

# How to match on a Mahalanobis distance

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In order to match on a Mahalanobis distance, or on a Mahalanobis distance within calipers, one has to first combine covariates into a matrix of Mahalanobis distances (or list of such matrices). R has some functions for creating Mahalanobis distances, but they seem to be oriented to applications other than Mahalanobis matching. This How To illustrates how those functions are adapted to this purpose.

First, here is an adaptation of the R function `mahalanobis`. It is specifically designed to be combined with `outer`, and may behave unexpectedly if used in isolation. Its arguments are `data`, a data frame containing all covariates to be combined in the distance; `inv.cov`, an inverted covariance for the  $k$  covariates, where  $k \geq 2$ ; and character vectors `Tnms`, `Cnms` containing subsets of the row names of `data` that correspond to treatment and control groups, respectively.

```
> myMH <- function(Tnms, Cnms, inv.cov, data) {  
+   stopifnot(!is.null(dimnames(inv.cov)[[1]]), dim(inv.cov)[1] >  
+     1, all.equal(dimnames(inv.cov)[[1]], dimnames(inv.cov)[[2]]),  
+     all(dimnames(inv.cov)[[1]] %in% names(data)))  
+   covars <- dimnames(inv.cov)[[1]]  
+   xdiffs <- as.matrix(data[Tnms, covars])  
+   xdiffs <- xdiffs - as.matrix(data[Cnms, covars])  
+   rowSums((xdiffs %*% inv.cov) * xdiffs)  
+ }
```

Before using it, one has to select the covariates, invert their covariance matrix, and isolate names of treated and control subjects.

```

> icv <- solve(cov(nuclear.nopt[, c("cap", "date")]))
> trtnms <- row.names(nuclear.nopt)[as.logical(nuclear.nopt$pr)]
> ctlnms <- row.names(nuclear.nopt)[!as.logical(nuclear.nopt$pr)]
> mdist <- outer(trtnms, ctlnms, FUN = myMH, inv.cov = icv, data = nuclear.nopt)
> dimnames(mdist) <- list(trtnms, ctlnms)
> round(mdist, 2)

```

	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
A	5.00	0.00	0.48	7.38	2.13	9.83	2.81	7.59	3.94	7.90	2.73	3.81	3.20	6.23	3.66
B	3.66	0.48	0.00	6.98	1.39	8.71	1.84	6.25	2.36	6.79	0.92	1.99	2.09	3.56	1.49
C	0.45	2.66	1.56	2.44	0.07	3.06	0.03	1.61	0.14	1.96	1.46	0.29	0.04	1.27	2.24
D	0.59	7.90	6.79	0.27	2.03	0.12	1.59	0.05	1.67	0.00	6.47	2.61	1.41	3.51	7.78
E	3.14	2.73	0.92	7.64	1.79	8.33	1.89	5.63	1.58	6.47	0.00	0.92	1.96	1.34	0.10
F	6.34	15.25	10.54	11.90	8.15	9.83	7.26	7.51	5.10	8.73	5.48	4.33	6.79	2.18	4.91
G	2.82	9.57	6.07	7.15	3.93	5.97	3.32	3.96	1.93	4.88	2.68	1.47	3.01	0.38	2.57
	W	X	Y	Z											
A	2.72	7.74	16.80	15.24											
B	1.15	4.83	12.79	10.31											
C	0.31	1.72	6.21	9.75											
D	3.48	3.17	4.31	15.79											
E	0.46	2.22	8.51	5.17											
F	5.26	1.72	2.19	2.12											
G	2.11	0.21	1.97	3.25											

```

> fullmatch(mdist)

```

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
m.1	m.2	m.3	m.4	m.5	m.6	m.7	m.3	m.1	m.2	m.4	m.3	m.4	m.3	m.4	m.3	m.4	m.5	m.3	m.3
U	V	W	X	Y	Z														
m.7	m.5	m.3	m.7	m.7	m.6														

This construction can be wrapped inside a `lapply` function, as described in the “listOfDistancesHowTo” vignette, for Mahalanobis matching within subclasses; and it can be combined with calipers, as explained in the “basicUses” vignette.