rtmpt: An R package for fitting response-time extended multinomial processing tree models

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Abstract

Response-time extended multinomial processing tree models (RT-MPT; Klauer and Kellen, *Journal of Mathematical Psychology*, 82, 111–130 2018) provide estimates of process-completion times for cognitive processes modeled by means of multinomial processing tree (MPT) models (Batchelder and Riefer, *Psychonomic Bulletin & Review*, 6, 57–86 1999). We present the R package `rtmpt` with which it is possible to fit RT-MPT models easily. The package is free and open source, it can be used with two established MPT syntaxes, and has a number of useful features, such as suppressing process-completion times for specific process outcomes, holding process probabilities constant, and changing some prior parameters. In the background of the R package, an altered version of the original C++ code is used for the MCMC sampling. We provide a guide to using `rtmpt`, validate the underlying hierarchical Bayesian algorithm of `rtmpt` using simulation-based calibration and show that previously reported results can be reproduced using `rtmpt`.

Keywords `rtmpt` · R package · RT-MPT · Response time · Multinomial modeling · Hierarchical modeling · Bayesian inference

For more than 150 years, researchers have tried to estimate completion times of cognitive processes. One of the earliest methods was proposed by Donders (1868) with his *method of subtraction*. Here, we consider a distant descendant of that method recently proposed by Klauer and Kellen (2018), called response-time extended multinomial processing trees (RT-MPTs). The method builds on the class of multinomial processing tree (MPT, Riefer & Batchelder 1988) models (see Batchelder & Riefer, 1999; Erdfelder et al., 2009; Hütter & Klauer, 2016, for reviews).

MPTs model categorical frequencies and estimate the probabilities with which assumed latent processes occur. Adding response-time data, the RT-MPT extension permits the estimation not only of process probabilities but also of process-completion times of every process involved in an MPT. In addition, the time required for encoding task stimuli and motor execution of the response is estimated. To simplify reading, we refer to process-completion time as *process time* and to encoding plus motor execution time as

motor time in what follows. The present article introduces and validates a software package called `rtmpt` for usage in the R programming environment (R Core Team, 2019) that implements the RT-MPT method.

This package enables one to fit RT-MPTs to observed data and has several advantages over a previous implementation (Klauer & Kellen, 2018). Most importantly, the previous implementation in C++ used the proprietary C library NAG (The Numerical Algorithms Group (NAG), 2017), limiting its accessibility to researchers who have access to the required licenses. In contrast, `rtmpt` is completely free and open source and accessible to every interested researcher. NAG routines are replaced by routines from the C library GSL (Galassi et al., 2018). Moreover, in `rtmpt`, we added the possibility to *suppress* the time of specific outcomes of a process with two possible outcomes. Suppressing a process time means setting the process time to zero and therefore holding it constant. Previously it was possible to suppress the time of either both outcomes of a process or none. Suppressing the time of only one outcome of a process can be useful whenever assuming a process either occurs with a certain probability or does not occur with the complementary probability such as the *activation of association* process in a process dissociation model (Jacoby, 1991). If activation does not occur, it often makes sense

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not to attach a time cost to this outcome. Furthermore, unlike the previous implementation, *rtmpt* can be easily used with established syntax for specifying MPT models such as the well-established *EQN* syntax (Hu, 1999; Heck et al., 2018a) or the one developed by Singmann and Kellen (2013)—referred to as *MDL* syntax.

RT-MPTs have several advantages when compared to traditional MPT analyses. Adding response times has the benefit that the estimates of process probabilities can be expected to become more accurate. Moreover, incorporating response times into the analysis renders identified many MPT models that are not identified on the basis of the frequency data alone. For explanations of these two points, see Klauer and Kellen (2018).

Furthermore, as elaborated on below, traditional MPT models can be specified in equivalent variants, differing in the orders in which the involved processes are assumed to occur. These different variants of the same MPT model lead to different predictions for the response times. Thus, RT-MPTs allow one to distinguish between two or more such variants of the same MPT model. In other words, the order in which the processes are assumed to occur does matter for RT-MPTs. This makes it possible to test two or more variants—or representations—of a traditional MPT model against each other (see Section “The RT-MPT model class”).

The new model class RT-MPT can also be seen as an alternative to diffusion models (Ratcliff, 1978) in some instances. As illustrated by Klauer and Kellen (2018), RT-MPTs can produce comparable results. Additionally, traditional diffusion model analyses are restricted to two-choice paradigms, whereas RT-MPTs are not.

In this paper, we evaluate the newly developed *R* package *rtmpt* by means of several approaches. A new procedure called simulation-based calibration (Talts et al., 2018) is used to validate the algorithm. This is one of the first times in psychology that simulation-based calibration has been used (see Section “Validation study (simulation-based calibration)”). A reproducibility study (Asendorpf et al., 2013) tests whether the results of analyses using the previous implementation can be reproduced. Finally, a small recovery study assesses the new features of the current

implementation, notably the suppression of individual process times.

In the next section, the RT-MPT model class is introduced more formally. We describe how MPTs are extended such that response latencies can be considered, what distributional assumptions are made, and discuss some of the advantages in more detail. Acknowledging that response-latency data are often too sparse to permit reliable estimation of the model parameters at the level of the individual participant, the *rtmpt* algorithm implements a hierarchical Bayesian model taking advantage of partial pooling of the individual data to obtain reliable group-level estimates while respecting and modeling any heterogeneity that may exist across participants. For a full description of the model class and estimation algorithm, interested readers are referred to the original paper by Klauer and Kellen (2018).

The RT-MPT model class

To understand this new RT-MPT model class, consider first the traditional MPT model class. In a nutshell, MPTs model the probabilities with which latent processes take place within a task (Erdfeiler et al., 2009). Usually such tasks comprise two or more response alternatives. For instance, in a simple word recognition task there are two possible responses, “old” or “new”, to indicate that a test word was either a word from a previously studied word list or not, respectively.

In using MPT models, assumptions are made about the processes believed to be involved in generating a given response. For example, one MPT model for the simple word recognition task is the popular two-high threshold model (2HTM; Snodgrass & Corwin, 1988). It assumes that a word from the studied word list can either be detected as previously studied—through a *detection process*—or guessed as previously studied or not—through a *guessing process*. The same holds for new words; they are either detected as new words or guessed. An error can only occur by wrong guessing.

Figure 1 shows a graphical representation of the model in terms of its processing trees. Detection is assumed to play

Fig. 1 2HTM (*Detect-Guess* variant). The rectangles indicate manifest states (i.e., item types and responses), and the gray circles indicate latent states (S_1 and S_2 are states of certainty and S_3 is a state of uncertainty). The double circles indicate the outcomes of the guessing

process where + denotes an “old” guess and – a “new” guess. The parameters D_O , D_N , and g refer to the probabilities of detecting an old item as old, a new item as new, and guessing “old”

Fig. 2 2HTM (*default-interventionist* variant). The rectangles indicate manifest states (i.e., item types and responses), and the gray circles indicate latent states (S_1 and S_2 are states of certainty and S_3 is a state of uncertainty). The double circles indicate the outcomes

a dominant role; if detection succeeds, the corresponding response is given (“old” for detecting a studied word with probability D_O and “new” for detecting a new word with probability D_N). If detection fails (with probability $1 - D_O$ or $1 - D_N$), the response corresponding to the guessing outcome is given. With probability g , “old” is guessed and “new” with probability $1 - g$.

Since MPT models are very flexible and relatively simple, they can be applied in many fields of psychology, such as recognition, source monitoring, immediate serial recall, implicit attitude measurement, and many more (for reviews see Erdfelder et al., 2009; Hütter & Klauer, 2016). One shortcoming is, however, that the order in which the processes occur cannot be tested (Klauer & Kellen, 2018). In most cases, several representations of one specific MPT model exist which are mathematically identical, but differ in the order and interaction of the processes in the graphical representation. For example, Fig. 1 shows only one variant of the 2HTM, which we call *Detect-Guess*. Another one, which leads to the same probability estimates, is shown in Fig. 2 and is called *default-interventionist*. In this variant of the model, guessing—or rather the *activation of a bias* in this case—takes place first and is overruled by the detection, if detection is successful. These two variants differ, however, in the predictions that they make for response times and hence give rise to different RT-MPT models.

Another shortcoming is that MPTs are often not identified (Klauer & Kellen, 2018). Only by restraining some parameters to be equal can identifiability be achieved. For example, our running example, the *Detect-guess* variant of the 2HTM, is one of these unidentified MPTs. We have three parameters to estimate (D_O , D_N , g), but only two equations; one for the hit rate and one for the false alarms (misses and correct rejections are redundant information). However, adding response times leads to an identified RT-MPT model (Klauer & Kellen, 2018).

There are two recent and prominent approaches that do consider RTs in the context of MPT models. The first

of the guessing process where + denotes an “old” guess and − a “new” guess. The parameters D_O , D_N , and g refer to the probabilities of detecting an old item as old, a new item as new, and guessing “old”

approach was proposed by Heck and Erdfelder (2016) and the second by Klauer and Kellen (2018).

Heck & Erdfelder’s (2016) approach uses a non-parametric method to model the RTs alongside frequencies. In this context, Starns (2018) recently proposed a discrete-race model that unlike (Heck & Erdfelder, 2016) accommodates a speed–accuracy trade-off for the 2HTM (but see Heck & Erdfelder, *in press*). Heck et al. (2018b) generalized Heck and Erdfelder’s (2016) approach to handle not only RTs, but also many types of continuous data together with frequencies. This class of models is called *generalized multinomial processing trees*.

Klauer & Kellen’s (2018) approach is a hierarchical Bayesian approach and builds on the method of Klauer (2010). It makes explicit assumptions about the distributions of each process time and motor time, and combines RTs and categorical data into a joint likelihood function. As already mentioned, RT-MPTs provide estimates of process times and also overcomes a number of limitations of MPTs. Note, however, that these benefits come at the cost of additional distributional assumption for process and motor times.

To introduce RT-MPTs, we use the following notations. Let p denote a process, o its possible outcomes, r the response, and s the subject. In our 2HTM example, p is either one of the detection processes or the guessing process, o is *success* or *failure* for the detection processes and *activation of a bias* towards r , which is either “old” or “new”. The probability parameters only depend on the process p and the subject s . Therefore, we denote them with $\theta_{p,s}$. In our example $\theta_s = (\theta_{D_O}, \theta_{D_N}, \theta_g)^T$.¹

Following Hu (2001), RT-MPTs assume that the observed response time is the sum of process times along the branch of the processing tree that generated the response and encoding plus motor execution time. Each process time is identified by its process name p and its outcome o . Again,

¹Note that we refer to person-level model parameters of MPT models by θ in the equations defining the model with a subscript identifying the process parameters referred to.

Fig. 3 Response-time extended 2HTM (*Detect-guess* variant). The rectangles indicate manifest states (i.e., item types and responses), and the gray circles indicate latent states (S_1 and S_2 are states of certainty and S_3 is a state of uncertainty). The double circles indicate the outcomes of the guessing process where + denotes an “old” guess and – a “new” guess. The parameters D_O , D_N , and g refer to

we have multiple subjects s and therefore denote a process time by $\tau_{p,o,s}$. The motor times are denoted by $\delta_{r,s}$, indicating their possible dependency on the response and the subject. In our 2HTM or rather RT-2HTM (see Fig. 3) we have $\tau_s = (\tau_{D_N}^-, \tau_{D_N}^+, \tau_{D_O}^-, \tau_{D_O}^+, \tau_g^-, \tau_g^+)_s^T$, where minus and plus signs denote the outcome (minus is either *failure* or a bias towards “new” and plus is either *success* or a bias towards “old”) added as superscript, and $\delta_s = (\delta_O, \delta_N)_s^T$, where O and N denote the two possible responses “old” and “new”, respectively.

Further assumptions regard the distributions of the process and motor times. The process times are assumed to follow exponential distributions and the motor times normal distributions truncated from below at zero. Taken together, the person-level model comprises three groups of parameters: the process probabilities $\theta_{p,s}$, the parameters governing the distributions of the process times $\tau_{p,o,s}$, and the motor times $\delta_{r,s}$. Previously we stated the following assumptions:

$$\begin{aligned} \tau_{p,o,s} &\sim \text{Exp}(\text{rate} = \lambda_{p,o,s}) \\ \delta_{r,s} &\sim \mathcal{TN}(\text{lower} = 0, \text{upper} = \infty, \mu = \gamma_{r,s}, \sigma = \sigma_s), \end{aligned} \quad (1)$$

where $\lambda_{p,o,s}$ are the corresponding rate parameters of the exponential distributions, and $\gamma_{r,s}$ and σ_s the mean parameters and the standard deviation parameters, respectively, of the truncated normal distributions ($\mathcal{TN}(\gamma_{r,s}, \sigma_s, 0, \infty)$). For the analysis, the process probabilities are probit-transformed $\alpha_{p,s} = \Phi^{-1}(\theta_{p,s})$, the rate parameters are used on the log scale $\beta_{p,o,s} = \log(\lambda_{p,o,s})$, and the mean parameters $\gamma_{r,s}$ are used on the original scale. The (transformed) parameters are further decomposed into a group-level parameter μ and a subject-specific deviation from it (marked by a prime as superscript):

$$\begin{aligned} \alpha_{p,s} &= \mu_p^{(\alpha)} + \alpha'_{p,s} \\ \beta_{p,o,s} &= \mu_{p,o}^{(\beta)} + \beta'_{p,o,s} \\ \gamma_{r,s} &= \mu_r^{(\gamma)} + \gamma'_{r,s} \end{aligned} \quad (2)$$

the probabilities of detecting an old item as old, a new item as new, and guessing “old”. The τ parameters denote the time for a process (*subscript*) to complete for each outcome (*superscript*). The δ_O and δ_N parameters denote the time for encoding and motor execution for responding “old” and “new”

Klauer and Kellen (2018). The process-related parameters (α and β) are allowed to correlate with each other across persons and the motor-related parameters (γ) are allowed to correlate with each other with variance-covariance matrices Σ and Γ , respectively. Both variance-covariance matrices are estimated. For further details see Klauer and Kellen (2018).

The R package `rtmpt`

With the R package `rtmpt` it is possible to fit RT-MPT models within the programming language R (R Core Team, 2019). It uses an altered version of the C++ code by Klauer and Kellen (2018) in the background to sample posterior samples with a Metropolis-Gibbs sampler. This means, within R the C++ program is called and executed, which returns quantities, such as the posterior samples to R. In the following, we describe how to use `rtmpt`, discuss an example (in Section “Example”) as well as provide installation notes (in Section “Installation”).

Specifying models

Specifying the MPT part of an RT-MPT model is possible by either using the well established *EQN* syntax (Hu, 1999; Heck et al., 2018a) for defining the MPT part of the RT-MPT model or the *MDL* syntax developed by Singmann and Kellen (2013). See Fig. 4 for the 2HTM written with the *EQN* syntax and Fig. 5 for the same model written with the *MDL* syntax. Both syntaxes are mathematically equivalent. The difference is that for the *EQN* syntax each branch and its branch probability are specified on a separate line while for the *MDL* syntax each response category and its probability are specified on a separate line. The probability of a response category is the sum of the branch probabilities of all branches leading to this category. As shown in Fig. 4, the *EQN* syntax separates *tree*, *category*,

```
# Tree ; # Category ; # EQN
Target ; hit ; Do
Target ; hit ; (1-Do)*g
Target ; miss ; (1-Do)*(1-g)
Lure ; f_a ; (1-Dn)*g
Lure ; c_r ; Dn
Lure ; c_r ; (1-Dn)*(1-g)
```

Fig. 4 *EQN* syntax for the *Detect-Guess* variant of the Two-High Threshold model adapted from Heck et al. (2018a). *f_a* and *c_r* stand for *false alarm* and *correct rejection*, respectively. *Do*, *Dn*, and *g* denote the process probabilities of detecting a target item, detecting a lure item, and guessing “old”, respectively

and *branch probability* with semicolons. Note that in both types of syntax, it is important that the parameters of a branch occur in the order in which the branch is traversed from the root of the tree to the leaf as their order matters for RT-MPT models. The syntax of both types can be provided either directly as a character object in *R* or by a text file. The former can be directly saved in an *R* object while the latter must be provided by a path to the text file.

For both kinds of syntax, process probabilities can be set to constants by adding one further line in the file with the keyword *constant* and a colon following it. In our example, this line would look like this

```
constant: g = .5
```

if we want to set the guessing probability to .5. Likewise, the process times can be suppressed by providing the label of the process and its outcome, like

```
suppress: g-, g+
```

if we want to suppress the process time of guessing in favor for “*new*” and the one for “*old*”. Process time parameters cannot be set to arbitrary constants.

The *EQN* and *MDL* syntax differ in how motor-time parameters are specified. For the *MDL* style it is a little bit easier: after each line specifying the probabilities of a response category, write a semicolon and a response-label number indexing the associated motor time. The numbering

```
# Target
Do+(1-Do)*g
(1-Do)*(1-g)

# Lure
(1-Dn)*g
Dn+(1-Dn)*(1-g)
```

Fig. 5 *MDL* syntax for the *Detect-guess* variant of the two-high threshold model. *Do*, *Dn*, and *g* denote the process probabilities of detecting a target item, detecting a lure item, and guessing “old”, respectively

```
# Target ; Response
Do+(1-Do)*g ; 0
(1-Do)*(1-g) ; 1

# Lure ; Response
(1-Dn)*g ; 0
Dn+(1-Dn)*(1-g) ; 1
```

```
constant: g = 0.5
suppress: g-, g+
```

Fig. 6 *MDL* syntax for the *Detect-guess* variant of the two-high threshold model with constant guessing probability of .5, suppressed process time of guessing for both outcomes and different motor times for the two possible responses. *Do*, *Dn*, and *g* denote the process probabilities of detecting a target item, detecting a lure item, and guessing “old”, respectively

should always include 0. If there are two different motor time distributions, then each line has either a 0 or 1 after the semicolon. This implies that different motor times will be estimated for the responses associated with the categories marked 0 and the ones marked 1; see Fig. 6 for an example of the 2HTM with all restrictions and specifications written in the *MDL* syntax. For the *EQN* syntax, one needs to specify the response mapping by means of a matrix with unique response categories using the keyword *resp* and a colon following it. For our 2HTM, the following lines need to be included if we assume different distributions of motor times for the “*old*” and “*new*” responses:

```
resp: Target ; hit ; 0
resp: Target ; miss ; 1
resp: Lure ; f_a ; 0
resp: Lure ; c_r ; 1
```

The order of the lines does not matter, but the labels of the *trees* (i.e., “Target” vs. “Lure”) and *categories* (i.e., “hit”, “miss”, “f_a”, or “c_r”) have to match the labels used in the data file. For an example of the 2HTM with all restrictions and specifications written in the *EQN* syntax see Fig. 7.

The `to_rtmt_model()` function needs to be applied in order to read and use the model. This function translates the syntax to a list of the class `rtmt_model` containing all the necessary information. For instance, the function call `to_rtmt_model(eqn_file = eqn)` is for using the *EQN* syntax with the character object (or path to the text file) named *eqn*. For the *MDL* syntax use the argument `mdl_file` instead.

With the `print()` function it is possible to check the model specifications. It also provides some notes and additional information on how to interpret its output.

If the restrictions/specifications of the process probabilities, the process times, and/or the motor time labels are not


```

# Tree ; # Category ; # EQN
Target ; hit ; Do
Target ; hit ; (1-Do)*g
Target ; miss ; (1-Do)*(1-g)
Lure ; f_a ; (1-Dn)*g
Lure ; c_r ; Dn
Lure ; c_r ; (1-Dn)*(1-g)

constant: g = 0.5
suppress: g-, g+

resp: Target ; hit ; 0
resp: Target ; miss ; 1
resp: Lure ; f_a ; 0
resp: Lure ; c_r ; 1

```

Fig. 7 EQN syntax for the *Detect-guess* variant of the two-high threshold model adapted from Heck et al. (2018a) with constant guessing probability of .5, suppressed process time of guessing for both outcomes and different motor times for the two possible responses. *Do*, *Dn*, and *g* denote the process probabilities of detecting a target item, detecting a lure item, and guessing “old”, respectively

correct, the model object of the class `rtmpt_model` can be altered. For the process parameters the `set_params()` function can be used and for the motor time labels the `set_resps()` function. Their use is further described in Appendix A.

Data transformation

The data must include five variables labeled *subj*, *group*, *tree*, *cat*, and *rt* encoding, in order, the subject number, the experimental group the subject belongs to, the tree of the current trial, the observed response category, and the observed response time. The variable *rt* must be provided in milliseconds. As previously mentioned the labels used in the model specification and the ones used in the data file must match. This is important if the data does not yet have the right format. For the main fitting function (see below) to work the data must only consist of numbers and except for *rt* all variables must have values starting from zero. For instance, with a total of 50 subjects, all numbers from 0 up to 49 must be included in the variable *subj*. The function `to_rtmpt_data()` takes care of that. It takes the *raw data* and transforms it into a list of the class `rtmpt_data`, which contains the transformed data as well as the transformations, which were used (old and new labels). In our previous example, we had two tree labels (Target and Lure) and four category labels (hit, miss, f_a, and c_r). These will be transformed into numbers according to the order in which they occur in the model file (Target → 0, Lure → 1, hit → 0, miss → 1, f_a → 2, c_r → 3). *subj* and *group* are transformed to numbers according to the order in which they occur in the raw data itself. For an example, see Section “Example”.

The function `to_rtmpt_data()` takes two arguments, *raw_data* and *model*. *raw_data* must either be the path to a text file with the necessary label names in the header or a `data.frame` with the necessary variable names included in the column names. The parameter *model* must be of class `rtmpt_model`.

Fitting models

With the main function `fit_rtmpt()` of the R package `rtmpt` it is possible to fit RT-MPT models to given data. A call of `fit_rtmpt()` does the MCMC sampling and returns the posterior samples. This function has two necessary arguments, *model* and *data*, and nine arguments with defaults.

The argument *model* must be a model list of class `rtmpt_model`. The argument *data* must either be the same as the *raw_data* in the `to_rtmpt_data()` function or the output of that function. Therefore it can be either a path to a file with a header, a `data.frame` or a data list `rtmpt_data`. If it is not a `rtmpt_data` object `to_rtmpt_data()` will be used automatically. To keep track of the transformations done in this function it is, however, advisable to use it beforehand and use the output of it in the *data* argument.

Four of the arguments with defaults are the well known arguments for MCMC sampling, namely the number of chains *n.chains*, number of samples *n.iter*, number of warm-up samples *n.burnin*, and thinning *n.thin*. The thinning is conducted at the end of the MCMC sampling.

An additional argument *Rhat_max* specifies a threshold for the *potential scale reduction factor* $\hat{R}$ (Gelman & Rubin, 1992). Once the maximal $\hat{R}$ of all the model parameters is (and stays) below this threshold, posterior samples are retained for the eventual output.² Note that these values calculated on the run differ from the “a posteriori” $\hat{R}$, since the latter are calculated on the basis of only the retained posterior samples.

Another additional argument is *Irep* which gives the frequency of intermediate outputs. Every *Irep* samples the number *Rhat_max* is recalculated and an intermediate output with $\hat{R}$ for the main parameters of the model as well as their current estimate is given.

In order to have some control over the priors, we included the *prior_params* argument. A number of prior parameters can thereby be specified, controlling the informativeness of the prior distributions required for the hierarchical Bayesian approach. Note that it is not necessary to set these prior parameters, since all of them have default

²Because the actual posterior sampling starts after the threshold is reached, the number of iterations in the MCMC sampling step is always larger or equal to $n.thin \times n.iter$.

values. These default values are comparable to those in Klauer and Kellen (2018), and they lead to rather broad prior distributions. The parameters controlling the prior distributions are explained in Appendix B. The last two arguments are `indices` and `save_log_lik`, which are both logical arguments, with functions explained in the next paragraph.

The output of the main function is a list consisting of at least the first three of the following objects.

1. `samples`: the MCMC samples saved as a `mcmc.list` class object of the *R* package `coda` (Plummer et al., 2006).
2. `diags`: a list of diagnostics with the 95% and 99% highest density intervals and the medians of the main parameters. Furthermore, the “a posteriori” $\hat{R}$, the deviance information criterion (Spiegelhalter et al., 2002) are part of this list, as well as posterior predictive checks of the first type (T_1 ; Klauer, 2010) for the frequencies as well as the latencies.
3. `specs`: a list of some specifications such as the model, the arguments of the function call, and the used data transformation.
4. `indices`: if `indices = TRUE`, the widely applicable information criterion (Watanabe, 2010) and leave-one-out cross-validation (Vehtari et al., 2017) saved in a list object.
5. `LogLik`: if `save_log_lik = TRUE`, the object `LogLik` containing the log-likelihood matrix of all samples and data points.

Table 1 gives an overview of all the functions. Note that only the first two are really necessary, but we recommend to use the remaining three for more control. For more detailed

Table 1 Overview of functions in `rtmpt`

Functions	Description
<code>fit_rtmpt</code> :	Fit RT-MPT models. Main output: posterior samples.
<code>to_rtmpt_model</code> :	Convert model file (<i>EQN</i> or <i>MDL</i>) to <code>rtmpt_model</code> .
<code>to_rtmpt_data</code> :	Convert data (text file or <code>data.frame</code>) to <code>rtmpt_model</code> .
<code>set_params</code> :	Restrict process parameters of an <code>rtmpt_model</code> .
<code>set_resps</code> :	Specify number of different motor times in an <code>rtmpt_model</code> .
<code>sim_rtmpt_data</code> :	Simulate data from an <code>rtmpt_model</code> object.
<code>fit_rtmpt_SBC</code> :	Simulate data and fit model to that data using the same priors. Main output: rank statistic (of all parameters) for simulation-based calibration.

Table 2 First six lines of a fictive data frame usable with the `rtmpt` function `fit_rtmpt()`

	subj	cat	tree	group	rt
1	1	miss	Target	1	699
2	1	miss	Target	1	655
3	1	c_r	Lure	1	651
4	1	c_r	Lure	1	676
5	1	hit	Target	1	753
6	1	f_a	Lure	1	1046

descriptions check out the help pages of these functions, for example by typing `?fit_rtmpt`, once `rtmpt` is installed.

Example

The first thing to do when trying to fit an RT-MPT to given data is to check what labels are used for `cat` and `tree` in the dataset. Table 2 shows how the first six lines of a data frame might look like. In order to find all labels of the two variable of interest one might execute these two lines

```
> unique(DF$cat)
> unique(DF$tree)
```

which will give the two outputs

```
[1] "c_r" "f_a" "hit" "miss"
[1] "Lure" "Target"
```

from which we can see the labels of the variables `cat` and `tree`, respectively.

If we wanted to use the *MDL* syntax, we would have to change these labels to numbers by hand first. Since we can use labels in the *EQN* syntax, it might be more convenient to define our model file using that format. Figure 8 shows the *EQN* file for the 2HTM with one common detection parameter for old and new items. It is important that the labels match the ones used in the data frame.

```
# Tree ; # Category ; # EQN
Target ; hit ; D
Target ; hit ; (1-D)*g
Target ; miss ; (1-D)*(1-g)
Lure ; f_a ; (1-D)*g
Lure ; c_r ; D
Lure ; c_r ; (1-D)*(1-g)
```

Fig. 8 Detect-guess variant of the restricted two-high threshold model (r2HTM.model) as *EQN* syntax. *D* and *g* denote the process probabilities of detecting an item correctly and guessing “old”, respectively

Once the model file is formulated we can transform it into an *R* object of the class `rtmpt_model` by typing

```
> model <- to_rtmpt_model(eqn_file="r2HTML.model")
```

To see the details of this model, call the model object by `model` to get an output like in Listing 1 in Appendix C. This output contains four important details about the model. First, we see what the *MDL* syntax of the model looks like, even if we defined the model with the *EQN* syntax. Remember, it was not possible to define it with the *MDL* syntax, because we used labels instead of numbers in the data, but now that the mapping of the data and the model is done using the *EQN* syntax, the model can also be represented with the *MDL* syntax. Second, it shows which of the process probability parameters will be estimated. Some notes and information about the parameters to estimate are also shown. Third, the process times to be estimated are shown. The latter two can be changed with the above mentioned function `set_params()`. Fourth, the response labels associated with specific motor times are shown. In the present state of the output in Listing 1 in Appendix C, all responses have the value 0, thus for all responses the motor times are assumed to follow the same distribution.

Even though our model and our data have matching labels, we cannot use the dataset as it is currently. We need to transform it first. This is not a necessary step since the main function takes care of it, but it is prudent to perform it and check with

```
> data <- to_rtmpt_data(DF, model)
> data
```

The function call in the second line produces an output of the data transformation—or rather the mapping from the raw data to the one usable for the main function (see Listing 2 in Appendix C). This mapping was only possible because of the matching labels of data and model.

The RT-MPT model can now be fitted by calling the main function. Here we use 10,000 posterior samples, a warm-up of 1000 samples, a thinning of two, a very small threshold for the maximal $\hat{R}$ of 1.01, an intermediate output after every 2000 samples, a prior precision ϵ of one, and choose to have WAIC and LOO as well.

```
> fit <- fit_rtmpt(model, data,
  n.iter = 10000, n.burnin = 1000,
  n.thin = 2, Rhat_max = 1.01,
  Irep = 2000,
  prior_params = list(prec_epsilon = 1),
  indices = TRUE, save_log_lik = TRUE)
```

Note that a prior precision ϵ of one is included for demonstration purposes only. This is the default value and

therefore will be used anyway if no other value is given. Executing the function starts the calculation of the initial values, then the sampling takes place. Intermediate outputs during the sampling show the progress by providing the $\hat{R}$ for the main parameters and the maximal $\hat{R}$ on the run. After the sampling a short output is given in the console, but all of it is saved in the *R* object `diags` as well.

Installation

`rtmpt` is on the Comprehensive R Archive Network (CRAN) and can be installed by entering

```
> install.packages("rtmpt")
```

in the command line of *R*. Alternatively, `rtmpt` can also be found on the software development platform [GitHub](https://github.com/RaphaelHartmann/rtmpt). We provide instructions on how to install `rtmpt` on <https://github.com/RaphaelHartmann/rtmpt>.

Reproducibility and simulation studies

The *C++* program underlying the package `rtmpt` has undergone many changes relative to the program used by Klauer and Kellen (2018). The most important change is that instead of the proprietary NAG library (The Numerical Algorithms Group (NAG), 2017), the open-source GSL library (Galassi et al., 2018) is used. In addition, some of the functions within the program are rewritten to make it more efficient. Additionally, the prior for the residual variance is changed from an improper prior to a proper gamma distribution. As just mentioned, it is now also possible to change certain prior parameters. Some minor changes include the routines for data and model-information input. All of these changes are potential sources for differences in the algorithm implemented by the program. Therefore, evaluating the program is desirable.

This is the purpose of the present section. The main part of this section is a simulation-based calibration (Talts et al., 2018) validating our implementation of the Bayesian algorithm. Next, we attempt to reproduce the major results of data analyses reported by Klauer and Kellen (2018) in their Tables 2 and 3 in a reproducibility study (Asendorpf et al., 2013). Finally, we present a small recovery study to test the partially new features of setting probability parameters constant and of suppressing individual process times.

Validation study (simulation-based calibration)

Simulation-based calibration (SBC) is a relatively new method for validating an algorithm for sampling from the

posterior distribution of model parameters given the data (Talts et al., 2018). Its idea is that if we repeatedly sample parameters from the prior distribution of the assumed model, generate data from these parameters, and then fit the model to these generated datasets, the resulting posterior samples should follow the same distribution as the priors (Talts et al., 2018). Histograms of a rank statistic (see later) are used to check whether this holds true.

As argued by Talts et al. (2018), traditional recovery studies using a single set of ground truth values (i.e., a fixed set of prior values) to generate data are limited because they may lead us to conclude that recovery has been successful even for misspecified algorithms. Conversely, a posterior that appears biased away from the ground truth need not necessarily reflect a malfunctioning algorithm. SBC overcomes these limitations by considering the performance of the algorithm over the entire joint distribution of data and parameters.

SBC is based on the *self-consistency* condition

$$p(\theta) = \int \int p(\tilde{\theta}) p(\tilde{y}|\tilde{\theta}) p(\theta|\tilde{y}) d\tilde{\theta} d\tilde{y}, \quad (3)$$

where $\tilde{\theta} \sim p(\theta)$ are the parameters—denoted as *ground truth*—sampled from the prior distribution and $\tilde{y} \sim p(y|\tilde{\theta})$ the data generated from the model using the ground truth. $\theta \sim p(\theta|\tilde{y})$ are the posterior samples.

The *rank statistic* mentioned above is defined as

$$r(\{f(\theta_1), \dots, f(\theta_L)\}, f(\tilde{\theta})) = \sum_{l=1}^L \mathbb{1}_{\{f(\theta_l) < f(\tilde{\theta})\}}, \quad (4)$$

where $f : \Theta \rightarrow \mathbb{R}$ is a one-dimensional function (Talts et al., 2018). In our case f is the function that picks one specific element of the posterior parameter vector θ_l or prior parameter vector $\tilde{\theta}$, meaning we calculate the rank statistic for each parameter separately.

By comparing the ground truth $\tilde{\theta}_n$ with the posterior samples $\{\theta_{n,1}, \dots, \theta_{n,L}\}$ using the rank statistic (4) for each

replication $n \in \{1, \dots, N\}$ we can test whether Eq. 3 holds true for one specific model $p(\tilde{y}|\tilde{\theta})$ (Talts et al., 2018). L is the number of effective samples, meaning we thin the original posterior samples to reduce autocorrelation following Algorithm 2 of Talts et al. (2018). If the algorithm implemented through `rtmpt` is valid, this rank statistic is uniformly distributed within $[0, L]$. We test the uniformity via histograms and χ^2 -tests. As Talts et al. (2018) showed, the SBC procedure thereby allows the detection of many biases in the posterior samples such as autocorrelation, over- and underdispersion, and under- and overestimation. In fact, in our first attempt, we observed an overestimation of the mean process rates $e^{\mu^{(\beta)}}$. This was due to the fact that we forgot to apply the above-mentioned precision parameter `prec_epsilon` in the code for sampling from the conditional distribution of these parameters given the data and the other parameters—a rather subtle mistake that might well have gone unnoticed without this validation study.

We perform this test for the *Detect-guess* variant of a restricted version of the 2HTM (see Fig. 9) that is the running example for this manuscript (see Section “The RT-MPT model class”). As is often done in applications of the 2HTM, the restricted model assumes that detection for new and old items are equivalent processes so that we use the same parameters for their probability and process times. Using a simplified model helped to keep the computing time required for the simulations manageable. For the same reason, we adapted the priors to be more informative than the broad default priors. The default priors often lead to categories with zero cells and to extreme ranges of response times in the simulated data which tends to cause slow convergence of the algorithm. The adapted priors, detailed in Appendix D, lead to simulated datasets with more realistic category frequencies and response times.

With this model and the 2000 ground truth vectors $\tilde{\theta}$ sampled from the (altered) prior distributions, we generate 2000 datasets $\tilde{y}$, one for each $\tilde{\theta}$. Each dataset simulates 40

Fig. 9 Restricted response-time extended 2HTM (*Detect-guess* variant). The rectangles indicate manifest states (i.e., item types and responses), and the gray circles indicate latent states (S_1 and S_2 are states of certainty and S_3 is a state of uncertainty). The double circles indicate the outcomes of the guessing process where + denotes an “old” guess and – a “new” guess. The parameters D , and g refer

to the probabilities of detecting an item as what it is and guessing “old”, respectively. The τ parameters denote the time for a process (in subscript) to complete for each outcome (in superscript). The δ_O and δ_N parameters denote the time for encoding and motor execution for responding “old” and “new”

subjects responding to 30 trials per condition (*studied items* and *new items*). For each such dataset, we fit the model with four chains, each with 4000 samples, a warm-up of 200 samples, and an $\hat{R}$ threshold of 1.025. For most of the 2000 datasets, a thinning of five was sufficient to have an effective sample size of at least 100 for the four times 4000 samples retained after thinning for each model parameter. If not, the fitting is repeated until the number of effective samples is at least 100 for each parameter. In cases where the number of effective sample size is still too low after three repetitions, we started the fitting anew with an increased thinning parameter of 15.

The parameters we check consist of the group-level parameters $(\mu_p^{(\alpha)}, \mu_{p,o}^{(\beta)}, \mu_r^{(\gamma)})^T$, the subject-specific deviations $(\alpha'_{p,s}, \beta'_{p,o,s}, \gamma'_{r,s})^T$, the variance-covariance matrices Σ and Γ , the individual variances of the motor times σ_s^2 , and the overall residual variance ω^2 . Since the subjects are replaceable, we only show the subject-specific SBC histograms for the first subject, meaning we exclude all subject-specific parameters other than $(\alpha'_{p,1}, \beta'_{p,o,1}, \gamma'_{r,1})^T$ and σ_1^2 , leading to a total of 42 parameters for which SBC histograms are shown. Histograms for all 393 parameters, including the other subject-specific parameters, are however reported in the OSF online materials.

Following the suggestions by Talts et al. (2018) we take $L = 99$ effective samples from the posterior samples of the parameters and $N = 2000$ replications (i.e., simulated datasets), such that we have a ratio of replications to bins of $20 = 2000/100$. Departing from Talts et al. (2018), we use two different approaches to take the 99 effective samples from the retained samples of the posterior distribution. First, the one also used by Talts et al. (2018), which is by thinning the retained samples to 99, meaning, for the cases where our sample is of the size 4×4000 every 161st sample is taken for the analysis. Second, we sample proportional to the effective sample size of each chain. This means that if one chain has clearly a higher minimal³ effective sample size than all others, more samples are taken from that chain than from the others.

The ranks of the samples of all 2000 replications cannot really be independent of each other, since knowing how many cases are in the first 99 ranks determines the number of cases in the 100th rank. Therefore the check for uniformity of ranks via histogram is an oversimplification: The Pearson's Chi-squared test takes that into account. For each of the 393 parameters (including all subject-specific parameters) we calculate the Chi-squared statistic with expected frequencies given by the expected uniform distribution (i.e., 20 per bin) and check how many of the

parameters are above the critical value of $\chi^2(p = .95, df = 99) = 123.23$. The degrees of freedom are just the number of possible ranks minus one.

Results

Problems with fitting the 2000 simulated datasets occurred in a few cases with regard to two types of diagnostics, minimal effective sample size and convergence. First, the minimal effective sample size ranged from about ten to a few thousand, depending on the simulated dataset. For datasets with low minimal effective sample size (about 15%), the thinning was increased from a factor of 5 to 15. This not only increased the effective sample sizes, but also decreased $\hat{R}$. Second, 20 (1%) of the datasets needed to be replaced because of severe convergence problems. About another 400 showed substantial differences between the “a posteriori” $\hat{R}$ and the threshold for $\hat{R}$ of the package for some of the sampled parameters, in which case fitting was repeated. Almost all of the cases with low minimal effective sample size are included in these 400 datasets.

Talts et al. (2018) propose to inspect histograms for systematic deviations from the uniform distribution. Figure 10 shows the histograms for the probit-transformed group-level process probability parameters $\mu^{(\alpha)}$ and for the group-level process rates $\mu^{(\beta)}$. Figure 11 shows the histograms of the rank statistic for the subject-specific deviations of the probit-transformed process probability parameters α' and the subject-specific deviations of the process rates β' . Figure 12 shows the histograms of the rank statistic for the variance and covariance parameters for the subject-specific deviations of the probit-transformed process probability parameters α' . The histograms of the rank statistic for the variance and covariance parameters for the subject-specific deviations of the process rates β' are shown in Fig. 13. Figure 14 shows the histograms of the rank statistic for the covariance parameters of the deviations of both the probit-transformed process probabilities and process rates.

Figure 15 shows the histograms of the rank statistic for the residual variance ω^2 , the variance of the motor times for the first subject σ_1^2 , the group-level motor time mean parameter $\mu^{(\gamma)}$ for both responses, the subject-specific deviations of the motor times γ' , and their variance and covariance parameters.

As can be seen, the histograms of the rank statistics show no deviations from the uniform distribution. This holds not only for the original sampling approach (proposed by Talts et al. 2018) for picking the 99 samples out of the generated 16,000 samples per dataset that underlies the shown histograms, but also for the proportional sampling method we used in addition. This means that there was no clear pattern in the histograms that indicate some kind of

³“Minimal” in the sense of minimal over all sampled model parameters.

Fig. 10 Histograms of the rank statistic for the group-level process-related parameters. On the *horizontal axes* are the rank statistics and on the *vertical axes* the relative frequencies (frequencies divided by $N = 2000$). μ^{α} denote the group-level parameters referring to the probabilities on the probit scale and μ^{β} to the process rates. *Lower* and

upper line specify the critical values of the exact two-tailed binomial test with $\alpha = .05$ for deviations between the observed and the expected frequency (*middle line*) of each individual bin. D and g denote the processes and $-$ and $+$ the outcomes for the process rates

Fig. 11 Histograms of the rank statistic for the first subject's deviation from the process-related parameters. α' denotes the deviation from the probit-transformed probabilities for the first subject and β' the

deviation from the process rates for the first subject. D and g denote the processes and $-$ and $+$ the outcomes for the process rates; see also caption of Fig. 10

Fig. 12 Histograms of the rank statistic for the variance and covariance parameters of the subject-specific deviations from the probit-transformed probability parameters α' . D and g denote the processes; see also caption of Fig. 10

Fig. 13 Histograms of the rank statistic for the variance and covariance parameters of the subject-specific deviations from the process rate parameters β' . D and g denote the processes and $-$ and $+$ the outcomes for the process rates; see also caption of Fig. 10

Fig. 14 Histograms of the rank statistic for the covariance parameters of the subject-specific deviations from both the probit-transformed process probability parameters and the process rate parameters. D and g denote the processes and $-$ and $+$ the outcomes for the process rates; see also caption of Fig. 10

bias—only some deviation from uniformity due to random fluctuations.

When using the original sampling method proposed by Talts et al. (2018), 4.07% of the parameters show a Chi-square statistic above the critical value and 5.60% when the proportional sampling is used. Both values are close to the expected percentage of 5% for Pearson’s Chi-squared tests with an α level of .05. This means that the Chi-squared tests show little indication for substantial deviations from a uniform distribution of the ranks.⁴

Considering the histograms with Chi-squared values larger than the critical value, most of these occurred for the subject-specific parameters (α' , β' , γ' , σ^2), which are the numerically largest class of parameters in the model. Under the proportional sampling procedure, there was also a variance and a covariance of the process-related parameters as well as one of the group-level motor times with high

Chi-squared values. Inspecting the corresponding histograms we can see no systematic pattern in the deviations, however. This suggests that these results just come from random fluctuations.

Discussion

No pattern in the histograms and about 5% of Chi-square statistics above the critical value suggest that the algorithm implemented by `rtmpt` passes Talts et al.’s (2018) strong and sensitive validity test. This is of course only true for the used model and needs to be validated anew for different models. In future versions of `rtmpt` we plan to implement the SBC approach, such that it can be used for every model.

The low minimal effective sample size of some of the posterior samples mentioned above reflects the liberal settings for fitting the model to the datasets chosen in the interest of keeping computing times for the simulation study at a manageable level. When analyzing individual experimental datasets, it is advised to specify more samples to be retained, higher thinning, and also a very low maximal $\hat{R}$, since the “a posteriori” $\hat{R}$ can differ substantially from the one calculated on the run.

⁴Note, however, that the 5% expectation strictly speaking holds for a set of independent Chi-squared tests, whereas the current Chi-squared tests are not independent from each other, because the different parameters are estimated from the same datasets.

Fig. 15 Histograms of the rank statistic for the residual variance ω^2 , variance of the motor times for the first subject σ^2 , group-level parameters for the motor times μ^{γ} , deviation of the motor times for the

first subject γ' , as well as variance and covariance parameters of the subject-specific deviations from the motor times. O and N refer to the response “old” and “new”, respectively; see also caption of Fig. 10

Reproducibility study

The goal of the reproducibility study is to test the reproducibility of the major results of the data analyses reported by Klauer and Kellen (2018) in their Tables 2 and 3. The datasets analyzed by Klauer and Kellen (2018) consist of the data from Arnold et al.’s (2015) Experiments 1, 2, and 3, as well as Dube et al.’s (2012) Experiments 1 and 2. In all of these studies, a word recognition task was used.

Arnold et al. (2015) used a base rate manipulation (change of ratio for old vs. new words) in the first experiment, a feedback manipulation (increase accuracy vs. increase speed) in the second experiment, and a manipulation of the frequency with which the words from the study list were presented during the study phase (half of them once and half of them twice) in the third experiment. Dube et al. (2012) conducted their first experiment with a mix of both, base rate and frequency manipulation. Their

second experiment was a mix of all three manipulations with a number of other minor modifications.

Parameter settings for the `rtmpt` fits mimic those employed by Klauer and Kellen (2018): We use four chains with 5000 samples each, an $\hat{R}$ threshold of 1.05, and a thinning parameter of 11. We use the same models as Klauer and Kellen (2018) for all the datasets, which are variations of the default-interventionist version of the 2HTM. Departing from Klauer and Kellen (2018), the prior for the residual variance is however changed from an improper prior to a gamma prior in `rtmpt` as already mentioned. For the gamma prior we use the default of the `R` package, namely a mean of 0.005 and a variance of .01.

Results and discussion

In Tables 3 and 4, we juxtapose the results from the `rtmpt` package and the original results reported by Klauer and

Table 3 Comparison of parameter estimates between the newly developed R package `rtmpt` and the old C++ program by Klauer and Kellen (2018)

Par.	Prog.	D_N	D_W	D_S	g_1	g_2	g_3	g_4	g_5
Exp. 1									
$\mu^{(\alpha)}$	<code>rtmpt</code>	.50 [.38, .63]	.35 [.27, .43]	.79 [.74, .85]	.21 [.14, .29]	.28 [.21, .36]	.44 [.35, .52]	.57 [.48, .65]	.63 [.57, .70]
	C++	.51 [.38, .63]	.35 [.27, .43]	.79 [.74, .85]	.21 [.14, .29]	.28 [.21, .36]	.44 [.35, .52]	.57 [.48, .65]	.63 [.57, .70]
$\mu_{-}^{(\beta)}$	<code>rtmpt</code>	203 [159, 248]	190 [154, 211]	160 [116, 211]	19 [10, 31]	63 [33, 101]	113 [66, 158]	116 [67, 174]	133 [85, 185]
	C++	203 [158, 245]	189 [150, 223]	160 [110, 212]	20 [10, 34]	62 [32, 101]	114 [68, 162]	118 [66, 179]	135 [85, 185]
$\mu_{+}^{(\beta)}$	<code>rtmpt</code>	128 [100, 158]	109 [69, 154]	79 [54, 108]	170 [120, 226]	162 [107, 220]	81 [42, 128]	33 [15, 56]	21 [10, 34]
	C++	127 [98, 156]	107 [67, 157]	78 [51, 107]	169 [115, 226]	163 [101, 223]	79 [40, 127]	33 [15, 57]	20 [10, 35]
Exp. 2									
$\mu^{(\alpha)}$	<code>rtmpt</code>	.48 [.34, .60]	.21 [.12, .30]	.72 [.63, .80]	.19 [.14, .24]	.29 [.23, .36]	.47 [.37, .56]	.58 [.50, .65]	.65 [.57, .71]
	C++	.48 [.34, .61]	.21 [.12, .30]	.72 [.63, .80]	.19 [.14, .24]	.29 [.23, .36]	.47 [.38, .57]	.58 [.50, .65]	.65 [.58, .71]
$\mu_{-}^{(\beta)}$	<code>rtmpt</code>	240 [190, 294]	201 [163, 244]	232 [170, 301]	208 [155, 260]	155 [109, 204]	137 [84, 198]	57 [34, 82]	24 [11, 43]
	C++	238 [188, 293]	199 [162, 242]	227 [165, 298]	205 [157, 255]	155 [112, 203]	136 [86, 193]	58 [35, 84]	24 [12, 42]
$\mu_{+}^{(\beta)}$	<code>rtmpt</code>	152 [110, 195]	104 [62, 153]	100 [71, 130]	177 [128, 232]	208 [165, 260]	88 [50, 130]	50 [27, 75]	17 [9, 32]
	C++	156 [117, 202]	103 [58, 152]	100 [72, 134]	177 [126, 234]	210 [164, 261]	89 [52, 133]	51 [28, 79]	18 [8, 33]

Note. The table shows the median and 95% HDIs (in square brackets) of the estimates for the Dube et al. (2012) datasets (two experiments) using the default-interventionist variant of the 2HTM. Par. = Parameter type. $\mu^{(\alpha)}$ are transformed to the probability scale and $\mu_{-}^{(\beta)}$ and $\mu_{+}^{(\beta)}$ to process times in milliseconds; Prog. = Program;

Kellen (2018) in their Tables 2 and 3. Tables 3 and 4 show the median of the posterior samples as well as the 95% highest density intervals in square brackets. As can be seen, the `rtmpt` and the original results are in close agreement. The largest differences occur for Experiment 2 by Arnold et al. (2015): One of its process probability estimates differs by about 47% and one of its process time estimates by about 17 ms between `rtmpt` and the original results.

Because the posterior samples from the original results were still available, a more formal test of agreement between the two fits was possible. For this purpose, both sets of samples obtained for a given dataset were numbered from 1 to 20,000. For each parameter, the difference in the values of given parameter was then computed for each pair of samples with equal numbers. We then checked whether the difference was credibly different from zero by computing 95% highest density intervals for the 20,000 difference values and by checking whether the interval did not contain the value zero. None of the calculated differences in the posterior samples of all parameters are credibly different from zero: All 95% highest density intervals include zero.

The numerically similar medians of the posterior samples and the highest density intervals for the differences of the posterior samples of both methods show that the new C++ code in the background of `rtmpt` allows one to reproduce the fits produced by the original code.

Recovery study

Finally, we conducted a small recovery study to assess the adequacy of our implementation of the above-mentioned two features of the `rtmpt` package, namely holding process probabilities constant and suppressing specific process times. We report the goodness of recovery for models in which either of these features or both are implemented as well as for a model without these constraints. Our rationale for assessing these features is the following: If recovery performance is about as well for the constrained models as for the model without these constraints, this raises one's confidence that the implementation of the constraints is correct.

We use a model that is rather difficult to fit: The default-interventionist of the 2HTM (see Fig. 16) with two distinct detection processes D_O and D_N and a guessing process g . This model is difficult to fit because it is not identified in the setting of traditional MPTs, whereas it becomes identified only through the inclusion of response times (Klauer & Kellen, 2018).

In total, we use six models from which to generate data. Model 6 is the model without restrictions. Models 1 to 5 implement combinations of the following three restrictions:

- holding g constant at .5,
- suppressing the process time of guessing with outcome in favor for “new”,

Table 4 Comparison of parameter estimates between the newly developed *R* package *rtmpt* and the old C++ program by Klauer and Kellen (2018)

Par.	Prog.	Exp. 1		Exp. 2		Exp. 3
		Low	High	Acc.	Speed	
Process probabilities						
D_N	rtmpt	.60 [.31,.78]	.55 [.40,.68]	.46 [.11,.62]	.47 [.32,.61]	.79 [.72,.85]
	C++	.59 [.28,.76]	.53 [.07,.67]	.43 [.06,.57]	.45 [.07,.59]	.79 [.73,.85]
D_O	rtmpt	.33 [.11,.53]	.14 [.01,.37]	.26 [.12,.50]	.06 [.00,.24]	.02 [.00,.11]; .55 [.42,.67] ^a
	C++	.34 [.14,.52]	.15 [.00,.58]	.28 [.13,.55]	.10 [.00,.40]	.01 [.00,.09]; .54 [.43,.68] ^a
g	rtmpt	.39 [.20,.55]	.66 [.52,.75]	.57 [.35,.67]	.58 [.46,.67]	.57 [.48,.66]
	C++	.38 [.20,.52]	.65 [.30,.74]	.55 [.30,.65]	.56 [.29,.64]	.58 [.49,.66]
Process times in ms for negative outcomes						
D_N	rtmpt	240 [197,288]	306 [239,366]	476 [386,574]	87 [51,113]	174 [130,220]
	C++	237 [187,287]	302 [83,363]	465 [362,568]	83 [39,109]	178 [136,224]
D_O	rtmpt	165 [110,240]	255 [219,294]	451 [380,522]	88 [58,110]	137 [114,160]; 153 [123,182] ^a
	C++	164 [49,191]	250 [97,291]	448 [377,532]	86 [43,109] ^c	138 [116,159]; 155 [127,183] ^{a,b}
g	rtmpt	135 [55,199]	94 [57,131]	47 [20,75]	46 [17,80]	55 [28,87]
	C++	136 [49,191]	97 [57,245]	49 [16,81]	45 [22,90]	55 [28,81]
Process times in ms for positive outcomes						
D_N	rtmpt	71 [41,122]	206 [150,259]	312 [151,388]	78 [53,101]	81 [59,104]
	C++	70 [35,118]	202 [39,258]	295 [129,385]	77 [49,102]	81 [61,104]
D_O	rtmpt	84 [30,156]	63 [20,134]	160 [78,282]	57 [23,113]	91 [21,207]; 59 [35,85] ^a
	C++	87 [34,160]	59 [16,166]	168 [84,305]	59 [20,98]	84 [17,203]; 56 [35,83] ^{a,b}
g	rtmpt	168 [122,213]	77 [34,143]	92 [47,152]	67 [37,98]	89 [69,110]
	C++	171 [119,216]	76 [37,287]	100 [55,197]	69 [40,106]	88 [68,107]
Motor times						
N	rtmpt	622 [597,647]	682 [655,710]	770 [729,815]	552 [509,591]	620 [589,650]
	C++	623 [597,650]	684 [652,711]	773 [722,819]	551 [510,591]	620 [593,648]
O	rtmpt	636 [612,662]	592 [566,617]	716 [671,763]	518 [477,562]	582 [559,605]
	C++	638 [613,663]	593 [568,618]	716 [667,765]	517 [475,560]	583 [560,607]

Note. The table shows the median and 95% HDIs (in square brackets) of the estimates for the Arnold et al. (2015) datasets (three experiments) using the default-interventionist variant of the 2HTM. Par. = Parameter; For the process parameters this is the process name and for the motor times the response; Prog. = Program; Low = Low base-rate; High = Highbase-rate; Acc. = Accuracy;

^aValues for weak and strong studied items, respectively

^bThe order of weak and strong were mistakenly switched in Table 2 of Klauer and Kellen (2018)

^cThe values from Table 2 in Klauer and Kellen (2018) were mistakenly reported as 168[84,304]

- suppressing the process time for both outcomes of the guessing process.

This leads to three models with constant g , which are actually identified on the basis of the response frequencies alone (Models 1 to 3), and to two models with only one guessing-process outcome time suppressed (Models 2 and 4), and two models with both guessing-process outcome times suppressed (Models 3 and 5). The *MDL* file for the model with all restrictions (Model 3) can be seen in Fig. 17.

For each model, we generate 100 datasets with 40 participants and 30 trials per tree (*studied item* and *new item*) and participant. Note that the small size of these datasets limits the precision with which parameters can be estimated so that the overall goodness of recovery cannot be expected to be excellent.

Ground-truth values for the group-level parameters were chosen from fits to real data in order to generate realistic datasets: Thus, for the variance-covariance matrices Σ and Γ , and for the residual variance ω^2 , we directly use the

Fig. 16 Response-time extended 2HTM (*default-interventionist* variant). The rectangles indicate manifest states (i.e., item types and responses), and the gray circles indicate latent states (S_1 and S_2 are states of certainty and S_3 is a state of uncertainty). The double circles indicate the outcomes of the guessing process where + denotes an “old” guess and – a “new” guess. The parameters D_O , D_N , and g

median of the rounded parameter estimates from fitting the default-interventionist variant of the 2HTM to the data of the first experiment by Arnold et al. (2015). The subject-specific deviations are sampled from a normal distribution with mean zero and variance-covariance matrices Σ or Γ , respectively. The subject-specific variances of the motor times σ_s^2 are sampled from a scaled inverse Chi-squared distribution with 10 degrees of freedom and ω^2 as scale parameter. This number of degrees of freedom was necessary, since using the default of 2 leads to many RTs with unrealistic values larger than 3500 ms.

Each model was fit to the 100 datasets generated from that model. Except for the degrees of freedom of the scaled inverse Chi-squared distribution (10) of σ^2 , the default priors of the *rtmpt* package are used. For each dataset, we fit the corresponding model with four chains, 4000 samples per chain, a thinning parameter of five, and an $\hat{R}$ threshold of 1.025.

# Target	; Response
$g * D_O + g * (1 - D_O) + (1 - g) * D_O$	; 0
$(1 - g) * (1 - D_O)$	; 1
# Lure	; Response
$g * (1 - D_N)$	; 0
$g * D_N + (1 - g) * D_N + (1 - g) * (1 - D_N)$	; 1
constant: $g = 0.5$	
suppress: g^-, g^+	

Fig. 17 MDL syntax for the *default-interventionist* variant of the two-high threshold model with constant guessing probability of .5, suppressed process time of guessing for both outcomes and different motor times for the two possible responses

refer to the probabilities of detecting an old item as old, a new item as new, and guessing “old”. The τ parameters denote the time for a process (*subscript*) to complete for each outcome (*superscript*). The δ_O and δ_N parameters denote the time for encoding and motor execution for responding “old” and “new”

In order to measure the recovery precision, we used the root mean squared error (RMSE) and the bias. The RMSE of an estimator $\hat{\theta}$ for a random variable θ is defined as

$$RMSE(\hat{\theta}) = \sqrt{\frac{1}{R} \sum_{r=1}^R (\hat{\theta}_r - \theta_r)^2},$$

and the bias as

$$bias(\hat{\theta}) = \frac{1}{R} \sum_{r=1}^R (\hat{\theta}_r - \theta_r),$$

where R denotes the number of replications, $\hat{\theta}_r$ the mean of the posterior samples, and θ_r the true value for the r^{th} replication.

Results and discussion

Table 5 shows the parameter recovery for all models. The estimates of the process probability parameters for the first three models are quite precise. The means of the posterior deviate from the true values by only about 1%. The RMSEs support that; the largest value being 0.06. The mean of the estimated process times is mostly also close to the true value. Typically, they differ from the true values by less than 10 ms. The largest difference is about 32 ms and the largest RMSE value is .045. Most process-related parameter estimates (18 of 21) have a slightly negative bias, indicating that the true values are slightly underestimated.⁵

⁵Considering process time-related parameters, the (relatively) largest cases of bias occur for the largest true values (such as 0.24 for $\mu_{(D_N, -)}^{\beta}$), suggesting that they to some extent reflect shrinkage towards the mean (0.1) of their somewhat informative prior.

Table 5 Parameter recovery study: Group-level means of process-related parameters

Par.	Proc.	True	Est.	RMSE	Bias	SE	SD
Model 1							
μ^α	D_N	0.60	0.59	0.045	−0.0066	0.0045	0.05
	D_O	0.35	0.34	0.061	−0.0121	0.0060	0.05
μ_-^β	D_N	0.24	0.20	0.045	−0.0330	0.0032	0.04
	D_O	0.16	0.15	0.029	−0.0194	0.0022	0.03
μ_+^β	g	0.14	0.14	0.023	0.0052	0.0023	0.03
	D_N	0.07	0.06	0.016	−0.0065	0.0016	0.02
	D_O	0.08	0.08	0.023	−0.0074	0.0022	0.03
	g	0.17	0.17	0.022	0.0002	0.0022	0.03
Model 2							
μ^α	D_N	0.60	0.59	0.050	−0.0095	0.0050	0.05
	D_O	0.35	0.35	0.047	−0.0034	0.0047	0.05
μ_-^β	D_N	0.24	0.22	0.028	−0.0149	0.0024	0.03
	D_O	0.16	0.16	0.015	−0.0031	0.0014	0.01
μ_+^β	D_N	0.07	0.07	0.013	−0.0004	0.0013	0.01
	D_O	0.08	0.08	0.024	−0.0097	0.0022	0.02
	g	0.17	0.17	0.019	−0.0044	0.0019	0.02
Model 3							
μ^α	D_N	0.60	0.60	0.051	−0.0029	0.0052	0.05
	D_O	0.35	0.34	0.049	−0.0054	0.0050	0.05
μ_-^β	D_N	0.24	0.23	0.022	−0.0048	0.0021	0.02
	D_O	0.16	0.16	0.012	−0.0030	0.0012	0.01
μ_+^β	D_N	0.07	0.07	0.010	−0.0015	0.0010	0.01
	D_O	0.08	0.08	0.016	−0.0067	0.0014	0.02
Model 4							
μ^α	D_N	0.60	0.54	0.098	−0.0559	0.0081	0.11
	D_O	0.35	0.35	0.065	−0.0023	0.0067	0.08
	g	0.40	0.38	0.060	−0.0233	0.0058	0.07
μ_-^β	D_N	0.24	0.22	0.031	−0.0127	0.0028	0.03
	D_O	0.16	0.16	0.012	−0.0031	0.0012	0.01
μ_+^β	D_N	0.07	0.07	0.016	0.0031	0.0015	0.02
	D_O	0.08	0.09	0.024	0.0100	0.0024	0.03
	g	0.17	0.16	0.024	−0.0109	0.0021	0.03
Model 5							
μ^α	D_N	0.60	0.59	0.065	−0.0090	0.0065	0.07
	D_O	0.35	0.32	0.070	−0.0317	0.0065	0.08
	g	0.40	0.41	0.057	0.0089	0.0058	0.06
μ_-^β	D_N	0.24	0.23	0.023	−0.0088	0.0021	0.02
	D_O	0.16	0.16	0.012	−0.0026	0.0012	0.01
μ_+^β	D_N	0.07	0.07	0.010	−0.0008	0.0010	0.01
	D_O	0.08	0.08	0.015	−0.0097	0.0012	0.02

Table 5 (continued)

Par.	Proc.	True	Est.	RMSE	bias	SE	SD
Model 6							
μ^α	D_N	0.60	0.56	0.095	−0.0393	0.0092	0.12
	D_O	0.35	0.30	0.100	−0.0478	0.0099	0.11
	g	0.40	0.40	0.075	0.0044	0.0083	0.09
μ_-^β	D_N	0.24	0.19	0.054	−0.0414	0.0037	0.04
	D_O	0.16	0.14	0.034	−0.0275	0.0022	0.03
	g	0.14	0.15	0.021	0.0104	0.0019	0.03
μ_+^β	D_N	0.07	0.06	0.018	−0.0090	0.0015	0.02
	D_O	0.08	0.08	0.020	−0.0080	0.0018	0.04
	g	0.17	0.17	0.024	0.0017	0.0025	0.03

Note: Par. and Proc.: parameter type and process; True and Est.: true and estimated value; RMSE and BIAS: root mean squared error and bias of the estimates; SE: standard error of posterior medians across simulated datasets. SD: posterior standard deviation (mean across simulated datasets). Model 1 to 3 have constant guessing probabilities. Model 2 to 5 have suppressed process times for guessing "new" and model 3 and 5 also for guessing "old". μ^α are transformed to process probabilities and μ_-^β and μ_+^β to process times in seconds

The last three models are not identified in the MPT setting without response times, and the process probability estimates are not as accurate as in the previous three. The largest difference between true and mean estimate is about 6%. The corresponding RMSE value is 0.098. Note, however, that goodness of recovery is comparable for the unconstrained Model 6 and the constrained Models 4 and 5. The process times are estimated as well or better for the constrained models than for the unconstrained model. The largest RMSE occurs for the unconstrained model with a value of about 0.055. The largest RMSE for the constrained models is 0.031. Again, most of the biases (18 of 24) are slightly lower than zero, indicating that the true values are slightly underestimated (see Footnote 5).

For the restricted models, the mean of the estimated motor times differ from about .7 ms to about 9.5 ms from the true values and have RMSE values ranging from about .009 to .015. Their biases are slightly larger than zero (ranging from .0007 to .009), meaning they are slightly overestimated. In contrast, for the unrestricted model the mean of the two estimated motor times differ about 12 ms and 9 ms from the true values and have RMSE values of about .018 and .015, respectively. The biases are also slightly larger than zero with values .009 and .012, respectively.

The results of the recovery study suggest that the two features, holding process probabilities constant and suppressing process times, work quite well in terms of

our evaluation criterion: Recovery was about as good or better for the models implementing the features as for the unconstrained model.

General discussion

Experience shows that the use of a new model such as the RT-MPT model class proposed by Klauer and Kellen (2018) hinges critically on the availability of user-friendly software. The purpose of this manuscript is to introduce and evaluate the R package `rtmpt` that aims to provide such software. The only previous implementation of the RT-MPT model class relied on a proprietary software library and was available only in the form of C++ code, severely limiting its accessibility. These shortcomings are overcome by `rtmpt` that completely uses open source and free software, as well as the R environment. Many changes in the underlying C++ code were however necessary to accomplish these goals, calling for an attempt to demonstrate that the Bayesian algorithm has been implemented correctly.

The results of the validation studies raise our confidence that `rtmpt` implements the Bayesian algorithm as intended. First and foremost, the `rtmpt` passed a strong and sensitive validity test in the form of simulation-based calibration. Moreover, `rtmpt` was able to recover the major results of analyses with the previous implementation by Klauer and Kellen (2018). Finally, a small recovery study suggested that two partially new features have been implemented correctly.

These results and our thorough and repeated scrutiny of the program code sufficiently raise our confidence in the correctness of the implementation of the RT-MPT model class via `rtmpt`. We feel secure to offer the R package for public usage. Nevertheless, additional validation studies are desirable based on additional and more complex models. In this vein, we intend to implement the simulation-based calibration procedure as a general feature of `rtmpt`.

One reviewer suggested to make the SBC procedure available in the R package. Therefore, we added two additional functions in `rtmpt` to simulate data (`sim_rtmpt_data()`) and to run one replication of the SBC procedure (`fit_rtmpt_SBC()`). The latter function in particular calculates the rank statistics for all the model parameters. These procedures are currently restricted to models such as the 2HTM with no more than two response categories for each tree. For more details, see the respective help files by entering

```
> ?sim_rtmpt_data()
> ?fit_rtmpt_SBC()
```

Is it possible to implement the RT-MPT model class in general-purpose software for Bayesian analyses such as Stan (Gelman et al., 2015) or JAGS (Plummer, 2003)? Being able to do so would come with considerable advantages. For example, prior distributions could be specified with more flexibility and variety than via `rtmpt`. Furthermore, an independent implementation, not relying on the original C++ code, however much modified, would further decrease the probability of undetected errors if it were shown to perform comparable to the implementation based on the C++ code. Accordingly, we invested considerable efforts into developing an implementation within Stan or JAGS.

As detailed in Klauer and Kellen (2018), the likelihood function of an RT-MPT model can be stated algebraically. Unfortunately, the likelihood is not differentiable, which is however a requirement in Stan. Therefore, implementing RT-MPT models in Stan was not possible. Another attempt consisted of implementing the model class via JAGS (Plummer, 2003). This entailed the construction of a so-called *JAGS module* (Wabersich & Vandekerckhove, 2014) for those factors of the likelihood not already implemented in JAGS. We successfully built such a module, but the resulting MCMC algorithm did not converge reliably for reasons that are not clear to us. It is possible that these problems can be overcome, for example, by clever use of data augmentation steps, and we would very much welcome such a contribution.

As it stands, the current implementation provides an accessible tool to make use of the RT-MPT model class that has passed a number of validity tests. The MPT model class

is popular and widely used. Moreover, in many research projects using MPT models response times are available over and above the responses themselves. Considering the advantages coming from modeling responses and response times jointly as outlined in the introduction, we are hoping for many researchers to take up the opportunity of using `rtmpt` for their purpose.

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Author Note All R scripts for the simulations and the empirical analysis, as well as experimental datasets, are available at the Open Science Framework: <https://osf.io/9a4jw/>.

Appendix A: `rtmpt` functions for model restrictions and specifications

The function `set_params()` takes four arguments. The first one is `model`, which is of the class `rtmpt_model` and names the model we want to alter. The second argument is `parameters`. This stands for the parameter we want to change—either “probs” for holding the probabilities constant, “tau_minus” for suppressing the process time(s) with negative outcome, or “tau_plus” for suppressing the process time(s) with positive outcome. The third argument is `names` and should be a character (vector) with the process name(s) to be changed. The last argument is `values`, which should be of the same length as `names` and provide numerical values; NA is used for estimating the given process parameters, values larger than zero and lower than one for holding process probabilities constant, and zero for suppressing a process time. Here are some examples:

- `> r2HTM <- set_params(model=r2HTM, parameters="probs", names="g", values=NA)` will take the model `r2HTM`, change the state of the probability parameter of the process ‘g’ to “to be estimated”, and save it again in `r2HTM`,
- `> r2HTM <- set_params(model=r2HTM, parameters="probs", names="g", values=0.5)` will take the model `r2HTM`, change the probability parameter of the process ‘g’ to the constant 0.5, and save it again in `r2HTM`,
- `> r2HTM <- set_params(model=r2HTM, parameters="tau_minus", names="g", values=0)` will take the model `r2HTM`, change the completion-time parameter τ_g^- of the process ‘g’ to 0 (meaning it will be suppressed), and save it again in `r2HTM`.

The function `set_resps()` takes four arguments. The first is again the `model` to be altered. The second is `tree`, which should be the label of the tree, for which we want to make a change, as a character (or number if numbers are used in the model). Third is `categories` which specifies the categories within the tree, for which we want to make changes. This should again be a vector of characters (or numbers if numbers are used in the model). The last argument `values` must be a vector of numbers corresponding to a certain response. For example,

```
> r2HTM <- set_resps(model=r2HTM,
  tree="Target", categories="miss",
  values=1)
> r2HTM <- set_resps(model=r2HTM,
  tree="Lure", categories="c_r",
  values=1)
```

will define a separate motor time label for all “new” responses if it was not already taken care of in the *EQN* or *MDL* file. This means, we would assume different motor time distributions for “old” and “new” responses.

Appendix B: Prior specifications in `rtmpt`

The settings concern the prior distributions of

- $\mu^{(\alpha)}$, the group-level means of the probit-transformed process probabilities (2), which are given a normal prior distribution with mean 0,
- $\mu^{(\beta)}$, the group-level means of the log-transformed process rates (2) with a gamma prior on the (original) exponential scale,
- Σ , the variance-covariance matrix estimated for the probit-transformed process probabilities α_s and the log-transformed process rates β_s from Eq. 2 with a scaled inverse Wishart prior distribution,
- $\mu^{(\gamma)}$, the group-level means of the motor times (2) with a normal distribution as prior,
- Γ , the variance-covariance matrix estimated for the mean person-level motor times, γ_s , from Eq. 2 with a scaled inverse Wishart prior distribution (Gelman et al., 2014),
- σ_s^2 , the person-level variances of motor times (1), with a scaled inverse Chi-squared distribution with scale factor ω^2 , and
- ω^2 , which can be interpreted as an estimate of the overall residual variance and is given a gamma prior.

The prior distributions of Σ and Γ are scaled inverse Wishart distributions with df degrees of freedoms as specified in Klauer and Kellen (2018). A matrix follows this distribution if it is distributed as $\xi^T A \xi$, with scale factors ξ distributed normally with mean 1 and prior variance ϵ^{-1} , and A distributed as an inverse Wishart distribution with scale matrix E . The scale factors ξ permit the variances in Σ and Γ to be estimated with fewer constraints than imposed by the unscaled Wishart distribution (Gelman et al., 2014). The user can set their variance, or rather their precision ϵ ; the default value is 1.0. Choosing smaller precision values results in less informative priors for the variances, choosing larger values results in priors more in line with the unscaled inverse Wishart distribution. Precision parameter ϵ , labelled `prec_epsilon` in the `prior_params` list argument of the function `fit_rtmpt()`, also applies to the variances of $\mu^{(\alpha)}$. The default value 1.0 implies a uniform prior distribution of these parameters on the original probability scale. Again, smaller precision values make their prior distributions even less informative, whereas larger values will make the prior distributions more focused around the mean value of 0.5 on the probability scale.

The just-mentioned inverse Wishart distributions also require a scale matrix E , which is the identity matrix by default. But via the list elements `sf_of_scale_matrix_SIGMA` and `sf_of_scale_matrix_GAMMA` of the `prior_params` list, the identity matrix can be scaled by a constant for Σ and Γ , respectively. Values smaller than the default 1.0 imply smaller a priori variances and less variability in samples from the prior distribution for Σ and Γ , values larger than 1.0 imply larger a priori variances and permit more variability in samples from the resulting prior distribution.

Additionally, the degrees of freedom df of the inverse Wishart distribution underlying the priors for Σ and Γ can be adjusted. df is by default the number of parameters plus k with k being 1. This ensures a priori uniformly distributed correlations between -1 and 1 corresponding to an uninformative prior distribution. With the `rtmpt` parameter `add_df_to_invWish` the user can change the value of k . With larger k , the expected values of the variances and covariances get closer to zero (Gelman et al., 2014).

The user can also specify mean and variance of $e^{\mu^{(\beta)}}$, the Gamma distributed group-level estimates of the process rates. For simplicity the user can set the mean and variance, instead of shape and rate, of the Gamma distribution via `mean_of_exp_mu_beta` and `var_of_exp_mu_beta` in the `prior_params` list. Note that shape and rate can be transformed unambiguously into mean and variance for

Table 6 Overview of prior parameters to set in the `prior_params` argument of the `fit_rtmt()` function

Name	Description	Default	Restriction
<code>prec_epsilon</code>	Precision of the normal distribution for $\mu^{(\alpha)}$ and ξ	10	> 0
<code>mean_of_exp_mu_beta</code>	Group-specific mean of the exponential rates	10	> 0
<code>var_of_exp_mu_beta</code>	Group-specific variance of the exponential rates	100	> 0
<code>mean_of_mu_gamma</code>	Group-specific mean of the motor times	0	
<code>var_of_mu_gamma</code>	Group-specific variance of the motor times	10	> 0
<code>mean_of_omega_sqr</code>	Mean of the residual variance	0.005	> 0
<code>var_of_omega_sqr</code>	Variance of the residual variance	0.01	> 0
<code>df_of_sigma_sqr</code>	Degrees of freedom for the individual variance of the response executions	2	≥ 2
<code>sf_of_scale_matrix_SIGMA</code>	Scaling factor of Σ	1	> 0
<code>sf_of_scale_matrix_GAMMA</code>	Scaling factor of Γ	1	> 0
<code>add_df_to_invWish</code>	Additional degrees of freedom (integer) in the scaled inverse Wishart distribution of Σ and Γ	1	> 0

the Gamma distribution. By default, these are given values of 10 and 100, implying a mean process time in the order of $(1/10) \text{ s} = .1 \text{ s}$ with a large prior variance.⁶

Similarly, the prior mean and variance of $\mu^{(\gamma)}$ (normally distributed group-specific mean of the person-level motor-times γ_s) can be set via `mean_of_mu_gamma` and `var_of_mu_gamma` of the `prior_params` list. Their default setting is 0 s and 10, respectively, which are reasonable values for the applications we studied so far, but can be adjusted according to the motor times expected in a given application and the amount of uncertainty that exists about them a priori.

Furthermore, the degrees of freedom for the prior distribution of σ_s^2 , the person-level variances of motor times, can be set. The default setting is 2, resulting in a relatively uninformative prior distribution. If little

heterogeneity between participants in the variability of motor times is expected, degrees of freedom can be set to higher values to reflect this, using `df_of_sigma_sqr` in `prior_params` list.

The scale factor of the scaled inverse χ^2 distribution of σ_s^2 is ω^2 , the residual variance in response times, not accounted for by the RT-MPT model. The residual variance is Gamma distributed and its prior mean and variance, instead of shape and rate, can be specified via `mean_of_omega_sqr` and `var_of_omega_sqr`, respectively of the `prior_params` list argument. By default, values of 0.005 and 0.01 are set on the basis of our experience using the model, implying a prior expectation of the mean residual variance in the order of 0.005 for response times specified in seconds with a reasonably large amount of a priori variability or uncertainty.

Table 6 lists all parameters of the `prior_params` argument list of the function `fit_rtmt()`. The table shows the name of the usable list elements, a short description, default values, and the restrictions for setting their values. The *R* help file for the `fit_rtmt()` function provides additional information on this named list argument `prior_params`.

⁶Remember that process times are exponentially distributed with rate parameter $e^{\mu^{(\beta)}}$ and the inverse of the rate parameter is the expected value of the process times. These settings seem reasonable for many applications, but when processes are expected to take much longer or much shorter to complete, the user is free to adjust the mean values and via the variance the prior uncertainty in the mean settings.

Appendix C: Outputs for model and data transformation

Listing 1 and 2 show the respective outputs of the model and the data transformation.

MODEL OVERVIEW

MDL syntax for the MPT part:

```
MDL_lines
1 # Target [ hit , miss ]
2           D+(1-D)*g
3           (1-D)*(1-g)
4
5 # Lure [ f_a , c_r ]
6           (1-D)*g
7           D+(1-D)*(1-g)
```

* NOTE 1: Each line in the MDL syntax represents one response category.

Process probability parameters:

```
D g
1 NA NA
```

* NOTE 1: NA means the parameter will be estimated.
 * NOTE 2: A value larger than 0 and smaller than 1 means it will be held constant.
 * INFO: 0 of the process probabilities will be held constant.

Process completion time parameters:

```
D g
minus NA NA
plus NA NA
```

* NOTE 1: "minus" refers to the negative outcome (1-P) and "plus" to the positive.
 * NOTE 2: NA means the parameter will be estimated. 0 means it will be suppressed.
 * INFO: 0 of the process completion times will be suppressed.

Number and membership of responses:

```
TREE CAT RESP
1 Target hit 0
3 Target miss 0
4 Lure f_a 0
5 Lure c_r 0
```

* NOTE 1: Unique representation of trees and categories.
 * NOTE 2: Each response number corresponds to a distinct encoding plus motor execution time.
 * INFO: 1 distinct response(s) assumed, namely [0].

Listing 1 Example model output via the R function `to_rtmtpt_model()`

DATA TRANSFORMATION OVERVIEW

```

Reordered variables:
subj, group, tree, cat, rt
* NOTE1: Additional variables are attached behind these
        five.
* NOTE2: To see your data frame use <object name>$data.
-----

Transformed variable(s):
"subj"
      old new
1      1   0
2      2   1
3      3   2
4      4   3
5      5   4
6      6   5
7      7   6
8      8   7
9      9   8
10     10   9
11     11  10
12     12  11
13     13  12
14     14  13
15     15  14
16     16  15
17     17  16
18     18  17
19     19  18
20     20  19
21     21  20
22     22  21
23     23  22
24     24  23
25     25  24
26     26  25
27     27  26
28     28  27
29     29  28
30     30  29
31     31  30
32     32  31
33     33  32
34     34  33
35     35  34
36     36  35
37     37  36
38     38  37
39     39  38
40     40  39

"group"
      old new
1      1   0

"tree"
      old new
1 Target   0
2  Lure    1

"cat"
      old new
1 hit     0
2 miss    1
3 f_a     2
4 c_r     3

* NOTE: "old" refers to the used labels and "new" to the
        ones that will be used.
-----

```

Listing 2 Example output of the data transformation via the *R* function `to_rtmt_data()`

Appendix D: Prior specification for the simulation-based calibration study

Since the original priors used in the program are too broad and lead to too many extreme RTs (RTs from zero to over 10,000 ms) and categories with no observations, some adjustments were required. First, the precision parameter ϵ for $\mu^{(\alpha)}$ (probit-transformed group-level process probabilities) and ξ (scale parameter for the scaled inverse Wishart distribution of the variance-covariance matrices) is increased from 1 to 10 to ensure that probability parameters are almost never zero or one and therefore the number of categories with zero observations is small. This also ensures that ξ is not too large, which is important because it can cause too large values in Σ and Γ , the variances-covariance matrices. Second, mean and variance of the Gamma distribution for $e^{\mu^{(\beta)}}$ (group-mean process rate) are changed from 10 and 100 to 10 and 10, respectively. Since the process times are exponentially distributed a group-mean rate of 10 corresponds to a mean process time of 100 milliseconds. The choice of the variance ensures that most of the group-mean process times are between 50 and 250 milliseconds. Third, the mean and variance parameter of $\mu^{(\gamma)}$ are changed from 0 and 10 to .5 and .0025, respectively, which ensures that most values of $\mu^{(\gamma)}$ fall roughly between 350 and 650 milliseconds. As a reminder, this is not the mean of the encoding and motor execution time δ , since $\delta \sim \mathcal{TN}(a = 0, b = \infty, \mu = \mathbb{E}[\gamma], \sigma^2 = \sigma^2)$, where $\mathbb{E}[\gamma] = \mathbb{E}[\mu^{(\gamma)}] = .5$ seconds, which means the actual expected encoding and motor execution time is higher. Fourth, we changed the prior distributions of two related parameters, ω^2 (residual variance) and σ^2 (variance of the motor times). Parameter ω^2 follows a gamma distribution with shape and rate set to values, such that the mean is .005 and the variance $4.0e - 6$. Parameter σ^2 follows a scaled inverse χ^2 distribution with 10 degrees of freedom (instead of two) and ω^2 as scale parameter. Since the mean of the overall residual parameter ω^2 is .005 the expected value of the σ^2 is .00625. Finally, the variance-covariance matrices, Σ and Γ , have scaled inverse Wishart priors. The first with $p + 5$ degrees of freedom, scale matrix $(.1 \times \mathbf{I}_p)$, and scale parameter ξ , where p is the number of process parameters (in our case six: two probability and four process rate/time parameters). The second has $r + 5$ degrees of freedom, scale matrix $(.01 \times \mathbf{I}_r)$, and also scale parameter ξ , where r is the number of responses (in our case two). This leads to less extreme correlations and variances. The reason for the difference in the scale matrices is that the process-related parameters are on a different scale than the encoding and motor execution times.

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