

Bug report from Dr. Guo

December 18, 2012

1 Using `fullmatch`'s `data` argument

This document attempts to recreate this issues reported by Dr. Guo with the latest version of `optmatch` (0.8-0). I think the problem is a documentation bug with the new `data` argument to `fullmatch`. This argument is optional, but when omitted, a warning is issued suggesting that the user include it. While this warning message is important, the somewhat ambiguous use of the word “data” might confuse users. Does “data” mean the distance matrix? Does “data” mean a propensity score object? Does “data” mean some sort of data vector or matrix that was used earlier in the process? The correct answer is the last one: a vector or matrix that establishes the proper order of the match vector, but from reviewing the error message and the `fullmatch` documentation, I can understand if users are not crystal clear on the nature of this important distinction.

The rest of this document attempts to mock up (using simulated data), a similar situation in the one reported by Dr. Guo. I show where the confusion over the `data` comes from, along with the proper usage of this argument. There may be other issues at play (and I'd like to get the original data to make sure that there are not multiple problems appearing simultaneously). The new version of `optmatch` certainly has a few outstanding bugs (and I discovered a new one in the process of writing this document), so it is possible that Dr. Guo's issue is not simply a documentation problem.

```
> library(optmatch)
```

Here will mock up some data in the style of (linear) propensity scores:

```
> set.seed(20121218)
> N <- 100
> X <- rnorm(N)
> Z <- rep(c(1,0), each = N/2)
> names(X) <- c(paste("T", 1:(N/2), sep = "."), paste("C", 1:(N/2), sep = "."))
> c(X[1:5], X[(N/2 + 1):(N/2 + 6)])
```

T.1	T.2	T.3	T.4	T.5	C.1
0.86362093	0.64588297	0.25532827	-0.99844199	0.09015015	-0.49596442

	C.2	C.3	C.4	C.5	C.6
	-0.92916171	-0.72465459	0.37861986	2.06783497	0.87281308

To make things interesting, let's shake up the order of the data vector. This will be important to illustrate a point later:

```
> rnd.order <- sample(1:N)
> X <- X[rnd.order]
> Z <- Z[rnd.order]
```

Now, we can rank the data and create a matrix. See Section 3 for another way to create this distance matrix:

```
> R <- rank(X)
> D <- abs(outer(R[Z == 1], R[Z == 0], '-'))
> D[1:3, 1:3]
```

	C.10	C.24	C.13
T.39	10	45	29
T.14	38	3	19
T.43	1	36	20

Now, we will perform a simple full match. If the length is zero, the match failed (or if it is all NA values):

```
> fm <- fullmatch(D, min.controls = 1, max.controls = 4)
> stopifnot(length(fm) > 0 & all(!is.na(fm)))
```

If you are reading this, the match worked. However, you might be worried when you see this warning:

```
Warning message:
In fullmatch(D, min.controls = 1, max.controls = 4) :
  Without 'data' argument the order of the match is not guaranteed
  to be the same as your original data.
```

This message does not mean that `fullmatch` failed (it is not a full error, just a warning). It is to warn the user that the output (our `fm` object) might be in an order that does not correspond to any previous data vector, matrix, or table. To illustrate, compare the names of the first 5 items in the `fm` object with the first 10 items in the `X` object:

```
> fm[1:10]

T.39 T.14 T.43 T.19 T.25 T.7 T.48 T.44 T.11 T.30
1.33 1.6 1.38 1.11 1.18 1.48 1.43 1.39 1.3 1.24

> X[1:10]
```

C.10	T.39	T.14	T.43	T.19	C.24	C.13
-0.2252463	-0.4707736	0.7526047	-0.2932224	-0.1929818	0.6506225	0.2255692
C.31	C.36	T.25				
-0.4760022	1.2832260	0.8433414				

Notice that the `fm` object is all treated units, while the original data had a random order of treated and control objects. If we tried to use `cbind` to join these two vectors, they would not correspond. This can be an even bigger issue if certain observations get dropped during the distance creation. Then result of `fullmatching` may have a different length than the original data.

In previous versions of `optmatch`, users had to manually match up names of the matched object to avoid this issue.

```
> fm.ordered_by_x <- fm[names(X)]
> fm.ordered_by_x[1:10]
```

C.10	T.39	T.14	T.43	T.19	C.24	C.13	C.31	C.36	T.25
1.11	1.33	1.6	1.38	1.11	1.1	1.12	1.4	1.48	1.18

In the latest version, the `data` argument helps with this issue by looking in an existing vector, matrix or `data.frame` to get the proper order (including any observations that got dropped in the process, say when fitting a `glm` object).

```
> fm.with_data <- fullmatch(D, min.controls = 1, max.controls = 4, data = X)
> fm.with_data[1:10]
```

C.10	T.39	T.14	T.43	T.19	C.24	C.13	C.31	C.36	T.25
1.11	1.33	1.6	1.38	1.11	1.1	1.12	1.4	1.48	1.18

The `fullmatch` documentation is somewhat brief on the usage of the `data` argument. We will improve it in the next version:

`data`: Optional `\code{data.frame}` or `\code{vector}` to use to get order of the final matching factor. If a `\code{data.frame}`, the `\code{rownames}` are used. If a vector, the `\code{names}` are first tried, otherwise the contents is considered to be a character vector of names. Useful to pass if you want to combine a match (using, e.g., `\code{cbind}`) with the data that were used to generate it (for example, in a propensity score matching).

What is most unclear in this help text is a more precise definition of where the `data` argument should come from; it is not the same as the `distance` argument! For this problem, either `X` or `R` (the original data and the rank transformed version) are valid choices. If the user were fitting a model it would look something like this:

```
> XZ <- data.frame(X, Z)
> rownames(XZ)[1:10]
```

```

[1] "C.10" "T.39" "T.14" "T.43" "T.19" "C.24" "C.13" "C.31" "C.36" "T.25"

> fm <- fullmatch(match_on(glm(Z ~ X, data = XZ, family = binomial)), data = XZ)
> names(fm)[1:10]

[1] "C.10" "T.39" "T.14" "T.43" "T.19" "C.24" "C.13" "C.31" "C.36" "T.25"

>

```

Future improvements to `optmatch` will be smarter about finding the `data` argument if possible and helping users avoid some of the nested calls (`match_on(glm(...))`) for common use cases.

2 Using Guo's data directly

```

> library(foreign)
> set.seed(10)
> cds <- read.dta("opt.dta")
> attach(cds)
> prank <- rank(ps)
> names(prank) <- id
> d1 <- outer(prank[aodserv==1], prank[aodserv==0], "-")
> d1 <- abs(d1)
> d1[1:3, 1:3]

      2      3      6
1 2283 1263  542
5 1886  866  145
8  354  666 1387

> #variable match, (vm1 - at least 1 at most 4)
> vm1 <- fullmatch(d1,min.controls=1,max.controls=4)
> vm1

      1      5      8      9     15     23     45     50     64     67     85     99    101    160    164    188
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887  899  952  956  960  970  971  979  982 1002 1009 1011 1014 1017 1025 1027
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```

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[illegible]

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```

```

> (vm1.d <- matched.distances(vm1,d1,pres=TRUE))

logical(0)

```

3 New Syntax

There many new improvements to the distance creation tools in `optmatch` _0.8. Specifically, the `match_on` function provides some convenient short cuts for common distance creation techniques. In addition creating distances from GLM objects (seen above), functions, and formulas (using Mahalanobis or Euclidean distance), this function also has a `numeric` method that performs absolute differences on a single dimension. Using the ranks from before, we can create the same distance matrix without using `outer`:

```

> D2 <- match_on(R, z = Z)
> all(D2 - D == 0)

[1] TRUE

```

(D2 is a child class of `matrix`, so to show that they are the same, I use subtraction and comparison to zero.)

One nice feature of the `match_on.numeric` is that for large problems where a caliper is required, the caliper value can be passed in and only the values that are less than the caliper will be computed, saving considerable computation time and memory.

```

> D[1:3, 1:3]

```

```

      C.10 C.24 C.13
T.39    10   45   29
T.14    38    3   19
T.43     1   36   20

```

```

> D3 <- match_on(R, z = Z, caliper = 20)
> optmatch:::as.matrix.InfinitySparseMatrix(D3)[ c("T.39", "T.14", "T.43"), c("C.10", "C.24", "C.13")]

```

	control			
treated	C.10	C.24	C.13	
T.39	10	Inf	Inf	
T.14	Inf	3	19	
T.43	1	Inf	20	

In writing this up, I see a small bug: we didn't properly export the `as.matrix` method for the special objects that `match_on` produces. Rest assured this will be addressed in the next maintenance release.

A R Session Info

```
> sessionInfo()

R version 2.15.2 (2012-10-26)
Platform: x86_64-apple-darwin12.2.1 (64-bit)

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] foreign_0.8-51 optmatch_0.8-1

loaded via a namespace (and not attached):
[1] tools_2.15.2
```