

## 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>.