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Bridging the Nomothetic and Idiographic Approaches to the Analysis of Clinical Data

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Abstract

The nomothetic approach (i.e., the study of interindividual variation) dominates analyses of clinical data, even though its assumption of homogeneity across people and time is often violated. The idiographic approach (i.e., the study of intraindividual variation) is best suited for analyses of heterogeneous clinical data, but its person-specific methods and results have been criticized as unwieldy. Group iterative multiple model estimation (GIMME) combines the assets of the nomothetic and idiographic approaches by creating person-specific maps that contain a group-level structure. The maps show how intensively measured variables predict and are predicted by each other at different time scales. In this article, GIMME is introduced conceptually and mathematically, and then applied to an empirical data set containing the negative affect, detachment, disinhibition, and hostility composite ratings from the daily diaries of 25 individuals with personality pathology. Results are discussed with the aim of elucidating GIMME's potential for clinical research and practice.

Keywords

connectivity map; group iterative multiple model estimation; idiographic; interindividual variation; intraindividual variation; nomothetic; personality disorder

From bench to bedside, the goal of clinical psychological science is to facilitate mental health by understanding disorders and implementing optimal prevention and treatment strategies (Kazdin, 2013). Achieving this goal requires the accurate description of current symptomatology and the accurate prediction of a disorder's future course, of methods for reducing and eliminating problematic behavior, and of ways to maintain psychological health. Accurate description and prediction, in turn, require tools that validly and reliably model clinical phenomena.

The aim of this article is to present an optimal statistical tool clinical scientists and practitioners can use for description and prediction: group iterative multiple model

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estimation, or GIMME (Gates & Molenaar, 2012). This is accomplished in several steps. First, the statistical idiographic (individual) and nomothetic (population) approaches are described. Second, the utility of the idiographic approach is elaborated via clinical examples and limitations are offered. Third, GIMME is introduced as a way to connect idiographic and nomothetic analyses, taking advantage of the strengths of each approach. Fourth, an example GIMME analysis is presented using daily diary reports from a heterogeneous sample of individuals with personality pathology. Personality pathology is consequently used as a prototype throughout the work. Fifth, the potential of GIMME for clinical research and practitioner implementation is explored.

The Idiographic Versus Nomothetic Approach

The traditional approach to statistical analysis in clinical (and all of psychological) science is nomothetic: The aim is to make *general predictions about the population* by examining *interindividual variation*, that is, variation between or across people (Molenaar, 2004; Molenaar & Campbell, 2009). The approach is appealing because it permits pooling across participants (e.g., members of a control or clinical group who share a disorder, risk factor, or treatment profile) for data collected in both cross-sectional and longitudinal designs.

In the idiographic approach to statistical analysis, however, the aim is to make *specific predictions about an individual* by examining *intraindividual variation*, that is, variation within a person over time (Molenaar, 2004; Molenaar & Campbell, 2009). Because this approach assumes heterogeneity across participants and time, each participant is intensively assessed at multiple time points, and then person-specific analyses are conducted; in other words, time series analyses are implemented (Lütkepohl, 2005). There are many types of data that are amenable to time series analyses, some of which clinical scientists and practitioners may have already collected but not coded or analyzed idiographically. Examples include observations of patient social interactions coded in 10-second intervals, a month of daily diaries containing patient-reported affect, functional neuroimaging scans, components of physiological health monitored with an actigraph (e.g., fitbit), and ecological momentary assessments, such as patient-reported cravings for a cigarette that are regularly entered into a smartphone application.

The difference between nomothetic investigations of interindividual variation and idiographic studies of intraindividual variation is shown in Figure 1. Each datum in Cattell's (1952) data box represents one variable measured at one point in time for one participant; see Figure 1A. When the data are concatenated across variables, a vector is formed that reflects all variables measured at a single time point for a single participant. When the variable vectors are then concatenated across participants, a plane is formed that houses all variables measured for all participants at a single time point; see Figure 1B. This is a data set used in nomothetic analyses of interindividual variation; it is based on the assumption that participants are homogeneous. When the variable vectors are concatenated across time points (instead of participants), a plane is formed that houses all variables measured at all time points for a single participant; see Figure 1C. This is a data set used in idiographic (time series) analyses of intraindividual variation; it is based on the assumption that participants are heterogeneous and change over time.

Ergodicity

Most psychological processes are nonergodic: They are heterogeneous across people and time because results obtained from analyses of interindividual variation are not equivalent to those obtained from analyses of intraindividual variation; these processes should, therefore, be studied with idiographic analyses (Molenaar, 2004). This is apparent in clinical data because individuals with the same disorder differ from each other and over time in nontrivial ways. The realization of individual differences in disorders partly underlies the motivation for the National Institute of Mental Health Research Domain Criteria (NIMH RDoC; Insel et al., 2010), which is an initiative to better understand, prevent, and treat mental illness by reconceptualizing psychopathology: Disorders do not reflect distinct, qualitative groups but rather manifestations of varying levels of multiple (often biologically influenced) behavioral dimensions. Also, disorders change over time, as seen in individuals who have the same disorder, but whose diagnosis resulted from unique triggers and symptomatology, and whose treatment profiles vary. For example, individuals with borderline personality disorder are heterogeneous, differing in levels of effortful control and types of interpersonal problems (Hoermann, Clarkin, Hull, & Levy, 2005; Wright et al., 2013). Change is also evident in those with personality disorders, including borderline personality disorder, with most people displaying fewer clinical symptoms as their personalities mature over time (Wright, Hopwood, & Zanarini, 2015). In cases such as these, where there is heterogeneity across participants and time, only idiographic analyses offer accurate results that reflect the *dynamic* psychological processes being studied (Molenaar, 2004).

Idiographic Analyses in Clinical Science

It is clear that the idiographic statistical approach should be taken to delineate the dynamics underlying mental health. This is true not only from a methodological perspective but also from a therapeutic perspective, so that clinical research can inform responses to national calls for personalized treatment (Insel, 2014). Idiographic analyses will have the greatest impact on personalized treatment when combined with idiographic assessment, or the measurement of behaviors that are most relevant to an individual's unique symptom profile or disease presentation (rather than using standardized questionnaires; see Haynes, Mumma, & Pinson, 2009). Even though a person-specific approach is by no means the typical approach, its influence is quickly growing within the medical and psychological sciences due to its accuracy and potential for unveiling novel results. For instance, it has been used to determine the timing of insulin injections for diabetes patients (Wang et al., 2014), genetic contributions to brain function (Molenaar, Smit, Boomsma, & Nesselroade, 2012), and sex differences in children's play (Beltz, Beekman, Molenaar, & Buss, 2013). Some insightful examples of clinically relevant person-specific approaches are also available in the literature; two studies are considered below.

Examples Concerning Personality

In the first example, 22 participants provided personality assessments for 90 consecutive days, each day reporting on the extent to which 30 adjectives (e.g., irritable, sociable, helpful, industrious, and knowledgeable) described their behavior (Borkenau & Ostendorf, 1998). The 30 adjectives were designed to reflect the Big Five personality factors. Using a

nomothetic approach to determine the structure of personality, in which single ratings of the 30 adjectives for all 22 participants were submitted to a standard factor analysis (r-technique), the expected results were found: The well-known Big Five structure emerged (Borkenau & Ostendorf, 1998). Results differed, however, when an idiographic approach was used, in which 22 different factor analyses were conducted, and in each, the person-specific structure of personality was determined from a participant's 90 ratings of the 30 adjectives (p-technique; Jones & Nesselroade, 1990; Molenaar & Nesselroade, 2009). In these analyses, the five-factor structure was not found for even one participant (Molenaar & Campbell, 2009). Eight participants had two-factor structures, 13 had three-factor structures, and one had a four-factor structure. Thus, personality appears to be nonergodic (i.e., its structure differs in analyses of inter- and intraindividual variation), with idiographic analyses using time series data capturing the heterogeneity across participants.

In the second example, daily covariation among different facets of internalizing and externalizing behavior problems was determined in four individuals with personality pathology (Wright, Beltz, Gates, Molenaar, & Simms, 2015). Four facets were defined by participants' behavioral ratings provided each day for nearly 100 days: negative affect, detachment, disinhibition, and hostility. Unified structural equation models (uSEMs; Gates, Molenaar, Hillary, Ram, & Rovine, 2010; Kim, Zhu, Chang, Bentler, & Ernst, 2007) mapped the covariation among the facets, such that each facet had the potential to predict or be predicted by the lagged and contemporaneous variation in the other facets. Figure 2 shows the result for one participant (Wright, Beltz, et al., 2015). Notice that variation in disinhibition was explained by the previous day's disinhibition (dashed line with $\beta = .37$), and that disinhibition substantially explained variation in hostility on the same day (solid line with $\beta = .70$); variation in hostility was also explained by detachment from the previous day (dashed line with $\beta = -.17$). One interpretation of the hostility result is that this individual's interactions with others are likely to have detrimental outcomes: The individual acts aggressively because he or she is irresponsible (high disinhibition) and his or her aggression is exacerbated around others (low detachment). Results shown in this map are person-specific: Even though they are unlikely to generalize to other participants, they have high clinical relevance for this individual; for example, they suggest that this individual's detachment is externally (interconnected with adverse interpersonal interactions) and not internally driven (propelled by a self-induced withdrawal), and thus, that a practitioner might consider targeting interpersonal interactions in treatment.

Criticisms of the Idiographic Approach

Despite its advantages for heterogeneous and time-varying data and its potential for personalized treatment, the idiographic approach has been criticized. One critique that is particularly relevant to clinical applications is that concentration on the individual-level undermines generalization (Spencer & Schöner, 2003). In other words, person-specific analyses provide detailed results that do not apply to other individuals or even to the same individual in a different situation. Other critiques stem from questions concerning the practicality of implementing an idiographic approach. How can behaviors be intensively measured across time? Are person-specific analyses too difficult for a non-methodologist to

use? How do clinical scientists present results in a manuscript? They cannot possibly create and interpret process models (e.g., versions of Figure 2) for each person in their sample.

These critiques of the idiographic approach are overcome by GIMME and a detailed discussion of its implementation. GIMME addresses the substantive critiques because it integrates the nomothetic and idiographic approaches: The group-level structure within GIMME facilitates generalization and results presentation, while the individual-level structure makes GIMME suitable for heterogeneous data. The practical critiques are addressed below through an accessible presentation of GIMME analysis procedures and results interpretation.

GIMME: Bridging Idiographic and Nomothetic Approaches

GIMME bridges nomothetic and idiographic analyses for data that are heterogeneous across people and time (Gates & Molenaar, 2012). It simultaneously analyzes each datum in Cattell's (1952) data box shown in Figure 1A. It does not separate the matrix into single coronal slices of time for nomothetic analyses (Figure 1B) or axial slices of people for idiographic analyses (Figure 1C). GIMME accomplishes this by mapping directed relations among a set of variables according to their temporal covariation, creating individual-level networks that include some group-level relations, that is, directed relations shared for everyone in the sample.

Conceptual Introduction to GIMME

GIMME generates a graph for each participant that can be conceptualized as a person-specific network or connectivity map. The graphs, networks, or maps can be behavioral (e.g., explaining associations among self-reported personality facets), biological (e.g., explaining links between cortisol and substance use), or neural (e.g., explaining connections among brain regions). They take advantage of the temporal ordering of measurements to show how one variable linearly affects or is affected by another.

GIMME was developed to map functional neuroimaging data, explaining how activity (usually the blood oxygen level–dependent signal collected via functional magnetic resonance imaging, or fMRI) in one neural region of interest was explained by activity in other region of interests (Gates & Molenaar, 2012). Large-scale simulation studies have shown that GIMME recovers more true parameters and generates fewer false positives than other connectivity mapping techniques, including correlations, principal components, Granger causality, Bayesian nets, and dynamic causal models; thus, it is an accurate, state-of-the-art approach for network mapping (Gates & Molenaar, 2012; Smith et al., 2011). This accuracy is due, in part, to GIMME's inclusion of group-level information in individual-level solutions. The group-level structure (i.e., set of relations among variables) is robust (in that it holds across participants) and helps ensure that network relations are not the result of statistical noise, as can be the case for relations in idiographic analysis approaches. GIMME also adds an individual-level structure, such that a network is created for each participant. This makes GIMME appropriate for heterogeneous data.

Another reason for GIMME's optimal performance is that it maps both lagged and contemporaneous relations among variables. Variables are predicted by other variables measured at the same time point and by variables measured at previous time points. GIMME accomplishes this by implementing a uSEM (introduced above in *Examples Concerning Personality* section; Wright, Beltz, et al., 2015) at both the group- and individual-levels (Gates et al., 2010; Kim et al., 2007). A uSEM is a structural vector autoregressive model (Lütkepohl, 2005) that is estimated by simultaneously fitting both lagged and contemporaneous weighted relations to the data.

A final reason for GIMME's optimal performance is that it is data-driven. It is an exploratory, bottom-up approach in which maps are built for participants based on their time series. This does not mean that relations are added randomly, though; only significant relations are added to the model using the validated sequential fitting procedure described in the Supplemental Materials (available online at http://asm.sagepub.com/content/by/supplemental-data). Exploratory work is advantageous because clinical science is in a period of discovery, as little is known about the dynamic processes underlying personality and psychopathology (Bringmann, Lemmens, Huibers, Borsboom, & Tuerlinckx, 2015; Cramer et al., 2012). Nonetheless, GIMME can also be implemented in a confirmatory way to test specific hypotheses; clinical scientists can specify which relations are included in a participant's network.

Mathematical Introduction to GIMME

In matrix notation, GIMME with constant mean (fixed at zero) is specified as

$$\eta_i(t)=(\mathrm{A}_i+\mathrm{A}^g)\eta_i(t)+(\Phi_{1,i}+\Phi_1{}^g)\eta_i(t-1)+\zeta_i(t),$$

where $\eta_i(t)$ is the p-variate series to be explained at time points $t = 1, 2, \ldots T$, with T the total number of time points; A is the (p,p)-dimensional matrix of contemporaneous relations among variables; Φ_1 is the (p,p)-dimensional matrix of lagged relations among variables; ζ_i is the p-variate error matrix, lacking sequential dependences and having zero mean and a diagonal covariance matrix; superscript g indicates group-level relations; subscript i indicates individual-level relations. GIMME is fit using a special sequential procedure that is described in the Supplemental Materials (see also Gates & Molenaar, 2012). This procedure involves Lagrange multiplier testing combined with Wald trimming and provides results consistent with those obtained through likelihood ratio testing (Chou & Bentler, 1990).

There are two assumptions of GIMME that must be satisfied for each data set. One is that the solution produced for each participant (that contains group- and individual-level relations) is unique; there are no other networks that similarly fit the data. This may not always be the case because the A matrix of contemporaneous relations is essentially a cross-sectional path model (e.g., SEM) embedded within GIMME, and multiple solutions are a characteristic of cross-sectional path models (MacCallum, Wegener, Uchino, & Fabrigar, 1993). To solve this potential problem, GIMME for multiple solutions (GIMME-MS; Beltz

& Molenaar, in press) can be used to generate all possible solutions so that an optimal one can be selected.

The other assumption is that there are no temporal dependencies in the error term, that is, that the residuals are white noise. GIMME is currently implemented with a lag of 1, meaning that each variable has the opportunity to be explained by the other variables (and itself) at the prior measurement (and concurrently), but each variable may also be related to other variables (and itself) from two measurements ago, three measurements ago, and so on. If this is the case, then a lag of 1 will be insufficient for the data (and residuals will not be white noise), and a lag of 2, 3, and so on must be included in the model (in Φ_2, Φ_3, and so on matrices). A posteriori model validation can be used to test the white noise assumption and to subsequently modify individual-level maps when lags greater than 1 are necessary (Beltz & Molenaar, 2015).

Exemplar GIMME Analysis

GIMME is easy to use. It has only a few data stipulations and is estimated within an SEM framework using a fully automated program. GIMME currently assumes continuous time series that are weakly stationary (i.e., with constant means and variances), and thus, obvious trends or cycles should be removed prior to analysis; there are several programs that facilitate this (see, e.g., Liu & Molenaar, 2014). Additional information is provided in the Supplemental Materials.

Method

Participants were 25 individuals (14 women) with a personality disorder selected from the daily diary portion of a parent study aimed at refining measurement in personality pathology (for details, see Wright, Beltz, et al., 2015). Participants had a mean age of 42 years (SD = 12.8) and were heterogeneous in their personality disorder diagnoses, with most receiving more than one diagnosis: 60% avoid-ant, 8% dependent, 52% obsessive compulsive, 24% narcissistic, 56% borderline, 4% histrionic, 12% antisocial, 48% paranoid, 16% schizotypal, and 8% schizoid.

Participants were instructed to complete diaries for 100 consecutive evenings (for further details, see Wright, Beltz, et al., 2015). The diaries were online surveys, consisting of questions related to clinically relevant behaviors. Participants included here provided a median of 95 diaries (M = 93.3, SD = 7.8). They received financial compensation for their participation.

Sixteen items from the daily diaries concerning behavioral manifestations of personality disorders were used in the present study, replicating procedures used in prior idiographic analyses with this sample (see *Examples Concerning Personality* section and Wright, Beltz, et al., 2015). On an 8-point scale from 0 (*not at all*) to 7 (*very much so*), participants endorsed statements about each behavior. The statements were designed to reflect the personality facets of negative affect (*I felt depressed*), detachment (*I didn't want to be around others*), disinhibition (*I did something on impulse*), and hostility (*I lost my temper*). Empirical work supports this organization: Multilevel structural equation models show that

the items load onto four factors at the within-person level (Wright, Beltz, et al., 2015). Items defining each facet were averaged for each participant at each time point; the resulting four-variate time series were used in subsequent analyses.

Data Analysis

The time series were submitted to GIMME-MS (Beltz & Molenaar, in press); analyses were conducted in MATLAB (MathWorks, 2010) and LISREL (Jöreskog & Sörbom, 1992). GIMME-MS was used because multiple solutions are present when contemporaneous relations are large with respect to lagged relations (Beltz & Molenaar, in press), and relatively large contemporaneous relations were expected in daily diary data, as the (long) 24-hour measurement interval reduces temporal correlations. When there were multiple solutions at the individual level, the Akaike Information Criterion (AIC; Akaike, 1974) was used to select the optimal one (see Wright, Beltz, et al., 2015). When there were multiple solutions at the group level, the optimal one was selected by evaluating the final maps using three decision metrics: (a) alternative fit indices to ensure all solutions fit the data well, (b) the AIC to determine which solution explained the most information using the fewest parameters, and (c) the maximum residual—an indicator of model misfit—to determine which solution best accounted for the variation in all variables (i.e., had the lowest maximum residual). These decision metrics have performed well in simulation studies, leading to the identification of the true model (Beltz & Molenaar, in press). Final maps (i.e., person-specific models containing group- and individual-level relations) were evaluated with alternative fit indices, with two of four required to indicate excellent fit (Brown, 2006): root mean square error of approximation (RMSEA) ≤ .05, standardized root mean square residual (SRMR) ≤ .05, comparative fit index (CFI) ≥ .95, and non-normed fit index (NNFI) ≥ .95.

Final models were then submitted to a posteriori validation (as described in Beltz & Molenaar, 2015). To ensure the lagged relations sufficiently accounted for the temporal dependencies in the time series, residuals were examined with white noise tests; the tests were evaluated with the same alternative fit indices and cutoffs as the final models. When residuals were not white noise, modification indices were used to add lag 2 individual-level relations to the map, and then white noise tests were repeated.

Results

GIMME-MS detected four group-level solutions and multiple solutions in some individual-level maps: 24% in the first group-level solution, 8% in the second group-level solution, 20% in the third group-level solution, and 12% in the fourth group-level solution. As shown in Figure S1, the group-level solutions each contained a contemporaneous relation between negative affect and detachment and between disinhibition and hostility, but they differed in the directions of the relations. Table 1 shows the decision metrics for each group-level solution, revealing that while all solutions fit the data well (i.e., had two of four alternative indices indicating excellent fit), the first was optimal according to the AIC and maximum residual, having the lowest values. Thus, the first solution was selected.

The final maps from the first solution were submitted to a posteriori model validation to ensure that their temporal order (i.e., the covariation accounted for by the contemporaneous

and lag 1 relations) was sufficient for capturing all sequential dependencies in the data. The relations were sufficient for 24 participants; only a single participant required two lag 2 relations. After estimating these lag 2 relations, all models testing white noise fit the residuals well, according to mean fit indices: RMSEA = .00, SRMR = .08, CFI = .99, and NNFI = .95.

GIMME-MS with a posteriori model validation generated a map for all 25 participants in the example data set, as shown for four individuals in Figure 3. (To aid comprehension, Figure S2 also shows the map for one participant depicted as a lead-lag-type diagram.) Each map contained the contemporaneous group-level relations uncovered by the first GIMME-MS solution shown in Figure S1, a unique pattern of contemporaneous, lag 1, and (for one participant) lag 2 individual-level relations, beta weights associated with all relations, excellent statistical fit to the data according to alternative indices, and white noise residuals.

Key elements of the results are considered below with respect to the maps in Figure 3, and they are listed in general terms applicable to all GIMME analyses in Table S1. First, the maps fit each participant's data well. Even the χ^2 tests were nonsignificant in Figure 3.

Second, all participants have the same two group-level contemporaneous relations (thick solid arrows), but the beta weights for the relations differ across participants. (Group-level lagged relations are possible, but none were detected.) These group-level relations reflect sample homogeneity, highlighting parameters that may be meaningful to examine in studies of interindividual variation using nomothetic analyses. They are positive in all instances in Figure 3 (e.g., increases in negative affect predict increases in detachment), but they can also be negative.

Third, participants have different individual-level relations (thin solid and dashed arrows). These individual-level relations reflect sample heterogeneity, highlighting the importance of analyzing intraindividual variation in idiographic analyses. These relations are statistically significant for each participant; significance is ensured by the trimming procedures employed within GIMME. They can also be positive or negative; for example, among other influences, increases in the negative affect of Participant C were predicted by previous-day increases in the same behavior, providing evidence for some carry-over effects.

Fourth, contemporaneous relations (solid arrows) show how personality facets are related on the same day, while the lagged relations (dashed arrows) show how facets are related on subsequent days. Returning to the negative affect of Participant C, increases in it are predicted by decreases in disinhibition from the previous day, increases in disinhibition on the same day, and increases in negative affect (itself) from the previous day. The self-prediction reflects an autoregressive component, and its interpretation is straightforward: The participant is likely to be in a bad mood today if he or she was in a bad mood yesterday. The prediction by both increases and decreases in disinhibition, however, is not as clear: They create a feed forward loop and underscore that complex temporal dynamics underlie the interplay between negative affect and disinhibition for this person. Moreover, Participant C's relations between disinhibition and hostility, with the former predicting the latter on the same day but the latter predicting the former on subsequent days, likely reflect a feedback

loop and underscore the perpetual interdependence between the behaviors. Potential clinical interpretations of these relations are elaborated in the next, closing section.

GIMME for Clinical Research and Practice

GIMME has the potential to provide insight into clinical research and practice. Although direct translations from network maps to therapeutic settings might be premature, there is little doubt that such notions are in the zeitgeist. So, some of the ideas presented below are speculative, but they are nonetheless important for urging science forward.

A detailed review of the four final person-specific maps presented in Figure 3 reveals some potential ways in which GIMME can inform clinical work. Two of the four participants (A and C) had maps with individual-level autoregressive components. In the full sample, 32% had one autoregressive component, 24% had two components, 12% had three components, and 0% had four components; 32% had no autoregressive components. These percentages are low compared with GIMME maps created from fMRI data, which usually contain group-level autoregressive components (e.g., Beltz, Gates, et al., 2013). Results may differ due to the measurement interval (seconds vs. 24 hours) or they may reveal something unique about personality disorders, such as low emotional continuity. This could be tested by replicating findings with data collected at a different measurement interval (e.g., 12 hours), comparing maps of those with a personality disorder to maps of healthy controls, or correlating the number of autoregressive components in current maps with behaviors assessed in the clinic. If this is indeed a novel clinical finding, then the number of autoregressive components could be used as a marker for disorder severity, daily functioning, or treatment responsiveness.

Three of the four participants in Figure 3 (A, B, and D) had maps in which hostility predicted negative affect (contemporaneous or lagged relation), but negative affect never predicted hostility. This generalized to the full sample, in which hostility predicted negative affect for 44% of the participants, but the reverse never occurred. There is high confidence in the direction of these relations because GIMME-MS was used with the purpose of accurately determining the direction of explanation between relations (see Beltz & Molenaar, in press). Thus, hostility's influence on negative affect is a potential clinical target that warrants further empirical investigation: Negative affect and hostility are known to co-occur (Watson & Clark, 1994), but the direction of their relation has received little attention.

Feed forward loops in the maps of Participants B and C signal possible areas for clinical intervention. For Participant B, hostility positively predicted negative affect contemporaneously and at a lag of 1. Colloquially, this is a “double whammy,” as negative affect increased with increases in same-day and previous-day hostility. For Participant C, negative affect increased with increases in same-day disinhibition and decreases in previous-day disinhibition. Although this initially seems counterintuitive, it might actually signal that the relations have different origins (i.e., that different variables exogenous to the network are responsible for them). The same-day positive relation might indicate that consequences of the impulsive behaviors sparked the participant's poor mood (e.g., upset over a speeding ticket), while the previous-day negative relation might suggest that the participant is in a bad

mood after exhausting all his or her emotional resources by inhibiting impulses the day before. Other explanations are also possible and could instigate future work.

Feedback loops between disinhibition and hostility in the maps of Participants C and D show the perpetual interdependence between behaviors that define externalizing problems. The contemporaneous group-level relation from disinhibition to hostility was accompanied by an individual-level relation from hostility to disinhibition in the maps of 40% of the sample; 80% of those individual-level relations were lagged and 90% were positive. Thus, for most participants, disinhibition and hostility fueled each other: for example, impulsivity heightened same-day aggression, while aggression, in turn, heightened impulsivity on the next day. But, the interpretation likely differs for the single participant who had a negative individual-level relation from hostility to disinhibition. For this person, as impulsivity increased aggression, aggression decreased impulsivity; this suggests that an unmodeled third variable, such as emotion regulation, may have moderated the relation. The unique pattern for this participant might also substantively mark recovery, and it emphasizes the methodological importance of the idiographic approach.

Opportunities for Integrating GIMME and Clinical Science

GIMME aligns with current thinking in clinical science. The recent revision of the *Diagnostic and Statistical Manual of Mental Disorders* reignited discussions about the heterogeneity of disorders and the need to study individuals and their symptoms over time (Olbert, Gala, & Tupler, 2014), a task that GIMME accomplishes. GIMME is also consistent with the aims of the NIMH RDoC to unpack disorders by delineating the dynamics (e.g., individual differences in continuously measured symptoms) that underlie them (Insel, 2014; Insel et al., 2010).

There are also many possibilities for combining GIMME and clinical research to benefit the patient–practitioner relationship. First, GIMME-MS could be incorporated into therapy sessions. In the empirical example presented here, statistical criteria (e.g., AIC) were used to select a single solution from the set of possible solutions generated by the program. Although this approach has been supported in simulations (see Beltz & Molenaar, in press), it may be unsatisfying from an applied perspective, especially when statistical differences are small. So, clinical criteria could be used to aid or determine model selection. A practitioner could collaborate with the patient to identify a solution, presenting the patient with the possibilities and asking for reactions to them. The patient could suggest which behavior he or she thinks is the cause and work to change it, with the practitioner's guidance. This may be particularly meaningful when used in combination with idiographic assessment (see Haynes et al., 2009).

Second, real-time map updates could be used to inform practitioners of changes that might signal a patient's recovery or regression. There is a movement in data science to increase participants' control of their own data. In this framework, participants regularly provide responses to questions using a smartphone application, creating a time series. Participants are then “pinged” by researchers to contribute to studies. If they opt in, then the researchers send a statistical model to be run locally on the participants' time series, and the model results (but not the raw data) are sent back to the researchers (see, e.g., Boker et al., 2015).

This could be extended to GIMME in clinical settings. For instance, the emergence of a relation from negative affect to disinhibition might signal that a patient is acting irresponsible in response to feelings of anxiety, and might prompt a practitioner to intervene with exercises to reduce the anxiety.

Third, GIMME maps could be linked to clinical data, and treated as a consequence of past actions or as a predictor of future outcomes. Map parameters, such as beta weights from group-level relations (which are estimated for everybody), the number of individual-level relations (which can be an indicator of behavioral complexity), or graph theoretical metrics (e.g., degree, which is the sum of a variable's incoming and outgoing relations) can be correlated with clinically relevant behaviors or examined for group differences. Moreover, GIMME could be extended to consider the influence of external influences, that is, exogenous variables or aspects of the context that might influence the network (Gates, Molenaar, Hillary, & Slobounov, 2011). For example, the relations among variables may differ on days when a patient visits his or her practitioner, family, or place of employment. This may be a meaningful way to identify triggers.

Fourth, GIMME could be leveraged to enhance understanding of the temporal nature of clinical phenomena. It is paramount that researchers consider the time course of client behaviors and that they plan their assessments accordingly. For example, the daily diary measurements used here may fail to capture alterations in the behavior of individuals with borderline personality disorder, whose affect changes by the minute. When in doubt, researchers should measure behavior as frequently and for as long as possible. If the resulting time series are not stationary, GIMME can still be used, but its implementation must be altered to accommodate time-varying relations. For example, separate models could be conducted for different sections of the time series, GIMME could be run on an individual's windowed data to see which relations are constant across time, nonstationary relations could be directly estimated using a second order extended Kalman filter/smoother (see Molenaar, Beltz, Gates, & Wilson, 2016), or analyses could be conducted in the frequency domain (see Molenaar & Lo, 2015).

Alternatives to GIMME

GIMME spans the idiographic and nomothetic analysis approaches and has been shown to be accurate with heterogeneous data (Gates & Molenaar, 2012), but there are also other analysis techniques that include both individual- and group-level parameters. These techniques may be more suitable than GIMME for particular research questions or data sets.

Most techniques that contain group- and individual-level parameters parse between- and within-person variation, taking advantage of group-level information to aid the estimation of individual-level parameters, but they do not provide person-specific results. For example, multilevel models contain both fixed (i.e., group means) and random (i.e., variations from the means) effects, but they generally take a nomothetic approach to longitudinal data and use interindividual variation to determine how participants change with respect to others in the sample (Ram & Grimm, 2007). One extension of multilevel modeling unpacks the random effects variation into between- and within-person effects (i.e., time invariant and time-varying predictors) in order to, respectively, mark differences among people that

consistently influence behavior and changes within a person that influence behavior differently across time (see Hoffman & Stawski, 2009). Such an approach might be better suited than GIMME for data sets with fewer than 20 measurement occasions. Multilevel structural equation models offer a similar approach for time series data (e.g., data sets with greater than 20 measurements), in which variation is parsed into between- and within-person structures, both of which require some pooling across participants (for an instance relevant to personality pathology, see Wright, Beltz, et al., 2015). Relatedly, multilevel dynamic factor models (Song & Zhang, 2014) have been used to capture between-person variation; they expand on p-technique and dynamic factor models (Jones & Nesselroade, 1990; Molenaar, 1985). Multilevel structural equation models and dynamic factor models do not generate person-specific results, but they may be better suited than GIMME for the analysis of behaviorally high-dimensional data sets (e.g., with more than 20 variables) that contain a latent structure.

Beyond p-technique and dynamic factor models, other person-specific modeling approaches have recently been extended to multiple subjects. A newly proposed machine learning algorithm (Karch, Sander, von Oertzen, Brandmaier, & Werkle-Bergner, 2015) is similar to GIMME in that it generates individual- and group-level results, but it requires many measurement occasions (over 1,000) in order to train and test a classifier. Thus, it currently holds the most promise for clinically relevant physiological measurements (e.g., obtained through electroencephalography) and not behavioral assessments. A promising area for future work also concerns examination of optimal ways to incorporate group-level parameters into other idiographic analysis approaches, such as dynamic time series regression and autoregressive moving-average models.

Finally, dynamic systems modeling techniques may hold particular promise for clinical science (e.g., Granic & Hollenstein, 2003; Pervin, 2001). They consider all influences on a person (i.e., system), including the temporal nature of behavior and how it changes with respect to context and in response to others (Thelen & Smith, 1998). The techniques can be challenging to implement and interpret, though, because a data set must be conceptualized in terms of dynamic systems constructs, such as attractors (system-preferred behavioral states) and repellors (system-averted behavioral states), and the richness of the person-specific results is often lost by implemented summary statistics. Thus, GIMME is optimal for research questions concerning individual differences in the pattern of covariation among a set of related brain or behavioral variables and time series data sets collected with many observations and variables. (Specific guidelines about observations and variables are made in the Supplemental Materials.)

Conclusions

GIMME is a data analysis method that holds great promise for clinical research and practice. Developed for analyzing neural networks, it can also be used with behavioral time series data (e.g., daily diaries, coded observations, physiological recordings) to create person-specific maps that contain a group-level structure by identifying contemporaneous and lagged directed relations among the behaviors. Thus, it combines the idiographic analysis approach concerned with person-specific models of intraindividual variation and the

nomothetic analysis approach concerned with population-generalizable models of interindividual variation. The maps not only provide insight into the heterogeneity among people, symptoms, and time courses underlying psychopathology, but they can also be leveraged in treatment (e.g., as representations of patient behavior problems that require discussion and possibly mediation and as real-time indicators of patient functioning that may signal the need for practitioner intervention).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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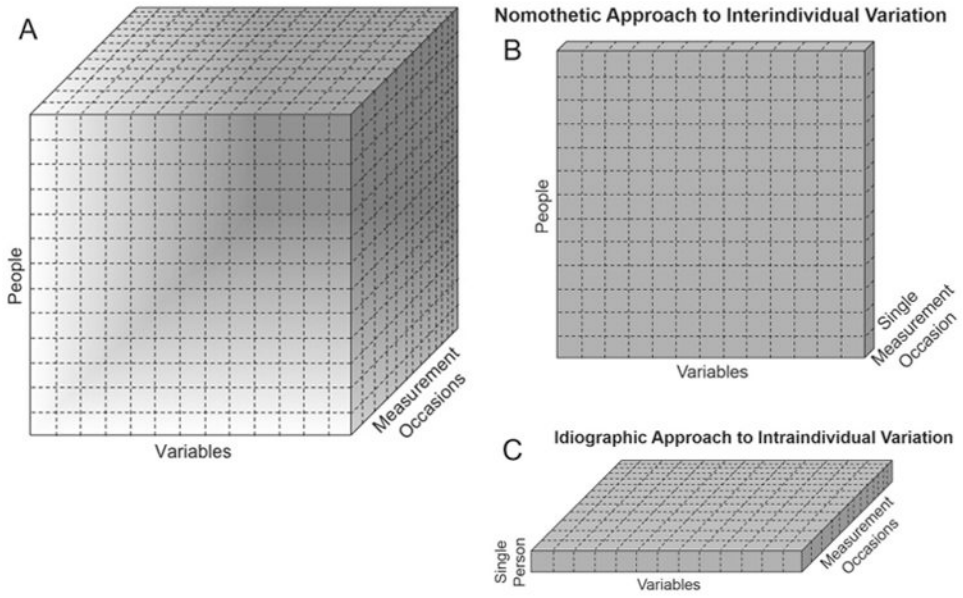

Figure 1.

A Cattell (1952; see also Ram & Nesselroade, 2007) data box illustrating the structure of data from multiple people, variables, and measurement occasions (i.e., time points). (A) A complete data box contains data from all people, variables, and measurement occasions; these data can be analyzed with GIMME (Gates & Molenaar, 2012), which accurately models both inter- and intraindividual variation. (B) A single coronal slice of the data box contains data from all people and variables at a single measurement occasion; these data can be analyzed with nomothetic analyses of interindividual variation that permit inferences about the population if people are homogeneous. (C) A single axial slice of the data box contains data from all variables and measurement occasions for a single person; these data can be analyzed with idiographic analyses of intraindividual variation that assume people are heterogeneous across time.

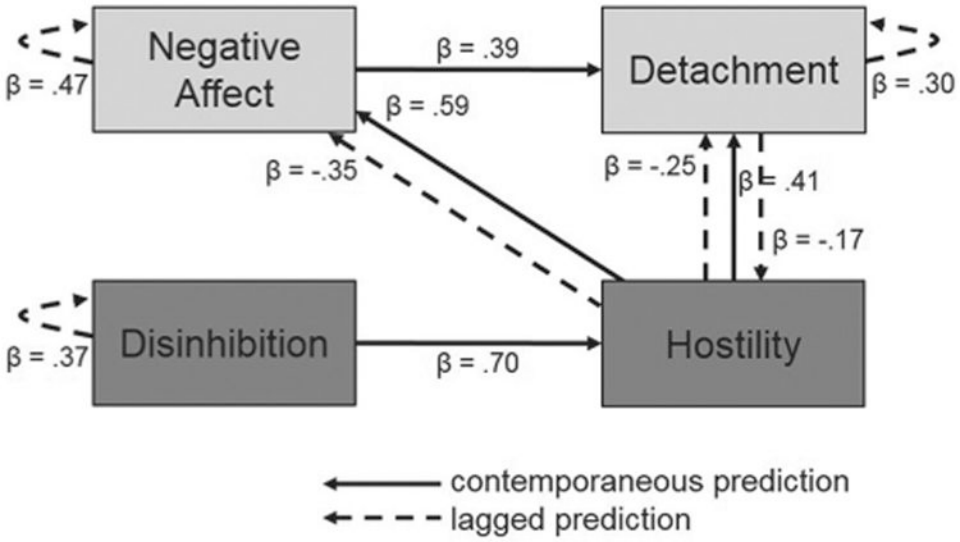

Figure 2.

Results of an idiographic analysis implementing a unified structural equation model (Gates et al., 2010; Kim et al., 2007) on a single participant's composite daily reports of negative affect and detachment (in light gray, reflecting internalizing problems) and disinhibition and hostility (in dark gray, reflecting externalizing problems). Variation is explained by contemporaneous (solid arrows) and lagged (dashed arrows) relations among the facets. For example, today's negative affect is predicted by yesterday's negative affect and hostility as well as today's hostility.

Note. Reproduced from Wright, Beltz, et al. (2015).

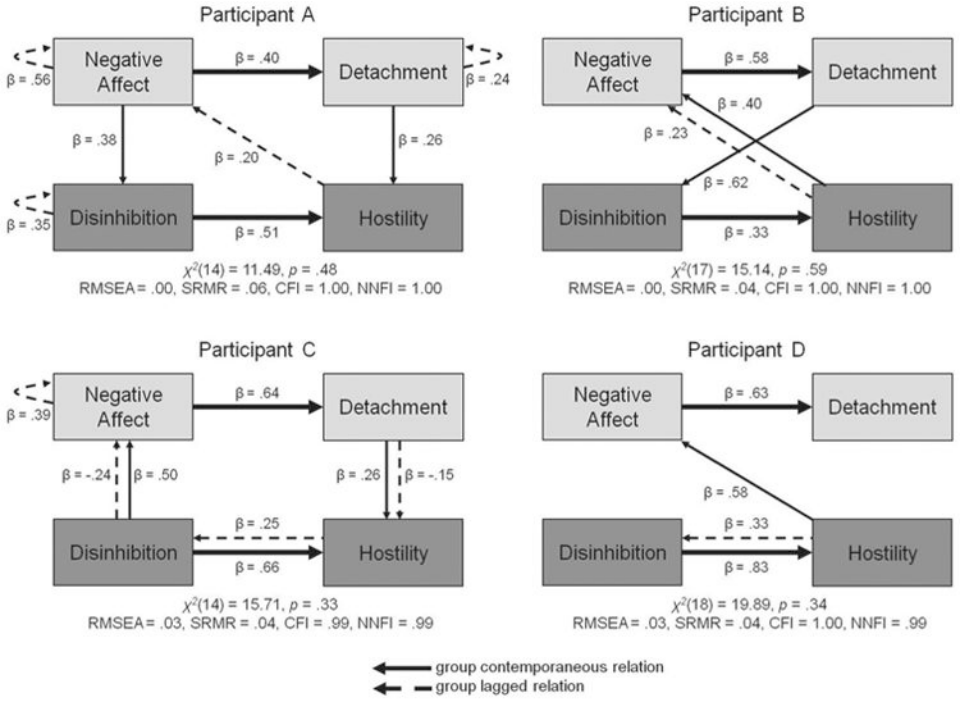

Figure 3.

Four final person-specific maps produced by GIMME-MS analysis of the example data set, containing the optimal group-level structure from the first solution; see Figure S1 and Table 1. All maps fit the data well, contain only significant relations at $p \leq .05$, and have white noise residuals indicating that temporal dependencies are sufficiently accounted for in the maps; models specifying that residuals were unrelated across time fit the data well: (A): $\chi^2(126) = 88.63$, $p = 1.00$, RMSEA = .00, SRMR = .09, CFI = 1.00, NNFI = 1.00. (B): $\chi^2(126) = 93.53$, $p = .99$, RMSEA = .00, SRMR = .07, CFI = 1.00, NNFI = 1.00. (C): $\chi^2(126) = 74.94$, $p = 1.00$, RMSEA = .00, SRMR = .07, CFI = 1.00, NNFI = 1.00. D: $\chi^2(126) = 86.21$, $p = 1.00$, RMSEA = .00, SRMR = .07, CFI = 1.00, NNFI = 1.00.

Note. GIMME-MS = GIMME for multiple solutions; RMSEA = root mean square error of approximation; SRMR = standardized root mean square residual; CFI = comparative fit index; NNFI = non-normed fit index.

Table 1

Decision Metrics of the Four Group-Level Solutions Generated by GIMME-MS for the Example Data Set, Averaged Across the Final Maps of all Participants ($N = 25$).

	Solution 1	Solution 2	Solution 3	Solution 4
Alternative fit indices				
RMSEA	.01	.01	.01	.02
SRMR	.06	.06	.05	.06
CFI	.99	.99	1.00	.99
NNFI	.99	.99	.99	.99
AIC	54.25	54.61	54.50	55.09
Maximum residual	.83 disinhibition	.87 detachment	.88 hostility	.88 detachment

Note. GIMME-MS = GIMME for multiple solutions; RMSEA = root mean square error of approximation; SRMR = standardized root mean square residual; CFI = comparative fit index; NNFI = non-normed fit index;

AIC = Akaike Information Criterion. See Figure S1 for maps illustrating each of the four solutions.