FAQs about the **network** suite for performing network meta-analysis in Stata

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# Installing, updating and citing

## How do I use the latest version?

In Stata:

1. type net from http://www.homepages.ucl.ac.uk/~rmjwiww/stata/
2. click on **meta**
3. click on **network**
4. click on “click here to install”

or (possibly better) use **adoupdate network**

## I’ve installed the latest version but it still isn’t working

1. An old version may be masking the newer version. In Stata, type

which network, all

The first version found should be 1.1.4 or later. If instead the new version is lower down, you need to remove the older version(s). See **help adoupdate** and **help ado** - in particular, try **ado uninstall mvmeta**.

1. You may not have the latest version of **mvmeta**. Follow the instructions [above](#_How_do_I) (but clicking on **mvmeta** instead of **network** in step 3).

## I get an error message that my mvmeta needs updating, but I've updated it

If you are running a version of **network** dated between 3jun2014 (v0.6) and 12mar2015 (v1.0) then you may see an error message like

network requires mvmeta version 2.10 or later

This is a bug that was corrected in **network** version 1.1, so the solution is to update **network**.

## I'm getting an unexpected error message

Send me the log file errorlog.txt created by running the following code:

log using errorlog.txt

which network, all

which mvmeta, all

set trace on

set tracedepth 2

<your command>

log close

## How should I cite the package?

The preferred citation is

* White IR (2015) Network meta-analysis. *Stata Journal* 15: 1–34.

Other possible citations are

* White, I. R. (2011). Multivariate random-effects meta-regression: Updates to mvmeta. Stata Journal, 11, 255–270.
* White, I. R., Barrett, J. K., Jackson, D., & Higgins, J. P. T. (2012). Consistency and inconsistency in network meta-analysis: model estimation using multivariate meta-regression. Research Synthesis Methods, 3, 111–125.

# Using the network suite

## How do I compare coefficients using lincom?

At present you have to do this by writing commands like

lincom [\_y\_C]\_cons - [\_y\_B]\_cons

I have drafted a command -**networkcompare**- to automate this.

## How does the network suite select the reference treatment?

If treatment is numeric, it uses the numerically first treatment; otherwise it uses the alphabetically first treatment. You can change this using the **ref()** option on **network setup**.

## Is the parameterisation of the inconsistency model arbitrary?

Yes, it's an arbitrary parameterisation. However, different parameterisations give the same overall model: in particular the test statistic for inconsistency is the same.

I think of this as being like regression with a categorical variable: depending on which level you take as the reference level, you will get different parameter estimates, but the model is the same and the overall test for differences between levels is the same.

## Is the network model a fixed or random effects model?

The term "fixed effects" is very confusing.

* In meta-analysis it has come to mean "no heterogeneity between studies", although for this meaning it should really be "fixed effect" or better still "common effect" (Higgins et al. A re-evaluation of random-effects meta-analysis. JRSSA 2009;172:137–159).
* In the rest of statistics it means that a set of parameters are to be estimated entirely separately, rather than being assumed to come from a particular distribution. We might better call this "fixed parameters" or "separate parameters" as opposed to "random parameters".

So my network package:

* allows heterogeneity between studies by default in all network meta-analysis (though the **fixed** option fits a homogeneity or "fixed-effect" model);
* when it allows for inconsistency, it does so using fixed parameters not random parameters.

## Is the confidence interval of the network estimate always at least as narrow as that of the direct estimate or the indirect estimate?

Yes under a fixed-effect model.

No under a random-effects model, since heterogeneity estimation across the network can have strange results.

## Do I need the commonparm option to perform meta-regression in NMA?

The commonparm option is a technical option of mvmeta; in the context of using mvmeta to do NMA, it is primarily used for analysing NMA data in the “standard” format.

Meta-regression is easier to do in “augmented” format. In fact if you look at the network meta help file you will see the option:

regress(varlist) Specify covariates for network meta-regression. Every treatment contrast is allowed to depend on the covariate(s) listed. This option is currently only allowed in augmented format.

For example, regress(gender) allows every treatment contrast to depend - in a different way - on gender. So for example gender might modify the A-B contrast but not the C-D contrast. [Gender is a poor example since we should be talking about study-level covariates - perhaps imagine all studies in our network were single-gender studies.]

It’s important to consider whether you want every treatment contrast to depend in a different way on gender. [Dias et al](http://journals.sagepub.com/doi/abs/10.1177/0272989X13485157) propose (1) Unrelated Treatment-Specific Interactions, (2) Exchangeable and Related Treatment-Specific Interactions, (3) Same Interaction Effect for All Treatments. They favour (3), which implies that if A is the reference treatment, all contrasts with A are modified by gender, but all other contrasts (B-C, D-E etc.) are NOT modified by gender. I prefer model (1), which handles all treatments symmetrically.

## How do I estimate the CI for a SUCRA?

You should not estimate a CI for SUCRA! This is because SUCRA is not a parameter (like a treatment effect) but a summary of the evidence (like a p-value).

This is discussed in [this article](https://www.sciencedirect.com/science/article/pii/S0895435617308016) - this commentary refrains from a definitive statement, "it is unclear whether it makes sense to report and interpret uncertainty intervals for SUCRA measures", but makes its views clear, "the interpretation of the SUCRA uncertainty intervals would be irrelevant".

## Why don't my results from pairwise MA agree with NMA?

In general, NMA includes more evidence than pairwise MA, so you don't expect to get the same answers.

However there are some cases where you might expect to get the same answer for a particular comparison, say B vs A:

1. If there is only direct evidence for B vs A.
2. If you run network sidesplit A B and compare the direct evidence with the pairwise MA result.

Whether you can expect the same answer depends on heterogeneity and the presence of multi-arm trials.

* If there are multi-arm trials involving A and B, then these may contribute indirect evidence.
* Otherwise, if you run a common-effect NMA (i.e. using the fixed option of network meta or network sidesplit), then you should indeed get perfect agreement.
* If you run a default random-effects NMA, then you won't get agreement. This is because these models assume the heterogeneity variance is the same for all comparisons, whereas when you do separate pairwise MAs you allow a different heterogeneity variance for each comparison.
* Finally if you run a random-effects NMA with the bscov(unstructured) option, then you should get agreement, since this allows a different heterogeneity variance for each comparison.