

Package ‘exteriorMatch’

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Type Package

Title Constructs the Exterior Match from Two Matched Control Groups

Version 1.0.0

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Description If one treated group is matched to one control reservoir in two different ways to produce two sets of treated-control matched pairs, then the two control groups may be entwined, in the sense that some control individuals are in both control groups. The exterior match is used to compare the two control groups.

License GPL-2

LazyData TRUE

NeedsCompilation no

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exteriorMatch-package *Constructs the Exterior Match from Two Matched Control Groups*

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Details

The DESCRIPTION file:

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Index of help topics:

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exteriorMatch-package  Constructs the Exterior Match from Two Matched
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```

Author(s)

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References

Rosenbaum, P.R. and Silber, J.H., 2013. Using the exterior match to compare two entwined matched control groups. *The American Statistician*, 67(2), pp.67-75.

Examples

```
#The example is Figure 3 in Rosenbaum and Silber (2013).
g1<-c("A", "C", "D", "E", "G", "H", "I", "K", "L")
g2<-c("B", "C", "E", "F", "H", "I", "J", "L", "K")
exterior(g1,g2)
```

exterior

Constructs the Exterior Match from Two Matched Control Groups

Description

If one treated group is matched to one control reservoir in two different ways to produce two sets of treated-control matched pairs, then the two control groups may be entwined, in the sense that some control individuals are in both control groups. The exterior match is used to compare the two control groups.

Usage

```
exterior(id1, id2)
```

Arguments

id1	id1 and id2 are vectors of the same length containing unique identifiers for the controls in control group 1 and control group 2. The first treated individual is paired with control id1[1] in the first control group, and with control id2[1] in the second control group. The <i>i</i> th treated individual is paired with control id1[<i>i</i>] in the first control group and with control id2[<i>i</i>] in the second control group, for $i = 1, 2, \dots, \text{length}(\text{id1})$.
id2	See id1.

Details

The identifiers in id1 are unique, $\text{length}(\text{id1}) == \text{length}(\text{unique}(\text{id1}))$, and the identifiers in id2 are unique, $\text{length}(\text{id2}) == \text{length}(\text{unique}(\text{id2}))$; however, some controls in id1 may also be in id2. The exterior match minimally adjusts the match to remove duplicates. It is used to compare the two control groups. The exterior match was proposed in Rosenbaum and Silber (2013), and the example below reproduces the example in Figure 3 of that paper.

Value

The value is a list containing a revised id1 and id2 with revised pairing and the removal of duplicates.

Note

If one treated group is matched to one control reservoir in two different ways to produce two sets of treated-control matched pairs, then the two control groups may be entwined, in the sense that some control individuals are in both control groups. The exterior match is used to compare the two control groups. The exterior match minimally adjusts the original match to remove duplicates. The exterior match was proposed by Rosenbaum and Silber (2013) and was used to study medical disparities in Silber et al. (2013, 2014).

An alternative to the exterior match is avoid duplicates when building the match using tapered matching; see Daniel et al. (2008). The control reservoir needs to be fairly large to obtain close matches without duplication. Additionally, in tapered matching, each control group alters or distorts the control population by removing controls used by other control group, a source of concern in some applications.

The exterior match can be used to study disparities. In Silber et al. (2013), the US black population with breast cancer was matched to several white groups with breast cancer. One control group was matched for age. Another group was matched for age, cancer characteristics such as stage and grade, and other health problems such as diabetes and congestive heart failure. Yet another control group matched for all of these variables plus cancer treatment, surgery, chemo, radiation. The exterior match is a tool that aids in understanding the extent to which the disparity changes as differences between the white and black populations are removed.

The exterior match can be used when a second control group is built with the hope of attenuating unmeasured biases; see Pimentel et al. (2016).

Figure 3 in Rosenbaum and Silber (2013) is better than any verbal description of the exterior match. Technically, the exterior match consists of the exterior nodes of the connected components of a bipartite graph.

Author(s)

Paul R. Rosenbaum

References

Daniel, S.R., Armstrong, K., Silber, J.H. and Rosenbaum, P.R., 2008. An algorithm for optimal tapered matching, with application to disparities in survival. *Journal of Computational and Graphical Statistics*, 17(4), pp.914-924.

Pimentel, S.D., Small, D.S. and Rosenbaum, P.R., 2016. Constructed second control groups and attenuation of unmeasured biases. *Journal of the American Statistical Association*, 111(515), pp. 1157-1167.

Rosenbaum, P.R. and Silber, J.H., 2013. Using the exterior match to compare two entwined matched control groups. *The American Statistician*, 67(2), pp.67-75.

Silber, J.H., Rosenbaum, P.R., Clark, A.S., Giantonio, B.J., Ross, R.N., Teng, Y., Wang, M., Niknam, B.A., Ludwig, J.M., Wang, W. and Even-Shoshan, O., 2013. Characteristics associated with differences in survival among black and white women with breast cancer. *JAMA*, 310(4), pp.389-397.

Silber, J.H., Rosenbaum, P.R., Ross, R.N., Niknam, B.A., Ludwig, J.M., Wang, W., Clark, A.S., Fox, K.R., Wang, M., Even-Shoshan, O. and Giantonio, B.J., 2014. Racial disparities in colon cancer survival: a matched cohort study. *Annals of Internal Medicine*, 161(12), pp.845-854.

Examples

#The example is Figure 3 in Rosenbaum and Silber (2013).

```
g1<-c("A", "C", "D", "E", "G", "H", "I", "K", "L")
g2<-c("B", "C", "E", "F", "H", "I", "J", "L", "K")
exterior(g1,g2)
```

The function is currently defined as

```
function (id1, id2)
{
  stopifnot(is.vector(id1))
  stopifnot(is.vector(id2))
  stopifnot(length(id1) == length(id2))
  stopifnot(length(id1) == length(unique(id1)))
  stopifnot(length(id2) == length(unique(id2)))
  n <- length(id1)
  ident <- id1 == id2
  nident <- sum(ident)
  id1 <- id1[!ident]
  id2 <- id2[!ident]
  inter <- intersect(id1, id2)
  while (length(inter) >= 1) {
    dup <- inter[1]
    w1 <- which(id1 == dup)
```

```
w2 <- which(id2 == dup)
id1 <- c(id1[w2], id1[-c(w1, w2)])
id2 <- c(id2[w1], id2[-c(w1, w2)])
if (id1[1] == id2[1]) {
  id1 <- id1[-1]
  id2 <- id2[-1]
}
inter <- intersect(id1, id2)
}
o <- order(id1)
id1 <- id1[o]
id2 <- id2[o]
list(id1 = id1, id2 = id2)
}
```

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