

Program Structural Equation Modeling: New Developments and Applications

Location: Tilburg University, S8

Online via Zoom:

<https://tilburguniversity.zoom.us/j/95093470822?pwd=N2dOeUtxejYwaUMzM5YMWtwV0VqZz09>

Wednesday 9 March 2022

10.00-13.00: workshop "Structural Equation Modeling with lavaan" (Yves Rosseel; online)

13.00-14.00: *lunch break*

14.00-17.00: workshop "Bayesian Structural Equation Modeling" (Sara van Erp; online)

Thursday 10 March 2022

09.00-09.25: *walk-in/coffee*

09.25-09.30: *welcome*

09.30-10.30: Keynote Rogier Kievit: Attach of the Psychometricians 2: They're coming for your brains (live)

10.30-10.45: *break*

10.45-11.15: Dandan Tang: Bayesian evaluation of approximate measurement invariance (online)

11:15-11:45: Andrej Srakar: Adaptive wavelet estimation of a latent variable model (online)

11.45-13.00: *lunch break*

13.00-14.00: Keynote Yves Rosseel: Small sample solutions for SEM (live)

14.00-14.15: *break*

14.15-14.45: Rebecca Kuiper: What's wrong with the null hypothesis? New methods for informative hypothesis testing (live)

14.45 - 15.15: Terrence D. Jorgensen: Pooled score tests for SEM with multiply imputed data (live)

15.15-15.30: *break*

15.30-16.00: Sacha Epskamp: Introducing psychonetrics, an R package for structural equation modelling and network psychometrics (live)

16:00-16:30: Kim de Roover: Mixture multigroup factor analysis for unraveling measurement non-invariance across many groups (live)

16:30-20:00: *drinks and dinner @ Boerke Mutsaers*

Friday 11 March 2022

09.00-09.30: *walk-in/coffee*

09.30-10.30: Keynote Suzanne Jak: Current opportunities and challenges in meta-analytic structural equation modeling (live)

10.30-10.45: *break*

10.45-11.15: Hannelies de Jonge: Using meta-analytic structural equation modeling to synthesize data of randomized controlled trials (live)

11.15-11.45: Xi Yu: A new approach for modeling aggregate constructs (live)

11.45-13.00: *lunch break*

13.00-14.00: Keynote Daniel Oberski: SEMs as computation graphs and other useful insights from machine learning (online)

14.00-14.30: Wen Wei Loh: Data-driven covariate selection for confounding adjustment by focusing on the stability of the effect estimator (online)

14.30-14.45: *break*

14.45-15.45: Keynote Sara van Erp: Bayesian regularized SEM: What, why, and how? (live)

15.45-16.00: *closing*

Abstracts

Attack of the Psychometricians II: They're coming for your brains

Rogier A. Kievit

Psychometric tools such as factor modeling, growth modeling and mixture model can and should have a substantial effect on the field of cognitive neuroscience – However, this impact has thusfar been limited. In this talk, I argue that both disciplines stand to gain by more interdisciplinary work. Developmental cognitive neuroscientists will gain the many benefits of psychometric tools including power, precision, measurement, novel parameters of interests and a flexible model selection approach. The benefits for psychometricians are arguably even greater. The novel questions and large, often freely available, idiosyncratic datasets offer a wealth of new questions often demanding novel methodological innovations and applications. I illustrate these arguments through several examples of modified or new psychometric tools in this field, including factor analysis for brain data, regularized SEM with many biological predictors, growth modeling of brain maturation and genomic SEM. I call for psychometricians to look to other fields for new inspiration and translational impact.

Bayesian Evaluation of Approximate Measurement Invariance

Dandan Tang, Xin Gu, Caspar van Lissa, and Herbert Hoijtink

Measurement invariance (MI) is of vital importance in multiple-group research with latent factors. In practice, the assumption of exact measurement is often not met. This article proposes a Bayesian testing approach to evaluate approximate MI in confirmatory factor analysis (CFA) models. Approximate MI is formulated using approximate hypotheses, in which loadings and intercepts are constrained by about equality. To make loadings and intercepts comparable across groups, a new measurement scale is placed on CFA models. When testing approximate hypotheses, researchers have to carefully specify the prior distribution for loadings and intercepts, as well as tolerant differences. Simulation studies explore the performance of different prior choices and tolerance differences to provide a recommendation for applied researchers and a flowchart of testing approximate MI. The accompanying R function BMI was implemented in bain package, and the real data example was illustrated the procedure.

Adaptive wavelet estimation of a latent variable model

Andrej Srakar

Latent variable models provide statistical tool for explaining and analyzing underlying structure of multivariate data by using the idea that observable phenomena are influenced by underlying factors which cannot be observed or measured directly. One possibility to fit them is to assume that the underlying distribution is Gaussian, and therefore it is uniquely determined by its covariance structure. This is commonly done using maximum likelihood and works under large sample asymptotics. In a recent article, first in developing non-parametric regression with latent variables, Kelava et al. (2017) used a two-step approach to

fit a non-parametric regression model: in the first step they have fitted a common factor analysis model and then applied B-spline nonparametric regression techniques to analyze the relation between the latent variables. Following this approach, we extend their article in multiple directions. Common factor analysis as key part of the approach is fit using non-parametric Bayesian approach following Piatek and Papaspiliopoulos (2018) and Knowles and Ghahramani (2011), allowing for correlated factors. Moreover, we extend the spline approach of Kelava et al. to adaptive (block-thresholded) wavelets which were shown to have good finite sample properties (Cai, 1999; 2009). This allows the estimation to be used for smaller samples. We derive asymptotic properties of the approach and show the estimator is consistent, asymptotically normal and efficient. The behaviour of the estimator is studied in Monte Carlo simulation comparing it to the generally used Latent Moderated Structural Equations (LMS) and Structural Equation Mixture Modeling (SEMM) estimators as well as to the Kelava et al. spline estimator. Short application studies relationship of subjective life satisfaction and financial indicators of the elderly using data of Survey of Health, Ageing and Retirement in Europe (SHARE).

Small sample solutions for SEM

Yves Rossee

In the frequentist framework, estimation and inference in structural equation modeling (SEM) is based on large-sample technology. As a result, when the sample size is (very) small, many problems may arise: nonconvergence, nonadmissible solutions, parameter bias, parameter instability, and test statistics that cannot be trusted. In this presentation, I will present several solutions for a some of these problems.

A first solution is called 'bounded estimation' and tries to avoid the frustrating problem of nonconvergence. Instead of using unconstrained optimization (using, for example, quasi-Newton methods), bounded estimation imposes simple data-driven lower and upper bounds on a selection of model parameters during optimization. By using well chosen bounds that are either on the boundary or just outside the admissible parameter space, we are able to stabilize regular ML estimation in (very) small samples.

A second solution targets the parameter bias by using resampling techniques. We will show that the jackknife and the bootstrap can be used to effectively decrease the finite sample bias that we typically observe in small samples, in particular for variance components.

A third solution is the so-called structural-after-measurement (SAM) approach. In this approach, estimation proceeds in two steps. In a first step, only

parameters related to the measurement part of the model are estimated. In a second step, parameters related to the structural part (only) are estimated. One application of SAM is to fit large models (with many latent variables) when the sample size is (in comparison) rather small. An attractive feature of the SAM approach is that non-iterative estimators can be used in both steps.

Finally, I will briefly demonstrate how these solutions can be used in the R package lavaan.

What's wrong with the null hypothesis? New methods for informative hypothesis testing

Caspar J. Van Lissa, Joris Mulder, Rebecca Kuiper, Herbert Hoijtink

The "Null Ritual" is deeply ingrained in applied research. In the context of SEM, researchers often gloss over model output, looking for parameters significantly different from zero. But this null-hypothesis is often a straw man hypothesis: it holds little credibility and exists purely for the purpose of being rejected. The outcome is a binary decision, indicating whether there is evidence against the null-hypothesis - but this says nothing about evidence in favor of the researcher's theoretical beliefs. What if researchers could explicitly test, and quantify the evidence in favor of, hypotheses of theoretical relevance? This presentation introduces the concept of informative hypotheses: theoretically derived statements about directional differences and equality constraints between (structural equation) model parameters. It explains the statistical underpinnings of Bayesian informative hypothesis evaluation and introduces the Bayes Factor as a measure of evidence in favor of one hypothesis over another. Finally, three open source software R-packages are presented: bain, which performs Bayesian evaluation of informative hypotheses, including about structural equation model parameters, and introduces a generalizable syntax for hypothesis specification; BFpack, which has specialized solutions e.g. for hypotheses about correlations and uses the same syntax; and gorica, a frequentist method for evaluating informative hypotheses based on a generalized AIC-type information criterion, which performs model comparison using AIC weights.

Pooled Score Tests for SEM with Multiply Imputed Data

Terrence D. Jorgensen, Maxwell Mansolf, & Craig K. Enders

Structural equation modeling (SEM) applications routinely employ a trilogy of significance tests that includes the likelihood ratio test (LRT), Wald test, and score test (or "modification index"). Researchers use these tests to assess global model fit, evaluate whether individual estimates differ from zero, and identify potential sources of local misfit, respectively. Until recently, only pooled Wald and LRT statistics have been proposed for multiply imputed data sets. We present a general pooled score test statistic for multiple imputations that follows the same logic as the pooled Wald test. Consistent with its complete-data counterpart, this

imputation-based score test provides an estimate of the expected change in a parameter estimate upon releasing the tested constraint(s). The new procedure is available for lavaan models using the R package semTools and naturally suited for identifying local misfit in SEM applications (i.e., a model modification index). A simulation study demonstrated the performance (Type I error rate, power) of the proposed score test relative to the score test produced by full information maximum likelihood (FIML) estimation. Due to the two-stage nature of multiple imputation, the score test exhibited slightly lower power than the corresponding FIML statistic in some situations but was generally well calibrated.

Introducing psychonetrics, an R package for structural equation modelling and network psychometrics.

Sacha Epskamp

In this talk, I introduce the R package psychonetrics (psychonetrics.org), which is a new open-source software package for structural equation modelling (SEM) and network psychometrics. The psychonetrics package currently includes multi-group (full-information) maximum likelihood estimation and weighted least squares estimation of (dynamic) latent variable models for cross-sectional, time-series and panel data. In addition, it includes the option for every variance-covariance matrix to be modelled as a Cholesky decomposition or a Gaussian graphical model (GGM; networks model of partial correlations). This allows for a large number of models that are closely related to SEM to be estimable: multi-level and meta-analytic GGMs (Epskamp et al., 2020), latent and residual network models (Epskamp et al., 2017), and latent-variable graphical vector-autoregression models for time-series and panel data (Epskamp, 2020). Finally, the package provides functionality to simplify exploratory estimation and model search for all included modelling frameworks. The talk will include a broad overview of the functionality of psychonetrics, a tutorial showcasing the syntax, and empirical examples showcasing its potential.

References

- Epskamp, S. (2020). Psychometric network models from time-series and panel data. *Psychometrika*. <https://doi.org/10.1007/s11336-020-09697-3>
- Epskamp, S., Isvoranu, A.-M., & Cheung, M. (2020). Meta-analytic Gaussian Network Aggregation. *PsyArxiv Preprint*. <https://doi.org/10.31234/OSF.IO/236W8>
- Epskamp, S., Rhemtulla, M. T., & Borsboom, D. (2017). Generalized Network Psychometrics: Combining Network and Latent Variable Models. *Psychometrika*, 82(4), 904–927. <https://doi.org/10.1007/s11336-017-9557-x>

Mixture multigroup factor analysis for unraveling measurement non-invariance across many groups

Kim De Roover

Psychological research often builds on between-group comparisons of (measurements of) latent variables, for instance, to evaluate cross-cultural differences in neuroticism or mindfulness. A critical assumption in such comparative research is that the same latent variable(s) are measured in exactly the same way across all groups (i.e., measurement invariance). Otherwise, one would be comparing apples and oranges. Nowadays, measurement invariance is often tested across a large number of groups by means of multigroup factor analysis. When the assumption is untenable, one may compare group-specific measurement models to pinpoint sources of non-invariance, but the number of pairwise comparisons exponentially increases with the number of groups. This makes it hard to unravel invariances from non-invariances and for which groups they apply, and it elevates the chances of falsely detecting non-invariance. An intuitive solution is clustering the groups into a few clusters based on the measurement model parameters. Therefore, we present mixture multigroup factor analysis (MMG-FA) which clusters the groups according to a specific level of measurement invariance. For instance, clusters of groups with metric invariance are obtained by making the loadings cluster-specific, whereas intercepts, factor (co)variances and residual variances are still allowed to differ between groups within a cluster.

Current opportunities and challenges in meta-analytic structural equation modeling

S. Jak

Meta-analytic structural equation modeling (MASEM) refers to fitting structural equation models (such as path models or factor models) to meta-analytic data. The meta-analytic data generally consists of correlations across the variables in the path or factor model, obtained from multiple primary studies. In this talk, I will contrast univariate MASEM to multivariate MASEM. Univariate MASEM refers to performing multiple univariate meta-analyses in order to obtain a synthesized correlation matrix as input in a SEM program. Multivariate MASEM in contrast involves using multivariate meta-analysis to synthesize correlation matrices across studies (e.g., GLS, TSSEM, one-stage MASEM). I will show that although univariate MASEM is the default MASEM method in for example organizational psychology, results obtained from univariate MASEM cannot be trusted. The reason that univariate MASEM is still often used, may be that fitting MASEMs may be challenging for researchers that are not accustomed to working with R software and packages. Therefore, we developed webMASEM; a web application for MASEM. This app implements the one-stage MASEM approach, and allows users to apply multivariate MASEM in a user-friendly way.

Using Meta-Analytic Structural Equation Modeling to Synthesize Data of Randomized Controlled Trials

Hannelies de Jonge, Kees-Jan Kan, & Suzanne Jak

Meta-analytic structural equation modeling (MASEM) is an increasingly popular method as it allows investigating multiple relations between variables simultaneously and to get the overall model fit of the hypothesized model (Becker, 1992, 1995; Cheung & Chan, 2005; Viswesvaran & Ones, 1995). Hypothesized models can include relationships between a grouping variable and several continuous variables. With current MASEM methods, it is not evident how one can include group data, such as dichotomous variables. In randomized control trials (RCT) the dichotomous variable typically represents whether the participants are in the experimental or control group. RCTs are applied in several research fields to gain knowledge on the effect of interventions. With RCTs, one could apply MASEM to evaluate the indirect effect of the intervention (X) on some outcome variable (Y) through a mediating variable (M). In RCTs, researchers typically report the Cohen's *d* (i.e., standardized mean difference), means of the groups on some outcome variable, and standard deviations. Cohen's *d* cannot directly be included in the MASEM-analyses as it is only possible to analyze correlation matrices. One way to include data of RCTs in MASEM is to transform the Cohen's *d* to a point-biserial correlation. McGrath and Meyer (2006) stress that even though Cohen's *d* and the point-biserial correlation can directly be transformed into each other, they are not automatically interchangeable and may lead to different conclusions. Moreover, in the meta-analytic literature there are various formulas to transform the Cohen's *d* to a pointbiserial correlation (see e.g., Borenstein, Hedges, Higgins, & Rothstein, 2009; Lakens, 2013; Lipsey and Wilson; 2001). Thus, it is not clear whether the use of these different transformation formulas lead to substantially different results when one includes Cohen's *d* to *r* transformed point-biserial correlations in MASEM. To investigate the effect of transforming effect sizes on the parameter estimates when applying MASEM to synthesize the results of RCTs in order to test mediational hypotheses, we will conduct a simulation study.

References

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A new approach for modeling aggregate constructs

Xi Yu, Georg Fassott, Florian Schuberth, Jorg Henseler

Aggregate constructs, i.e., constructs that are composed of their dimensions, are studied in various disciplines. However, limitations of existing approach to structural equation modeling (SEM) such as the two-stage approach and the conventional approach, prevent researchers from studying aggregate constructs with the flexibility that they are accustomed from SEM when used to study other types of constructs. To overcome this issue, we introduce the Henseler-Ogasawara (H-O) specification of aggregate constructs. Inspired by principal component analysis, in the H-O specification not only a single composite, but a set of composites is formed from the aggregate construct's dimensions. A scenario analysis which compares the performance of the H-O specification to existing approaches demonstrates the efficacy of our proposed specification.

SEMs as computation graphs and other useful insights from machine learning

Daniel Oberski

Data-driven Covariate Selection for Confounding Adjustment by Focusing on the Stability of the Effect Estimator

Wen Wei Loh and Dongning Ren

Valid inference of cause-and-effect relations in observational studies necessitates adjusting for common causes of the focal predictor (i.e., treatment) and the outcome. When such common causes, henceforth termed confounders, remain unadjusted for, they generate spurious correlations that lead to biased causal effect estimates. But routine adjustment for all available covariates, when only a subset are truly confounders, is known to yield potentially inefficient and unstable estimators. In this article, we introduce a data-driven confounder selection strategy that focuses on stable estimation of the treatment effect. The

approach exploits the causal knowledge that after adjusting for confounders to eliminate all confounding biases, adding any remaining non-confounding covariates associated with only treatment or outcome, but not both, should not systematically change the effect estimator. The strategy proceeds in two steps. First, we prioritize covariates for adjustment by probing how strongly each covariate is associated with treatment and outcome. Next, we gauge the stability of the effect estimator by evaluating its trajectory adjusting for different covariate subsets. The smallest subset that yields a stable effect estimate is then selected. Thus, the strategy offers direct insight into the (in)sensitivity of the effect estimator to the chosen covariates for adjustment. The ability to correctly select confounders and yield valid causal inference following data-driven covariate selection is evaluated empirically using extensive simulation studies. Furthermore, we compare the proposed method empirically with routine variable selection methods, including penalized or regularized SEM methods implemented in the `regsem` and `IsIx` R packages. Finally, we demonstrate the procedure using two publicly available real-world datasets.

Preprint: <https://psyarxiv.com/zkdqa/>

Bayesian regularized SEM: What, Why, When, and How?

Sara van Erp

The main goal of structural equation modeling (SEM) is to find a model that explains the phenomenon under investigation good enough while still being as parsimonious as possible. A recent development in SEM is to use regularization or penalization to attain such a model (Jacobucci, Grimm, McArdle, 2016). The basic idea of this approach is that some penalty function is applied to certain parameters in the model that will pull the estimates to zero if the parameter is zero in reality.

The idea of regularization in SEM can also be achieved using the Bayesian framework. In this case, a so-called *shrinkage prior* takes over the role of the penalty function. Many different shrinkage priors exist (van Erp, Oberski, & Mulder, 2019) and an active area of research is the implementation of these shrinkage priors in SEM. In this talk, I will explain the idea behind Bayesian regularized SEM as well as its advantages over classical regularized SEM. I will summarize the current state of research and illustrate its potential using different shrinkage priors. I will also discuss (current) limitations and potential areas for future research.

References

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