

Package ‘healthcare.antitrust’

January 9, 2024

Type Package

Title Healthcare Antitrust Analysis

Version 0.1.4

Description Antitrust analysis of healthcare markets. Contains functions to implement the semiparametric estimation technique described in Raval, Rosenbaum, and Tenn (2017) “A Semiparametric Discrete Choice Model: An Application to Hospital Mergers” <[doi:10.1111/ecin.12454](https://doi.org/10.1111/ecin.12454)>.

License CC0

Copyright As a work of the United States government, this project is in the public domain within the United States. Additionally, we waive copyright and related rights in the work worldwide through the CC0 1.0 Universal public domain dedication.

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Imports methods, stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.2.3

URL <https://github.com/mpanhans/healthcare.antitrust>

NeedsCompilation no

Author Matthew T Panhans [aut, cre] (<<https://orcid.org/0000-0001-7874-6740>>)

Maintainer Matthew T Panhans <mpanhans@gmail.com>

Repository CRAN

Date/Publication 2024-01-09 00:20:02 UTC

R topics documented:

cell_defn	2
discharge_data	3
div_calc	4
wtp_calc	5

Index	8
--------------	----------

cell_defn	<i>Allocate Observations to Cells</i>
-----------	---------------------------------------

Description

Take a dataset of hospital discharges, and assigns them to cells that meet a minimum threshold cell size.

Usage

```
cell_defn(data, min_size, layers, count = "count", expandLayers = FALSE)
```

Arguments

data	Dataset of discharges.
min_size	Minimize cell size.
layers	A list of lists. Each layer is a list of the variables on which observations will be allocated to cells. The layers should be ordered in decreasing refinement, so that observations not assigned to a cell meeting the minimum size threshold can be assigned by a more coarse layer.
count	Name of variable which indicates the number of admissions represented by an observation. Default variable name is count.
expandLayers	logical; if only a single layer is given, setting this to TRUE will expand the layer to a set of layers where each layer drops the last variable in the list of the previous layer.

Details

If the variable count is not available, the function will assume that each observation represents one admission, and a variable count will be created in the output data frame to indicate this.

When assigning observations to cells in a given layer, this function only assigns observations that have not been previously assigned in a finer layer. That is, the function assigns observations without replacement. Assignment with replacement is currently not supported.

For more details see the example vignette by typing: `vignette("semipar_example", package = "healthcare.antitrust")`

Value

A list of data frames. The first component in the list, assigned, is the original data frame, with observations assigned to cells, and excluding observations that were not assigned. The assigned cells are designated by the variable `cell`, and the layer number in which the observation is assigned to the cell is given by the variable `cell_type`. The second component of the list, unassigned, is a data frame with the unassigned observations.

Examples

```
data(discharge_data, package = "healthcare.antitrust")

list1 <- c("drg", "age", "zip5")
layers <- list(list1)
th <- 15
discharge_data$count <- 1

outList <- cell_defn(discharge_data, th, layers)
```

discharge_data	<i>A simulated dataset of hospital discharges</i>
----------------	---

Description

A simulated dataset of hospital discharges containing patient characteristics.

Usage

```
discharge_data
```

Format

A data frame with 1,200 rows (one for each discharge) and 7 variables:

drg diagnosis related group (drg) code for the admission

age patient age

zip5 patient 5 digit zip code of residence

hosp_id hospital identifier

hospital hospital name

sys_id system identifier

system system name

Source

Created as part of healthcare.antitrust package.

div_calc

*Diversion Ratio Calculator***Description**

Calculates provider-level diversion ratios, once cells have been defined.

Usage

```
div_calc(
  data,
  cell = "cell",
  provider_id = "provider_id",
  provider = "provider",
  sys_id = "sys_id",
  focal_sys_id = NULL,
  party_ind = "party_ind",
  count = "count",
  dropDegenerateCell = TRUE,
  hosp_id = NA,
  hospital = NA
)
```

Arguments

data	Dataset of patient choices, with required variables: cell, provider_id, hospital, sys_id, party_ind, count. Use other function arguments to indicate alternative variable names to the default names.
cell	Name of variable specifying cell to which each observation has been allocated. Default variable name is cell. Can be created by cell_defn function.
provider_id	Name of variable specifying (numeric) provider identifier. Default variable name is provider_id.
provider	Name of variable specifying (string) provider name. Default variable name is provider.
sys_id	Name of variable specifying (numeric) system identifier. Default variable name is sys_id.
focal_sys_id	numeric; list of sys_id's specifying systems of interest for which diversions will be calculated from. For a merger, this will typically be the system identifies of the merging parties.
party_ind	deprecated; use focal_sys_id instead.
count	Name of variable indicating the number of admissions represented by the observation. Set = 1 for every row if each observation represents one admission.
dropDegenerateCell	logical; specifies how to treat cells with a 100 percent within-system share. If TRUE, observations in degenerate, 100 percent share cells will be ignored in the

diversion ratio calculation. If FALSE, any such individuals will be assigned to the outside option, but still included in the denominator, so that the inside-option diversion will total less than 100 percent.

`hosp_id` deprecated; use `provider_id` instead.
`hospital` deprecated; use `provider` instead.

Details

For system-to-system diversions, set `provider_id` and `provider` equal to corresponding system-level identifiers. Diversions then reflect that patients are not allowed to divert to within-system alternative providers

For more details see the example vignette by typing: `vignette("semipar_example", package = "healthcare.antitrust")`

Value

A list with two components. The first component, `provider_level`, is a matrix giving provider-level diversions from party providers to all other providers. The second object, `sys_level`, is a matrix that aggregates party providers to systems, thus giving diversions from party systems to all other providers

Examples

```
data(discharge_data, package = "healthcare.antitrust")

list1 <- c("drg", "age", "zip5")
layers <- list(list1)
th <- 15
discharge_data$count <- 1

outList <- cell_defn(discharge_data, th, layers)
D0 <- outList$assigned

out <- div_calc(D0, provider_id = "hosp_id", provider = "hospital",
               focal_sys_id = c(1,5))
```

wtp_calc

Willingness-to-Pay Calculator

Description

This function calculates the system-level Willingness-To-Pay.

Usage

```
wtp_calc(
  data,
  cell = "cell",
  sys_id = "sys_id",
  count = "count",
  weight = "weight",
  dropDegenerateCell = TRUE
)
```

Arguments

<code>data</code>	Dataset of hospital discharges. Required variables: <code>cell</code> and <code>sys_id</code> . Use other function arguments to indicate alternative variable names to the default names.
<code>cell</code>	Name of variable specifying cell to which each observation has been allocated. Default variable name is <code>cell</code> . Can be created by <code>cell_defn</code> function.
<code>sys_id</code>	Name of variable specifying (numeric) system identifier. Default variable name is <code>sys_id</code> .
<code>count</code>	Name of variable indicating the number of admissions represented by the observation. Set = 1 for every row if each observation represents one admission.
<code>weight</code>	Name of variable indicating designated weight of admission; =1 if observations should be equally weighted.
<code>dropDegenerateCell</code>	logical; specifies how to treat cells with a 100 percent within-system share. If TRUE, observations in degenerate, 100 percent share cells will be ignored in the WTP calculation. If FALSE, an adjustment is made where any cells with > 99 percent share at a single hospital have the share set to 99.0 percent.

Details

This function calculates the system-level WTP. For use in a WTP simulation exercise of the "WTP/Q Method" described in Brand and Balan (2018) [doi:10.2139/SSRN.3153109](https://doi.org/10.2139/SSRN.3153109). Hospital systems need to be numbered by `sys_id`, with a distinct `sys_id` for each independent hospital.

The weight input might for example be a DRG weight for each inpatient hospital admission.

For more details see the example vignette by typing: `vignette("semipar_example", package = "healthcare.antitrust")`

Value

A data frame with the number of rows equal to the number of systems in the input data frame, and the following variables: `sys_id` is the system identifier, `WTP_s` is the system's WTP, `N_s` is the number of admission for the system, and `WTP_s_wt` is the weighted WTP for the system if the weight input is provided.

Examples

```
data(discharge_data, package = "healthcare.antitrust")

list1 <- c("drg", "age", "zip5")
layers <- list(list1)
th <- 15
discharge_data$count <- 1

outList <- cell_defn(discharge_data, th, layers)
D0 <- outList$assigned

out <- wtp_calc(D0)
```

Index

* datasets

discharge_data, 3

cell_defn, 2

discharge_data, 3

div_calc, 4

wtp_calc, 5