RT-MPTs: Process Models for Response-Time Distributions Based on Multinomial Processing Trees with Applications to Recognition Memory

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Abstract

Multinomial processing tree models have been widely used for characterizing categorical responses in terms of a finite set of discrete latent states, and a number of processes arranged serially in a processing tree. We extend the scope of this model class by proposing a method for incorporating response times. This extension enables the estimation of the completion times of each process and the testing of alternative process orderings. In line with previous developments, the proposed method is hierarchical and implemented using Bayesian methods. We apply our method to the two-high-threshold model of recognition memory, using previously published data. The results provide interesting insights into the ordering of memory-retrieval and guessing processes and show that the model performs at least as well as established benchmarks such as the diffusion model.

Keywords: Multinomial Models, Response Times, Hierarchical Models

Response time is perhaps the most important measure used to investigate 1 hypotheses about mental processes in experimental psychology, going back to the pioneering work of Franciscus Donders in the nineteenth century (for reviews, see Luce, 1986; Jensen, 2006; Townsend & Ashby, 1983; Van Zandt, 2002). From a data-analytic perspective, this predominance has raised important challenges: For instance, response time distributions are positively skewed, with longer tails on the right sight of the probability density function than on the left side. Moreover, reaction-time means and variances are often found to be linearly related (Wagenmakers & Brown, 2007). These two features alone are enough to see that response times do not mesh well with the general class of statistical linear models traditionally used to analyze data. 11 As a response to this challenge, several approaches have been developed, 12 which can be roughly divided into two research strands: One has focused 13 on fitting response-time data to a suitable parametric distribution (e.g., the ex-Gaussian distribution; Matzke & Wagenmakers, 2009) in order to pro-15 vide economical summaries of the data in terms of a few parameters (e.g., 16 Schmiedek, Oberauer, Wilhelm, Süß, & Wittman, 2007; for an overview, see Balota & Yap, 2011). The second research strand, which is quite active to 18 this date, instead focuses on the development of mathematical models as 19 psychological accounts for the data in terms of specific mental processes that 20 unfold across time (e.g., Brown & Heathcote, 2008; Ratcliff & Rouder, 1998; Townsend & Nozawa, 1995; for reviews, see Luce, 1986; Townsend & Ashby, 22 1983; Schweickert, Fisher, & Sung, 2012; Van Zandt, 2002). 23 Beyond response times, another widely applicable tool for the study of 24 mental processes is given by the class of multinomial-processing tree models (MPT models; Riefer & Batchelder, 1988). MPT models characterize cat-26 egorical (frequency) data in a given paradigm by postulating a finite set of latent states. For each item type, the observed responses are the outcome of a mixture of the different latent states and associated state-to-response mappings. The probability of each state being reached is generated from a processing tree, the edges of which represent the outcomes of different processes. MPT models are usually tailored to a particular experimental paradigm, with trees specifying the most important processes believed to be involved in the generation of responses. The family of process-dissociation models (Jacoby, 1991) used in many lines of psychological research (Klauer, Dittrich, Scholtes, & Voss, 2015) is one prominent member of the MPT model class among many others.

Figure 1 illustrates another simple and well-known MPT model, the twohigh-threshold model (2HT) for recognition memory (Snodgrass & Corwin, 1988). In recognition-memory research, participants study a list of items and later see these items intermixed with new items. Their task is to decide for each item whether it was previously studied or not. The 2HT model assumes three latent states:

- S_1 : Item is detected as having been previously studied
- S_2 : Item is detected as being new.
- S_3 : The status of the item could not be determined

 \mathcal{S}_1 and \mathcal{S}_2 are memory-certainty states that can only be reached by studied and non-studied items, respectively, whereas the uncertainty state \mathcal{S}_3 can be reached by both item types. Each item type is associated with a processing subtree. Each process in the subtree can complete with one of two possible outcomes, represented by two edges, one for each outcome. The likelihood of each of the two process outcomes is governed by a parameter assigned to the respective edge. 1

For a studied item, participants first attempt to recognize the item, which 54 succeeds with probability D_O and fails with probability $1-D_O$. In the former case, participants enter state S_1 and respond "old". In the latter case, they 56 enter the uncertainty state S_3 , which in turn triggers a guessing process. 57 With probability g, the item is guessed as having been previously studied, 58 resulting in an "old" response. With probability 1-g, the items is instead guessed as being absent from the study list, leading to a "new" response. For 60 a new item, participants again attempt to recognize the item, but according 61 to the model, they cannot succeed in recognizing it. Instead, with probability D_N , participants can sometimes infer that the item is new, based on, for example, its overall dissimilarity from the studied items (e.g., Mewhort & Johns, 2000) or memorability expectations that were not met (e.g., Strack & Bless, 1994). A successful inference of this kind, which corresponds to state \mathcal{S}_2 , leads to the response "new". If participants cannot infer a test item's true status, they enter the uncertainty state S_3 and the same guessing process as described for old items is assumed to operate. Based on participants' recognition judgments, we can estimate the 2HT model's parameters and 70 test some of its properties (e.g., Dube & Rotello, 2012; Kellen & Klauer, 71 2014, 2015; Kellen, Singmann, Vogt, & Klauer, 2015; Province & Rouder, 72 2012). Although not as ubiquitous as response-time analyses, MPT models such 74

as the 2HT model have been found useful in an enormous range of psycho-

logical inquiries (for reviews, see Batchelder & Riefer, 1999; Erdfelder et

¹The two possible outcomes associated with each process are often referred to as "success" and "failure", respectively. This nomenclature is intuitive in some cases; e.g., succeeding/failing to retrieve an item from memory, but it is completely arbitrary in others; e.g., when referring to guessing processes.

Response Frequencies

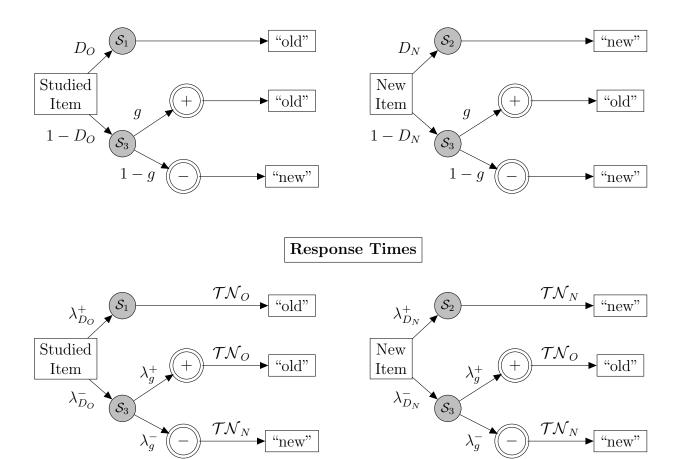


Figure 1: 2HT Model ("Detect-Guess" Variant). The rectangles indicate manifest states (i.e., item type and responses), and the gray circles indicate the latent states \mathcal{S} . The double circles provide a reference for the outcome of the guessing process, terminating with either an "old" or a "new" guess (denoted by + and -, respectively). The parameters D_o , D_n , and g refer to the probabilities of, in order, detecting an old item as old, a new item as new, and guessing "old". The λ parameters are exponential-rate parameters governing the time for these processes to complete for each outcome. \mathcal{TN}_O and \mathcal{TN}_N refer to truncated normal distributions governing encoding and response-execution times for response "new" and "old", respectively. Note that only nodes with process parameters attached to outgoing edges count as nodes in the technical sense detailed in Section 2.2. (i.e., the root node and the node for \mathcal{S}_3).

al., 2009; Hütter & Klauer, 2016). In addition to the ongoing stream of proposals for new substantive models (e.g., Gawronski, Conway, Armstrong,

Friesdorf, & Hütter, 2016; Meissner & Rothermund, 2013), the current fruitfulness of this model class is attested by its growing methodological toolbox: From hierarchical and mixed-model extensions (Klauer, 2010; Matzke, Dolan, Batchelder, & Wagenmakers, 2015), to sophisticated model-selection indices 82 (Klauer & Kellen, 2015; Wu, Myung, & Batchelder, 2010), and inequality-83

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constraint applications (Klauer, Singmann, & Kellen, 2015). But as useful as this model class may be, there are limits to what one can 85 achieve on the basis of response frequencies alone. For instance, the charac-86 terization of the observed responses as a function of a mixture of latent states 87 is ultimately silent about the duration of each of the processes that govern the access to these states, as well as about their exact order. Let us go back 89 to the 2HT example: The tree structure of the model illustrated in Figure 90 1 suggests that the guessing responses occur after a failed attempt to recognize the test item. We can refer to this as the "detect-guess" variant of the 2HT. Alternatively, we can conceive 2HT models in which guessing occurs prior to any attempt to recognize the test item. For example, according to a "default-interventionist" variant of the 2HT shown in Figure 2, the participant first guesses whether the test item is old or new.² Only after this process is completed does the participant engage in a memory-retrieval process that 97 — if successful — takes precedence over the previously established guess. 98

Although the original detect-guess and the default-interventionist variants of

the 2HT are very distinct in terms of mental-processing assumptions, they

are formally equivalent in the sense that they yield the exact same range of

predictions with the same parameters and parameter values.

²In this respect, the default-interventionist variant resembles the diffusion model of recognition memory (Dube, Starns, Rotello, & Ratcliff, 2012) in which a starting point for the diffusion process, governing response biases, is set prior to any attempt to recognize the test item.

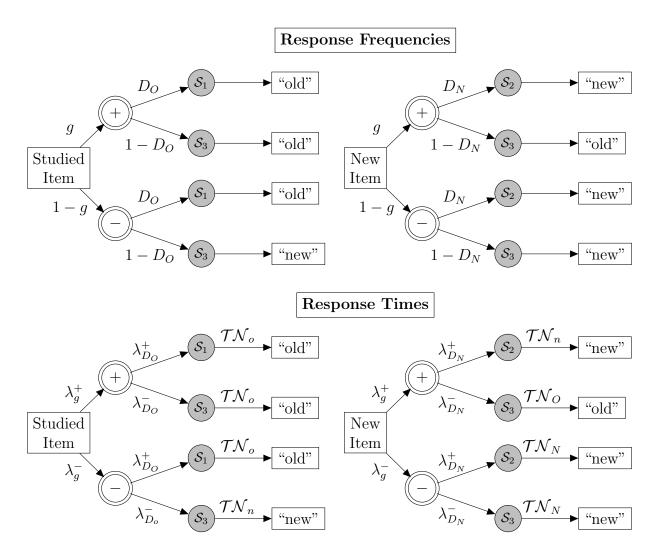


Figure 2: 2HT Model ("Default-Interventionist" Variant). The rectangles indicate overt states (i.e., item type and responses), and the gray circles indicate the latent states \mathcal{S} . The double circles provide a reference for the outcome of the guessing process, terminating with either an "old" or a "new" guess (denoted by + and -, respectively). The parameters are described in the caption of Figure 1. Note that only nodes with process parameters attached to outgoing edges count as nodes in the technical sense detailed in Section 2.2. (i.e., the root node and the double circles).

In order to test alternative tree structures and estimate the duration of the different processes they postulate, we need to extend the MPT model so that it can provide a joint characterization of response frequencies and their respective times. We present a framework within which different distributional assumptions can be explored and fully elaborate one model in this framework. The method can be applied to data from any identified MPT model if response times have been recorded along with the responses. It even extends the class of models that can be investigated because models that are not mathematically identified based on only the response frequencies can become so by the inclusion of the response times as illustrated below.

In line with modern developments, the new method is hierarchical, which 113 is advantageous in two different ways: First, it enables models to accommo-114 date the substantial heterogeneity that usually stems from individual differ-115 ences. These differences can be expressed in many ways such as accuracy, response bias, response speed, and speed-accuracy trade-offs, among others. 117 Second, each participant's parameter estimates are thereby informed by the 118 other participants' estimates, which is particularly valuable when the data 119 per individual are sparse, and group-level estimates generalize across them 120 (Katahira, 2016; Klauer, 2010). In terms of substantive psychological ap-121 plications, the proposed method can provide us with deeper insights into 122 the architecture of processes in the modeled tasks, enabling the testing of 123 theoretical predictions regarding the temporal characteristics of the involved 124 processes, and the development of more diagnostic measurement models. In 125 light of these contributions, the proposed method can be cast as a principled 126 alternative to the currently dominant paradigm of simple diffusion-model accounts. 128

1. Precursors and State of the Art

Relatively direct precursors of the present approach are mixture models postulating probabilistic mixtures of response-time distributions (e.g., Falmagne, 1965; Ollman, 1966; Yantis, Meyer, & Smith, 1991). Mixture models

are naturally related to MPT models if each processing-tree path terminating 133 in an observable response category is considered as giving rise to a distinct 134 path-specific response-time distribution. Another important precursor is the 135 study of complex cognitive architectures that followed the seminal work of 136 Sternberg (1969). For instance, Schweickert (1978) showed how the selective 137 influencing of processes could be used to gain insights into their arrangement 138 (e.g., are two processes serial or concurrent?) along an acyclical network (see 139 also Dzhafarov & Schweickert, 1995; Goldstein & Fisher, 1991; Townsend & 140 Nozawa, 1995; for a review, see Schweickert et al., 2012). 141

Hu (2001) applied some of these earlier ideas in the context of the MPT model class, noting that any tree structure belonging to this class is a special 143 type of acyclical network. Specifically, Hu investigated under what condi-144 tions it is possible to decompose mean response latency for each response 145 category into mixtures of different path-specific means, which are further decomposed into additive components for each edge along the path, each such 147 component describing the mean completion time of the process (and pro-148 cess outcome) associated with it. The inclusion of response times under this framework enabled Hu to compare two variants of the famous high-threshold 150 source-memory model (Batchelder & Riefer, 1990) that postulate distinct 151 relationships between the retrieval of item and source memory. Among the 152 limitations of Hu's approach is the fact that it only operates at the level of mean response times, ignoring higher-order moments of the response-time 154 distributions. In addition, the method does not develop tools for statis-155 tical inference. Finally, it assumes that process-completion times and the 156 probability of a process succeeding are independent, a highly implausible 157 assumption. 158

An approach based on mixture models was recently developed by Heck

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and Erdfelder (2016). It is based on setting up a number of response-latency 160 bins: For example, when using two bins the responses might be split into fast 161 and slow responses based on the overall median. A new branching is then 162 added at the end of each path of the MPT model, distributing the responses 163 generated along that path into the different bins. The probabilities associated 164 with each new binary branching are governed by a path-specific parameter 165 L. For example, in the case of the 2HT, the "old" responses emerging from 166 state \mathcal{S}_1 are mapped into 'slow old' and 'fast old' bins with probabilities L_{D_O} 167 and $1 - L_{D_O}$, respectively. The L parameters for the different paths order 168 them in terms of their relative speed, using the overall median as benchmark. One key advantage of Heck and Erdfelder's (2016) approach is that the 170 binning of response times sidesteps the need to impose any parametric as-171 sumptions on the shape of the response-time distributions. Additionally, the 172 models resulting from their approach are still members of the MPT model 173 class as formalized by Hu and Batchelder (1994), which means that the en-174 tire methodological toolbox developed so far for MPTs can be applied with-175 out any modification. One limitation, however, is that the models resulting from this approach will often not be identified, with pathwise L parameters 177 that cannot be uniquely estimated. Additional simplifying assumptions are 178 needed to achieve identifiability: For example, for the 2HT model, Heck and 179 Erdfelder assume that "old" responses to old items generated by a recognition failure and an "old" guess (with probability $[1 - D_O]g$) have the same 181 response-time distribution as "old" responses to new items generated by a 182 failure to infer that they are new and followed by an "old" guess (with prob-183 ability $[1 - D_N]g$). An analogous assumption is made for recognition and 184 inference failures that are followed by a "new" guess. These simplifying as-185 sumptions allow for the L parameters of the corresponding paths to be set

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equal, yielding an identifiable model.

Further simplifying assumptions are usually required to link the path-188 specific L parameters to individual processes along the different paths. For 189 example, for the 2HT model, the L parameter attached to the processing 190 path $(1 - D_O)g$ is interpreted as capturing the relative speed of guessing 191 "old" although in terms of processes, the failure to recognize (with probability 192 $(1-D_O)$ is also involved. Finally, it is difficult in this kind of model to integrate 193 temporal differences across stimuli, responses, or experimental conditions 194 due to encoding and/or response-execution processes. Such components are 195 routinely accommodated by most response-time models usually in the form of an additive response-time component t_0 (Luce, 1986). Nevertheless, where 197 applicable the approach by Heck and Erdfelder (2016) is relatively easy to 198 use and has the potential to provide valuable insights into the relative speed 199 of cognitive processes involved in the generation of the observed responses. 200 These advantages have been spelt out in a large application by Heck and 201 Erdfelder (2017). 202

The present approach pursues an alternative but complementary route 203 by imposing specific parametric assumptions on the processes along with a 204 serial interpretation of the processing paths as describing a succession or at 205 least a cascade of processing steps (McClelland, 1979). In this latter respect, 206 the present approach builds on the one by Hu (2001) and follows the intuition 207 of many modelers in formulating MPT models. The downside of imposing 208 parametric assumptions and a serial or cascade interpretation of processing 209 paths is that the resulting method cannot be expected to be useful in situ-210 ations where there are substantive deviations from such assumptions. More 211 generally speaking, parametric response-time models such as the diffusion 212 model (Ratcliff & Rouder, 1998) are most interesting where they provide a

good description of observed data. Such an outcome implies that the model 214 and its ensemble of assumptions provide one viable theoretical account of 215 the data. A failure to describe given data is less interesting, inasmuch as 216 it is often difficult to diagnose whether the failure goes back to a violation 217 of central structural assumptions (e.g., the idea of a diffusion process or a 218 particular MPT model architecture) or to a violation of ancillary parametric 219 assumptions (e.g., the assumption of normally distributed residual encoding 220 and response-execution times t_0). For this reason, it is desirable to develop 221 these models for different sets of parametric assumptions, but in the present 222 manuscript we focus on only one such set.

As will be shown below, the approach proposed here provides complete de-224 scriptions of the observed joint distribution of responses and response times, 225 including accounts of the differences between individuals, and the correlations 226 between the parameters governing responses and response times related to 227 these individual differences. The methods presented here can be applied to 228 any identifiable MPT model as well as to many MPT models that are not 229 identified based on only the response frequencies without imposing further 230 restrictions. 231

232 2. Model Assumptions

233 2.1. Overview

In its simplest form, the present method builds on binary multinomial processing trees (only two branches go out from each node) in which each processing path represents a succession of processing stages for which processcompletion times add up (Sternberg & Backus, 2015). An additional additive component summarizes encoding and response-execution times. The processcompletion times of different processes are assumed to be independently dis-

tributed (i.e., conditional independence is assumed), and process-completion time distributions leading to the same outcome of the same process are assumed to be identical wherever that process occurs in the processing tree.

For example, in the bottom part of Figure 1, the process of guessing "old" associated with parameter g in the tree for old items has two completion-time distributions depending upon whether it completes successfully or not. The same process occurs in the tree for new items, where it is assumed to have the same completion-time distributions.

A complete model of response-time distributions needs specific parametric assumptions (Van Zandt, 2002), where limited data are available per participant. Consider three sets of assumptions in increasing order of psychological plausibility and decreasing order of tractability:

- 1. Each completion-time distribution is exponentially distributed with a separate rate parameter λ for each process outcome (see the bottom part of Figures 1 and 2). The distribution of encoding and response-execution times follows a truncated Gaussian distribution \mathcal{TN} (truncated so that only positive values can occur). There are separate parameters for the probabilities with which the processes complete with either of the two outcomes.
- 2. Like Option 1, but each completion-time distribution follows a Wald distribution (first-passage time distribution of a Brownian motion with positive drift) with separate threshold and drift-rate parameters. The encoding and response-execution times follow an exponential distribution.
- 3. Each process and its joint distribution of outcomes and completion times is modeled by a diffusion model with a minimal set of parameters.

 There is a separate distributional assumption for the distribution of

encoding and response-execution times.

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Further options can of course be considered such as that processes com-268 plete as the outcome of a race between separate counters. The options listed 269 here were motivated by models figuring importantly in the literature on response-time distributions. Option 1 is motivated by the ex-Gaussian dis-271 tribution often used for modeling response times (Matzke & Wagenmakers, 272 2009), whereas Option 2 is motivated by the ex-Wald distribution proposed by Schwarz (2001). There are critical discussions of these distributions that 274 focus on their empirical adequacy as well as on their psychological plausibil-275 ity (e.g., Burbeck & Luce, 1982; Matzke & Wagenmakers, 2009; Sternberg 276 & Backus, 2015). Most of these criticisms are dealt with through Option 3, motivated by the diffusion-model literature, which is however in all like-278 lihood the most difficult to implement mathematically.³ Note that Option 279 1 models, permitting different exponential-rate parameters for each process 280 outcome, accommodate reaction-time distributions that differ as a function of response category. This means that none of the models is bound to assume 282 that responses and their respective times are independent, a (problematic) 283 property known as separability (Marley & Colonius, 1992; see also Brown, 284 Marley, & Heathcote, 2012). 285 In the present manuscript, we develop a Bayesian hierarchical version of 286 the Option 1 model with participants as random effects. Thus, each par-287 ticipant is associated with different parameters for the process probabilities and completion-time distributions. These parameters are constrained by a

³Although in its simplest form, the proposed approach assumes sequential additive stages along each processing path, it can easily accommodate technical parameters in any given path (e.g., Klauer, Singmann, et al., 2015) to which no completion-time component is attached. Furthermore, stages with overlapping or parallel processes can often be modeled by concatenating two sequential stages and assigning only one common completion-time distribution to them.

prior distribution with population means and variance-covariance structure,
parameters that are also estimated from the data. The resulting models provide process-oriented accounts of the joint distribution of response categories
and response times.

294 2.2. The Person-Level Model for Responses and Response Times

MPT models usually consist of several subtrees. For example, in the most 295 simple 2HT model, there are two subtrees, one for trials involving studied items, and one for trials involving new items. Each tree has internal nodes, 297 referred to simply as nodes in the following, and leaves. The leaves correspond 298 to observable response categories such as "old" or "new". Categories for different subtrees are, however, considered different categories. For example, 300 the category "old" is also indexed by the subtree from which it stems and 301 thus, to be precise, there are four response categories in the most simple 2HT 302 model. The categories are mapped on actual responses such as left or right keypresses so that responses are a function of categories. For example, the 304 two "old" response categories may be mapped on the left key, and the two 305 "new" response categories on the right key. We consider only binary MPT 306 models in which each node has two children. But note that non-binary MPT 307 models can be transformed into binary MPT models (Hu & Batchelder, 1994; 308 see Appendix for more details). 309

To each node n in the tree, a process p = p(n) is attached with two outcomes. For example, p might be a guessing process with two outcomes 'guess old' versus 'guess new'. The two outcomes correspond to two edges going out from the node, and we will refer to an outcome o generically as the '+' outcome, o = +, or the '-' outcome, o = -. Furthermore, let plus(o) be a function of the outcome with plus(+)=1 and plus(-)=0.

Under Option 1, each process is characterized by three parameters: θ_p, λ_p^+ ,

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and λ_p^- . Parameter θ_p models the probability that the process p completes with the '+' outcome with completion time governed by the exponential rate parameter λ_p^+ . The probability of the '-' outcome is given by $1 - \theta_p$ with completion time described by parameter λ_p^- .

We consider paths B from root to one of the leaves and represent them in terms of the internal nodes n traversed from root to leave along with the outcomes, + or -, attached to the edges along the path and thus, as a set of edges (n, o). The probability of path B is a product of the MPT model parameters, such as D_o and g, and their complements, as encountered along the path. Thus,

$$P(B) = \prod_{(n,o)\in B} \theta_{p(n)}^{\text{plus}(o)} (1 - \theta_{p(n)})^{1-\text{plus}(o)}.$$
 (1)

The response latency of a response generated along path B is the sum of 327 an encoding and response-execution time δ , that follows a truncated normal 328 distribution, and exponentially distributed process-completion times of the 329 processes along that path. It is reasonable to assume that the encoding 330 and response-execution time δ with mean γ and variance σ^2 depends on the 331 particular motor response r, r = 1, ..., R, such as a left or right keypress⁴ and thus, we permit its mean $\gamma = \gamma_r$ to differ between different responses. 333 Each path B ends in a category c = c(B), which is mapped on a response 334 r = r(c). For a path B with only one node n, attached process p = p(n), and 335 outcome o that leads to response r = r(c(B)), the distribution of response latency thus follows the familiar ex-Gaussian distribution with truncation at 337 zero carried over from the truncated normal component:

⁴For example, responses made with the right hand are often executed faster than left-handed responses by persons with dominant right hand; frequent responses are often executed faster than infrequent responses, etc. (see Voss, Voss & Klauer, 2010).

$$f(t|B) = \operatorname{ex-Gauss}_{\geq 0}(t|\lambda_p^o, \gamma_r, \sigma^2)$$

$$= \lambda_p^o \exp\left[\lambda_p^o(\gamma_r + \frac{1}{2}\lambda_p^o\sigma^2 - t)\right] \left\{\Phi\left(\frac{t - \gamma_r - \lambda_p^o\sigma^2}{\sigma}\right) - \Phi\left(\frac{-\gamma_r - \lambda_p^o\sigma^2}{\sigma}\right)\right\}$$

$$\times \left(1 - \Phi\left(\frac{-\gamma_r}{\sigma}\right)\right)^{-1}.$$
(2)

For longer paths, the response latencies are the sum of several exponentials and a truncated normal. The sum of exponentials is distributed as what is known as a hypoexponential or generalized Erlang distribution (Johnson, Kotz, & Balakrishnan, 1994), which after convolution with the truncated normal yields the following density:⁵

$$f(t|B) = \sum_{(n,o)\in B} \left(\text{ex-Gauss}_{\geq 0}(t|\lambda_{p(n)}^o, \gamma_r, \sigma^2) \prod_{(m,q)\in B, (m,q)\neq (n,o)} \frac{\lambda_{p(m)}^q}{\lambda_{p(m)}^q - \lambda_{p(n)}^o} \right). \tag{3}$$

Hence, the joint distribution of categories c for a given subtree (such as the category "new" for old items) and response latencies t is characterized by

$$f(c,t) = \sum_{B:B \text{ ends in } c} f(t|B)P(B). \tag{4}$$

⁵This formula assumes that the same process and outcome is not attached to two different nodes in the path. It needs to be modified if the same process is repeated along a path.

347 2.3. Priors and Hyperpriors

348 2.3.1. Priors for process-related parameters.

The parameters of the above person-level model, θ_p , λ_p^o , γ_r , and σ^2 , can 349 assume different values for each individual s and thus, they carry the ad-350 ditional index s, which has so far been suppressed for ease of exposition. 351 Like in Klauer (2010), the person-level MPT parameters $\theta_{p,s} \in (0,1)$ are 352 transformed via an inverse-probit link to the real line, yielding new param-353 eters $\alpha_{p,s} = \Phi^{-1}(\theta_{p,s})$, where Φ is the cumulative distribution function of 354 a standard normal distribution. Analogously, the exponential rate parame-355 ters $\lambda_{p,s}^o \geq 0$ are transformed via a log link to the entire real line, yielding 356 transformed parameter $\beta_{o,p,s} = \log(\lambda_{p,s}^o)$. 357 Furthermore, we decompose the person-level parameters into the sum of 358 a population mean μ and (zero-centered) person-level deviations from that 359 mean: 360

$$\alpha_{p,s} = \mu_p^{(\alpha)} + \alpha'_{p,s},$$

$$\beta_{o,p,s} = \mu_{o,p}^{(\beta)} + \beta'_{o,p,s},$$

$$\gamma_{r,s} = \mu_r^{(\gamma)} + \gamma'_{r,s}.$$
(5)

The parameters $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ characterize the accuracy and speed, respectively, of the processes specified in the MPT model. It is reasonable to assume that they can correlate across persons and thus, we assume that they are jointly distributed as a multivariate normal with variance-covariance structure $\boldsymbol{\Sigma}$ that is to be estimated from the data. Stacking the person-level deviations into vectors $\boldsymbol{\alpha}'_s = (\alpha'_{p,s})_{(p=1,\ldots,P)}$ and $\boldsymbol{\beta}'_s = (\beta'_{o,p,s})_{(o=+,-;p=1,\ldots,P)}$, their prior distribution is given by

$$\begin{pmatrix} \boldsymbol{\alpha}_s' \\ \boldsymbol{\beta}_s' \end{pmatrix} \sim \mathcal{N}\left(\mathbf{0}_{3P}, \boldsymbol{\Sigma}\right), \tag{6}$$

where $\mathbf{0}_n$ is a vector of zeros of length n and P is the number of different processes in the MPT model. This structure constrains the person-level deviations to follow a normal distribution with variances and covariances 370 estimated from the data. 371 Person-level statistical information is thereby aggregated in the popula-372 tion means $\boldsymbol{\mu}^{(\alpha)} = (\mu_p^{(\alpha)})_{(p=1,\dots,P)}$ and $\boldsymbol{\mu}^{(\beta)} = (\mu_{o,p}^{(\beta)})_{(o=-,+;p=1,\dots,P)}$ for each 373 parameter. Variances across persons, and correlations between parameters 374

2.3.2. Hyperpriors for process-related parameters. 376

for different processes, are estimated by Σ .

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Hyperpriors are needed for the prior parameters $\mu^{(\alpha)}$, $\mu^{(\beta)}$, and Σ . Like 377 in Klauer (2010), the hyperprior for $\mu^{(\alpha)}$ is a normal distribution 378

$$\boldsymbol{\mu^{(\alpha)}} \sim \mathcal{N}(\mathbf{0}_P, \epsilon^{-1} \boldsymbol{I}_P)$$

where I_P is the $P \times P$ identity matrix and the precision ϵ is set to one here 379 and below for the analyses presented in this paper, implying a uniform prior 380 distribution for the $\mu_p^{(\alpha)}$ on the probability scale. The hyperpriors for pa-381 rameters $\mu_{o,p}^{(\beta)}$ are specified on the original (not log-transformed) scale and 382 thus in terms of parameters $\exp(\mu_{o,p}^{(\beta)})$ as independent Gamma distributions 383 with shape and rate parameters set to 1.0 and 0.1 for the analyses presented 384 below, implying a mean and variance of 10 and 100, respectively. A mean of 385 10 was chosen because a mean exponential rate of 10 implies a mean process-386 completion time of 0.1 s or 100 ms, which seemed a reasonable prior setting 387 for process-completion times for the applications considered in this paper. A 388 variance of 100 ensures that the hyperprior is nevertheless reasonably unin-389

390 formative.

Following Klauer (2010), the hyperprior for Σ is a scaled Inverse-Wishart 391 distribution with 3P + 1 degrees of freedoms, scale matrix I_{3P} , and scale 392 factors $\boldsymbol{\xi}^{(\alpha)}$ and $\boldsymbol{\xi}^{(\beta)}$ for parameters $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$, respectively. As discussed by 393 Gelman and Hill (2007, Chap. 13), setting the degrees of freedom to 3P+1, 394 that is, one plus the number of parameters in the multivariate normal distri-395 bution of Equation 6, has the effect of imposing a uniform prior distribution 396 on the individual correlation coefficients implied by Σ , a reasonably unin-397 formative prior setting for the correlations. This distribution does, however, 398 impose stronger constraints on the variances. To relax these constraints as well as to speed up convergence in Markov Chain Monte Carlo (MCMC) 400 estimation, Gelman and Hill (2007) propose to use a scaled Inverse-Wishart 401 distribution in which unidentified scale parameters ξ are introduced. Details 402 are described in the Appendix. 403

2.3.3. Priors and hyperpriors for encoding and response-execution times.

The person-level model describes the encoding and response-execution 405 times δ in terms of person-level means $\gamma_{r,s}$ and variances σ_s^2 . It is reasonable 406 to assume that the $\gamma_{r,s}$ pertaining to different responses are correlated across 407 persons. Thus, we assume a multivariate normal distribution with popula-408 tion means $\mu_r^{(\gamma)}$ and variance-covariance matrix Γ as prior. The hyperpriors 409 for $\mu_r^{(\gamma)}$ are again independent normal distributions with zero mean. For the 410 application reported below, we chose a variance of 10 for these hyperpriors, 411 which for response latencies in the range of at most a few seconds seemed to be a reasonably uninformative choice for the variance of person-level mean 413 values, especially when considering that the variances of means are necessar-414 ily smaller than variances for individual latencies. The hyperprior for Γ is 415 the above-discussed scaled Inverse-Wishart distribution with R+1 degrees 416

of freedom and scale matrix I_R , R being the number of different responses that can occur.

For the variances σ_s^2 , a scaled inverse chi-squared distribution with scale factor ω^2 and df=2 was chosen as prior, which again imposes few constraints on the variances. For ω^2 , an improper uninformative prior was chosen, $p(\omega^2) \propto \frac{1}{\omega^2}$. The posterior estimate of population-level parameter ω^2 provides an overall estimate of the residual variance in response latencies that is not accounted for by the model.

425 3. Algorithm

The resulting model does not fall into the scope of standard software for MCMC estimation such as JAGS (Plummer, 2003), primarily because the 427 kernel density in Equation 3 is not implemented in such software (but see 428 Annis, Miller, & Palmeri, 2017). We devised a Gibbs sampler, more precisely 429 a Metropolis-within-Gibbs sampler, for fitting the model that uses three steps 430 of data augmentation.⁶ The first two steps of data augmentation constitute 431 an adaptation of the approach by Albert and Chib (1993) to replace observed 432 categorical responses by an underlying Gaussian structure tailored to the 433 special structure of multinomial processing trees (Klauer, 2010). 434 The first step is to augment each observed category c by the path B along 435 which it was generated. Let \mathcal{B}_c be the set of paths B that end in category 436 c. The probability that an observed category c and response latency t was generated by a specific member B of \mathcal{B}_c is then given by 438

$$p(B \mid c, t) = \frac{p(B)f(t \mid B)}{\sum_{B' \in \mathcal{B}_c} p(B')f(t \mid B')},$$
(7)

 $^{^6}$ Program (C++) scripts of this implementation calling the NAG library can be obtained from the first author.

where p(B) and $f(t \mid B)$ are given by Equations 1 and 3, respectively. Thus, the observed data of each trial can be augmented given the person-level parameters by sampling a path B from \mathcal{B}_c based on a multinomial distribution with the above $p(B \mid c, t)$ as parameters.

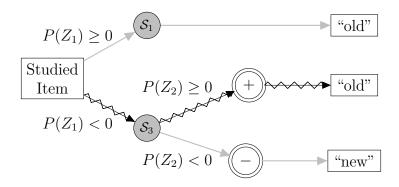
The second step of data augmentation is illustrated in Figure 3. For each 443 trial from each subtree of the model administered to person s, values $z_{n,s}$ of 444 latent normal variables $Z_{n,s}$ are sampled for each node n of the subtree, given 445 the person-level parameters α_s and the path B sampled in the first step. The 446 $z_{n,s}$ are sampled from normal distributions with means $\alpha_{p(n),s} = \Phi^{-1}(\theta_{p(n),s})$ 447 and variance one. For (n, o) in B, the $Z_{n,s}$ variable is truncated from below at zero with $Z \geq 0$ for the + outcome, o = +, and truncated at zero from 449 above with Z < 0 for the - outcome, o = - (Albert & Chib, 1993). For 450 edges in the subtree but not on the path B, the Z variate is not truncated.⁷ 451 The helpful aspect of this double data augmentation, by paths B and Z452 variates, is that it allows us to estimate the person-level parameters α as in 453 a standard hierarchical linear model in a Bayesian framework as elaborated 454 in the Appendix. 455

The third step of data augmentation is also illustrated in Figure 3. For each trial from each subtree of the model administered to person s, latent process-completion times $\tau_{n,s}^o$ are generated for each edge (n,o) of the subtree along with residual encoding and motor-execution component $\delta_{r(c(B)),s}$, given the person-level parameters α_s , β_s , γ_s , and σ_s as well as the path Bsampled for the trial on the basis of the category c and the response latency

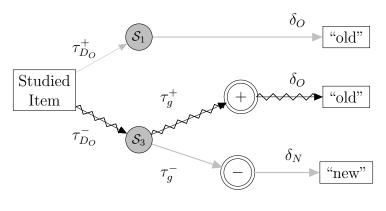
⁷As discussed by Klauer (2010), these non-constrained Z variates seem redundant. Leaving them out, the number of such variates is, however, itself a random variable that takes on different values in each cycle of the resulting sampler, which in consequence would no longer be a Gibbs sampler. In consequence, the strong convergence results known for the MCMC sampler (Gill, 2008, Chap. 9) do no longer apply, and a new theoretical foundation would be required to justify the algorithm without the unconstrained Z.

For a given response "old" to a studied item with latency t:

Data Augmentation: Second Step



Data Augmentation: Third Step



With
$$t = \tau_{D_O}^- + \tau_g^+ + \delta_O$$

Figure 3: Illustration of the second and third steps of data augmentation. The zigzag arrows indicate the tree path that was sampled. In the second step of data augmentation (upper panel), the multinomial probability parameters are encoded in terms of (truncated) normal variates. In the third step, process completion times τ and encoding and response-execution times δ are added. For further details, see the body of text.

t that was observed on that trial. For edges (n, o) in the subtree, but not on the path B, the process-completion time is sampled from an exponential

distribution with rate parameter $\lambda_{p(n),s}^o = \exp(\beta_{o,p,s})$. For links on the path 464 B, sampling is constrained by the fact that the sums of τ -values and residual 465 component δ along the path B have to add to the observed response latency (see Appendix for details). The helpful aspect of this data augmentation is 467 that it allows us to estimate the exponential-rate parameters and the param-468 eters governing the encoding and response-execution times as though we had 469 directly observed the process-completion times τ and residual components δ . 470 With the observed and augmented data, most of the conditional distribu-471 tions of the Gibbs sampler turn out to stem from relatively standard families 472 of distributions for which it is easy to generate random values. One exception is the just-mentioned constrained sampling of process-completion times 474 τ and residual component δ , which required a rejection-sampling step. A 475 second exception is the sampling of the exponential-rate parameters $\lambda_{p,s}^o$, 476 which required an adaptive rejection-sampling step (Gilks & Wild, 1992). A 477 third exception concerns the sampling of parameters related to the encod-478 ing and response-execution times, which required Metropolis-Hastings steps. 479 The joint model likelihood and details on the Gibbs sampler are provided in the Appendix. 481

482 4. Identifiability and Model Checks

483 4.1. Identifiability

The resulting model is identifiable whenever the underlying MPT model is identified. From Equation 4, it is easy to see that the distribution of response latencies given category c is a mixture of hypoexponential distributions convoluted with a truncated normal distribution with mixture weights given by $\frac{P(B)}{\sum_{B':B'} \text{ ends in } c}P(B')$, where B is a path that ends in c. If the multinomial model is identified, these mixture weights are identified (see Equation

1). Even without this extraneous identification stemming from the categor-490 ical responses, mixtures of members of parameterized families of continuous 491 distributions are usually identified as shown by Titterington, Smith, and 492 Makov (1985, Chap. 3). One way to see this is to note that expressing the 493 n—th moments of the predicted response time distribution in terms of model 494 parameters will usually yield as many non-redundant equations relating the 495 model parameters to the moments as there are independent model parame-496 ters. Conversely, this implies that the model parameters are identified only 497 from the higher-order moments of the RT distributions although they are 498 further constrained by structural constraints as discussed below.

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The extraneous identification of the mixture weights even deals with a remaining problem known as the *labeling problem*: When members from the same family of distributions (such as normal distributions) are mixed, the different components are exchangeable. That is, the order in which the different components are mixed makes no difference for the resulting mixture distribution. Hence, we can permute mixture weights and parameter values of the associated mixture components without changing the probability distributions predicted by the model. This possibility is however preempted when mixture weights are already identified from the categorical data alone.

These labeling problems again need to be considered where the underlying model is not identified. For example, in the basic 2HT model applied to data from a basic recognition-memory experiment, a model with parameters D_N , D_O and g will not be identified when only categorical "old"/"new" responses are available. Mixtures of pathwise response-latency distributions, including mixture weights, will nevertheless usually be identified. Even the labeling problem will usually not pose a problem, because the paths give rise to distinct families of distributions as a function of the number of edges upon

them. For example, in the 2HTM, the "new" category for new items is 517 reached via two paths, one with one edge labeled by D_N , the other one with 518 two edges, labeled $1-D_N$ and 1-g, respectively. The first path generates an ex-Gaussian distribution, the second a hypoexponential distribution with two 520 exponential components convoluted with a truncated normal distribution. 521 The labeling problem arises only if (at least some of) the different mixture 522 components stem from families of distributions with overlap (i.e., sharing 523 some distributions) and if such components fall into this area of overlap. 524 There is, however, no overlap between the ex-Gaussian family of distributions 525 and the distribution of the sum of two exponential variates and a truncated Gaussian variate. It follows that the mixture is completely identified with 527 the relabeling possibility ruled out and hence that the mixture weights D_N 528 and $(1 - D_N)(1 - g)$ are also identified in this case (and, mutatis mutandis, 529 D_O and $[1 - D_O]g$). Analogous arguments show that most RT-MPT models 530 will be identified even if the underlying MPT model is not. It is, however, 531 possible to construct special cases in which the resulting model still suffers 532 from the labeling problem. 533

How the observed reaction times are carved up into process-completion 534 times and response-execution components depends in part on the distribu-535 tional assumptions. In this respect, RT-MPTs are no different from other 536 process-oriented models of reaction times such as the diffusion model (Jones & Dzahafarov, 2014; Heathcote, Wagenmakers, & Brown, 2014). The issue 538 is somewhat mitigated by the fact that the same process-completion compo-539 nents and response-execution components appear in different combinations in different processing paths of the model, imposing structural constraints on 541 these components and associated parameters. Nevertheless, due to such is-542 sues, estimation of the model should be accompanied by assessments of model

fit as well as by selective-influence studies. In selective-influence studies manipulations are implemented that are believed to affect only one process on 545 theoretical grounds. The model is thereby validated not only in terms of fit, but also in terms of whether or not it maps the effects of the manipulation on 547 only this process (Heathcote, Brown, & Wagenmakers, 2015; Klauer, Stahl, 548 & Voss, 2012). Success in these validation steps will increase one's confidence 549 in the assumption that the parameter estimates are not unduly biased by in-550 appropriate distributional assumptions. We illustrate both validation steps 551 in the application below. 552

553 4.2. Model Checks

One way to assess the adequacy of a model for describing a given dataset 554 is to conduct posterior predictive model checks (for an overview, see Gelman 555 & Shalizi, 2013). Given the data \mathbf{x} , new data \mathbf{x}^{pred} can be generated from the 556 predictive posterior distribution. Referring to the collection of person-level parameters as $\boldsymbol{\eta} = (\boldsymbol{\eta}_1, \dots, \boldsymbol{\eta}_S)$, such model checks are based on a goodness-558 of-fit quantity $T(\mathbf{x}, \boldsymbol{\eta})$ defined as a function of the (new or old) data and of 559 the parameters such that it quantifies specific deviations of the data from 560 the model predictions. The probability p of $T(\mathbf{x}^{\text{pred}}, \boldsymbol{\eta}) > T(\mathbf{x}, \boldsymbol{\eta})$ is then 561 estimated under the joint distribution of $(\mathbf{x}^{\text{pred}}, \boldsymbol{\eta})$ given the observed data. 562 The model is considered adequate with regard to the deviations quantified 563 by T if p is not small. Specifically, for each of the retained parameter sets generated via the MCMC sampler, a new dataset of the same size, \mathbf{x}^{pred} , is 565 generated from the distribution specified in Equation 4, and the estimate of 566 p is simply the proportion of cases with $T(\mathbf{x}^{\text{pred}}, \boldsymbol{\eta}) > T(\mathbf{x}, \boldsymbol{\theta})$. 567

One way to think of this procedure is by analogy to parametric Bootstrap assessments of model fit (Efron, 1982). The observed value of a test statistic is evaluated with reference to the distribution of the statistic generated from the model given the current parameter estimates. For a critique of posterior predictive model checks, see, however, O'Hagan and Forster (2004, chap. 8), Bayarri and Berger (1998), among others.

For the applications below, we routinely compute posterior predictive 574 model checks based on three statistics, X_1 , X_2 , and X_3 . Statistics X_1 and 575 X_2 assess the fit of the data to the mean frequencies per category and the 576 mean latencies per category, respectively, using statistics of the Pearson's 577 chi-squared type, $\sum \frac{(O-E)^2}{E}$. X_3 is a summary measure of the fit of the joint 578 distribution of categories and latencies based on the SSE statistic proposed 579 by Van Zandt (2002). Let $F(c, t \mid \boldsymbol{\eta_s}) = \int_0^t f(c, x \mid \boldsymbol{\eta_s}) dx$ be the defective cumulative distribution function of response latencies from category c given 581 person s along with that person's person-level parameters collected in η_s , 582 where the joint density f is given by Equation 4. Let N be the total number 583 of trials across all participants, and N(subtree(c), s) the number of trials 584 administered to the s-th participant from the subtree to which category c585 belongs. Furthermore, let the observed response latencies from category c be 586 ordered from smallest to largest such that $t_{c,1} < t_{c,2} < \ldots < t_{c,N(c)}$, where N(c) is the observed frequency of category c across trials and participants. 588 Then, 589

$$X_3 = \sum_{c}^{C} \sum_{j=1}^{N(c)} \left(\frac{j}{N} - \sum_{s=1}^{S} \frac{N(\operatorname{subtree}(c), s)}{N} F(c, t_j \mid \boldsymbol{\eta_s}) \right)^2.$$

590 5. Application

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We apply the method to the analysis of several datasets from recognition memory using the 2HT model.⁸ The datasets stem from three experiments

⁸For all analyses reported below, we exclude extreme outliers in an individual's distribution of response latencies using Tukey's outlier criterion (Clark-Carter, 2004, Chap. 9);

by Arnold, Bröder, and Bayen (2015) and from two experiments by Dube et 593 al. (2012) to which diffusion models have been fitted. These data contribute 594 to an ongoing debate (Bröder & Schütz, 2009; Chen, Starns, & Rotello, 2015; Dube & Rotello, 2012; Dube et al., 2012; Kellen & Klauer, 2014, 2015; 596 Kellen, Klauer, & Bröder, 2013; Province & Rouder, 2012) about whether 597 or not memory-based judgments in recognition memory are better described 598 in terms of discrete memory states as in the 2HT model or in terms of a 599 continuous familiarity signal as in signal detection models (Kellen & Klauer, 600 in press). In particular, Dube et al. (2012) argued that diffusion models 601 are dynamic extensions of standard signal-detection models, and they were found to fit the frequencies of old/new decisions and associated response 603 latencies reasonably well in two experiments. Here, we evaluate whether the 604 2HT model is also capable of providing a reasonable fit of these data with 605 meaningful parameter values.

Arnold et al. (2015) manipulated baserate of old and new items (believed 607 to selectively influence guessing g; Experiment 1), the emphasis on accuracy 608 versus speed (Experiment 2), and studied-item strength by presenting strong items several times in the study list and weak items only once (believed to 610 selectively influence detection parameters D_O). Baserate was also manipu-611 lated in five steps by Dube et al. (2012) along with studied-item strength. 612

An overview of these datasets is provided in Table 1.

We sampled posterior parameter distributions using the algorithm de-614 scribed above to generate four MCMC chains in parallel. Note that the 615 2HT model is not identified based on only the categorical responses for the

that is, trials with latencies 3.0 times the interquartile range below the first quartile or above the third quartile in the individual's distribution of latencies were excluded prior to fitting the model

datasets without baserate manipulation within participants. Convergence 617 was monitored following the recommendations by Gelman, Carlin, Stern, 618 and Rubin (2004, Chap. 11). Specifically, the \hat{R} statistic was computed for 619 all model parameters (all population-level parameters and all scaled person-620 level parameters) with the exception of the unidentified scale parameters ξ . 621 Sampling was continued until all of the \hat{R} statistics were smaller than 1.05. 622 Subsequently, every 11th sample from each MCMC chain was retained for 623 analyses until a total N of 20,000 retained samples was reached. 624

5.1. Model Selection and Model Checks

Table 1 also shows the deviance information criterion (DIC) and the 626 Bayesian p values for the summary model-check statistics X_1 , X_2 , and X_3 627 for the "detect-guess" (DG) and "default-interventionist" (DI) variants of 628 the 2HT model shown in Figures 1 and 2. Note that, for both models, we 629 allowed response-execution times to differ for the "old" and the "new" re-630 sponses. Both models are equivalent in terms of their account of the response 631 frequencies, but they imply different predicted response-latency distributions. 632 As can be seen in Table A1, the DI variant of the 2HT model is associated 633 with the smaller DIC value in four of five cases. Moreover, its model checks 634 are generally satisfactory, especially when considering that X_3 checks the 635 entire joint distribution of responses and latencies. There is, however, some 636 room for improvement for the Dube et al. (2012) data. Due to its superior 637 performance, we will focus on the DI variant model in the discussion below.⁹ 638 To place the success of the DI model in perspective, Figure 4 compares 639 its fit of Dube et al.'s (2012, Experiment 1) data with the fit obtained with a

⁹We also fitted the same models with response-execution-times set equal across "old" and "new" responses. As detailed in the Appendix (Table A1), this resulted in much larger DIC values uniformly across datasets and for both the DG and the DI model.

Table 1
Reanalyzed Data Sets, DIC values, and Model Checks (Posterior p Values) for the DG
and the DI Models

			DG Variant			DI Variant				
Data	S	Manipulation	$\Delta { m DIC}$	X_1	X_2	X_3	$\overline{\Delta { m DIC}}$	X_1	X_2	X_3
— Arnold et al. (2015) —										
Exp. 1	60	Baserate (b.p.)	22.12	.50	.47	.63	0.00	.50	.40	.66
Exp. 2	60	Speed-accuracy	0.00	.50	.33	.49	41.19	.48	.48	.40
		tradeoff (b.p.)								
Exp. 3	30	Target strength (w.p.)	23.55	.48	.65	.51	0.00	.50	.66	.45
		— 1	Dube et	al. (2012)) —					
Exp. 1	21	Base-rate (w.p.) \times	62.58	.0001	.01	.04	0.00	.29	.008	.11
		target strength (w.p.)								
Exp. 2	26	Base-rate (w.p.) \times	81.40	<.0001	.04	.31	0.00	.0001	.01	.44
		target strength (w.p.)								

Note. DG = "Detect-Guess"; DI = "Default-Interventionist"; b.p. = Between participants; w.p. = Within participants; S = Number of participants in the dataset. $\Delta DIC = DIC$ difference from the lowest DIC.

diffusion model under the maximum-likelihood parameter estimates reported 641 by Dube et al. Specifically, Figure 4 shows the model fits to the response 642 frequency data (panel "ROC"), and mean correct and false response latencies for the three kinds of items (strong studied-items, weak studied-items, and 644 new items). As can be seen, both models capture the major trends in the 645 data. The mean frequencies and latencies are generally well captured by the DI model's posterior predictions, whereas the diffusion model encounters 647 difficulties in accounting for false-response latencies to new items (see points 648 for "errors" in the lower right panel). The analogous figure for Dube et al.'s 649 Experiment 2 shows the same patterns and is therefore omitted.

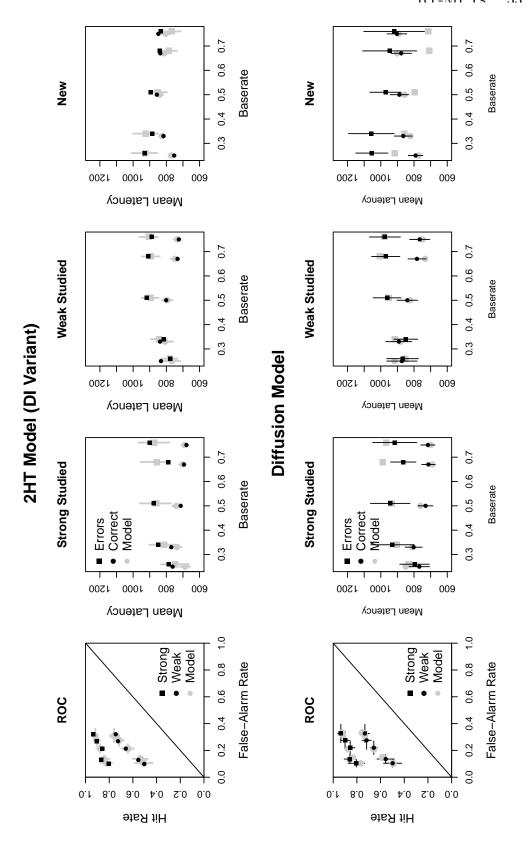


Figure 4: Fits of the 2HT model to false-alarm and hit rates (upper left panel) and to correct and false response latencies for strong studied-items, weak studied-items, and new items (upper right panels) per baserate condition. Lower panels: Fits of the diffusion model. In the upper panels, the error bars give the 95% HDIs of the model predictions, whereas in the lower panels the error bars correspond to the 95% confidence intervals associated with each observed data point. Note that the data points differ slightly between upper and lower panels due to differences in outlier treatment (see Footnote 7).

The superior fit of the DI variant of the 2HT model only serves as an ex-651 ample of the feasibility of the RT-MPT approach, not as a direct comparison 652 against the diffusion model. One confounding factor is the difference in the number of parameters between the two models. The DI model requires more 654 parameters per person than the diffusion model: the former needs to capture 655 the outcomes and completion times of three separate two-outcomes processes 656 (2 detection processes, one guessing process), whereas the latter model needs 657 to characterize the outcomes and completion times of only one such pro-658 cess (the diffusion process). For a basic recognition-memory paradigm, the 659 2HT models used here require, per process, three parameters (one parameter governing accuracy, two parameters governing completion times), and three 661 parameters to model response-execution times (two for the means of old and 662 new responses and one for the variance), for a total of twelve parameters per 663 person. The diffusion model uses only seven parameters in this situation (although the model could be extended to include additional components such 665 as drift criterion; see Starns, Ratcliff, & White, 2012). A formal comparison 666 of the fits of the 2HT model and the diffusion model should therefore take differences in flexibility into account via an adequate quantification of model 668 parsimony (e.g., Vandekerckhove, Matzke, & Wagenmakers, 2015). 669

5.2. Parameter Estimates and Effects of Experimental Manipulations

Tables 2 and 3 report the median posterior population-level parameters and their respective 95% highest-density intervals (HDI, reported in square brackets) for the data from Arnold et al. (2015) and Dube et al. (2012), respectively. The parameters governing process-completion times were retransformed to the original millisecond scale for ease of interpretation.

Consider the detection parameters. Detection failures (see rows/columns for D parameter under $\mu_{-}^{(\beta)}$) generally required more time than detection

successes (see $\mu_{+}^{(\beta)}$), perhaps reflecting multiple retrieval attempts before an uncertainty state is entered. This result could be interpreted in light of the notion that successful detection emerges from a self-terminating process, whereas the failure to detect corresponds to an exhaustive process (for a general discussion, see Cox & Criss, 2017).

The effects of studied-item strength. Moreover, detection parameters for 683 studied items $(D_O, D_S, \text{ and } D_W)$ were sensitive to studied-item strength, 684 as captured by their respective population means $\mu^{(\alpha)}$. There was, how-685 ever, little evidence for an effect of study strength on the process-completion 686 times of the detection process, whatever its outcome (see $\mu_{-}^{(\beta)}$ and $\mu_{+}^{(\beta)}$). 687 This result is in line with previous studies showing that response speed-ups 688 observed in study-strength manipulations can be largely attributed to differ-689 ences in the mixture of detection (S_1 and S_2) and uncertainty (S_3) states (see 690 Kellen et al., 2015; Province & Rouder, 2012), as reflected in the differences in $\mu^{(\alpha)}$ parameters for the detection parameters. 692

The effects of baserate. The baserate manipulation had the expected effect of increasing $\mu^{(\alpha)}$ for the guessing parameters as the proportion of old items increased. This pattern was present in in both Arnold et al.'s (2015) Experiment 1 and Dube et al.'s (2012) datasets. The 95% HDI of the contrast between low and high base rate in the former experiment contains zero, however (see the respective column Δ in Table 2). Furthermore, in Dube et al.'s (2012) datasets, the process-completion time for the guessing process increases for guessing "new" $(\mu_{+}^{(\beta)})$ and decreases for guessing "old" $(\mu_{+}^{(\beta)})$

 $^{^{10}\}mathrm{Because}$ Dube et al.'s (2012) studies always involved a within-participant manipulation of study strength, in Table 3 we denote the detection probabilities for weak and strong items by D_W and D_S , respectively. In the case of Arnold et al. (2015), only Experiment 3 included such a manipulation, but between subjects. We therefore denote all detection probabilities as D_O in Table 2.

Table 2
Parameter Estimates and 95% HDIs for the Arnold et al. (2015) Data

			a		RT-MPTs
Exp. 3		.79 [.73, .85] .01 [.00, .09]; .54 [.43, .68] ^a .58 [.49, .66]	$187 [136, 224]$ $155 [127, 183]; 138 [116, 159]^a$ $55 [28, 81]$	$81 [61, 104]$ $56 [35, 83]; 84 [17, 203]^a$ $88 [68, 107]$	New 623 [597, 650] 684 [652, 711] $[-97, -21]$ 773 [722, 819] 551 [510, 591] [155, 282] 620 [593, 648] Old 638 [613, 663] 593 [568, 618] [10, 79] 716 [667, 765] 517 [475, 560] [134, 263] 583 [560, 607] Note. Par. = Parameter: Low= Low base-rate: High base-rate: Acc. = Accuracy: $\Delta = 95\%$ HDI of the group
Exp. 2		[32, .18] [04, .43] [21, .13]	[285, 483] [285, 456] [-49, 41]	[50, 307] [17, 251] [-27, 113]	[155, 282] [134, 263] acv: $\Delta = 95\%$
	Speed	.45 [.07, .59] .10 [.00, .40] .56 [.29, .64]	83 [39, 109] 168 [84, 304] 45 [22, 90]	77 [49, 102] 59 [20, 98] 69 [40, 106]	551 [510, 591] 517 [475, 560] 5: Acc. = Accur
	Acc.	$egin{array}{ll} &oldsymbol{\mu}^{(lpha)} & oldsymbol{\mu}^{(lpha)} & -43 \ .28 \ [.13, .55] \ .55 \ [.30, .65] \end{array}$	$-\frac{\mu_{-}^{(\beta)} \text{ (ms)}}{465 [362, 568]}$ $448 [377, 532]$ $49 [16, 81]$	$-\mu_{+}^{(\beta)} \text{ (ms)} 295 [129, 385] 168 [84, 305] 100 [55, 197]$	$-\mu^{(\gamma)} \text{ (ms)}$ 773 [722, 819] 716 [667, 765] = High base-rate
		[20, .55] [26, .39] [44, .07]	[-144, 143] [-157, 80] [-126, 118]	[-196, 32] [-75, 123] [-113, 150]	[-97, -21] $[10, 79]$ se-rate: High =
Exp. 1	High	.53 [.07, .67] .15 [.00, .58] .65 [.30, .74]	302 [83, 363] 250 [97, 291] 97 [57, 245]	202 [39, 258] 59 [16, 166] 76 [37, 287]	684 [652, 711] 593 [568, 618] r: Low= Low ba
	Low	.59 [.28, .76] .34 [.14, .52] .38 [.20, .52]	237 [187, 287] 164 [49, 191] 136 [49, 191]	70 [35, 118] 87 [34, 160] 171 [119, 216]	623 [597, 650] 638 [613, 663] ar. = Paramete
	Par.	$egin{array}{c} D_N \ D_O \ g \end{array}$	$egin{array}{c} D_N \ D_O \ g \end{array}$	$egin{array}{c} D_N \ D_O \ g \end{array}$	New Old

Note. Par. = Parameter; Low = Low base-rate; High = High base-rate; Acc. = Accuracy; Δ =95% HDI of the group

difference. $^a\mathrm{Values}$ for weak and strong studied items, respectively.

Table 3

Parameter Estimates and 95% HDIs for the Dube al. (2012) Data

95		.65 [.58, .71]	135 [85, 185]	20 [10, 35]		.63 [.57, .70]	208 [155, 260]	18 [8, 33]	R
g_4		.58 [.50, .65]		$\begin{array}{c} 33 \ [15, 57] \\ , -91 \end{array}$.57 [.48, .65] .44]	155 [109, 204] 190]	51 [28, 79] -110]	
g_3		.29 [.23, .36] .47 [.38, .57] .58 [.50, .65] Linear Trend: [29 79]	62 [32, 101] 114 [68, 162] 118 [66, 179] Linear Trend: [49, 132]	163 [101, 223] 79 [40, 127] 33 Linear Trend: [-179, -91]		.28 [.21, .36] .44 [.35, .52] .57 Linear Trend: [.32, .44]	$57 \left[34,82 \right] 137 \left[84,198 \right] 155 \left[109,204 \right]$ Linear Trend: $\left[105,190 \right]$	210 [164, 261] 89 [52, 133] 51 Linear Trend: [-190,-110]	
g_2		.29 [.23, .36]	62 [32, 101] Line	163 [101, 223] Linea		.28 [.21, .36] Line	57 [34, 82] Lines	210 [164, 261] Linear	
g_1	— Exp. 1—	.19 [.14, .24]	20 [10, 34]	169 [115, 226]	— Exp. 2	.21 [.14, .29]	24 [11, 43]	177 [126, 234]	
D_S		.79 [.74, .85]	a a a a a a a a a a	78 [51, 107] ak: [-70, 10]		.72 [.63, .80] ak: [.42, .62]	232 [170, 301] ak: $[-19, 87]$	100 [72, 134] ak: $[-50, 44]$	
D_W		.35 [.27, .43] .79 [.74, .85] Strong vs Weak: [36, 52]	189 [150, 223] 160 [110, 212] Strong vs. Weak: [-76, 21]	107 [67, 157] 78 [51, 107] Strong vs. Weak: [-70, 10]		.21 [.12, .30] .72 [.63, .80] Strong vs. Weak: [.42, .62]	201 [163, 244] 232 [170, 301] Strong vs. Weak: [-19, 87]	103 [58, 152] 100 [72, 134 Strong vs. Weak: [-50, 44]	
D_N		.51 [.38, .63]	203 [158, 245]	127 [98, 156]		.48 [.34, .61]	240 [190, 294]	156 [117, 202]	
Par.		$ ho_{m{\mu}}^{(lpha)}$	$rakebox{2}_{-eta}^{(eta)}$	${{\stackrel{\bullet}{\mathcal{L}}}}^{+}_{(\beta)}$		$ ho_{m{\mathcal{H}}^{(lpha)}}$	$ abla_{-}^{(eta)}$	$\triangleright_{\boldsymbol{\mathcal{E}}_{(\widehat{\boldsymbol{\mathcal{G}}})}}^{+}$	

detection for strong studied items. $\mu^{(\gamma)}$ for new and old responses were, respectively, 518 ms [490, 547] and 554 ms [531, 578] in Exp. 1; 534 ms [505, 563] and 557 ms [518,594] in Exp. 2. Note. Par. = Parameter; $\Delta = 95\%$ HDI of planned contrasts, D_w =target detection for weak studied items, D_s =target

as the proportion of old items increases (from g_1 to g_5). This agrees well with 701 the idea of the DI version of the 2HT model that guessing first suggests a 702 default response and that a clear default is available to the extent to which 703 the baserate departs from 50%. There is, however, no such trend in Exper-704 iment 1 by Arnold et al. (2015) in which a baserate manipulation was also 705 implemented, perhaps because response-execution times for "old" and "new" 706 responses and completion times for guessing "old" and "new" are strongly 707 confounded in Arnold et al.'s design, making it difficult to estimate guessing 708 completion-times with precision. 709

The effects of speed-accuracy instructions. We did not have clear expectations for the effects of the speed-accuracy instructions other than that we expected an emphasis on speed to speed up response execution and perhaps detection processes, as participants might refrain from continuing their retrieval efforts after a certain period. Furthermore, an emphasis on speed should not increase the probability of detection (e.g., Ludwig & Davies, 2011).

As can be seen in Table 2, an emphasis on accuracy (Arnold et al., 2015, Exp. 2) has relatively little effect on the accuracy parameters relative to an emphasis on speed. The only exception was a trend for better detection of studied items ($\mu^{(\alpha)}$ for D_O) in Arnold et al.'s (2015) Experiment 2. This is in line with the absence of a significant effect of the manipulation on signal-detection sensitivity in traditional analyses (Arnold et al., 2015).

However, an emphasis on speed led to a speed-up of all process-completion times as well as response execution relative to an emphasis on accuracy. For example, detection processes under accuracy instructions might be based on repeated retrieval attempts, which do not add much to accuracy over and above the first attempt, whereas fewer retrieval attempts might be performed under speed instructions. Only the completion times for the guessing pro-

cesses are not affected, in line with the idea that guessing always provides a fast first response proposal in the DI variant of the 2HT model.¹¹

Summary. Taken together, the DI model provides a reasonable fit of the
data, and its parameters react meaningfully to the different experimental
manipulations. This suggests that a discrete-state model is able to provide a
process account of extant response-time data in recognition memory at least
to a similar extent as the diffusion model does. Limitations of the RT-MPT
account are considered in the General Discussion.

736 5.3. Correlations

One advantage of the present hierarchical approach is the possibility to 737 model and estimate correlations between the person-level process param-738 eters across persons. To illustrate, we consider correlations between the 739 person-level parameters $\beta'_{+,p,s}$, averaged across processes p, and $\beta'_{-,p,s}$, averaged across processes p based on the estimated variance-covariance ma-741 trix Σ . For Arnold et al.'s (2015) Experiments 1 to 3, they amounted to 742 (95% HDIs in brackets), in order, 0.71 [0.38, 0.93], 0.82 [0.61, 0.96], and 0.35 743 [-0.24, 0.81]. For Dube et al.'s (2012) Experiments 1 and 2, they amounted to 0.41 [-0.24, 0.81], and 0.79 [0.59, 0.92], respectively. Thus, there is some 745 evidence for a general speed factor, such that persons completing processes 746 with a '+' outcome fast also tend to arrive at the '-' outcome fast.

We also probed for speed-accuracy trade-off between persons by computing the correlations between the person-level parameters governing accuracy, $\alpha'_{p,s}$ corresponding to the detection parameters D_N and D_O , averaged across

¹¹It is worth noting that our evidence for selective influence with Arnold et al.'s (2015) Experiment 2 data is not replicated when fitting the data with the diffusion model. Arnold et al. reported differences in the boundary-separation parameters (as expected) but also in the drift rates for new items.

the different detection processes on the one hand and the person-level parameters governing the speed of responses $\beta'_{+,p,s}$ and $\beta'_{-,p,s}$ averaged across these same detection processes on the other hand. None of these correlations was substantial, however, ranging from -0.15 to 0.28, and all 95% HDIs contained zero. Thus, there is little evidence for speed-accuracy trade-offs between persons in these datasets.

Based on the posterior distribution of the variance-covariance matrix Γ for response-execution parameters, the speed of executing "old" and "new" responses correlated positively across participants with correlations ranging from 0.35 to 0.91 across studies. None of the associated 95% HDIs contained the value zero.

5.4. Precision of Estimates

Another advantage of the present approach is that the precision of the 763 estimation of the traditional MPT parameters governing the categorical data 764 can be expected to increase as a side effect of including the response-time 765 data. To see this, consider the population mean parameters $\mu_p^{(\alpha)}$ for process p. 766 The MCMC algorithm samples from the distribution of this parameter given 767 the categorical frequency data C and the response-time data T, that is from 768 $P(\mu_p^{(\alpha)} \mid C, T)$, and the estimate of $\mu_p^{(\alpha)}$ is a measure of the central tendency 769 of that distribution. The measurement precision can thus be quantified in 770 terms of the variability of $\mu_p^{(\alpha)}$. 772

The traditional Bayesian approach without response-time data (e.g., Klauer, 2010) samples from $P(\mu_p^{(\alpha)} \mid C)$. It is well known that the variances of these distributions, $P(\mu_p^{(\alpha)} \mid C, T)$ and $P(\mu_p^{(\alpha)} \mid C)$, are related via var $(\mu_p^{(\alpha)} \mid C) = \mathbb{E}_T[\text{var}(\mu_p^{(\alpha)} \mid C, T)] + \text{var}_T(\mathbb{E}[\mu_p^{(\alpha)} \mid C, T])$, where \mathbb{E}_T and \mathbb{E}_T refer to taking the expectation and variance with respect to T (Gelman et al., 2004, p. 24). This implies that the variance of $\mu_p^{(\alpha)}$ given C and T,

var $(\mu_p^{(\alpha)} | C, T)$, can be expected to be smaller than the variance given only C by the variance of the expected value of $\mu_p^{(\alpha)}$ given C and T, across repeated response-time measurements, T. In other words, including the response-time data can be expected to decrease the variability of the posterior distribution of $\mu_p^{(\alpha)}$.

To illustrate, we computed the lengths of the HDI's for the 16 $\mu_p^{(\alpha)}$ pa-783 rameters in the two experiments by Dube et al. (2012) under the DI variant 784 (see Tables 2 and 3). In these experiments, the 2HT model is also identified 785 on the basis of only the categorical data, and we applied the hierarchical 786 Bayesian approach on the basis of only the categorical data using exactly 787 the same priors and hyperpriors as in the present approach to estimate these 788 same parameters. HDIs based on categorical data and response times were 789 shorter than those based on only the categorical data for 13 of the 16 param-790 eters. The mean saving in the length of the HDIs across the 16 parameters 791 was 39%. 792

⁷⁹³ 6. Recovery Study

Strong theoretical results on MCMC estimation guarantee that the pos-794 terior estimates will approach the true underlying values as the sample size 795 increases. However, such results do not excuse researchers from investigat-796 ing the recoverability of parameters under any new modeling development 797 (Heathcote, Brown, & Wagenmakers, 2015). Ideally, these recovery studies 798 should be based on realistic datasets. We therefore conducted a recovery 799 study based on the parameters of Dube et al.'s (2012) Experiment 1. We chose this dataset because it is the smallest one in terms of numbers of partic-801 ipants (S = 21) with a large number of process-related parameters (P = 8)802 and few trials per cell of the baserate × item-type design (between 12 and 803

48 trials per person). Recovery results in this framework are thereby likely to provide a lower baseline of the estimation accuracy to be expected.

Based on the population-level parameters estimated for Dube et al.'s (2012) Experiment 1, we generated 2000 artificial datasets of the same size as the original data in terms of participants and numbers of trials per participant. Each dataset was then submitted to the present algorithm.

Table 4 presents recovery results for the population-level process pa-810 rameters. It can be seen that the estimates tend to track the underlying 811 values quite closely, but there is a tendency to overestimate small process-812 completion times. The 50% and 95% HDIs for each parameter appear to be reasonably well calibrated as quantifying estimation uncertainty inasmuch as 814 the underlying value tends to fall into the respective interval with approxi-815 mately the nominal percentages. There are, however, again larger deviations 816 for small process-completion times, and in general there is a tendency for the 817 actual intervals to contain the true value somewhat less often than suggested 818 by their nominal percentages even for large estimated process-completion 819 times. The standard deviation of parameter values in the posterior sample provides an adequate estimate of the standard deviation of the posterior 821 median across simulated datasets. 822

Table 5 presents the same information for the population-level standard deviations of the process parameters as estimated in Σ . Despite the small size of the underlying datasets, the model performs quite well in estimating the underlying standard deviations in the person-level process parameters and succeeds well in quantifying estimation uncertainty in terms of the HDIs. Again, the standard deviation of parameter values in the posterior sample provides a good estimate of the standard error of the posterior median across the board.

Table 4
Parameter Recovery Study: Population-level Means of Process
Parameters

Par.	True	Est.	$50\%^{a}$	$95\%^{a}$	SE^b	SD^c					
$-oldsymbol{\mu}^{(lpha)}-$											
D_N	.51	.51	46.35	92.85	0.06	0.06					
D_W	.35	.36	48.50	94.40	0.04	0.04					
D_S	.79	.79	49.30	95.35	0.03	0.03					
g_1	.21	.21	47.05	93.65	0.04	0.04					
g_2	.28	.28	51.70	94.45	0.03	0.04					
g_3	.44	.44	46.70	93.25	0.04	0.04					
g_4	.57	.57	49.25	94.90	0.04	0.04					
g_5	.63	.63	49.45	94.20	0.03	0.03					
$- \boldsymbol{\mu}_{-}^{(\beta)} -\!\!\!\!\!-$											
D_N	202.70	194.23	μ_{-} 43.25	90.15	21.53	21.96					
D_W	189.20	184.63	47.05	92.45	15.95	16.44					
D_S	159.90	151.09	43.15	89.70	21.04	21.12					
g_1	19.94	34.82	10.70	60.50	7.83	8.97					
g_2	62.26	77.18	44.95	91.40	17.84	19.89					
g_3	114.30	118.46	51.50	95.20	20.66	22.42					
g_4	117.80	126.89	49.80	95.05	26.46	28.17					
g_5	134.70	139.46	49.40	94.40	23.09	23.79					
			(β)								
D	100.00	100 50	$-\mu_+^{(eta)}-$	-	10.70	10.00					
D_N	126.90	120.53	43.85	90.05	12.73	12.86					
D_w	107.20	99.51	40.90	88.75	18.75	18.27					
D_s	78.40	73.51	42.85	89.40	12.50	12.58					
g_1	168.60	174.91	46.95	93.35	29.57	29.40					
g_2	162.60	167.59	49.25	94.50	27.54	28.42					
g_3	79.10	93.72	46.95	92.70	21.11	22.61					
g_4	33.11	51.89	23.95	77.40	12.46	14.32					
g_5	20.46	36.24	10.50	64.30	8.32	9.96					

Note. Par. = Parameter; Est. = posterior median (mean across simulated datasets).

 $[^]a\mathrm{Percent}$ of simulated datasets with true value in the HDI of this percentage.

 $[^]b$ Standard error of posterior medians across simulated datasets. c Posterior standard deviation (mean across simulated datasets).

Table 5
Parameter Recovery Study: Standard Deviations of Person-Level
Process Parameters

$-\alpha'$ — D_N 0.57 0.61 52.45 96.05 0.12 D_w 0.27 0.30 48.95 92.55 0.10 D_s 0.33 0.38 47.70 92.65 0.09 g_1 0.48 0.51 50.85 94.10 0.12 g_2 0.34 0.34 46.80 91.90 0.11	0.13 0.10 0.09 0.13 0.11 0.10											
$egin{array}{cccccccccccccccccccccccccccccccccccc$	0.10 0.09 0.13 0.11 0.10											
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0.10 0.09 0.13 0.11 0.10											
D_s 0.33 0.38 47.70 92.65 0.09 g_1 0.48 0.51 50.85 94.10 0.12	0.09 0.13 0.11 0.10											
g_1 0.48 0.51 50.85 94.10 0.12	0.13 0.11 0.10											
0.24 0.24 40.22 0.4.02	0.11 0.10											
a = 0.34 + 0.34 + 46.80 + 01.00 + 0.11	0.10											
32												
$g_3 = 0.28 0.26 51.10 91.85 0.10$	0.11											
$g_4 = 0.29 0.29 48.40 92.35 0.11$												
$g_5 = 0.19 0.20 45.75 95.55 0.09$	0.10											
Q!												
$-oldsymbol{eta'}$	0.10											
$D_N = 0.42 = 0.46 = 50.85 = 95.85 = 0.09$	0.10											
D_w 0.30 0.32 48.90 94.55 0.08	0.08											
D_s 0.40 0.43 46.50 92.90 0.15	0.15											
g_1 1.09 0.86 30.70 82.70 0.27	0.26											
g_2 1.08 1.03 49.00 94.95 0.21	0.23											
g_3 0.70 0.72 52.10 96.70 0.16	0.17											
g_4 0.83 0.85 52.70 96.65 0.18	0.20											
$g_5 = 0.56 0.58 52.20 95.25 0.16$	0.17											
a.												
$-\beta'_{+}$ $-D_{N}$ 0.24 0.26 46.70 94.80 0.11	0.12											
D_w 0.52 0.52 47.70 92.50 0.19	0.19											
D_s 0.60 0.65 50.75 95.00 0.15	0.16											
g_1 0.46 0.46 49.80 93.65 0.17	0.18											
g_2 0.53 0.54 51.55 92.40 0.17	0.18											
g_3 0.96 0.90 48.80 93.65 0.20	0.22											
g_4 1.21 1.01 33.75 85.75 0.27	0.27											
g_5 1.19 0.94 32.10 82.70 0.29	0.28											

Note. Par. = Parameter; Est. = posterior median (mean across simulated datasets).

 $[^]a\mathrm{Percent}$ of simulated datasets with true value in the HDI of this percentage.

 $[^]b$ Standard error of posterior medians across simulated datasets. c Posterior standard deviation (mean across simulated datasets).

Table 6 presents the same information for selected correlations, specifi-831 cally for the eight lowest, eight median, and eight highest correlations. Con-832 sidering the small number of persons across which these correlations are esti-833 mated and the small numbers of trials per cell of the design, the correlations 834 are estimated reasonably well. The estimates faithfully track the sign of the 835 underlying correlations. Perhaps not surprisingly, given the small sizes of 836 the datasets, they underestimate the absolute sizes of the true correlations, 837 and standard deviations of posterior medians across simulated datasets are 838 systematically smaller than the posterior standard deviation of parameter 839 values. Nevertheless, the HDIs quantify the estimation uncertainty reasonably well. 841

A reviewer suggested to provide information on model discrimination via 842 simulation. Specifically, the concern was that the DI model might outper-843 form the DG model due to greater flexibility. To assess this possibility, we 844 generated 100 more datasets from the DI model as well as 100 datasets from 845 the DG model using the same parameters and procedures as just described, 846 and fitted these datasets with the DG and the DI model, computing DIC for both models. When generating from the DI model, DIC was higher for 848 the DG model than for the DI model for all 100 artificial datasets; when 849 generating from the DG model, DIC was higher for the DI model than the 850 DG model in 98 cases. The mean differences in DIC values in favor of the 851 generating model were 379.02 and 197.79, respectively. Not surprisingly, the 852 differences were significant in a t test across the 100 datasets in both cases: 853 t = 40.34, df = 99, p < .001 and t = 20.11, df = 99, p < .001, respectively. These DIC differences indicate that none of the models is particularly apt 855 in mimicking the other, providing additional support for the present results 856 favoring the DI variant of the 2HT model.

Table 6
Parameter Recovery Study: Selected Correlations of Person-Level
Process Parameters

Pars.	True	Est.	$50\%^{a}$	$95\%^{a}$	SE^b	SD^c
	_	_		Correla	tions -	
$\alpha'_{D_s}, \beta'_{g_5,-}$	53	23	37.95	95.45	0.17	0.28
$\alpha'_{D_s}, \beta'_{g_5,+}$	51	21	38.25	96.15	0.17	0.29
$\alpha'_{g_1}, \beta'_{D_N,-}$	50	33	50.05	94.95	0.17	0.22
$\alpha'_{g_1}, \beta'_{g_5,-}$	50	30	50.25	96.60	0.17	0.24
$\beta'_{g_1,-}, \beta'_{g_5,+}$	48	20	41.90	94.90	0.18	0.28
$\alpha'_{g_1}, \beta'_{D_s,-}$	47	24	46.95	96.90	0.17	0.26
$\alpha'_{g_3}, \beta'_{D_N,-}$	47	23	48.10	95.75	0.18	0.27
$\beta'_{g_1,-}, \beta'_{g_5,-}$	44	21	49.85	95.10	0.19	0.27
		Fight	Median	Correla	ations -	
$\beta_{g_5,-}',\beta_{D_w,+}'$.03	.04	59.20	99.30	0.20	0.29
$\alpha'_{D_s}, \beta'_{g_5,+}$.03	.00	58.30	98.85	0.19	0.27
$lpha_{g_5}', eta_{D_N,-}'$.03	.09	60.25	99.35	0.18	0.29
$eta'_{g_2,-},eta'_{g_1,+}$.03	.02	65.70	99.50	0.18	0.28
$\alpha'_{g_4}, \beta'_{g_1,+}$.04	.02	74.85	99.95	0.15	0.30
$\beta'_{g_1,-}, \beta'_{D_s,+}$.04	.01	55.40	97.75	0.21	0.27
$\alpha'_{g_3}, \beta'_{D_w,+}$.04	.00	68.90	99.65	0.17	0.30
$\beta'_{q_2,-}, \beta'_{D_s,+}$.04	.03	55.20	96.85	0.20	0.24
$g_2, D_s,+$						
		Eight	Largest	Correla	ations -	_
$\beta'_{D_N,-}, \beta'_{g_3,-}$.48	.35	55.95	97.40	0.17	0.22
$\beta'_{D_w,-},\beta'_{g_3,-}$.48	.34	58.50	98.15	0.16	0.23
$\alpha'_{D_w}, \beta'_{D_w,-}$.48	.21	40.30	94.20	0.17	0.27
$\beta'_{D_w,+}, \beta'_{D_s,+}$.51	.27	47.70	96.45	0.18	0.27
$\beta'_{D_N,-},\beta'_{g_5,-}$.53	.37	57.10	97.05	0.16	0.23
$\beta'_{g_3,-}, \beta'_{g_5,-}$.54	.35	51.65	95.70	0.17	0.23
$\alpha'_{g_3}, \beta'_{g_1,-}$.56	.21	28.60	92.90	0.17	0.29
$\beta'_{D_N,-},\beta'_{D_w,-}$.60	.41	50.80	95.00	0.15	0.22

Note. Pars. = Parameters; Est. = posterior median (mean across simulated datasets).

 $[^]a\mathrm{Percent}$ of simulated datasets with true value in the HDI of this percentage.

^bStandard error of posterior medians across simulated datasets. ^cPosterior standard deviation (mean across simulated datasets).

7. General Discussion

The modeling tools currently available in researchers' toolboxes constitute 859 a major source of constraint for the type of experimental paradigms that are 860 ultimately adopted. In the case of response-time modeling, the need for a 861 large number of observations has been relaxed due to recent advances in 862 hierarchical Bayesian methods, making them available to a large number 863 of applications (e.g., Rouder, Province, Morey, Gomez, & Heathcote, 2015; Vandekerckhove, Tuerlinckx, & Lee, 2011). However, most response-time 865 models like the prominent diffusion model (Ratcliff & Rouder, 1998) are 866 restricted to two-choice paradigms (one exception being the family of linear-867 ballistic accumulator models; Brown & Heathcote, 2008), which limits their 868 overall usefulness. No such limitations exist in the case of MPT models. 869

The present work aims to enrich the current toolbox by proposing a 870 method for combining two long-standing modeling traditions that are typi-871 cally seen as somewhat disjoint — process-oriented response-time modeling 872 and multinomial-processing-tree modeling. As traditionally assumed in MPT 873 models, the probability of observing a certain response corresponds to a mix-874 ture of different processing paths. We propose that the latencies associated with a given response can be captured by ascribing a completion-time dis-876 tribution to each process outcome included in the different paths that lead 877 to that response, in addition to encoding and response-execution times. Because our proposed method can be applied to any existing member of the 879 MPT model class, it imposes no a priori constraints on the type of MPT 880 paradigm that one can consider, as long as response times can be reliably 881 recorded. In fact, the inclusion of response time might even lead to less constrained model accounts, as parameters that were not identified can become 883 so. 884

As an application example, we extended two variants of the well-known 885 2HT model and tested their ability to capture recognition-memory data 886 across a range of experimental manipulations. Interestingly, we found that 887 a "default-interventionist" variant of the 2HT, in which the guessing process 888 precedes the attempts to retrieve the item from memory, provided the best 889 account of the datasets considered here. This tree structure deviates from 890 the way the 2HT is typically conceptualized, namely in terms of the "detect-891 guess" variant. However, it should be emphasized that the two variants are 892 indistinguishable on the basis of the typical categorical data collected and 893 analyzed in recognition-memory experiments. The conceptualization of the model in terms of the "detect-guess" variant has therefore been a convention 895 based on tacit and previously untestable assumptions about processing order. 896 Future work is required to determine whether the processing-tree structure 897 found to be most adequate here depends on the characteristics of the experimental design, a likely possibility in any complex faculty such as human 899 memory (e.g., Humphreys, Bain, & Pike, 1989; Meyer & Kieras, 1997). One 900 indication in this direction may be the finding that the traditional "detect-901 guess" variant outperformed the "default-interventionist" variant in one of 902 the analyzed datasets in which instructions emphasized either speed or ac-903 curacy. In any case, the present results demonstrate that by incorporating 904 response times, one can overcome a long-standing inability to distinguish between different processing tree structures (e.g., Kellen & Singmann, in press; 906 Kellen, Singmann, & Klauer, 2014). 907 The applications also illustrate two additional advantages of incorporating 908 response times in the present framework: First, models that are not identifiable on the basis of only categorical responses will typically be identified when 910

response times are included via assumptions about process-completion dis-

tributions and distributions of encoding and response-execution components. 912 For example, in the above applications, models with different detection pa-913 rameters D_N and D_O for detecting new and old items, respectively, could 914 be fit even where this would not have been possible in the traditional MPT 915 analysis. Second, the present method provides a principled alternative to the 916 currently dominant diffusion-model analyses (e.g., Matzke & Wagenmakers, 917 2009; Voss, Voss, & Lerche, 2015), at least in the many cases in which theory-918 driven and validated MPT models have been formulated for the accuracy 919 data in the experimental paradigm under scrutiny. In such cases, RT-MPT 920 models establish a principled competitor for process-oriented accounting of 921 the data. RT-MPT models build on the MPT models that were successful 922 in describing the accuracy data, now addressing the same range of data at 923 the same level of detail as the diffusion-model analyses of them as illustrated 924 here for recognition-memory paradigms. 925

Note, however, that RT-MPT models and diffusion models differ in the 926 breadth and depth of the process accounts they provide. RT-MPT models 927 postulate that several processes are at work and aim at quantifying the dif-928 ferent processes' relative contributions to observed responses and response 929 times, conditional on the constellation of the processes' interactions as coded 930 in the tree structure. This is especially helpful in modeling paradigms in 931 which multiple processes are likely involved. These processes are, however, 932 not modeled in any more detail beyond what they contribute to the fre-933 quencies of responses and the observed response times. In contrast, dif-934 fusion models postulate one (diffusion) process, which they model in more 935 depth. For example, the threshold parameter in diffusion models allows one 936 to model speed-accuracy trade-offs in a parsimonious and compact way, and 937 the starting-point parameter captures negative correlations between response

frequency and response time in a natural fashion. Options 2 and 3 discussed 939 in the introduction for alternative distributional assumptions may enable one to graft some of this elegance onto response-time extensions of MPT models. The proposed approach is also likely to be valuable in areas in which 942 the incorporation of response times into existing MPT models represents a 943 major development. One such area of research is implicit social cognition — 944 which includes prominent paradigms such as the Implicit Association Test 945 or the Weapon Identification Task — where several MPT models captur-946 ing a diverse set of automatic and controlled processes have been proposed 947 (e.g., Bishara & Payne, 2009; Meissner & Rothermund, 2013; for reviews, see Hütter, & Klauer, 2016; Sherman, Klauer, & Allen, 2010). Despite their 949 merits, these models currently ignore response times, a key aspect of partici-950 pants' judgments (e.g., decide as quickly as possible whether the object being 951 held by a Black or White person is a gun) and a key aspect in traditional 952 analyses of such data. Incorporating response times into the model analyses 953 would allow the MPT literature on social-cognition paradigms to speak more 954 directly to the vast social-cognition literature relying on response times as the major dependent variable. One important question that response times 956 can help answering concerns the relative temporal sequencing of controlled 957 detection and inhibition processes and their dominance over automatic pro-958 cesses. Another contribution is that the present method, by disentangling process-completion times, allows one to characterize the speed of the differ-960 ent modeled processes and to test theoretical predictions about their different 961 speeds. For example, one defining characteristic of automatic processes such 962 as the activation of response proposals based on stereotypic associations in the Implicit Association Task or the Weapon Identification Task is that they 964 are believed to complete faster than the controlled detection and inhibition processes that are also assumed to operate in these tasks. Efforts to incorporate response times into some of these models from social cognition are ongoing.

Finally, since its inception, the MPT model class has been framed as a way 969 to obtain theoretically motivated and empirically validated decompositions 970 of the major processes at work, which can be useful when characterizing 971 individuals from different populations (Riefer & Batchelder, 1988). When 972 used as a measurement tool, a MPT model can provide important insights, 973 such as the attribution of a given cognitive deficit to differences in a specific 974 parameter (e.g., Riefer, Knapp, Batchelder, Bamber, & Manifold, 2002). By providing simultaneous descriptions of accuracy and response-time data, the 976 extended RT-MPT models obviously make use of more information than tra-977 ditional MPT models thereby likely enhancing the usefulness of such models 978 as measurement tools. For example, the precision of the estimation of the traditional MPT parameters governing the categorical data can be expected 980 to increase as a side effect of including the response-time data. As another 981 simple example, the new RT-MPT method can accommodate differences be-982 tween persons in the relative emphasis an individual puts on accuracy at 983 the expense of speed and vice versa — individual differences to which tradi-984 tional MPT models, relying on only the accuracy data, are vulnerable. For 985 instance, it would now be possible to diagnose cognitive deficits that are revealed primarily in processing speed rather than processing accuracy and 987 to pinpoint the processes most affected, addressing important issues in, for 988 example, the study of cognitive aging (e.g., Kliegl, Mayr, & Krampe, 1994). 989 To conclude, consider just one more area where measurement modeling 990 using the RT-MPT method seems especially promising — the characteri-991 zation of workload capacity conceptualized in terms of processing speed as

a function of the number of concurrent stimuli (Miller, 1982). The assess-993 ment of individual workload capacity can often be challenging due to the 994 need for a considerable number of trials per person, as well as the possibility of contamination by guessing-based responses (for an overview, see 996 Gondan & Minakata, 2016). Alternatively, one could follow up on Ollman's 997 (1966) earlier work and build an RT-MPT that estimates the latencies of 998 the stimulus-dependent and stimulus-independent (i.e., guessing) processes. 999 Such an approach has the advantage of capturing information in the response-1000 time distributions in a small number of parameters, with workload capacity 1001 being assessed by comparing process-latency parameters across conditions 1002 (see Eidels, Donkin, Brown, & Heathcote, 2010). Moreover, the RT-MPT 1003 method is hierarchical, which improves parameter estimation by allowing in-1004 dividual estimates to inform each other, an advantage of critical importance 1005 when data are sparse (Katahira, 2016; Klauer, 2010). 1006

Reaping these benefits rests on these models fitting the to-be-analyzed 1007 data well and on successfully passing a validation program based on selective-1008 influence studies (Heathcote et al., 2015; Klauer et al., 2012) as tentatively 1009 illustrated here for the response-time extension of the 2HT model. Selective-1010 influence studies implement experimental manipulations believed to affect 1011 only one process in the model. The question then is whether each such 1012 manipulation will be reflected primarily in the parameters for the targeted 1013 process while leaving parameters pertaining to non-manipulated processes 1014 unaffected. As already mentioned, one limitation of the present develop-1015 ment in this context is that like diffusion models, RT-MPTs rely on a set of 1016 specific auxiliary assumptions about the distributions of process-completion 1017 times and encoding and response-execution times. It is likely that cases ex-1018 ist in which these specific auxiliary assumptions do not even approximately describe the data-generating process, leading to misfit and failure of demonstrating selective influence, even though the core structural and psychological assumptions of the underlying MPT model as such may still be viable. We hope to be able to relax this limitation to some extent through future work in which we aim to develop the model for the alternative sets of distributional assumptions outlined above (see Section 2.1.).

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1343 Appendix

1344

A.1. Non-Binary MPT Models

Models containing nodes with more than two children can be transformed 1345 into binary MPT models. For that purpose, each node with more than two 1346 children is replaced by a sequence of linked nodes each of which has only 1347 two children. Hu and Batchelder (1994) show how to parameterize the links 1348 to achieve equivalence between the original non-binary MPT model and the resulting binary MPT model. To maintain equivalence of the response-time 1350 predictions, the technical links connecting the series of binary nodes that re-1351 place a non-binary node should not be assigned a completion-time component 1352 so that having such links in a processing path does not add to the response 1353 times. This guarantees equivalence of the person-level models. In hierarchical 1354 models, priors and hyperpriors also need to be adjusted to guarantee equiv-1355 alence for the entire hierarchical model following parameter transformations 1356 (Gelman et al., 2004, Chap. 2; see also Heck & Wagenmakers, 2016). 1357

1358 A.2. The Likelihood of the Joint Distribution of Parameters and Data

On each trial x, administered to subject s=s(x), a category c=c(x) with response r=r(c(x)) and latency t=t(x) is observed from one of the subtrees of the models, denoted subtree(x). Subtree(x) is represented as the set of edges (n,o) in the subtree; the set of nodes n in the subtree will be referred to as nodes(subtree(x)).

The data observed for each trial x are augmented as described above by the path B_x along which the category c(x) was reached, by z-variates $\mathbf{z}_x = (z_{n,x})_{n \in \text{nodes(subtree}(x))}$ for each node of the relevant subtree, and processcompletion times $\mathbf{\tau}_x = (\tau_{n,x}^o)_{(n,o) \in \text{subtree}(x)}$ for each edge of that subtree along with the residual encoding and motor-execution component δ_x . Let 1_C be an indicator function that takes on the value one if the condition C is satisfied and the value zero otherwise. Let θ be a vector that stacks all of the model parameters. For N trials x, the probability function for the joint distribution of parameters and observed and augmented data is given by:

$$p(\quad (B_{x}, \boldsymbol{z}_{x}, \boldsymbol{\tau}_{x}, \delta_{x})_{x=1,\dots,N}, (c_{x}, t_{x})_{x=1,\dots,N}, \boldsymbol{\theta})$$

$$\propto \prod_{x=1}^{N} \left[\left(\prod_{n \in \text{nodes(subtree}(x))} \frac{1}{\sqrt{2\pi}} e^{-\frac{1}{2} \left(z_{n,x} - \alpha_{p(n),s(x)} \right)^{2}} \right) \left(\prod_{n,o) \in B_{x}: o = +} 1_{\{z_{n,x} \geq 0\}} \right) \left(\prod_{n,o) \in B_{x}: o = -} 1_{\{z_{n,x} < 0\}} \right) 1_{\{B_{x} \text{ ends in } c_{x}\}} \left(\prod_{n,o) \in \text{subtree}(x)} \lambda_{p(n),s(x)}^{o} e^{-\lambda_{p(n),s(x)}^{o} \tau_{n,x}^{o}} \right) \left(\sqrt{2\pi\sigma_{s(x)}^{2}} \Phi\left(\frac{\gamma_{r(c(x)),s(x)}}{\sigma_{s(x)}}\right) \right)^{-1} e^{-\frac{1}{2} \frac{\left(\delta_{x} - \gamma_{r(c(x)),s(x)}\right)^{2}}{\sigma_{s(x)}^{2}}} 1_{\{\delta_{x} \geq 0\}} 1_{\{\delta_{x} + \sum_{(n,o) \in B_{x}} \tau_{n,x}^{o} = t_{x}\}} \right] g(\boldsymbol{\theta}), \tag{A1}$$

where g summarizes the prior and hyperprior distributions as unpacked below. The likelihood is the product of five factors:

- 1. The product of the densities of the independent normal variables $z_{n,x}$ with means $\alpha_{p,s} = \mu_p^{(\alpha)} + \alpha'_{p,s}$,
- 2. the product of indicator variables coding whether z_x is consistent with the path B_x and whether the path B_x is consistent with the observed category c_x ,
- 3. exponential densities for the process-completion times $\tau_{n,x}^o$ with rate parameters $\lambda_{p,s}^o = \exp(\mu_{o,p}^{(\beta)} + \beta_{o,p,s}')$ and the truncated normal density for the residual encoding and motor-execution time δ_x with parameters

1384
$$\gamma_{r,s} = \mu_r^{(\gamma)} + \gamma_{r,s}'$$
 and σ_s^2 ,

- 4. an indicator function coding whether these times are consistent with the observed response latency, and
- g 5. the function g characterizing the prior and hyperprior distributions.

In this equation, we suppressed, as is usual for exponential variates, indicator functions coding that the individual process-completion times must be non-negative, but we will need this fact below where we consider the conditional distribution of $(\tau_x, \delta_x)_{x=1,...,N}$.

1392 A.3. The Gibbs Sampler

The Gibbs sampler is an MCMC algorithm for sampling from the posterior distribution of the model parameters given the data $(c_x, t_x)_{x=1,...,N}$. It cycles through blocks of parameters. For each block, one sample is drawn from the conditional distribution of the parameters of the block given the data and the remaining parameters. In what follows, we characterize the conditional distributions involved and briefly describe how we sampled from them for non-standard distributions.

1400 A.3.1. The Augmented Data

The conditional distribution of $(B_x, \mathbf{z}_x, \mathbf{\tau}_x, \delta_x)_{x=1,\dots,N}$ is sampled trial by 1401 trial. For a given trial x, we first sample B_x from the conditional dis-1402 tribution of paths B with normal variates z_x and process-completion and 1403 encoding/response-execution times (τ_x, δ_x) integrated out, followed by sam-1404 pling from the conditional distribution of z_x given B_x , the other parameters, 1405 and the data, with (τ, δ_x) integrated out, followed by sampling from the con-1406 ditional distribution of $(\boldsymbol{\tau}_x, \delta_x)_{x=1,\dots,N}$ given B_x , \boldsymbol{z}_x , the other parameters, 1407 and the data. 1408

Like in Klauer (2010), it can be shown that the distribution of B_x end-1409 ing in c_x is given by Equation 7 in the body of the paper. This defines a 1410 multinomial distribution from which paths were sampled. Given a path B_x , 141 the normal variates z_x can be sampled from truncated and non-truncated 1412 normal distributions as described in the paper (Section "Algorithm"). 1413 Consider next the conditional distribution of (τ, δ_x) given the path B_x , 1414 z_x , and the other parameters. For a given trial x and path B_x , the conditional 1415 distribution of (τ_x, δ_x) is a function of the exponential rates $\lambda_{p(n), s(x)}^o$ attached 1416 to the edges (n, o) of the path as well as the parameters $\gamma_{r(c(x)),s(x)} = \mu_{r(c(x))}^{(\gamma)} +$ 1417 $\gamma'_{r(c(x)),s(x)}$ and $\sigma_{s(x)}$ governing the residual time δ_x . Process-completion times $\tau_{n,x}^o$ for edges (n,o) in subtree(x), but not on 1419 the given path B_x can be sampled from the exponential distribution with 1420 rate $\lambda_{p(n),s}^o$ without further constraint (see also Footnote 7 in the body of 1421 the paper). The process-completion times and the residual time along the 1422 given path B_x must, however, add up to t_x . This means that one of these 1423 component times can be expressed in terms of the other times. Let (m,q)1424 be one of the edges (n, o) in B_x with minimum rate parameter: $\lambda_{p(m), s(x)}^q =$ 1425 $\min_{(n,o)\in B_x} \lambda^o_{p(n),s(x)}$. We sample $((\tau^o_{n,x})_{(n,o)\in B_x},\delta_x)$ in three steps. 1426 First, we sample process-completion times $\tau_{n,x}^o$ for edges other than (m,q)1427 from the conditional distribution with δ_x integrated out, followed by sampling 1428 δ_x from the conditional distribution of δ_x given τ_x , all other parameters and 1429 the data. Finally, $\tau_{m,x}^q$ is set to $t_x - \delta_x - \sum_{(n,o) \in B_x: (n,o) \neq (m,q)} \tau_{n,x}^o$. 1430 Collecting the other parameters and data in \mathcal{P} , the conditional distribu-1431 tion $p = p((\tau_{n,x}^o)_{(n,o) \in B_x:(n,o) \neq (m,q)}, \delta_x) | \mathcal{P})$ of $((\tau_{n,x}^o)_{(n,o) \in B_x:(n,o) \neq (m,q)}, \delta_x)$ given 1432 \mathcal{P} is characterized by: 1433

$$p \propto \lambda_{p(m),s(x)}^{q} e^{-\lambda_{p(m),s(x)}^{q} \tau_{m,x}^{q}} \prod_{\substack{(n,o) \in B_{x}: (n,o) \neq (m,q)}} \lambda_{p(n),s(x)}^{o} e^{-\lambda_{p(n),s(x)}^{o} \tau_{n,x}^{o}}$$

$$1_{\{\delta_{x} \geq 0\}} 1_{\{\tau_{m,x}^{q} \geq 0\}} e^{-\frac{1}{2} \frac{\left(\delta_{x} - \gamma_{r(c(x)),s(x)}\right)^{2}}{\sigma_{s(x)}^{2}}}$$

$$\propto \prod_{\substack{(n,o) \in B_{x}: (n,o) \neq (m,q)}} (\lambda_{p(n),s(x)}^{o} - \lambda_{p(m),s(x)}^{q}) e^{-(\lambda_{p(n),s(x)}^{o} - \lambda_{p(m),s(x)}^{q}) \tau_{n,x}^{o}}$$

$$1_{\{0 \leq \delta_{x} \leq t_{x} - \sum_{(n,o) \in B: (n,o) \neq (m,q)} \tau_{n,x}^{o}\}} e^{-\frac{1}{2} \frac{\left(\delta_{x} - (\gamma_{r(c(x)),s(x)} + \lambda_{p(m),s(x)}^{q} \sigma_{s(x)}^{2}\right)^{2}}{\sigma_{s(x)}^{2}}},$$

where components in the above product of exponential densities with rate parameters $\lambda_{p(n),s(x)}^o - \lambda_{p(m),s(x)}^q$ and $\lambda_{p(n),s(x)}^o = \lambda_{p(m),s(x)}^q$ should be replaced by a constant. The second expression in the above characterization of p is obtained by replacing $\tau_{m,x}^q$ by $t_x - \delta_x - \sum_{(n,o) \in B_x:(n,o) \neq (m,q)} \tau_{n,x}^o$ and simple manipulations. Integrating out δ_x , the conditional distribution of $(\tau_{n,x}^o)_{(n,o) \in B_x:(n,o) \neq (m,q)}$ given the other parameters and data is proportional to:

$$p((\tau_{n,x}^{o})_{(n,o)\in B_{x}:(n,o)\neq(m,q)} | \mathcal{P}) \propto \prod_{\substack{(n,o)\in B_{x}:(n,o)\neq(m,q)}} (\lambda_{p(n),s(x)}^{o} - \lambda_{p(m),s(x)}^{q}) e^{-(\lambda_{p(n),s(x)}^{o} - \lambda_{p(m),s(x)}^{q})\tau_{n,x}^{o}}$$

$$\left[\Phi \left(\frac{t_{x} - \sum_{(n,o)\in B:(n,o)\neq(m,q)} \tau_{n,x}^{o} - (\gamma_{r(c(x)),s(x)} + \lambda_{p(m),s(x)}^{q}\sigma_{s(x)}^{2})}{\sigma_{s(x)}} \right) - \Phi \left(\frac{-(\gamma_{r(c(x)),s(x)} + \lambda_{p(m),s(x)}^{q}\sigma_{s(x)}^{2})}{\sigma_{s(x)}} \right) \right] 1_{\{t_{x} - \sum_{(n,o)\in B:(n,o)\neq(m,q)} \tau_{n,x}^{o} \geq 0\}}.$$

To sample from this distribution, we sequentially sample the τ values along the edges (n,o) of B_x other than (m,q) from the respective exponential distribution with rate parameters $\lambda_{p(n),s(x)}^o - \lambda_{p(m),s(x)}^q$ truncated from above

by t_x (or from a uniform distribution on $[0, t_x]$ in the event that $\lambda_{p(n), s(x)}^o =$ $\lambda_{p(m),s(x)}^q$). If in this process, the sum of values already sampled exceeds t_x , we start afresh, amounting to rejection sampling to satisfy the constraint encoded in the indicator function $1_{\{t_x - \sum_{(n,o) \in B: (n,o) \neq (m,q)} \tau_{n,x}^o \ge 0\}}$. A complete set 1447 of τ values for (n, o) in B_x with $(n, o) \neq (m, q)$ emerging from this sampling 1448 scheme follows a distribution with density proportional to the above (nonnormalized) density without the factor given by the difference of the two 1450 cumulative normal distributions, which we refer to as $\Phi_1 - \Phi_2$. We can thus 1451 "add" this factor in a final rejection-sampling step by drawing a random 1452 value u from a uniform distribution, accepting the set of τ -values if 1453

$$u < \frac{\Phi_1 - \Phi_2}{\Phi\left(\frac{t_x - (\gamma_{r(c(x)),s(x)} + \lambda_{p(m),s(x)}^q \sigma_{s(x)}^2)}{\sigma_{s(x)}}\right) - \Phi_2}$$

and starting anew otherwise.

Next, from the above expression for the conditional distribution of $((\tau_{n,x}^o)_{(n,o)\in B_x:(n,o)\neq(m,q)},\delta_x)$, it is easy to see that the conditional distribution of δ_x given the τ -values other than $\tau_{m,x}^q$ and given the other parameters and data is a doubly truncated normal distribution with mean $\gamma_{r(c(x)),s(x)} + \lambda_{p(m),s(x)}^q \sigma_{s(x)}^2$, variance $\sigma_{s(x)}^2$, lower bound zero, and upper bound $t_x - \sum_{(n,o)\in B:(n,o)\neq(m,q)} \tau_{n,x}^o$. Having sampled a new δ_x from this distribution, the new $\tau_{m,x}^q$ is finally set to $t_x - \delta_x - \sum_{(n,o)\in B:(n,o)\neq(m,q)} \tau_{n,x}^o$.

1462 A.3.2. The Person-Level Process Parameters

Sampling $(\alpha'_s)_{s=1,\dots,S}$. Following Gelman and Hill (2007), we implement the scaled inverse Wishart distribution for the variance-covariance matrix Σ of $\begin{pmatrix} \alpha'_s \\ \beta'_s \end{pmatrix}$ by further decomposing $\alpha'_{p,s}$ and $\beta'_{o,p,s}$ into $\alpha'_{p,s} = \xi_p^{(\alpha)} \alpha''_{p,s}$ and $\beta'_{o,p,s} = \xi_p^{(\alpha)} \alpha''_{p,s}$ and $\beta'_{o,p,s} = \xi_p^{(\alpha)} \alpha''_{p,s}$

 $\xi_{o,p}^{(\beta)}\beta_{o,p,s}''$ using the scale factors $\boldsymbol{\xi} = \begin{pmatrix} \boldsymbol{\xi}^{(\alpha)} \\ \boldsymbol{\xi}^{(\beta)} \end{pmatrix}$. A multivariate normal with zero mean and variance-covariance matrix \boldsymbol{Q} is assumed as prior for the unscaled person-level parameters $\begin{pmatrix} \alpha_s'' \\ \boldsymbol{\beta}_s'' \end{pmatrix}$, and normal priors with mean 1.0 and variance ϵ^{-1} are assumed for the scale factors. $\boldsymbol{\Sigma}$ is thereby decomposed into

$$\Sigma = \operatorname{Diag}(\boldsymbol{\xi}) \boldsymbol{Q} \operatorname{Diag}(\boldsymbol{\xi}),$$

where Diag is a diagonal matrix of dimension $3P \times 3P$ with the elements 1471 of the vector it takes as argument as diagonal elements. If Q follows the 1472 Inverse-Wishart distribution (with the identity matrix as scale matrix and 1473 3P+1 degrees of freedom), then Σ is distributed as a scaled Inverse-Wishart 1474 distribution as desired. Reflecting this decomposition, we separately sample 1475 from the conditional distributions of $(\alpha_s'')_{s=1,...,S}$ and $\boldsymbol{\xi}^{(\alpha)}$. Denote by $\mathcal{T}(p,s)$ the subset of pairs of nodes and trials, (n,x), with 1477 trial x administered to participant s(x) = s and node n stemming from the 1478 trial's subtree, $n \in \text{subtree}(x)$, such that process p is attached to the node, p(n) = p. It follows: 1480

$$p((\boldsymbol{\alpha_s''})_{s=1,\dots,S} \mid \mathcal{P}) \propto \prod_{s=1}^{S} \left[\prod_{p=1}^{P} \prod_{(n,x)\in\mathcal{T}(p,s)} \frac{1}{\sqrt{2\pi}} e^{-\frac{1}{2} \left(z_{n,x} - \xi_p^{(\alpha)} \alpha_{p,s}'' - \mu_p^{(\alpha)} \right)^2} \right]$$

$$e^{-\frac{1}{2} \begin{pmatrix} \boldsymbol{\alpha_s''} \\ \boldsymbol{\beta_s''} \end{pmatrix}^t} Q^{-1} \begin{pmatrix} \boldsymbol{\alpha_s''} \\ \boldsymbol{\beta_s''} \end{pmatrix}$$

Partition Q^{-1} as follows:

$$oldsymbol{Q}^{-1} = \left(egin{array}{cc} (oldsymbol{Q}^{-1})_{11} & (oldsymbol{Q}^{-1})_{12} \ (oldsymbol{Q}^{-1})_{21} & (oldsymbol{Q}^{-1})_{22} \end{array}
ight)$$

where the dimensions of $(\boldsymbol{Q}^{-1})_{11}$, $(\boldsymbol{Q}^{-1})_{12}$, and $(\boldsymbol{Q}^{-1})_{22}$ are, in order, $P \times P$, $P \times 2P$, and $2P \times 2P$. Let N(p,s) be the number of pairs (n,x) in $\mathcal{T}(p,s)$.

Finally, let $\boldsymbol{R} = [(\boldsymbol{Q}^{-1})_{11} + \mathrm{Diag}\left((N(p,s)(\xi_p^{(\alpha)})^2)_{p=1,\dots,P}\right)]^{-1}$. Standard manipulations show that the conditional distribution of $\boldsymbol{\alpha}_s''$ for a given s is a multivariate normal with mean

$$\boldsymbol{R} \left[\left(\begin{array}{c} \dots \\ \xi_p^{(\alpha)} \sum_{(n,x) \in \mathcal{T}(p,s)} (z_{n,s,x} - \mu_p) \\ \dots \end{array} \right) - (\boldsymbol{Q}^{-1})_{12} \boldsymbol{\beta}_s'' \right]$$

and variance-covariance matrix R. Standard methods exist for sampling from multivariate normal distributions.

The conditional distribution of $\boldsymbol{\xi}^{(\alpha)}$, on the other hand, is given by

$$p(\boldsymbol{\xi^{(\alpha)}} \mid \mathcal{P}) \propto \prod_{p=1}^{P} \left[\prod_{s=1}^{S} \prod_{(n,x) \in \mathcal{T}(p,s)} \frac{1}{\sqrt{2\pi}} e^{-\frac{1}{2} \left(z_{n,s,x} - \xi_{p}^{(\alpha)} \alpha_{p,s}^{"} - \mu_{p}^{(\alpha)} \right)^{2}} \right] e^{-\frac{1}{2} \epsilon (\xi_{p}^{(\alpha)} - 1)^{2}},$$

where ϵ is the prior precision. It is easy to see that the $\xi_p^{(\alpha)}$ thereby follow independent normal distributions with posterior variance $\sigma_{\text{post}}^2 = \sum_{s=1}^{S} N(p,s)(\alpha_{p,s}'')^2 + \epsilon^{-1}$ and mean $\sigma_{\text{post}}^2(\sum_{s=1}^{S} \alpha_{p,s}'')\sum_{(n,x)\in\mathcal{T}(p,s)}(z_{n,s,x} - \mu_p) + \epsilon$.

Sampling $(\beta'_s)_{s=1,...,S}$. Again, we sample separately from the conditional distribution of β'' and from the conditional distribution of $\xi^{(\beta)}$. Consider β'' first:

$$p((\boldsymbol{\beta_s''})_{s=1\dots,S} \mid \mathcal{P}) \propto \prod_{s=1}^{S} \left[\left(\prod_{p=1}^{P} \prod_{(n,x)\in\mathcal{T}(p,s)} \prod_{o=-,+} \exp(\xi_{o,p}^{(\beta)} \beta_{o,p,s}'') e^{-\exp(\mu_{o,p}^{(\beta)} + \xi_{o,p}^{(\beta)} \beta_{o,p,s}'') \tau_{n,x}^{o}} \right) e^{-\frac{1}{2} \left(\boldsymbol{\alpha_s''} \right)^{t}} e^{-\frac{1}{2} \left(\boldsymbol{\alpha_s''} \right)^{t}} Q^{-1} \begin{pmatrix} \boldsymbol{\alpha_s''} \\ \boldsymbol{\beta_s''} \end{pmatrix} \right].$$

There is no easy way to sample from this distribution. We proceeded by sampling from the conditional distribution of each individual $\beta''_{o,p,s}$ given the other β'' —parameters, and the other model parameters and data \mathcal{P} . It is not difficult to show that the density of this distribution is log-concave throughout and hence, amenable to adaptive rejection sampling (Gilks & Wild, 1992), which is the sampling method adopted.

The conditional distribution of $\boldsymbol{\xi}^{(\beta)}$ on the other hand is proportional to:

$$p(\boldsymbol{\xi}^{(\beta)}|\mathcal{P}) \propto \prod_{p=1}^{P} \prod_{o=-,+} e^{-\frac{1}{2}\epsilon(\xi_{o,p}^{(\beta)}-1)^2} \left(\prod_{s=1}^{S} \prod_{(n,x)\in\mathcal{T}(p,s)} \exp(\xi_{o,p}^{(\beta)}\beta_{o,p,s}'') e^{-\exp(\mu_{o,p}^{(\beta)}+\xi_{o,p}^{(\beta)}\beta_{o,p,s}'')\tau_{n,x}^o} \right)$$

Again, there is no easy way to sample from this distribution, and we employed adaptive rejection sampling to sample from the conditional distribution of each $\xi_{o,p}^{(\beta)}$ given the other parameters using adaptive rejection sampling.

1508 A.3.3. The Population-Level Process-Related Parameters

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The conditional distribution of $\boldsymbol{\mu}^{(\alpha)}$. Using standard manipulations, it is not difficult to see that the $\mu_p^{(\alpha)}$ follow independent normal distributions with means

$$\frac{\sum_{s=1}^{S} \sum_{(n,x) \in \mathcal{T}(p,s)} (z_{n,x} - \xi_p^{(\alpha)} \alpha_{p,s}'')}{\sum_{s=1}^{S} N(p,s) + \epsilon}$$

and variance $(\sum_{s=1}^{S} N(p,s) + \epsilon)^{-1}$. Sampling proceeded from these normal distributions.

Sampling $\mu^{(\beta)}$. We sample the parameters $\mu^{(\beta)}$ on the original (not log-transformed) scale and thus in terms of parameters $\rho_p^o = \exp(\mu_{o,p}^{(\beta)})$. The conditional distribution of ρ_p^o given the other parameters and data, collected in \mathcal{P} is characterized by:

$$p(\rho_p^o \mid \mathcal{P}) \propto (\rho_p^o)^{\left[\sum_{s=1}^S N(p,s)+1\right]-1} e^{-\rho_p^o \left(\left[\sum_{s=1}^S \exp(\xi_{o,p}^{(\beta)} \beta_{o,p,s}'') \sum_{(n,x) \in \mathcal{T}(p,s)} \tau_{n,x}^o\right] + \frac{1}{10}\right)},$$

which defines a Gamma distribution with shape parameters $\sum_{s=1}^{S} N(p,s) + 1$ and rate parameter $\left[\sum_{s=1}^{S} \exp(\xi_{o,p}^{(\beta)} \beta_{o,p,s}'') \sum_{(n,x) \in \mathcal{T}(p,s)} \tau_{n,x}^{o}\right] + \frac{1}{10}$. Sampling proceeded from these Gamma distributions.

The conditional distribution of Q. The conditional distribution is an Inverse-Wishart with S+3P+1 degrees of freedom and I+C as scale matrix, where C is the sum of cross-products of the person-level deviations:

$$C = \sum_{s=1}^{S} \begin{pmatrix} \alpha_s'' \\ \beta_s'' \end{pmatrix} \begin{pmatrix} \alpha_s'' \\ \beta_s'' \end{pmatrix}^t.$$

1524 A.3.4. The Person-Level Encoding and Response-Execution Parameters

Sampling γ_s' . Like before, we implement the scaled Wishart distribution for the variance-covariance matrix Γ of the person effect parameters γ_s' by further decomposing $\gamma_{r,s}'$ into $\gamma_{r,s}' = \xi_r^{(\gamma)} \gamma_{r,s}''$ using the scale factors $\boldsymbol{\xi}^{(\gamma)}$. A multivariate prior with zero mean and variance-covariance matrix \boldsymbol{S} is assumed for the unscaled person-level parameters γ_s'' , and as before, independent normal priors with mean 1.0 and variance ϵ^{-1} are assumed for the scale factors.

Denote by $\mathcal{U}(r,s)$ the subset of observed trials x administered to participant s(x) = s with response r = r(c(x)), and by $N_{r,s}$ the number of such trials. It follows:

$$p((\boldsymbol{\gamma_s''})_{s=1,\dots,S} \mid \mathcal{P}) \propto \prod_{s=1}^{S} \left[\prod_{r=1}^{R} \left(\Phi(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}''}{\sigma_s}) \right)^{-N_{r,s}} \right]$$

$$\prod_{x \in \mathcal{U}(r,s)} \frac{1}{\sqrt{2\pi}\sigma_s} e^{-\frac{1}{2} \frac{\left(\delta_x - \xi_r^{(\gamma)} \gamma_{r,s}'' - \mu_r^{(\gamma)}\right)^2}{\sigma_s^2}} \right] e^{-\frac{1}{2} \left(\boldsymbol{\gamma_s''}\right)^t \mathbf{S}^{-1}(\boldsymbol{\gamma_s''})}$$

If it were not for the factors $\left(\Phi\left(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{p,s}^{"}}{\sigma_s}\right)\right)^{-N_{r,s}}$, the parameters $\gamma_s^{"}$ could be sampled for each participant s from a multivariate normal analogous to the sampling of $\alpha_s^{"}$. We sample from this multivariate distribution, using it as the proposal distribution for a Metropolis-within-Gibbs step, in which we accept the proposal γ_s^* , if for a random value u drawn from a uniform distribution

$$u \leq \frac{\prod_{r=1}^{R} \left(\Phi\left(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}^*}{\sigma_s}\right) \right)^{-N_{r,s}}}{\prod_{r=1}^{R} \left(\Phi\left(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}''}{\sigma_s}\right) \right)^{-N_{r,s}}},$$

and keep the old values γ_s''' otherwise. Because the person-wise mean of residual encoding and response-execution times $\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}''$ is usually large relative to the residual variance, σ_s , the factors $\left(\Phi(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}''}{\sigma_s})\right)^{-1}$ are very close to one both in the nominator and in the denominator of the above fraction so that the fraction itself is close to one and most proposals are accepted.

The conditional distribution of $\xi^{(\gamma)}$, on the other hand, is given by

$$p(\boldsymbol{\xi}^{(\gamma)} \mid \mathcal{P}) \propto \prod_{r=1}^{R} \left[\prod_{s=1}^{S} \left(\Phi(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}^{"}}{\sigma_s}) \right)^{-N_{r,s}} \right]$$

$$\prod_{x \in \mathcal{U}(r,s)} \frac{1}{\sqrt{2\pi}\sigma_s} e^{-\frac{1}{2} \frac{\left(\delta_x - \xi_r^{(\gamma)} \gamma_{r,s}^{"} - \mu_r^{(\gamma)}\right)^2}{\sigma_s^2}} e^{-\frac{1}{2}\epsilon(\xi_r^{(\gamma)} - 1)^2},$$

where ϵ is the prior precision. If it were not for the factors involving Φ , the parameters $\boldsymbol{\xi}^{(\gamma)}$ could be sampled from independent normal distributions for each response r analogous to parameters $\boldsymbol{\xi}^{(\alpha)}$. Like before, we sample proposal values from these normal distributions and "add" the factors involving the Φ through a Metropolis-within-Gibbs step.

The conditional distribution of $(\sigma_s^2)_{s=1,\dots,S}$. Let N_s be the number of trials x administered to participant s. It is not difficult to see that the conditional distribution of σ_s^2 is proportional to:

$$p(\sigma_s^2 \mid \mathcal{P}) \propto \left(\frac{1}{\sigma_s^2}\right)^{\left[\frac{N_s+2}{2}+1\right]} e^{-\frac{N_s+2}{2\sigma_s^2} \left(\frac{\sum_{x:s(x)=s} \left(\delta_x - \xi_r^{(\gamma)} \gamma_{r,s}'' - \mu_r^{(\gamma)}\right)^2 + 2\omega^2}{N_s+2}\right)}$$

$$\prod_{x:s(x)=s} \left(\Phi\left(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}''}{\sigma_s}\right)\right)^{-1},$$

where r=r(c(x)) is the response attached to trial x. If it were not for the last factors involving Φ , σ_s^2 could thus be sampled from a scaled inverse χ^2 -distribution with degrees of freedom N_s+2 and scale factor $\left(\frac{\sum_{x:s(x)=s}\left(\delta_x-\xi_r^{(\gamma)}\gamma_{r,s}'-\mu_r^{(\gamma)}\right)^2+2\omega^2}{N_s+2}\right)$. Again, we used this distribution to generate a proposal value and "add" the factors via a Metropolis-within-Gibbs step.

1561 A.3.5. The Population-Level Encoding and Response-Execution Parameters

The conditional distribution of $\boldsymbol{\mu}^{(\gamma)}$. It is not difficult to see that the conditional distribution of $\boldsymbol{\mu}_r^{(\gamma)}$ is proportional to a normal distribution with variance $\sigma_{\mathrm{post}}^2 = (\sum_s \frac{N_{r,s}}{\sigma_s^2} + \frac{1}{10})^{-1}$, and mean $\sigma_{\mathrm{post}}^2 \sum_s \frac{\sum_{x \in \mathcal{U}(r,s)} (\delta_x - \xi_r^{(\gamma)} \gamma_{r,s}^{"})}{\sigma_s^2}$ up to the factor $\prod_s \Phi(\frac{\mu_r^{(\gamma)} + \xi_r^{(\gamma)} \gamma_{r,s}^{"}}{\sigma_s})^{-N_{r,s}}$. We sample from the normal distribution to generate a proposal value and again "add" the factors via a Metropoliswithin-Gibbs step.

The conditional distribution of Γ . Like for the person-level parameters α' and β' , the decomposition of $\gamma'_{r,s}$ into $\gamma'_{r,s} = \xi_r^{(\gamma)} \gamma''_{r,s}$ implies that Γ is decomposed into

$$\Gamma = \operatorname{Diag}\left(oldsymbol{\xi}^{(\gamma)}\right) oldsymbol{S} \ \operatorname{Diag}\left(oldsymbol{\xi}^{(\gamma)}
ight).$$

The conditional distribution of S is Inverse-Wishart with S+R+1 degrees of freedom and I+C as scale matrix, where C is the sum of cross-products of the person-level deviations:

$$C = \sum_{s=1}^{S} (\boldsymbol{\gamma_s''}) (\boldsymbol{\gamma_s''})^t$$
.

The conditional distribution of ω^2 . It is not difficult to see that the conditional distribution of ω^2 is a Gamma distribution with shape and rate parameters equal to $\frac{S\times df}{2}$ and $\frac{df}{2}\sum_s \frac{1}{\sigma_s^2}$, respectively, where df=2 for the applications presented in the main body of the text.

1578 A.4. Model Selection for the Models with Equal Response-Execution Times

for Old and New Responses

Table A1 shows DIC values and the Model Checks for DG and DI Models 1580 with response-execution times for old and new responses set equal for the 1581 datasets analyzed in the body of the paper (see Table 1). As can be seen, 1582 DIC is uniformly larger than for the same models with unequal responseexecution times for old and new responses. The model checks are often, but 1584 not always associated with smaller p values. The relatively smaller impact 1585 of setting equal the response-execution times on the model checks than on 1586 the DIC values suggests that having separate parameters for old and new responses was less important for fitting the mean frequencies and response 1588 times averaged across participants – as also suggested by the fact that the 1589 HDI's of the $\mu_r^{(\gamma)}$ for old and new responses in most cases overlap (see Tables 1590 2 and 3) – than for accounting for individual differences, perhaps due to 1591 differences in handedness, between participants. 1592

Table A1 DIC values and Model Checks (Posterior p Values) for the DG and the DI Models with Equal Response-Execution Times for the Old and the New Response

	DG Variant				DI Variant						
Data	$\overline{\Delta { m DIC}}$	X_1	X_2	X_3	$\overline{\Delta { m DIC}}$	X_1	X_2	X_3			
— Arnold et al. (2015) —											
Exp. 1	267.70			,	283.63	.44	.44	.28			
Exp. 2	189.27	.49	.37	.37	203.62	.48	.29	.44			
Exp. 3	243.99	.40	.57	.08	218.22	.43	.64	.05			
— Dube et al. (2012) —											
Exp. 1	157.80	<.0001	.02	.15	106.25	.27	.01	.23			
Exp. 2	224.66	<.0001	.05	.48	133.31	.0001	.01	.62			

Note. DG = "Detect-Guess"; DI = "Default-Interventionist"; Δ DIC = DIC difference from the lowest DIC of the dataset from Table 1 in the body of the text.