

0.1 `match.data`: Output matched data sets

Description

The code `match.data` creates output data sets from the `matchit` matching algorithm.

Usage

```
match.data <- match.data(object, group = "all")
```

Arguments

<code>object</code>	Stored output from <code>matchit</code> .
<code>group</code>	Which units to output. Selecting "all" (default) gives all matched units (treated and control), "treat" gives just the matched treated units, and "control" gives just the matched control units.

Value

The `match.data` command generates a matched data set from the output of the `matchit` function, according to the options selected in the `group` argument. The matched data set contains the additional variables:

<code>pscore</code>	The propensity score for each unit.
<code>psclass</code>	The subclass index for each unit (if applicable).
<code>psweights</code>	The weight for each unit (generated from the matching procedure).

See the `matchit` documentation for more details on these items.

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See Also

The complete documentation for `matchit` is available online at <http://gking.harvard.edu/matchit>.