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From Behavioral Genetics to Idiographic Science: Methodological Developments and Applications Inspired by the Work of Peter C. M. Molenaar

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ABSTRACT

This special issue is a collection of papers inspired by Dr. Molenaar's work and innovations – a tribute to his passion for advancing science and his ability to ignite a spark of creativity and innovation in multiple generations of scientists. Following Dr. Molenaar's creative breadth, the papers address a wide variety of topics – sharing of new methodological developments, ideas, and findings in idiographic science, study of intraindividual variation, behavioral genetics, model inference/identification/selection, and more.

KEYWORDS

Peter Molenaar; granger causality; GIMME; idiographic; dynamic models; model equivalence

Dr. Peter Molenaar has made field-altering, transformational contributions to developmental science, cognitive science, behavioral and quantitative genetics, modeling of time-intensive brain/behavioral/physiological/developmental/cognitive processes, and quantitative psychology. He served on the faculty of the University of Amsterdam as head of the Department of Methodology before joining the faculty of Penn State in 2005. Throughout his career, Dr. Molenaar has received numerous accolades and awards, including the Sells Award for Distinguished Multivariate Research from the Society of Multivariate Experimental Psychology, the Pauline Schmitt Russell Distinguished Research Career Award from Penn State, and the Aston-Gottesman Award from the University of Virginia. He was editor of this journal, Multivariate Behavioral Research, from 2016 to 2020.

Dr. Molenaar's legacy of scientific contributions is complemented by the profound impact he has had on the lives of the many students and colleagues who have learned from him—through his papers, in classes, in lectures, in conversations, and by working alongside him. In every setting, Dr. Molenaar shares a lively passion for exploring a wide diversity of ideas, knowledge, and worldviews. His intellectual curiosity extends from statistics through all areas of psychology and deep into biology, physics, and philosophy. He is often encountered returning from the library with an armful of books—joyfully engaged each week with new readings that fuel new ideas and perspectives as he discovers connections between and among seemingly disparate areas of science and ways of thinking. Over the decades, Dr. Molenaar's deep engagements and wealth of knowledge have enriched and inspired everyone around him. Across the globe, his mentees and colleagues describe him as a visionary thinker—and note the astounding frequency at which the bold concepts and wild ideas he shares during casual hallway conversations later prove to be major innovations in how data are analyzed and what is learned from them. His continual pushing past the boundaries of traditional research methods has inspired a large community of mentees/peers to new thoughts, ideas, and discoveries.

This special issue is a collection of papers inspired by Dr. Molenaar's work and innovations—a tribute to his passion for advancing science and his ability to ignite a spark of creativity and innovation in multiple generations of scientists. Following Dr. Molenaar's creative breadth, the papers address a wide variety of topics—sharing of new methodological developments, ideas, and findings in idiographic science, study of intraindividual variation, behavioral genetics, model inference/identification/selection, and more. We hope that the collection honors the multitude of foundations that Dr. Molenaar has built and his unending encouragement to explore.

Pushing forward from Molenaar's contributions on alternative sources of developmental differences beyond standard decomposition of genetic and environmental influences (Molenaar et al., 1993), Bruins et al. (2024) introduce and test performance of a genotype-environment interaction model based on polygenic scores. This new model further grows the body of methods that can be used to test hypotheses about individuals' differential sensitivity to environmental circumstances depending on their genotype. Extending from Molenaar's work on children's cognitive development (Molenaar & Raijmakers, 2000), Lichtenberg et al. (2024) use hidden Markov models to identify and examine the variety of cognitive processes that manifest in young children's learning. The analyses artfully illustrate how advances in dynamic modeling that integrate intraindividual process models and interindividual differences models facilitate testing of detailed hypotheses about learning processes and development. Continuing Molenaar's explorations of multiple time-scale dynamics (Molenaar et al., 1992), Boker et al. (2024) introduce and check viability of a model wherein a differential equation model of individuals' long-term adaptation processes is combined with a second-order differential equation model for individuals' short-term regulatory dynamics. The analyses illustrate newly expanded possibility to examine and test hypotheses about intraindividual variations. Extending from Molenaar's explications of Granger causality in time-series models (Liu & Molenaar 2016; Molenaar & Lo, 2016), Oravecz & Vandekerckhove (2024) derive and implement the Bayes factor to quantify evidence in favor or against Granger causality among multivariate processes, including novel extensions to allow for test of no association from single- to multilevel frameworks. Together this set of papers propel new ideas about how to consider, incorporate, and interpret behavioral genetic, developmental, self-regulation, and affective processes that are manifested across the life course.

When highlighting the possibilities afforded by a new data analysis approach, Molenaar is a master at using extreme case scenarios to illustrate the consequential nature of traditional modeling assumptions. Leveraging this approach, Perez & Loken (2024) demonstrate that overall model fit as indicated by standard diagnostic tools fails to detect person-specific differential item functioning, thereby impacting the quality of the parameter and factor score estimates. In line with Molenaar's prior work on standard factor models (Kelderman & Molenaar, 2007), these simulations illustrate how serious departures from the model's homogeneity assumptions might be missed and thus compromise assessment of individuals' abilities. Parallel to this examination of across-person heterogeneity in measurement, Liu et al. (2024) suggest and demonstrate a taxonomy for describing the extent of across-person heterogeneity in the temporal relations among variables. Using an empirical demonstration, they show how qualification of how the data exhibit strict, pattern, weak, or no homogeneity in the intraindividual dynamics can help inform and clarify analytical choices and inferences. Pulling from Molenaar's Houdini transformation (Molenaar, 2003; Rovine & Molenaar, 2005), an algebraic framework wherein any latent variable model could be transformed into an observed variable model, Rovine & McDermott (2024) reify how the search for equivalences among models (e.g., RM ANOVA, latent growth, simplex, and non-stationary auto-regressive models of change) provides touchstones that transform seemingly qualitatively different models into nested models that can be directly compared with likelihood ratio tests. This subset of papers highlights both the need to acknowledge and affirm heterogeneity in both measurement and dynamic processes, while also reminding us that models/people that look quite different may, when we shift our perspective, actually be quite similar.

The next subset of papers drew inspirations from Dr. Molenaar's now-classic manifesto on idiographic science (Molenaar, 2004) where he outlined the ergodicity assumptions, how unlikely it is they are ever met, and suggested that understanding of individuals' behavior requires that we prioritize idiographic analysis of intra-individual variations over nomothetic analysis of interindividual differences. Focusing specifically on the implications for interpretation of cross-sectional correlation when ergodicity is absent, Hamaker (2024) derives the analytical expressions, showing how the often-interpreted cross-sectional correlation is a function of both between-person correlation (i.e., the correlation of stable between-person differences), and within-person correlation (i.e., the correlation between temporal within-person deviations from person-specific means). The expressions demonstrate exactly why care should be taken when interpreting cross-sectional modeling results. Borsboom &

Haslbeck (2024) deconstruct the idiographic-nomothetic divide, arguing that formal theories provide opportunity to make inferences about the interindividual and/or intraindividual phenomena manifested in the statistical patterns of empirical data. The paper argues that we can, with careful and precise theory, propel discovery of both types of phenomena. Tackling some of the concerns often leveled at the $N = 1$ idiographic analyses, Ram et al. (2024) suggest that the concept of generalizability is simply a subset of and can be replaced by notions of transferability that are core to modern artificial intelligence research and propose how explicit consideration of model transferability might proceed as newly available transformer models are applied to super-intensive time series data that are streaming continuously into myriad data repositories around the world. Together, these papers outline how formal tools might be used to advance theories by careful alignment of models, data, and assumptions that underlie those theories.

The final set of papers propel forward the ways that idiographic and nomothetic models can be combined. Each of these papers proposes and illustrates how to engage analysis of data obtained from multiple individuals can be analyzed simultaneously. Hunter (2024) presents a state-space mixture model in which subgroup or subpopulation differences in temporal structures are represented as distinct latent classes characterized by unique state-space models. Such a mixture approach provides an alternative way to reconcile idiographic and nomothetic variations compared, for instance, to the group iterative multiple model estimation (GIMME) framework, another important benchmark of Molenaar's scientific contributions. Central to the GIMME framework is the structural vector autoregressive model (SVAR; Chen et al., 2011; Gates et al., 2010), a multivariate dynamic network capturing contemporaneous and lagged (e.g., from yesterday to today) relations among multivariate time series processes, and is a variant of the vector autoregressive (VAR) model also considered in other papers in this issue (e.g., Oravecz and Vandekerckhove, 2024). GIMME begins by estimating individualized networks of contemporaneous and lagged relations, followed by iterative searches for relations or paths that are common across the majority of the participants, as well as individual-specific paths that, when freed up, yield significant improvements in fit. Lee & Gates (2024) outline one-stage and two-stage random effects meta-analysis for single-case experimental designs and show that the latter provides possibility to generate population inferences from a collection of person-specific SVAR models. The SVAR model has some inherent identifiability issues especially under weak directionality of influence, however, which motivated the development of GIMME for multiple solutions (GIMME-MS; Beltz & Molenaar, 2016) to highlight alternative GIMME solutions. Beltz & Kelly (2024) present an application of GIMME-MS to intensive longitudinal data on gender self-concept and cognition from young adults. GIMME-MS revealed notable heterogeneity in the presence, direction, and nature of relations from gender self-concept to cognition, underscoring the ambiguity that may arise in inferences for dynamic networks in the absence of strong assumptions. Park et al. (2024) evaluated results from applying two approaches developed by Molenaar and colleagues for subgrouping discrete-time processes such as VAR and SVAR, specifically subgrouped chain graphical VAR (scgVAR; Park et al., 2024) and subgrouping within GIMME (S-GIMME; Henry et al., 2019), to data realized by continuous-time processes. Fisher et al. (2024) propose yet a different approach, multi-VAR modeling, which serves similar goals as the scgVAR and S-GIMME, but rather than starting with individual modeling followed by iterative refinements of common paths characterizing the majority of individuals and subgroups of individuals with similar paths, multi-VAR uses cross-validation with penalized estimation to determine, in a single sweep, common, subgroup-specific, and individual-specific VAR paths. Together, these papers expand the variety of ways idiographic and nomothetic models can be combined and the types of intraindividual and interindividual phenomena that can be studied and theorized about.

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