Multiple Parallel Networks

Sample from Population of Networks

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).

Several approaches are possible for combining such data:

1. Multi-group analysis:
   - assume all parameters are identical.
2. Integrated hierarchical approach:
   - Assumption: population of networks, normal distribution.
3. Meta analysis:
   - Assumption: population of networks, no distributional assumptions: 
     two-stage meta analysis.
4. Meta analysis: no population assumption:
   - Fisher combination of independent tests.
Multilevel analysis...

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


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

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

Left one-sided testing.

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 $H_1 : \mu > 0$.

$\begin{align*}
\text{mean} &= 0.36, \text{s.d.} = 1.18, t_{99} = 3.40, p = 0.0003 \\
\text{linear model (ols): yes}
\end{align*}$

$\begin{align*}
\text{multilevel } t_4 = 1.49, p = 0.12 \\
\text{multilevel model: no}
\end{align*}$

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

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

\textit{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.

We treat how this can be handled with SAOMs, using the package \texttt{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.

\[
\begin{align*}
G_1 & \rightarrow G_1 & \rightarrow G_1 & \rightarrow G_2 & \rightarrow G_2 & \rightarrow G_3 & \rightarrow G_3 \\
G_1 & \rightarrow t_1 & \rightarrow t_2 & \rightarrow t_3 & \rightarrow t_1 & \rightarrow t_2 & \rightarrow t_3
\end{align*}
\]

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.

Integrated hierarchical random effects models

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 \( \theta_j^{(1)} \sim N(\mu, \Sigma) \).
3. On the global level there is a population of networks with either a multivariate normal distribution \( N(\mu, \Sigma) \) 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.

1. mixed effects:
some parameters varying, others constant across groups: restricted integrated hierarchical approach.
2. random effects:
all parameters varying across groups: integrated hierarchical approach
   but it is unusual to specify all parameters as randomly varying.
**Integrated hierarchical random effects models**

**Integrated procedure:**  
Estimate the distribution 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. Some explanation follows later; frequentist methods would also be possible.

For SienaBayes, however, a somewhat large number of random parameters seems not to be a problem.

But note the important distinction:  
**For fixed parameters (\( \eta \)), there is much more information than for the means and variances of random parameters (\( \mu, \Sigma \)).**

Therefore, the posterior distribution will be more concentrated (smaller variance) for the \( \eta \) parameters than for \( \mu \).

**Hierarchical model: restricted variation**

Terminology here:  
**fixed parameters** have the same value across groups;  
**random parameters** have different values across groups, with a priori a normal distribution.

From regular hierarchical linear models (HLMs) we know that ‘random slopes’ require a lot from the data.

In practice, HLMs have only a few random slopes.

The Bayesian MCMC procedure produces, when/if there is convergence (i.e., hopefully, after a burn-in period), a sample from the posterior distribution of all the parameters, both the \( \theta_j \) referring to the individual sampled networks, and \( \eta, \mu \) and \( \Sigma \) referring to the population of networks.

The inference is based on the sampled posterior distributions.

Two kinds of plot are important:

1. *trace plots*, representing successive draws from the posterior distribution (after thinning),

2. *density plots*, representing the plausible values of the parameters, given the observed data.
Prior distributions

For a smallish number of groups, the prior is consequential. It is given to SienaBayes as priorMu, priorSigma, priorDf.

For rate parameters, SienaBayes uses a data-dependent prior.

For evaluation function do not use the defaults (mean=0, var.=1) but use your prior experience; in particular, prior between-group variances can usually be much smaller than 1, because the Siena effects are calibrated to be usually less than 1 in absolute value.

For parameters that are the focus of research questions, use prior mean = 0.

Example: data Andrea Knecht

As an example, we use friendship networks in 21 school classes from the study by Andrea Knecht (PhD thesis Utrecht, 2008); see Knecht, Snijders, Baerveldt, Steglich, & Raub, ‘Friendship and Delinquency: Selection and Influence Processes in Early Adolescence’, Social Development, 2010.

We consider a model for a longitudinal study with 2 waves, dependent variables friendship and delinquent behavior.

Model specification

In addition to the regular effects, for multilevel models we should think about group-level effects.

1. The groups may have different numbers $n$ of actors. Snijders (2005; Section 11.13(B)) derives that for the empty model the outdegree parameter will have a component approximately $-\frac{1}{2} \log(n)$. Therefore it is recommendable to include $\log(n)$ as a covariate; the expected regression coefficient is something like $-0.5$, but for non-empty models the value is not really known.

2. Other group-level variables may also be relevant.

However, the number of level-2 variables should not be too large! The same considerations apply as for the number of covariates, given sample size, in linear regression models.

Within- and between-group regressions

Similar to the Hierarchical Linear Model of multilevel analysis, we should be aware that within-group regression coefficients may differ from between-group coefficients. The group mean of covariates, or dependent behavior variables, may be included in the model to account for this. By implication, cross-level interactions may be included.

In this case, we include the group mean of delinquency (ego) and the interaction of this group mean with delinquency alter.
Effects of delinquency on network evolution

From Snijders & Lomi (Network Science, 2019), we know that actor variables (here: delinquency) may have a variety of effects on networks, because such effects imply a level transition monadic ⇒ dyadic.

In a first analysis, the five-parameter model was used: $V(\text{ego}), V(\text{alter}), V^2(\text{ego}), V^2(\text{alter}), (V(\text{ego}) - V(\text{alter}))^2$.

From a provisional analysis it seemed that delinquency alter, for given ego, has approximately a linear effect. Therefore the model was reduced to four parameters: $V(\text{ego}), V(\text{alter}), V^2(\text{ego}), V(\text{ego}) \times V(\text{alter})$.

Random / fixed

The choice for which parameters to define as random was based on a preliminary multi-group analysis by MoM (siena07) where all parameters were assumed fixed, followed by sienaTimeTest to test parameter homogeneity; parameters with the largest test statistics were defined as random.

Network dynamics:
outdegree; reciprocity; transitive triplets; indegree popularity; outdegree activity; reciprocal degree-activity; delinquency ego; same sex;

Delinquency dynamics:
linear shape; quadratic shape.

Prior distributions

Prior for rates: data dependent, calculated internally;
other prior means for $\mu$: outdegree -2, same sex 0.4, others 0;
other prior variances for $\mu$: 0.01;
prior covariances: all 0;
prior variances for $\eta$: 2, but for group-level variables 1;
prior $\kappa$: 0.01.

This means that the between-group differences of parameters $\theta^{(1)}_j$ are thought to be in the order of magnitude of $\sqrt{0.01} = 0.1$, and the uncertainty about the value of the prior means of $\theta^{(1)}_j$ is of the order of $\sqrt{0.01/0.01} = 1$. 
For the MCMC algorithm, we used:

1. groupwise number of MH iterations for sampling micro-steps varies between 100–600 depending on distance between observed networks;
2. ⇒ 500 iterations sampling $\theta_j^{(1)}, \eta, \mu, \Sigma$ for warmup ⇒ 1000 iterations sampling $\theta_j^{(1)}, \mu, \Sigma$

and 3000 for sampling $\eta$ for estimation, with a thinning ratio of 1:40.

The results are provisional, because a good convergence check was not carried out.
Trace plots for means ($\mu$) of covariate network effects

Trace plots for fixed parameters ($\eta$) of covariate network effects

Trace plots for means ($\mu$) of behavior effects

Trace plots for fixed parameters ($\eta$) of behavior effects
Conclusion: non-stationarity mainly in warming phase, but up to run 800 there still seems some non-stationarity. A longer run is necessary!

The following page shows posterior means and standard deviations with 95% credibility intervals of $E(\theta_j)$, computed from runs 801-1500, for Bayesian estimation of friendship and delinquency dynamics in 21 classrooms (data Andrea Knecht).

### Friendship dynamics

<table>
<thead>
<tr>
<th>Effect</th>
<th>posterior mean (s.d.)</th>
<th>interval from to</th>
<th>varying</th>
</tr>
</thead>
<tbody>
<tr>
<td>outdegree (density)</td>
<td>-1.932 (0.145)</td>
<td>-2.208 -1.648</td>
<td>+</td>
</tr>
<tr>
<td>reciprocity</td>
<td>2.132 (0.133)</td>
<td>1.895 2.405</td>
<td>+</td>
</tr>
<tr>
<td>transitive triplets</td>
<td>0.493 (0.037)</td>
<td>0.421 0.565</td>
<td>+</td>
</tr>
<tr>
<td>indegree-popularity</td>
<td>-0.052 (0.030)</td>
<td>-0.113 0.004</td>
<td>+</td>
</tr>
<tr>
<td>outdegree-activity</td>
<td>-0.004 (0.024)</td>
<td>-0.051 0.042</td>
<td>+</td>
</tr>
<tr>
<td>recip. degree - activity</td>
<td>-0.175 (0.037)</td>
<td>-0.251 -0.105</td>
<td>+</td>
</tr>
<tr>
<td>old ties</td>
<td>0.368 (0.083)</td>
<td>0.200 0.534</td>
<td>-</td>
</tr>
<tr>
<td>deling alter</td>
<td>0.035 (0.037)</td>
<td>-0.035 0.111</td>
<td>-</td>
</tr>
<tr>
<td>deling ego</td>
<td>0.053 (0.088)</td>
<td>-0.114 0.234</td>
<td>+</td>
</tr>
<tr>
<td>deling squared ego</td>
<td>-0.043 (0.045)</td>
<td>-0.127 0.046</td>
<td>-</td>
</tr>
<tr>
<td>deling ego x deling alter</td>
<td>0.045 (0.044)</td>
<td>-0.042 0.127</td>
<td>-</td>
</tr>
<tr>
<td>deling group-average ego</td>
<td>-0.863 (0.690)</td>
<td>-1.857 0.727</td>
<td>-</td>
</tr>
<tr>
<td>del gr-av ego x del alter</td>
<td>-1.532 (0.535)</td>
<td>-2.522 -0.463</td>
<td>-</td>
</tr>
<tr>
<td>same sex</td>
<td>0.498 (0.078)</td>
<td>0.356 0.646</td>
<td>+</td>
</tr>
<tr>
<td>log(n) ego</td>
<td>-0.152 (0.539)</td>
<td>-1.264 0.833</td>
<td>-</td>
</tr>
</tbody>
</table>

Post. means, standard devs, and 95% credibility intervals for $\mu, \eta$; varying between classrooms: + = "yes", – = "no".

### Delinquency dynamics

<table>
<thead>
<tr>
<th>Effect</th>
<th>posterior mean (s.d.)</th>
<th>interval from to</th>
<th>varying</th>
</tr>
</thead>
<tbody>
<tr>
<td>linear shape</td>
<td>-0.068 (0.059)</td>
<td>-0.178 0.047</td>
<td>+</td>
</tr>
<tr>
<td>quadratic shape</td>
<td>-0.264 (0.054)</td>
<td>-0.368 -0.155</td>
<td>+</td>
</tr>
<tr>
<td>average alter</td>
<td>0.268 (0.147)</td>
<td>-0.030 0.546</td>
<td>–</td>
</tr>
<tr>
<td>effect from sex</td>
<td>0.212 (0.104)</td>
<td>0.007 0.421</td>
<td>–</td>
</tr>
</tbody>
</table>

Posterior means, standard deviations, and 95% credibility intervals for $\mu, \eta$; varying between classrooms: + = "yes", – = "no".

The hierarchical multilevel approach gives much more information: for each group, the posterior distribution of the parameters (which are constant across groups for the fixed parameters).

In the following plots, for the varying parameters, note the difference between the posterior density of $\mu$ and that of average $\theta_j$; the average $\theta_j$ has a bearing on this sample only; for $\mu$, there is the extra uncertainty due to generalisation from sample to population.
The MDS plot of the previous page can be used as a diagnostic. Based on this, we select groups 1–8 and 12 for plotting.
Integrated hierarchical random effects models
Andrea Knecht's data

Density plot for reciprocity

Density plot for transitive triplets

Density plot for transitive reciprocated triplets

Density plot for indegree-popularity
Density plot for outdegree-activity

Density plot for reciprocal degree-activity

Density plot for old ties

Density plot for delinquency alter
Density plot for delinquency ego

Density plot for delinquency squared ego

Density plot for delinquency group-average ego

Density plot for delinquency group-average ego
Density plot for delinquency group-average ego × delinquency alter

Density plot for same sex

Density plot for log(n) ego

Density plot for linear shape
Conclusion

The method seems to work well.

It is promising for analyzing collections of small networks; however, time-consuming.

The posterior uncertainty about parameters is much larger when they are assumed to vary between groups.

Thus, prior assumptions do matter...

Making inference about a population of networks is associated with much larger uncertainty than making inference about a single network.

Especially if there are not so many groups.
Random effects: two-stage procedure

Meta-Analysis \sim Random Effects Model
\theta_1, \ldots, \theta_j, \ldots, \theta_N \text{ are drawn randomly}
from a population \mathcal{P}\{\text{net}\} \text{ of networks,}
no further distributional assumptions are made.

Two-stage procedure:
estimate each \theta_j \text{ separately,}
combine the results in a meta-analysis (Cochran 1954),
(‘V-known problem’ in multilevel analysis)
which allows testing hypotheses about \mathcal{P}\{\text{net}\}
such as, for a coordinate \textit{k} ,
\begin{align*}
H_0^{\text{total}} : \quad & \text{all } \theta_{kj} = 0; \\
H_0^{\text{mean}} : \quad & \mathbb{E}\{\theta_{kj}\} = 0; \\
H_0^{\text{spread}} : \quad & \text{var}\{\theta_{kj}\} = 0.
\end{align*}

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Random effects: two-stage procedure

Meta-Analysis \sim 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 \rho^* \text{ approach});
Baerveldt, van Duijn, Vermeij, van Hemert (2004):
homophily in 20 schools, 1317 students;
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.

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Random effects: two-stage procedure

The input for the meta-analysis consists of
estimates \hat{\theta}_j \text{ and their standard errors } s.e.j.
The meta analysis is constructed based on the model
\begin{align*}
\hat{\theta}_j = \mu + U_j + E_j,
\end{align*}
where \mu is the population mean,
U_j \text{ is the true effect of group } j,
and E_j \text{ is the statistical error of estimation.}

U_j \text{ and } E_j \text{ are independent residuals with mean 0,}
the \text{ } U_j \text{ are i.i.d. with unknown variance } \sigma^2,
and \text{var}(E_j) = s.e.j^2 \text{ (‘V-known’)}.

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

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Random effects: two-stage procedure

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
Viechtbauer (2005): REML is somewhat better than WLS.

Fixed effects: conclusion only about the average of these \textit{N}
groups (usually weighted inversely by variances);
random effects: generalization to population of groups.
Therefore: the advice is to use metafor,
which also has a lot more options than siena08.
siena08 \text{ can be used for what is not provided by metafor:}
overall test of \text{ } H_0^{\text{total}} \text{; Fisher combination (see below).}

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Therefore: the advice is to use metafor, which also has a lot 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).


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 is somewhat better than WLS.

Example: Chris Baerveldt’s data


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


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.
Random effects: two-stage procedure  Example: Chris Baerveldt’s data

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

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 $p_\hat{\mu} = 0.23$, which can be explained by tests not producing certainty, and the test for $\mu$ being more focused.

For ‘positive in all groups’, think of $\hat{\mu} \pm 2\hat{\sigma}$.

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.

The funnel plot produced by metafor shows groupwise estimates and standard errors.

Important to get a feeling for what’s going on!
Meta-Analysis without a population assumption

\[ \theta_1, \ldots, \theta_j, \ldots, \theta_N \] are arbitrary values, 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?’


Meta-Analysis \sim 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

\[ H_1 : \theta_{kj} = 0 \text{ for at least one } j \, . \]

RSiena: first estimate for all groups, then use \texttt{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.
Without a population assumption  Double one-sided test

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
   $H_0':$ For all groups $j$ we have $\theta_{kj} \leq 0$
   with the alternative right-sided hypothesis;
   $H_1':$ 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
   $H_0':$ For all groups $j$ we have $\theta_{kj} \geq 0$
   with the alternative left-sided hypothesis;
   $H_1':$ 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 $p_l$.

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 $p_l$ are significant (e.g., for a combined $\alpha = 0.05$, that $p_r$ as well as $p_l$ are $< 0$).

This means that some groups have positive, 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 $\mu$.

Without a population assumption  Example@ Chris Baerveldt’s data

<table>
<thead>
<tr>
<th>$N$</th>
<th>$\hat{\mu}$</th>
<th>$\text{se}(\hat{\mu})$</th>
<th>$p_\mu$</th>
<th>$p_l$</th>
<th>$p_r$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Friendship dynamics</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>outdegree (density)</td>
<td>16</td>
<td>-2.955</td>
<td>0.149</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>reciprocity</td>
<td>16</td>
<td>3.588</td>
<td>0.253</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>GWESP</td>
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<td>2.377</td>
<td>0.120</td>
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<td>0.00</td>
</tr>
<tr>
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<td>-0.118</td>
<td>0.024</td>
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<td>1.00</td>
</tr>
<tr>
<td>outdegree - activity</td>
<td>16</td>
<td>0.121</td>
<td>0.024</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>rec. degree - activity</td>
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<td>-0.204</td>
<td>0.067</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
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<td>0.072</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>same ethnicity</td>
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<td>-0.005</td>
<td>0.089</td>
<td>0.96</td>
<td>0.36</td>
</tr>
<tr>
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<td>0.086</td>
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<td>1.00</td>
</tr>
<tr>
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<tr>
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<tr>
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<tr>
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<tr>
<td>reciprocity x GWESP</td>
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<td>-0.568</td>
<td>0.272</td>
<td>0.04</td>
<td>0.98</td>
</tr>
</tbody>
</table>

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 x 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.


