# Multilevel analysis of network dynamics

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cases studies of single networks.

However, it is preferable to generalize to a <span style="color:red">population</span> of networks.

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However, it is preferable to generalize to a population of networks.

This can be achieved, in principle,
by multilevel network analysis in the sense of analyzing
multiple similar networks, mutually independent.

This was proposed by Snijders & Baerveldt (*J. Math. Soc. 2003*).

Also see Entwisle, Faust, Rindfuss, & Kaneda (*AJS*, 2007)
who gave on overview of empirical work until then
involving multiple networks.

## Sample from Population of Networks

Suppose we have a sample indexed by $j = 1, \ldots, N$
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in the following sense:

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Suppose we have a sample indexed by $j = 1, \ldots, N$
from a population of networks on disjoint node sets,
where the networks are 'replications' of each other
in the following sense:

they all are regarded as realizations of processes obeying the same model,
but having different parameters $\theta_1, \ldots, \theta_j, \ldots, \theta_N$ .

Each disjoint network is called a group.
We assume we have network panel data for each group,
and wish to analyze these by fitting
Stochastic Actor-Oriented Models ('SAOMs', RSiena).

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   no distributional assumptions:
   *two-stage 'meta analysis'*.

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3. Two-step approach like in meta analysis:
   Assumption: population of networks,
   no distributional assumptions:
      *two-stage 'meta analysis'*.

4. Two-step approach without population assumption:
      *Fisher combination of independent tests.*

Such data sets have multilevel structure;
all caveats and considerations from usual multilevel analysis apply!

See T.A.B. Snijders & R.J. Bosker,
'Multilevel Analysis' (2nd ed., Sage, 2012);

T.A.B. Snijders, 'The Multiple Flavours of Multilevel Issues for Networks',
in E. Lazega & T.A.B. Snijders, 'Multilevel Network Analysis' (Springer, 2016).

# Multilevel designs, generalization, and the risks of having few groups

In 'standard' multilevel analysis, we have several populations.

Consider a data set with individuals nested in groups:
then we wish to generalize
to the population of individuals as well as the population of groups.
Often, we only have small number of groups,
which may jeopardize generalization.

For some basic intuitive understanding of the relevant issues,
consider the simplest case:
estimation of the population mean $\mu$ of some variable.

We have $N = 5$ randomly drawn groups each of size $n = 20$.
Data range from –2.5 to +3.5, as in the histogram (next page).
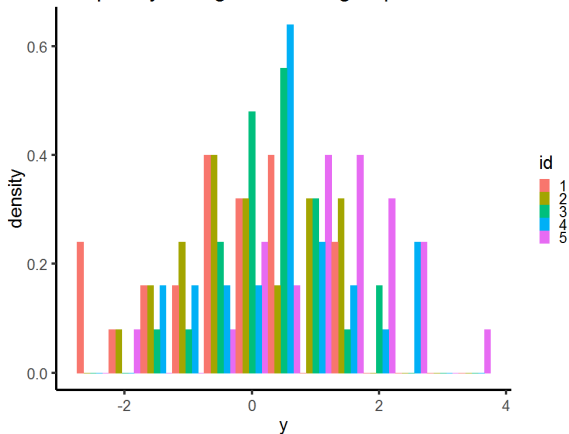Is there evidence that the population mean is positive?

Test $H_0 : \mu = 0$ against $H_1 : \mu > 0$ (one-sided).

Frequency histogram of 100 data points
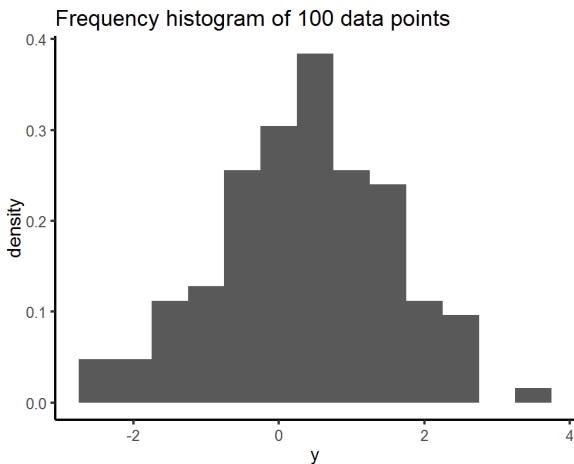
mean = 0.36, s.d. = 1.18, $t_{99}$=3.40, $p = 0.0003$

*linear model (OLS): yes*
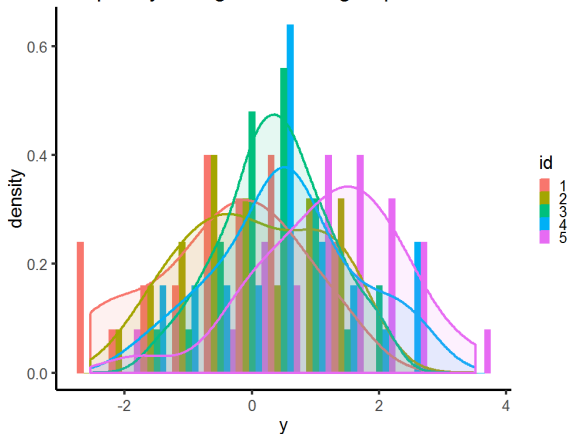
Frequency histogram of five groups

multilevel $t_4 = 1.49$, $p = 0.12$

*multilevel model: no*

but by group $p = 0.11, 0.84, 0.034, 0.021, 0.00002$

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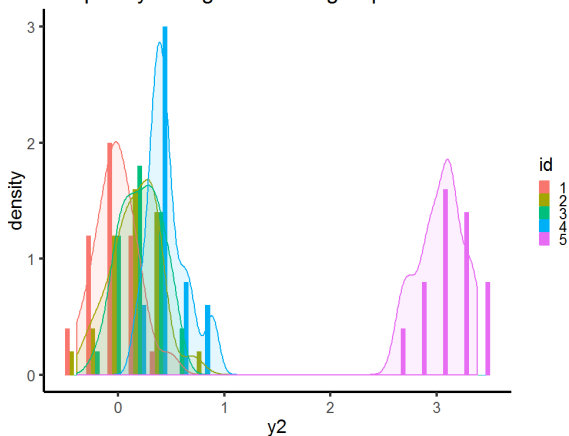
Frequency histogram of five groups

An even more extreme example:
OLS $t_{99} = 7.9$, $p \approx 0$; multilevel $t_4 = 1.50$, $p = 0.12$

by group $p = 0.64,\ 0.002,\ 0.000012,\ < 0.0001,\ < 0.0001$

The conclusion for both data sets is not only, that
the multilevel model tells us $\mu$ is not significantly positive.

There is also significant heterogeneity between the groups:
$\mu$ is not zero in all groups
(this can be concluded already from an OLS analysis by group).

And one of the groups has such a small $p$,
that the significance survives multiple testing with Bonferroni.

*If we wish to generalize to the population of all groups,
there is no evidence of a positive mean;
but there is evidence that
at least one of these groups has a positive mean,
and that the mean of these five groups is positive.*

After this sensitization, on with the four approaches:

1. Multi-group analysis:
   assume all parameters are identical.

2. Integrated hierarchical approach:
   Assumption: population of networks, normal distribution.

3. Two-stage approach:
   Assumption: population of networks,
   no distributional assumptions:
   > *first analysis by group, then combination 'meta-analysis'.*

4. Two-stage approach without population assumption:
   > *first analysis by group,*
   > *then Fisher combination of independent tests.*
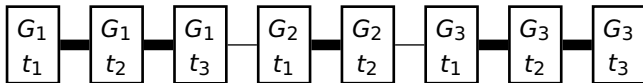
We treat how this can be handled with SAOMs,
using the package RSiena.

## Multi-group analysis

Multi-group analysis (sienaGroupCreate, siena07)
assumes all parameters are the same.
The groups are treated just like subsequent waves, strung in a sequence,
where (of course) transitions between groups are not analyzed.



Example for 3 groups, with 3 / 2 / 3 waves;
the analyzed 2+1+2 periods are indicated as bold lines.

Groups can have different sizes,
must have same variables and a common model specification.

(Earlier approaches combined all networks in one big network with structural zeros
between them; this is now superseded by multi-group analysis.)

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sienaTimeTest() can be used to test homogeneity assumption.

# Random effects:
# hierarchical multilevel structure

1. On the tie level there is a dynamic process governed by the SAOM.

2. On the network level there is a Stochastic Actor-Oriented Model (SAOM) with parameter vector $(\theta_j^{(1)}, \eta)'$ for group $j$.

   Here $\theta_j^{(1)} \sim \mathcal{N}(\mu, \Sigma)$.

3. On the global level there is a population of networks with either a multivariate normal distribution $\mathcal{N}(\mu, \Sigma)$ for the randomly varying parameters $\theta_j^{(1)}$, and a common parameter $\eta$ for the rest; or without distribution assumption.

# Hierarchical multilevel analysis

Assumption: population of networks;

$\theta_j \sim$ multivariate normal distribution,
perhaps conditionally on network-level covariates.

*integrated hierarchical approach*:
some parameters varying, others constant across groups.

(cf. random slopes and fixed effects
in Hierarchical Linear Model of standard multilevel analysis.)

multiSiena: *multi-level option*, sienaBayes()

*Integrated procedure:*
Estimate the <u>distribution</u> of $\theta_j$ and consider the
'posterior' distribution of $\theta_j$ given the data.

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Estimate the <u>distribution</u> of $\theta_j$ and consider the
'posterior' distribution of $\theta_j$ given the data.

*Advantage*:
The analysis of the separate networks draws strength from
the total sample of networks by regression to the mean.

*Useful especially for many rather small networks.*

The method implemented in sienaBayes is in the paradigm
of *Bayesian* as opposed to *frequentist* statistics.

Further explanation is in the set of slides
*'Multilevel analysis of network dynamics using sienaBayes '* .

(Frequentist methods would also be possible, but have not been elaborated.)

## Two-stage approach ∼ Random Effects Model

$\theta_1, \ldots, \theta_j, \ldots, \theta_N$ are drawn randomly
from a *population* $\mathcal{P}$[net] of networks,
no further distributional assumptions are made.

Parameter $\theta_j$ can be written as

$$\theta_j = \Big(\theta_{1j}, \theta_{2j}, \ldots, \theta_{Kj}\Big).$$

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Parameter $\theta_j$ can be written as

$$\theta_j = \left( \theta_{1j}, \theta_{2j}, \ldots, \theta_{Kj} \right).$$

*Two-stage procedure:*
estimate each $\theta_j$ separately,
combine the results in a meta-analysis (Cochran 1954),
('*V-known problem*' in multilevel analysis)
which allows testing hypotheses about $\mathcal{P}$[net]
such as, for a coordinate $k$ ,

$$\begin{aligned}
H_0^{\text{total}} &: \quad \text{all } \theta_{kj} = 0; \\
H_0^{\text{mean}} &: \quad \mathsf{E}\{\theta_{kj}\} = 0; \\
H_0^{\text{spread}} &: \quad \text{var}\{\theta_{kj}\} = 0.
\end{aligned}$$

The meta-analysis is directed at one particular coordinate $k$ (e.g., average alter).

The input for the meta-analysis consists of estimates $\hat{\theta}_{kj}$ and their standard errors s.e.$_{kj}$.

The meta analysis is constructed based on the model

$$\hat{\theta}_{kj} = \theta_{kj} + E_{kj} = \mu_k + U_{kj} + E_{kj} \, ,$$

where $\mu_k$ is the population mean for parameter coordinate $k$, $\theta_{kj}$ is the true coordinate $k$ of the parameter in group $j$, $U_{kj}$ is the true effect of group $j$ as deviation from $\mu_k$, and $E_{kj}$ is the statistical error of estimation.

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$\theta_{kj}$ is the true coordinate $k$ of the parameter in group $j$,
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and $E_{kj}$ is the statistical error of estimation.

$U_{kj}$ and $E_{kj}$ are independent residuals with mean 0,
the $U_{kj}$ are i.i.d. with unknown variance $\sigma^2$,
and var$(E_{kj}) = $ s.e.$_{kj}^2$  ('V–known').

Implemented in MLwiN, HLM, R package Metafor,
RSiena function siena08(); Snijders & Baerveldt (2003).

## Meta-Analysis ~ Random Effects Model (contd.)

This has been applied in quite many studies. Examples:

Lubbers (2003):
homophily in 57 classrooms with 1466 students
(also with random coefficient $p^*$ approach);

Baerveldt, van Duijn, Vermeij, van Hemert (2004):
ethnic homophily in 20 schools, 1317 students;

Valente, Fujimoto, Chou, and Spruit-Metz (2009):
friendship & obesity, 17 classrooms with 617 students;

Mercken, Snijders, Steglich, & de Vries (2009):
fr. & smoking, 7704 adolescents, 70 schools, 6 countries;
also other studies by Liesbeth Mercken.

Kruse & Kroneberg (2022):
liking & school grades, 40 schools, 4293 students.

There are a variety of R packages for meta-analysis.
For example: metafor, mvmeta.

RSiena also includes the function siena08 for meta-analysis.
This carries out meta-analysis according to S & B (2003),
but with an iterated weighted least squares ('WLS') method. metafor calls
this *WLS analysis* of the *random effects* model.

metafor also has more options than siena08.

siena08 can be used for what is not provided by metafor:
overall test of $H_0^{\text{total}}$; Fisher combination (see below).

Wolfgang Viechtbauer, 'Conducting meta-analyses in R with the metafor package', *Journal of Statistical Software*, 2010.

Some terminology:

The method carried out by siena08 is, in the language of metafor, the *WLS analysis* of the *random effects* model.

*Fixed effects*: conclusion only about the average of
these *N* groups (usually weighted inversely by variances);
*random effects*: generalization to population of groups.

Viechtbauer (2005): REML (one of the methods implemented in metafor) is somewhat better than WLS (implemented in siena08).

# Example: Chris Baerveldt's data

Houtzager and Baerveldt (1999): *Dutch Social Behavior study*.

19 classrooms in secondary schools,
evolution of friendship network and delinquent behavior.

Also used in Snijders & Baerveldt (*J. Math. Soc.*, 2003) and
Baerveldt, Völker & Van Rossem (*Can. J. Crim. Crim. Just.*, 2008).

3 classrooms had difficulties for convergence and were dropped;
in 2 further classrooms,
one parameter had to be fixed to 0 for stable convergence.

Number of pupils per group varied 33–91.
Average degrees per wave 1.0–3.2 (low!)
Jaccards 0.24–0.38.

The following pages show a table that was produced
as a hybrid from `metafor` and `siena08` results.

It has results for the global parameters, $\mu$ as well as $\sigma$.

Note: it is important for a meta-analysis
to present results for mean tendency as well as between-group variability!!!

(Many researchers unfortunately present only the former.)

All results in the table are from `metafor`,
except $p_T$ , the $p$-value for $H_0^{\text{total}}$ from `siena08`.

| | $N$ | $\hat{\mu}$ | se($\hat{\mu}$) | $p_\mu$ | $\hat{\sigma}$ | $p_\sigma$ | $p_T$ |
|---|---|---|---|---|---|---|---|
| *Friendship dynamics* | | | | | | | |
| outdegree (density) | 16 | –2.955 | 0.149 | 0.00 | 0.00 | 0.65 | 0.00 |
| reciprocity | 16 | 3.588 | 0.253 | 0.00 | 0.44 | 0.52 | 0.00 |
| GWESP | 16 | 2.377 | 0.120 | 0.00 | 0.18 | 0.27 | 0.00 |
| indegree - popularity | 16 | –0.118 | 0.024 | 0.00 | 0.02 | 0.42 | 0.00 |
| outdegree - activity | 16 | 0.121 | 0.024 | 0.00 | 0.00 | 0.91 | 0.00 |
| rec.degree - activity | 16 | –0.204 | 0.067 | 0.00 | 0.08 | 0.63 | 0.10 |
| indegree - activity | 16 | –0.204 | 0.072 | 0.00 | 0.05 | 0.70 | 0.17 |
| same ethnicity | 16 | –0.005 | 0.089 | 0.96 | 0.19 | 0.21 | 0.20 |
| sex (M) alter | 16 | –0.329 | 0.086 | 0.00 | 0.00 | 0.64 | 0.03 |
| sex (M) ego | 16 | –0.169 | 0.173 | 0.33 | 0.42 | 0.08 | 0.05 |
| same sex | 16 | 0.554 | 0.080 | 0.00 | 0.14 | 0.39 | 0.00 |
| crimi alter | 16 | –0.053 | 0.046 | 0.24 | 0.00 | 0.83 | 0.74 |
| crimi ego | 16 | 0.074 | 0.080 | 0.35 | 0.16 | 0.22 | 0.15 |
| crimi ego × alter | 16 | 0.006 | 0.057 | 0.92 | 0.11 | 0.22 | 0.21 |
| reciprocity × GWESP | 14 | –0.568 | 0.272 | 0.04 | 0.00 | 0.96 | 0.68 |

| | N | $\hat{\mu}$ | se($\hat{\mu}$) | $p_\mu$ | $\hat{\sigma}$ | $p_\sigma$ | $p_T$ |
|---|---|---|---|---|---|---|---|
| *Delinquency dynamics* | | | | | | | |
| linear shape | 16 | 0.015 | 0.108 | 0.89 | 0.00 | 0.93 | 0.93 |
| quadratic shape | 16 | −0.295 | 0.048 | 0.00 | 0.05 | 0.70 | 0.00 |
| outdegree | 16 | 0.042 | 0.047 | 0.37 | 0.00 | 0.99 | 0.99 |
| total alter | 16 | 0.076 | 0.064 | 0.23 | 0.00 | 1.00 | 1.00 |
| sex (M) | 16 | 0.610 | 0.139 | 0.00 | 0.00 | 0.99 | 0.09 |

- $N$: number of groups combined;

- $\hat{\mu}$, se($\hat{\mu}$), $p_\mu$ : inference for $\mu$;

- $\hat{\sigma}$ , $p_\sigma$ : inference for $\sigma$;

- $p_T$ : $p$-value for $H_0^{\text{total}}$.

It may be noted that $\sigma^2$ never is significantly positive.

However, sienaTimeTest, which uses a more powerful test
(multivariate, and using also information used for estimation)
concludes that the parameters are significantly different.

Some example conclusions:

- reciprocity: strongly significant,
  but also quite variable across groups;

- reciprocal degree-activity: clearly significant,
  variability across groups might exist;
  if so, no or hardly any groups with positive parameter;

- same sex: strongly significant,
  variable across groups, will be positive in all groups;

- total alter: not significant;
  if non-zero, then more likely to be positive;
  note that $p_\sigma = p_T = 1$ but $p_\mu = 0.23$,
  which can be explained by the fact that tests do not produce certainty,
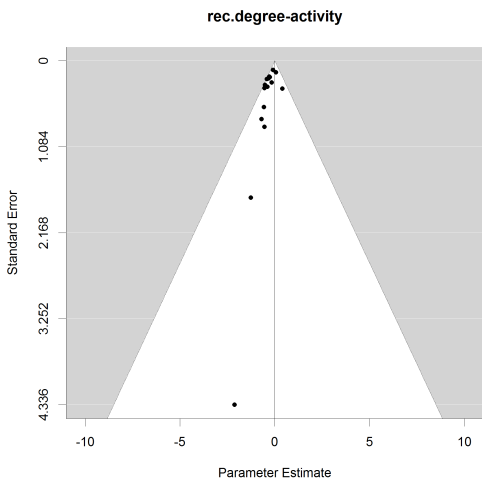  and that the test for $\mu$ is more focused.

For 'positive in all groups', think of $\hat{\mu} \pm 2\hat{\sigma}$.
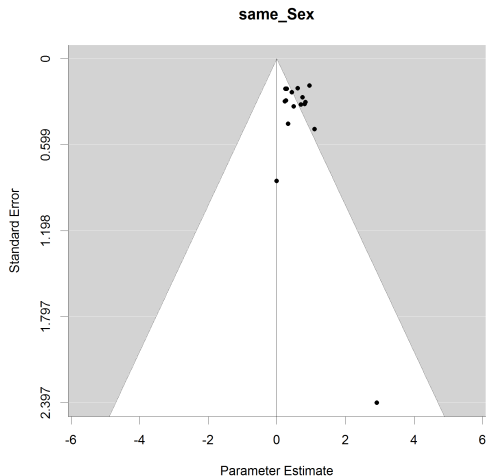
The *funnel plot*
produced by metafor
shows
groupwise estimates
and standard errors.

Important to get a feeling
for what's going on!

RSiena also has a function
<funnelPlot>.

**rec.degree-activity**

Note that for the reciprocated degree-activity effect,
none of the individual estimates is significant,
but jointly the effect is strongly significant.

**Crimi_total_alter**
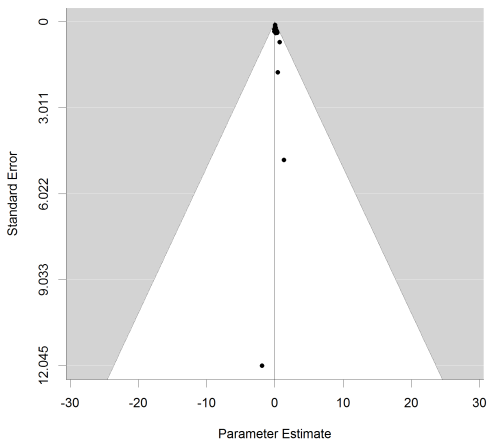
# Meta-Analysis without a population assumption

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no assumption about a population is made.

*two-stage procedure:*
estimate each $\theta_j$ separately, combine the results by
*Fisher's procedure for combining independent tests*:

'*is there any evidence for a hypothesized effect?*'

See, e.g., Snijders & Bosker, "Multilevel Analysis", Section 3.7.

*Meta-Analysis ∼ without population assumption (contd.)*:

For coordinate $k$ of the parameter, test null hypothesis

$$H_0 : \theta_{kj} = 0 \text{ for all } j$$

against alternative hypothesis

$$H_1 : \theta_{kj} \neq 0 \text{ for at least one } j .$$

RSiena: first estimate for all groups, then use siena08().
Useful when there are few groups.

Mercken, Snijders, Steglich, & de Vries (2009)
applied this in a study of smoking initiation:
7704 adolescents in 70 schools in 6 countries.

This principle here is applied in a double test for $\theta_{kj}$
(for each given effect $k$)

**1** for detecting if any groups $j$ have $\theta_{kj} > 0$,
the null hypothesis tested is
$H_0^r$ : For all groups $j$ we have $\theta_{kj} \leq 0$
with the alternative right-sided hypothesis;
$H_1^r$ : For at least one group $j$ , $\theta_{kj} > 0$;

**2** for detecting if any groups $j$ have $\theta_{kj} < 0$,
the null hypothesis tested is
$H_0^\ell$ : For all groups $j$ we have $\theta_{kj} \geq 0$
with the alternative left-sided hypothesis;
$H_1^\ell$ : For at least one group $j$ , $\theta_{kj} < 0$;

For each effect, `siena08` gives the right-sided $p$-value $p_r$,
and the left-sided $p$-value $p_\ell$.

To account for the double testing, the significance level $\alpha$
should be divided by 2;
corresponding to doubling the $p$-values.

It is very well possible that $p_r$ as well as $p_\ell$ are significant
(e.g., for a combined $\alpha = 0.05$, that $p_r$ as well as $p_\ell$ are $< 0$).

This means that some groups have positive,
others negative parameter values;
a perfectly possible conclusion.

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others negative parameter values;
a perfectly possible conclusion.

The following pages present
the two one-sided $p$-values for the Baerveldt data
for comparison combined with the earlier results for $\mu$.

|  | $N$ | $\hat{\mu}$ | $se(\hat{\mu})$ | $p_\mu$ | $p_\ell$ | $p_r$ |
|---|---|---|---|---|---|---|
| *Friendship dynamics* | | | | | | |
| outdegree (density) | 16 | –2.955 | 0.149 | 0.00 | 1.00 | 0.00 |
| reciprocity | 16 | 3.588 | 0.253 | 0.00 | 0.00 | 1.00 |
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| indegree - popularity | 16 | –0.118 | 0.024 | 0.00 | 1.00 | 0.00 |
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| same ethnicity | 16 | –0.005 | 0.089 | 0.96 | 0.36 | 0.42 |
| sex (M) alter | 16 | –0.329 | 0.086 | 0.00 | 1.00 | 0.00 |
| sex (M) ego | 16 | –0.169 | 0.173 | 0.33 | 0.66 | 0.04 |
| same sex | 16 | 0.554 | 0.080 | 0.00 | 0.00 | 1.00 |
| crimi alter | 16 | –0.053 | 0.046 | 0.24 | 0.88 | 0.31 |
| crimi ego | 16 | 0.074 | 0.080 | 0.35 | 0.09 | 0.73 |
| crimi ego × alter | 16 | 0.006 | 0.057 | 0.92 | 0.25 | 0.52 |
| reciprocity × GWESP | 14 | –0.568 | 0.272 | 0.04 | 0.98 | 0.13 |

|  | N | $\hat{\mu}$ | se($\hat{\mu}$) | $p_\mu$ | $p_\ell$ | $p_r$ |
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| *Delinquency dynamics* | | | | | | |
| linear shape | 16 | 0.015 | 0.108 | 0.89 | 0.65 | 0.77 |
| quadratic shape | 16 | −0.295 | 0.048 | 0.00 | 1.00 | 0.00 |
| outdegree | 16 | 0.042 | 0.047 | 0.37 | 0.55 | 0.93 |
| total alter | 16 | 0.076 | 0.064 | 0.23 | 0.38 | 0.99 |
| sex (M) | 16 | 0.610 | 0.139 | 0.00 | 0.00 | 1.00 |

In this case, the results of Fisher's combination of tests
are in line with the random-effects meta-analysis;
there is a difference in 'significance' only for reciprocity × GWESP.

This is related to the small variability between the groups,
and the fact that no parameters have ambiguous signs.

In other cases, it may well be different!
Statistical reasoning gives no certainty...

See the manual for further explanation.

# Literature

The example using Chris Baerveldt's data is in the script *RscriptMultipleGroups_meta.R* on the Siena website.

*References*

RSiena manual: Chapter 11.

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DOI: https://doi.org/10.48550/arXiv.2201.12713<br> To be published (in revised form) in *Journal of the Royal Statistical Society, vol. A*.

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Wolfgang Viechtbauer (2010). 'Conducting meta-analyses in R with the metafor package', *Journal of Statistical Software*.