

# Package ‘scqe’

October 14, 2022

**Title** Stability Controlled Quasi-Experimentation

**Version** 1.0.0

**Date** 2021-4-19

**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>](https://doi.org/10.1002/sim.8717).

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**Imports** AER, ggplot2, stats, utils

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**NeedsCompilation** no

**Author** Kirsten Landsiedel [cre],  
Hazlett Chad [aut],  
Wulf Ami [ctr],  
Pinkelman Colleen [ctr],  
Christopher Gandrud [ctr]

**Maintainer** Kirsten Landsiedel <kirstenlandsiedel@gmail.com>

**Repository** CRAN

**Date/Publication** 2021-05-14 09:10:03 UTC

## R topics documented:

scqe-package . . . . .	2
delta.optim.scqe . . . . .	2
delta.optim.scqe.1cfull . . . . .	3
delta.optim.scqe2 . . . . .	4

delta_optim_SCQE_2C . . . . .	5
plot.scqe . . . . .	6
scqe . . . . .	7
scqe.1cfull . . . . .	10
scqe.1csumm . . . . .	11
scqe.2cfull . . . . .	12
scqe.2csumm . . . . .	13
scqemethod . . . . .	14
summary.scqe . . . . .	15

<b>Index</b>	<b>17</b>
--------------	-----------

---

scqe-package	<i>scqe: Stability Controlled Quasi-Experimentation</i>
--------------	---

---

## Description

The scqe package contains several function 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

Hazlett, C. (2019), 'Estimating causal effects of new treatments despite self-selection: The case of experimental medical treatments.' *Journal of Causal Inference*.

---

delta.optim.scqe	<i>Delta optimization method for scqe 1 cohort, summary statistics</i>
------------------	--

---

## Description

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

**Usage**

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

**Arguments**

Y_T0	Y
untreated	Number of untreated individuals.
Y_untreated	Outcome for untreated individuals.
treated	Number of treated individuals.
Y_treated	Outcome for treated individuals.
obj	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**

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

```

    specified = NULL,
    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).
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

```

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

```

**Arguments**

post	Binary vector corresponding to T=0,1 for each observation.
treatment	Binary or continuous vector corresponding (usually) to 0,1.
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.
alpha	Numeric alpha for confidence intervals (default alpha=.05).
specified	Specified optional arguments.
...	Extra optional arguments.

**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	scqe 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**

```
## 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**

```
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)
```

---

 scqe

*Stability controlled quasi-experiment (scqe)*


---

**Description**

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

**Usage**

```
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,
```

```

    Y_untr_post,
    Y_tr_pre,
    Y_untr_pre,
    untr,
    tr,
    Y_tr,
    Y_untr,
    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.
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

Hazlett, C. (2019), 'Estimating causal effects of new treatments despite self-selection: The case of experimental medical treatments.' *Journal of Causal Inference*.

### Examples

```
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)
```

---

 scqe.1cfull

*Stability controlled quasi-experiment (scqe) for 1 cohort case, full data*


---

### 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))
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)

# 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)
```

---

scqe.lcsumm	<i>Stability controlled quasi-experiment (scqe) for 1 cohort case, summary statistics</i>
-------------	---

---

## Description

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

## Usage

```
scqe.lcsumm(
  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**

```

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	<i>Stability controlled quasi-experiment (scqe) for 1 cohort case, summary statistics</i>
-------------	---

---

**Description**

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

**Usage**

```

scqe.2csumm(
  untr_pre,
  untr_post,
  tr_post,
  tr_pre,
  Y_tr_post,
  Y_untr_post,
  Y_tr_pre,
  Y_untr_pre,
  min_delta,
  max_delta,
  delta,
  alpha = 0.05,
  ...
)

```

**Arguments**

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).
min_delta	Minimum delta. Optional, not used if delta is supplied.
max_delta	Maximum delta. Optional, not used if delta is supplied.
delta	Numeric scalar or numeric vector of possible values for change in average non-treatment outcome between cohorts (if applicable).
alpha	Numeric alpha for confidence interval (default is alpha=.05).
...	Extra optional arguments.

**Value**

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

**Examples**

```
# 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)
```

---

 scqemethod

*Stability controlled quasi-experiment (scqe)*


---

**Description**

Dispatches to correct scqe function

**Usage**

```
scqemethod(...)
```

**Arguments**

... Arguments from `scqe`

**Value**

`scqe` object of class "scqe", results table

---

summary.scqe	<i>Summary method for scqe</i>
--------------	--------------------------------

---

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

**Usage**

```
## 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**

```
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))
scqe.2cohort.full
print(scqe.2cohort.full)
```



# Index

`delta.optim.scqe`, [2](#)  
`delta.optim.scqe.1cfull`, [3](#)  
`delta.optim.scqe2`, [4](#)  
`delta_optim_SCQE_2C`, [5](#)

`plot.scqe`, [6](#)  
`print.scqe (summary.scqe)`, [15](#)

`scqe`, [2](#), [7](#), [7](#), [15](#)  
`scqe-package`, [2](#)  
`scqe.1cfull`, [10](#)  
`scqe.1csumm`, [11](#)  
`scqe.2cfull`, [12](#)  
`scqe.2csumm`, [13](#)  
`scqemethod`, [14](#)  
`summary.scqe`, [15](#)