```
HOW TO INSTALL:


Copy the ado files into an appropriate directory:
    (a)      I recommend to create a direcory w in the ado/plus directory of stata (if it
             does not exist yet).
    (b)      Unzip the files into this directory.



HOW TO USE:

The program can be used in two ways:

1. Using the integrating program wh_matching. It is called integrating because it integrates
the matching and the output generation.


wh_matching _treatvar_, n(#={1..4}) cov(_XVARLIST_) out(_YVARLIST) [ties met(#={1,2})
e(#={1..4}) bias(#={1,2}) cal(#=real) rob(#={1..4}) noreplacement desc ate ]

_treatvar_             : Treatment variable
n(#={1..4})            : Number of neighbors (max 4)
cov(_XVARLIST_)        : Covariates (order matters for exact matching)
out(_YVARLIST)         : Outcomes (more than one outcome can be specified)
met(#={1,2})           : Method to calculated distance metric 1: inverse variance  2: Mahalanobis
e(#={1..n})            : "exact" matching for the first # of covariates
bias(#={1,2})          : bias adjustment (same as in nnmatch)
cal(#=real)            : caliper if not used no caliper is assumed.
rob(#={1..4})          : robust variance (n is the number of neighbors used to calculate the
                         robust variance – same as in nnmatch)
noreplacement          : no replacement (only if the number of neighbors is set to 1)
desc                   : descending (only useful if noreplacement is used)
ate                    : if provided ATE is calculated, otherwise ATT (default); ATC can be
                         calculated by inverting the treatment variable


Examples:

wh_matching treat, n(4) cov(t1 t2 t3 m1 m2 m3) out(out1 out2 out3) met(1) e(1) bias(1) cal(0)
rob(4)

wh_matching treat, n(1) cov(t1 t2 t3 m1 m2 m3) out(out1 out2 out3) met(2) e(2) bias(1)
cal(0.1) rob(4) ate




2. Using the lower-level programs that prepare the data and calculate the statistics.

2a. Preparation of the dataset:
wh_match_prep sets up the dataset and contains the determination of the synthetic control
group. This part of the matching routine is time-consuming.

wh_match_prep _treatvar_, n(#={1..4}) cov(_XVARLIST_) [ties met(#={1,2}) e(#={1..4})
cal(#=real) rob(#={1..4}) noreplacement desc ate ]

_treatvar_             : Treatment variable
n(#={1..4})            : Number of neighbors (max 4)
cov(_XVARLIST_)        : Covariates (order matters for exact matching)
met(#={1,2})           : Method to calculated distance metric 1: inverse variance  2: Mahalanobis
e(#={1..n})            : "exact" matching for the first # of covariates
cal(#=real)            : caliper if not used no caliper is assumed.
rob(#={1..4})          : robust variance (n is the number of neighbors used to calculate the
                         robust variance – same as in nnmatch)
noreplacement          : no replacement (only if the number of neighbors is set to 1)
desc                   : descending (only useful if noreplacement is used)
ate                    : if provided ATE is calculated, otherwise ATT (default); ATC can be
                         calculated by inverting the treatment variable
```

Example:

```
wh_match_prep treat, n(4) cov(t1 t2 t3 m1 m2 m3) met(1) e(1) cal(0) rob(4)
```

2b. Statistical analysis based on the prepared dataset

The second part of the routine wh_match_execute contains the statistical analysis. Please note that >out< is in this case a single variable!

```
wh_match_execute _treatvar_, out(n(#={1..4}) cov(_XVARLIST_) [ties met(#={1,2}) e(#={1..4})
cal(#=real) rob(#={1..4}) noreplacement desc ate ]
```

```
_treatvar_           : Treatment variable

out(_YVARLIST)       : Outcome variable (only one outcome can be specified)
cov(_XVARLIST_)      : Covariates
n(#={1..4})          : Number of neighbors (max 4)
e(#={1..n})          : "exact" matching for the first # of covariates
rob(#={1..4})        : robust variance (n is the number of neighbors used to calculate the
                       robust variance – same as in nnmatch)
bias(#={1,2})        : bias adjustment (same as in nnmatch)
cal(#=real)          : caliper if not used no caliper is assumed.
met(#={1,2})         : Method to calculated distance metric 1: inverse variance  2: Mahalanobis
ate                  : if provided ATE is calculated, otherwise ATT (default); ATC can be
                       calculated by inverting the treatment variable
```

```
wh_match_execute  treat , out(out1)cov(t1 t2 t3 m1 m2 m3) e(1) n(1) rob(2) bias(1)
```

wh_match_execute can be used without having to run wh_match_prep, when chaning

1. the outcome variabe
2. setting bias on and off
3. rob(#) can be turned on or off and modified up the the value provided when wh_match_prep
   was run.

All other information cannot be modified by using wh_match_execute alone.