

Program 30th IOPS Winter Conference 2020

Thursday December 3rd 13:00 - 17:30 hours

13.00 – 13.15 Official opening and welcome

Rob Meijer (Chair IOPS) *University of Groningen*
Susan Niessen *University of Groningen*

13.15 – 13.40 Presentation Leonie Vogelsmeier *Tilburg University*

Latent Markov Factor Analysis: A mixture modeling approach for evaluating within- and between-person measurement model differences in intensive longitudinal data

When studying intensive longitudinal data (e.g., with Experience Sampling Methodology), drawing conclusions about dynamics of psychological constructs (e.g., well-being) over time requires the measurement model (MM; indicating which items measure which constructs) to be invariant between subjects and within subjects over time. However, there might be heterogeneity or “non-invariance” in the MM, for instance, due to subject-specific differences and changes in item interpretation or response styles. Mixture modeling approaches have proved to be powerful tools to detect unobserved heterogeneity, but methodology to evaluate measurement invariance for multiple time-points and subjects simultaneously was lacking. To fill this gap, we built upon common mixture modeling approaches and proposed latent Markov factor analysis (LMFA), which combines a discrete- or continuous-time latent Markov model (that clusters observations into separate states, according to state-specific MMs) with mixture factor analysis (that evaluates which MM applies for each state). In my talk, I introduce this novel methodology and present the latest extension, latent Markov latent trait analysis (LMLTA), that adequately deals with ordinal responses.

13.40 – 14:05 Presentation Elise Crompvoets *Tilburg University*

Pairwise comparison for educational measurement

Pairwise comparison is becoming increasingly popular as a holistic measurement method in education. Unfortunately, many comparisons are required for reliable measurement. To reduce the number of required comparisons, we developed two adaptive selection algorithms that select the most informative comparisons while taking the uncertainty of the object parameters into account. In a simulation study, we compared the performance of the algorithms with the commonly-used semi-random selection algorithm with respect to the object standard errors and reliability. In general, our Bayesian selection algorithm performed best. Our results revealed another concern for using pairwise comparison for educational measurement: can the SSR reliability estimate be trusted

14:05 - 14:25 Invited Speaker, Denny Borsboom *University of Amsterdam*

*Methodological contributions to research on COVID-19:
The RIVM-IOPS Task Force Psychometrics and other initiatives*

14:25 - 14:45 Break

14:45 - 15:15 Presentation Anton Olsson-Collentine *Tilburg University*

Meta-analyzing the multiverse: A peek below the hood of selective reporting

Any research process includes many decisions about how best to plan, run, analyze, and report a study. Unfortunately, the details of many decisions in a research project are often unclear, because typically the research process is only described in a short retrospective summary. Such lack of detail may hide biased decision-making and selective reporting. This concern is well recognized in the systematic review literature, and reporting guidelines (e.g., PRISMA, MARS) recommend reviewers to examine included studies for 'risk of bias'. However, it can be unclear what labels such as 'high' or 'some' risk of reporting bias mean practically and how concerned one should be. We show empirically what may underlie such labels, and what this means for resulting meta-analyses.

15:15 - 15:40 Presentation Wouter van Loon *Leiden University*

Selecting views in multi-view learning

Integrating information from different feature sets describing the same set of objects or persons is known as multi-view learning. In biomedical research, such feature sets (views) may correspond to different data sources such as medical imaging modalities, questionnaires, and omics data. Views can also be defined within data obtained from the same source, for example as different feature sets derived from the same image, as different brain regions, or as gene sets. Integrating the information from different views can increase the accuracy of medical classification models. However, collection of biomedical data can be expensive and/or burdening for patients. Identifying the views that are most important for prediction can improve the understanding of disease and can contribute to reducing the amount of required data collection. This leads to a group-wise feature selection or 'view selection' problem. In this talk I will discuss this view selection problem and a method we have been developing to tackle it.

15:40 - 15:55 Break

15:55 - 16:40 Poster Presentations (pitches)

Angelika Stefan *University of Amsterdam*

Eliciting Prior Distributions from Experts: Does Disagreement Matter?

Damiano D'Urso *Tilburg University*

Scale Length Does Matter: Recommendations for Measurement Invariance Testing with Categorical Factor Analysis and Item Response Theory

Edoardo Costantini *Tilburg University*

Multiple Imputation for High Dimensional Data: a Resampling Study Comparing State-of-the-Art Methods

Max Linde *University of Groningen*

Decisions About Equivalence: A Comparison of TOST, HDI-ROPE, and the Bayes Factor

Merle-Marie Pittelkow, *University of Groningen*

Are we there yet? Evidential strength of efficacy data for psycho-pharmacological treatments

Mingyang Cai *Utrecht university*

Predictive mean matching based on canonical regression analysis (PMM-CRA)

Sebastián Castro Alvarez, *University of Groningen*

Dynamic Item Response Theory (DIRT): Cleaning up the dirt in time series data

Sebastián Mildiner Moraga, *Utrecht University*

Bayesian multilevel hidden Markov models: data complexity and what researchers can do about it

Soogeun Park *Tilburg University*

Sparse Common and Distinctive Covariates Regression

16:40 - 17:25 Poster Breakout Sessions (4)

17:25 - 17:30 Closing

Rob Meijer