1)

# Two cohorts, full data
scqe.2cohort.full = scqe(post = post, treatment = tx, outcome = y,
        delta = seq(from = -0.1, to = 0.1, by = 0.05))
plot(scqe.2cohort.full)
summary(scqe.2cohort.full)

# One cohort, full data
scqe.1cohort.full = scqe(treatment = tx, outcome = y,
        delta=seq(from = -0.1, to = 0.1, by = 0.05))
plot(scqe.1cohort.full)
summary(scqe.1cohort.full)

# Two cohorts, summary data only
scqe.2cohort.sum = scqe(untr_pre = 200,untr_post = 150, tr_post = 50,
        tr_pre = 0, Y_tr_post = 20, Y_untr_post = 1,
        Y_tr_pre = 0, Y_untr_pre = 5, min_delta = 0.1,
        max_delta = 1)
plot(scqe.2cohort.sum)
summary(scqe.2cohort.sum)

# One cohort, summary data only
scqe.1cohort.sum = scqe(untr = 100, tr = 200, Y_untr = 5, Y_tr = 50,
        min_delta= 0.1, max_delta = 1)
plot(scqe.1cohort.sum)
summary(scqe.1cohort.sum)
```
Description

This function returns the scqe estimates and confidence intervals for the 1 cohort case (ie there is not 'post' input) when the user inputs full data.

Usage

scqe.1cfull(treatment, outcome, delta, min_delta, max_delta, alpha = 0.05, ...)

Arguments

treatment Binary or continuous vector corresponding (usually) to 0,1 (no treatment or treatment) for each observation.
outcome Continuous vector representing the outcome for each observation.
delta Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).
min_delta Minimum delta. Optional, not used if delta is supplied.
max_delta Maximum delta. Optional, not used if delta is supplied.
alpha Numeric alpha for confidence interval (default is alpha = 0.05).
... Extra optional arguments.

Value

scqe object of class "scqe." Returns results table for the 1 cohort, full data case.

Examples

set.seed(1234)
post = c(rep(0,100), rep(1,100))
rx = c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y = rbinom(n = 200, prob = 0.1 + 0.02 * post - 0.05 * tx, size = 1)

# One cohort, full data
scqe.1cohort.full = scqe(treatment = tx, outcome = y,
                          delta=seq(from = -0.1, to = 0.1, by = 0.05))
plot(scqe.1cohort.full)
supply(scqe.1cohort.full)
scqe.1csumm

Stability controlled quasi-experiment (scqe) for 1 cohort case, summary statistics

Description
This function returns the scqe estimates and confidence intervals for the 1 cohort case when the user inputs only summary statistics.

Usage
scqe.1csumm(
  untr_1C,
  Y_untr_1C,
  tr_1C,
  Y_tr_1C,
  delta,
  min_delta,
  max_delta,
  alpha = 0.05,
  ...
)

Arguments
untr_1C          Number of untreated individuals.
Y_untr_1C        Outcome for untreated individuals.
tr_1C            Number of treated individuals.
Y_tr_1C          Outcome for treated individuals.
delta            Single value or vector of possible values for change in average non-treatment outcome between cohorts (if applicable).
min_delta        Minimum delta. Optional, not used if delta is supplied.
max_delta        Maximum delta. Optional, not used if delta is supplied.
alpha            Numeric alpha for confidence interval (default is alpha = 0.05).
...               Extra optional arguments.

Value
scqe object of class "scqe." Returns results table for the 1 cohort, summary statistics case.
Examples
    # One cohort, summary data only
    scqe.1cohort.sum = scqe(untr=100, tr=200, Y_untr=5, Y_tr=50,
                              min_delta=.1, max_delta=1)
    plot(scqe.1cohort.sum)
    summary(scqe.1cohort.sum)

    scqe.2cfull

    Stability controlled quasi-experiment (scqe) for 2 cohort case, full data

Description
    This function returns the scqe estimates and confidence intervals for the 2 cohort case when the user
    inputs full data.

Usage
    scqe.2cfull(
        post, treatment, outcome, delta, 
        min_delta, max_delta, alpha = 0.05, 
        ...
    )

Arguments
    post          Binary vector corresponding to T = 0,1 for each observation.
    treatment     Binary or continuous vector corresponding (usually) to 0,1 (no treatment or 
                   treatment) for each observation.
    outcome       Continuous vector representing the outcome for each observation.
    delta         Single value or vector of possible values for change in average non-treatment 
                   outcome between cohorts (if applicable).
    min_delta     Minimum delta. Optional, not used if delta is supplied.
    max_delta     Maximum delta. Optional, not used if delta is supplied.
    alpha         Numeric alpha for confidence interval (default is alpha = 0.05).
    ...           Extra optional arguments.

Value
    scqe object of class "scqe." Returns results table for the 2 cohort, full data case.
Examples

```r
set.seed(1234)
post = c(rep(0,100), rep(1,100))
tx = c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y = rbinom(n = 200, prob = 0.1 + 0.02 * post - 0.05 * tx, size = 1)

# Two cohorts, full data
scqe.2cohort.full = scqe(post = post, treatment = tx, outcome = y,
delta = seq(from = -0.1,to = 0.1, by = 0.05))
plot(scqe.2cohort.full)
summary(scqe.2cohort.full)
```

---

### scqe.2csumm

**Stability controlled quasi-experiment (scqe) for 1 cohort case, summary statistics**

**Description**

This function returns the scqe estimates and confidence intervals for the 2 cohort case when the user inputs only summary statistics.

**Usage**

```r
scqe.2csumm(
    untr_pre,  # Integer number of untreated patients in the first cohort if applicable (summary statistics input) (T=0).
    untr_post, # Integer number of untreated patients in the second cohort if applicable (summary statistics input) (T=1).
    ...)
```

**Arguments**

- `untr_pre`  
- `untr_post`
### Description

Dispatches to correct scqe function

### Usage

scqemethod(...)

### scqemethod

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tr_post</td>
<td>Integer number of treated patients in the second cohort if applicable (T=1).</td>
</tr>
<tr>
<td>tr_pre</td>
<td>Integer number of treated patients in the first cohort if applicable (T=0).</td>
</tr>
<tr>
<td>Y_tr_post</td>
<td>Outcome for patients who received treatment at time T=1 (summary statistics input).</td>
</tr>
<tr>
<td>Y_untr_post</td>
<td>Outcome for patients who did not receive treatment at time T=1 (summary statistics input).</td>
</tr>
<tr>
<td>Y_tr_pre</td>
<td>Outcome for patients who did receive treatment at time T=0 (summary statistics input).</td>
</tr>
<tr>
<td>Y_untr_pre</td>
<td>Outcome for patients who did not receive treatment at time T=0 (summary statistics input).</td>
</tr>
<tr>
<td>min_delta</td>
<td>Minimum delta. Optional, not used if delta is supplied.</td>
</tr>
<tr>
<td>max_delta</td>
<td>Maximum delta. Optional, not used if delta is supplied.</td>
</tr>
<tr>
<td>delta</td>
<td>Numeric scalar or numeric vector of possible values for change in average non-treatment outcome between cohorts (if applicable).</td>
</tr>
<tr>
<td>alpha</td>
<td>Numeric alpha for confidence interval (default is alpha=.05).</td>
</tr>
<tr>
<td>...</td>
<td>Extra optional arguments.</td>
</tr>
</tbody>
</table>

### Value

scqe object of class "scqe." Returns results table for the 2 cohort, summary statistics case.

### Examples

```r
# Two cohorts, summary data only
scqe_2cohort_sum <- scqe(untr_pre = 200, untr_post = 150, tr_post = 50, 
                         tr_pre=0, Y_tr_post = 20, Y_untr_post = 1, 
                         Y_tr_pre=0, Y_untr_pre = 5, min_delta = 0.1, 
                         max_delta = 1)

plot(scqe_2cohort_sum)
summary(scqe_2cohort_sum)
```
**summary.scqe**

**Arguments**

... Arguments from scqe

**Value**

scqe object of class "scqe", results table

---

**summary.scqe**  
*Summary method for scqe*

**Description**

The summary method provides several statements that summarize important values of delta requires to make different conclusions about the treatment's effect on patient outcome.

The `print` method provides the result table that includes the given delta values and their conclusions about the treatment's effect on patient outcome.

**Usage**

```r
## S3 method for class 'scqe'
summary(object, ...)

## S3 method for class 'scqe'
print(x, ...)
```

**Arguments**

- `object` an object of class `scqe`
- `...` Extra optional arguments
- `x` an object of class `scqe`

**Value**

Text interpretations of your results from scqe method results table.

Results table.

**Examples**

```r
set.seed(1234)
post <- c(rep(0, 100), rep(1, 100))
tx <- c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y <- rbinom(n = 200, prob = 0.1 + 0.02 * post - 0.05 * tx, size = 1)

# Two cohorts, full data
scqe.2cohort.full = scqe(post = post, treatment = tx, outcome = y,
                           delta=seq(from = -0.1, to = 0.1, by = 0.05))
summary(scqe.2cohort.full)
```
set.seed(1234)
post = c(rep(0,100), rep(1,100))
tx = c(rep(0, 100), rbinom(n = 100, prob = 0.27, size = 1))
y = rbinom(n= 200, prob = 0.1 + 0.02 * post - 0.05 * tx, size = 1)

# Two cohorts, full data
scqe.2cohort.full = scqe(post = post, treatment = tx, outcome = y, 
                          delta = seq(from = -0.1, to = 0.1, by = 0.05))
print(scqe.2cohort.full)
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