

1 Event History Analysis for psychological time-to-event data: A tutorial in R with examples  
2 in Bayesian and frequentist workflows

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11

## Abstract

12 Time-to-event data such as response times and saccade latencies form a cornerstone of  
13 experimental psychology, and have had a widespread impact on our understanding of  
14 human cognition. However, the orthodox method for analyzing such data – comparing  
15 means between conditions – is known to conceal valuable information about the timeline of  
16 psychological effects, such as their onset time and how they evolve with increasing waiting  
17 time. The ability to reveal finer-grained, “temporal states” of cognitive processes can have  
18 important consequences for theory development by qualitatively changing the key  
19 inferences that are drawn from psychological data. Luckily, well-established analytical  
20 approaches, such as event history analysis (EHA), are able to evaluate the detailed shape  
21 of time-to-event distributions, and thus characterize the time course of psychological states.  
22 One barrier to wider use of EHA, however, is that the analytical workflow is typically more  
23 time-consuming and complex than orthodox approaches. To help achieve broader uptake of  
24 EHA, in this paper we outline a set of tutorials that detail one distributional method  
25 known as discrete-time EHA. We touch upon several key aspects of the workflow, such as  
26 how to process raw data and specify regression models, and we also consider the  
27 implications for experimental design. We finish the article by considering the benefits of  
28 the approach for understanding psychological states, as well as its limitations. Finally, the  
29 project is written in R and freely available, which means the approach can easily be  
30 adapted to other data sets.

31       *Keywords:* response times, event history analysis, Bayesian multilevel regression  
32 models, experimental psychology, cognitive psychology

33       Word count: 10115 (body) + 1742 (references) + 3442 (body supplemental material)  
34       + 393 (refs suppl. mat.)

## 35           **1. Introduction**

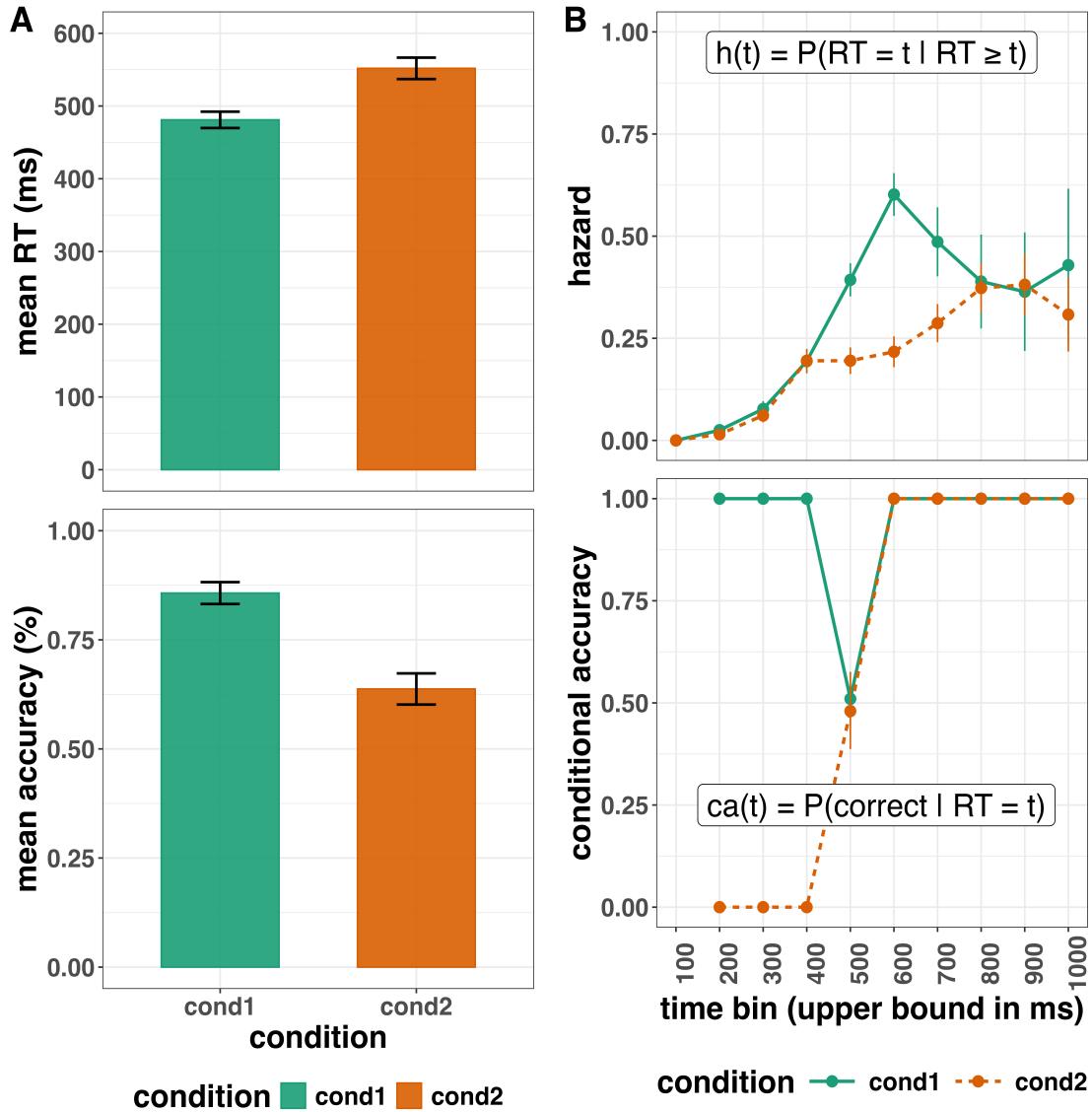
### 36   **1.1 Motivation and background context: Comparing means versus 37   distributional shapes**

38         In experimental psychology, it is standard practice to analyse response times (RTs),  
39   saccade latencies, and fixation durations by calculating average performance across a series  
40   of trials. Such comparisons between means have been the workhorse of experimental  
41   psychology over the last century, and have had a substantial impact on theory development  
42   as well as our understanding of the structure of cognition and brain function. Indeed, the  
43   view that mean values represent truth and variations around the mean are error is deeply  
44   ingrained in experimental psychology (Bolger, Zee, Rossignac-Milon, & Hassin, 2019).

45         However, differences in mean RT conceal important pieces of information, such as when an  
46   experimental effect starts, how it evolves with increasing waiting time, and whether its  
47   onset is time-locked to other events (Panis, 2020; Panis, Moran, Wolkersdorfer, & Schmidt,  
48   2020; Panis & Schmidt, 2016, 2022; Panis, Torfs, Gillebert, Wagemans, & Humphreys,  
49   2017; Panis & Wagemans, 2009; Wolkersdorfer, Panis, & Schmidt, 2020). Such absolute  
50   timing information is useful not only for the interpretation of experimental effects under  
51   investigation, but also for cognitive psychophysiology and computational model selection  
52   (Panis, Schmidt, Wolkersdorfer, & Schmidt, 2020).

53         As a simple illustration, Figure 1 summarises simulated data for one subject that  
54   shows how comparing means between two conditions can conceal the shapes of the  
55   underlying RT and accuracy distributions. Indeed, compared to the aggregation of data  
56   across trials (Figure 1A), a distributional approach offers the possibility to reveal the time  
57   course of psychological states (Figure 1B). Here we apply a distributional method known as  
58   event history analysis (EHA) extended with speed-accuracy tradeoff (SAT) analysis. For  
59   example, Figure 1B shows a first state (up to 400 ms after target onset) for which the early  
60   upswing in the hazard of response occurrence is equal for both conditions, and the emitted

61 responses are always correct in condition 1 and always incorrect in condition 2. In a second  
62 state (400 to 500 ms), the hazard of response occurrence is higher in condition 1, and  
63 conditional accuracies are close to .5 in both conditions. In a third state (>500 ms), the  
64 effect disappears in hazard, and all conditional accuracies are equal to 1. Note that we will  
65 always refer to a time bin by its upper bound. For example, time bin “500” in Figure 1B  
66 refers to the time interval running from 400 ms to 500 ms, with the lower bound of 400 ms  
67 excluded, and the upper bound of 500 ms included. Importantly from a face-validity  
68 perspective, this pattern of simulated data can be seen in the experimental psychology  
69 literature (Panis & Schmidt, 2022).



*Figure 1.* Simulated single-subject data showing mean performance versus a distributional analysis. (A) The mean RT (top) and overall accuracy (bottom) for two conditions are plotted. Two hundred trials are simulated in each condition. (B) The discrete-time hazard functions (top) and conditional accuracy functions (bottom) are plotted for the same data. The first second after target stimulus onset (time zero) is divided in ten time bins of 100 ms (indexed by  $t = 1$  to 10). The hazard and conditional accuracy estimates are plotted at the upper bound of each time bin. The definitions of discrete-time hazard and conditional accuracy are further explained in section 2.1.2. Error bars represent  $\pm 1$  standard error of the mean (A) or proportion (B).

70            Why does this matter for research in psychology? For many psychological questions,  
 71    the estimation of such “temporal states” information can be theoretically meaningful by

72 leading to more fine-grained understanding of psychological processes. Because EHA adds  
73 a relatively under-used but ever-present dimension – the passage of time – to the theory  
74 building toolkit, it provides one possible response to the recent call for a temporal science  
75 of behavior (Abney, Fausey, Suarez-Rivera, & Tamis-LeMonda, 2025).

76 **1.2 Aims**

77 Our ultimate aim in this paper is twofold. First, we want to convince readers of the  
78 many benefits of using EHA when dealing with psychological RT data. Second, we want to  
79 provide a set of practical tutorials, which provide step-by-step instructions on how you  
80 actually perform a (single event) discrete-time EHA on RT data, as well as a  
81 complementary discrete-time SAT analysis on timed accuracy data in case of choice RT  
82 data (Figure 1B).

83 Even though EHA is a widely used statistical tool and there already exist many  
84 excellent reviews (Allison, 1982; Blossfeld & Rohwer, 2002; Box-Steffensmeier, 2004;  
85 Hosmer, Lemeshow, & May, 2011; Mills, 2011; Singer & Willett, 2003; Teachman, 1983)  
86 and tutorials (Allison, 2010; Elmer, Van Duijn, Ram, & Bringmann, 2023; Landes,  
87 Engelhardt, & Pelletier, 2020; Lougheed, Benson, Cole, & Ram, 2019; Stoolmiller, 2015;  
88 Stoolmiller & Snyder, 2006), we are not aware of any tutorials that are aimed specifically  
89 at psychological RT (+ accuracy) data, and which provide worked examples of the key  
90 data processing and Bayesian multilevel regression modelling steps.

91 Set within this context, our overall aim is to introduce a set of tutorials, which  
92 explain **how** to do such analyses in the context of experimental psychology, rather than  
93 repeat in any detail **why** you may do them. Therefore, we hope that our tutorials will  
94 provide a pathway for research avenues in experimental psychology that have the potential  
95 to benefit from using EHA in the future.

### 96 1.3 Structure

97 In what follows, the paper is organised in three main sections. In Section 2, we  
98 provide a brief overview of EHA to orient the reader to the basic concepts that we will use  
99 throughout the paper and why such an approach might be relevant for research in  
100 experimental psychology. In Section 3, we outline a series of tutorials, which are written in  
101 the R programming language and publicly available on our Github page  
102 ([https://github.com/sven-panis/Tutorial\\_Event\\_History\\_Analysis](https://github.com/sven-panis/Tutorial_Event_History_Analysis)), along with all of the  
103 other code and material associated with the project. The tutorials provide hands-on,  
104 concrete examples of key parts of the analytical process, such as data wrangling, plotting  
105 descriptive statistics, model fitting and planning future studies, so that others can apply  
106 EHA to their own time-to-event data measured in RT tasks. In Section 4, we discuss the  
107 strengths and weaknesses of the approach for researchers in experimental psychology.

108 **2. What is event history analysis and why is it relevant to research in  
109 experimental psychology?**

110 **2.1 A brief introduction to event history analysis**

111 EHA is a class of statistical approaches to study the occurrence and timing of events,  
112 such as disease onset, marriages, arrests, and job terminations (Allison, 2010). In this  
113 section, we want to provide an intuition regarding how EHA works in general, as well as in  
114 the context of experimental psychology. For those who want more detailed treatment of  
115 EHA and/or regression equations, we refer the reader to several excellent textbooks on  
116 these topics (Allison, 2010; Gelman, Hill, & Vehtari, 2020; Mills, 2011; Singer & Willett,  
117 2003; Winter, 2019). We also supply relevant regression equations in section E of the  
118 Supplemental Material.

119 **2.1.1 Terminology and minimum requirements for EHA.** To avoid possible  
120 confusion in terminology used, it is worth noting that EHA is known by various labels,

121 such as survival analysis, hazard analysis, duration analysis, failure-time analysis, and  
122 transition analysis (Singer & Willett, 2003). In this paper, we choose to use the term EHA  
123 throughout.

124 In terms of minimum requirements to apply EHA, one must be able to:

- 125 1. define an event of interest that represents a qualitative change - a transition from one  
126 discrete state to another - that can be situated in time (e.g., a button press, a  
127 saccade onset, a fixation offset, etc.);
- 128 2. define time point zero in each trial (e.g., target stimulus onset, fixation onset, etc.);
- 129 3. measure the passage of time between time point zero and event occurrence in discrete  
130 or continuous time units in each trial.

131 These minimal requirements are fulfilled by the RT data obtained in single-button  
132 detection tasks, where the time-to-response is repeatedly measured in different trials in the  
133 same individual. In section A of the Supplemental Material we visualize this and other  
134 types of time-to-event data which are typically obtained in discrimination and bistable  
135 perception tasks.

136 **2.1.2 Types of EHA.** There are different types of modeling approaches in EHA.  
137 For example, the definition of hazard and the type of models employed depend on whether  
138 one is using continuous or discrete time units. As a lab, and mainly for practical reasons,  
139 we have much more experience using discrete-time EHA, and that is the approach that we  
140 describe and focus on in this paper. This choice may seem counter-intuitive, given that RT  
141 is typically treated as a continuous variable. However, continuous forms of EHA require  
142 much more data to reliably estimate the continuous-time hazard (rate) function (Bloxom,  
143 1984; Luce, 1991; Van Zandt, 2000). Thus, by trading a bit of temporal resolution for a  
144 lower number of trials, discrete-time methods seem ideal for dealing with typical  
145 psychological RT data sets for which there are less than ~200 trials per condition per

<sup>146</sup> participant (Panis, Schmidt, et al., 2020). Moreover, as indicated by Allison (2010),  
<sup>147</sup> learning discrete-time EHA methods first will help in learning continuous-time methods, so  
<sup>148</sup> it seems like a good starting point.

<sup>149</sup> To apply discrete-time EHA, one divides the within-trial time in discrete, contiguous  
<sup>150</sup> time bins indexed by  $t$  (e.g.,  $t = 1$  to 10; Figure 1B). Then let  $RT$  be a discrete random  
<sup>151</sup> variable denoting the rank of the time bin in which a particular person's response occurs in  
<sup>152</sup> a particular trial across a repeated measures design. For example, a response in one trial  
<sup>153</sup> might occur at 546 ms and it would be in time bin 6 (any RTs from 501 ms to 600 ms).  
<sup>154</sup> One then calculates the sample-based estimate of the discrete-time hazard function of  
<sup>155</sup> event occurrence for each experimental condition (Figure 1B upper panel). The  
<sup>156</sup> discrete-time hazard function gives you, for each time bin, the conditional probability that  
<sup>157</sup> the event occurs (sometime) in bin  $t$ , given that the event does not occur in previous bins.  
<sup>158</sup> In other words, it reflects the instantaneous risk that the event occurs in the current bin  $t$ ,  
<sup>159</sup> given that it has not yet occurred in the past, i.e., in one of the prior bins ( $t-1, t-2, \dots, 1$ ).

<sup>160</sup> In the context of experimental psychology, it is often (but not always), the case that  
<sup>161</sup> responses can be classified as correct or incorrect. In those cases, one can also calculate the  
<sup>162</sup> conditional accuracy function (Figure 1B lower panel). The conditional accuracy function  
<sup>163</sup> gives you for each time bin the conditional probability that a response is correct given that  
<sup>164</sup> it is emitted in time bin  $t$  (Allison, 2010; Kantowitz & Pachella, 2021; Wickelgren, 1977).  
<sup>165</sup> The conditional accuracy function is also known as the micro-level speed-accuracy tradeoff  
<sup>166</sup> (SAT) function. We refer to this extended (hazard + conditional accuracy) analysis for  
<sup>167</sup> choice RT data as EHA/SAT. The definitions of these and other discrete-time functions are  
<sup>168</sup> given in section B of the Supplemental Material.

**169 2.2 Benefits of event history analysis for research in experimental psychology**

170 Statisticians and mathematical psychologists recommend focusing on the hazard  
171 function when analyzing time-to-event data for various reasons (Holden, Van Orden, &  
172 Turvey, 2009; Luce, 1991; Townsend, 1990). We do not cover these benefits in detail here,  
173 as these are more general topics that have been covered elsewhere in textbooks (see also  
174 section G of the Supplemental Material). Instead, here we focus on the benefits as we see  
175 them for common research programmes in experimental psychology.

176 We highlight three benefits that we think are relevant to the domain of experimental  
177 psychology. First, as illustrated in Figure 1, compared to averaging data across trials,  
178 integrating results between hazard functions and their associated conditional accuracy  
179 functions for choice RT data can be informative for understanding psychological processes,  
180 in terms of inferences about the microgenesis and temporal organization of cognition and  
181 theoretical development. As such, the approach permits different kinds of questions to be  
182 asked, different inferences to be made, and it holds the potential to discriminate between  
183 theoretical accounts of psychological and/or brain-based processes. For example, what kind  
184 of theory or set of mechanisms could account for the shape of the functions and the  
185 temporally localized effects reported in Figure 1B (Panis & Schmidt, 2016)? Are there new  
186 auxiliary assumptions that computational models need to adopt (Panis, Moran, et al.,  
187 2020)? Will the temporal effect patterns align nicely with EEG findings (Panis & Schmidt,  
188 2022)? And are there new experiments that need to be performed to test the novel  
189 predictions that follow from these analyses?

190 Second, compared to more conventional analytical approaches, EHA uses more of the  
191 data because it deals with missing data differently. It is conventional with RT data to  
192 either (a) use a response deadline and discard all trials without a response, or (b) wait in  
193 each trial until a response occurs and then apply data trimming techniques, i.e., discarding  
194 too short or too long RTs (and perhaps also erroneous responses) before calculating a mean

195 RT (Berger & Kiefer, 2021). Discarding data can introduce biases, however. Rather than  
196 treat non-responses as missing data, EHA treats such trials as *right-censored* observations  
197 on the variable RT, because all we know is that RT is greater than some value.  
198 Right-censoring is a type of missing data problem and a nearly universal feature of survival  
199 data including RT data. For example, if the censoring time was 1 second, then some trials  
200 result in observed event times (those with a RT below 1 second), while the other trials  
201 result in response times that are right-censored at 1 second. The fact that EHA can deal  
202 with right-censoring, therefore, presents a analytical strength of the approach compared to  
203 many common approaches in experimental psychology (e.g., ANOVA, linear regression,  
204 delta plots).

205 Third, the approach is generalisable and applicable to many tasks that are commonly  
206 used in experimental psychology, such as detection, discrimination and bistable perception  
207 tasks, and to a range of common experimental manipulations, such as  
208 stimulus-onset-asynchrony (see section A of the Supplemental Material). The upshot is  
209 that one general analytical approach, which holds several potential advantages, is widely  
210 applicable to many substantive use-cases in the RT domain of experimental psychology,  
211 irrespective of the analyst's current view on the nature of cognition (Barack & Krakauer,  
212 2021).

### 213 2.3 Implications for research design in experimental psychology

214 Performing EHA in experimental psychology has implications for how experiments  
215 are designed. More specifically, we consider three implications that researchers will need to  
216 consider when using discrete-time EHA. First, because EHA deals with right-censored  
217 observations, one can use a fixed response deadline in each trial. This will increase design  
218 efficiency as one does not need to wait for very long RTs that would be trimmed anyway.

219 Second, since the number of trials per condition are spread across bins, it is

220 important to have a relatively large number of trial repetitions per participant and per  
221 condition. Accordingly, experimental designs using this approach typically focus on  
222 factorial, within-subject designs, in which a large number of observations are made on a  
223 relatively small number of participants (so-called small-*N* designs). This approach  
224 emphasizes the precision and reproducibility of data patterns at the individual participant  
225 level to increase the inferential validity of the design (Baker et al., 2021; Smith & Little,  
226 2018). Note that because statistical power derives both from the number of participants  
227 and from the number of repeated measures per participant and condition, small-*N* designs  
228 can still achieve what are generally considered acceptable levels of statistical power, if they  
229 have a sufficient amount of data overall (Baker et al., 2021; Smith & Little, 2018).

230 Third, the width of each time bin will need to be determined. For instance, in Figure  
231 1B we chose 100 ms in an arbitrary manner. In reality, however, bin width will need to be  
232 set by considering a number of factors simultaneously. The optimal bin width will depend  
233 on (a) the length of the observation period in each trial, (b) the rarity of event occurrence,  
234 (c) the number of repeated measures (or trials) per condition per participant, and (d) the  
235 shape of the hazard function. Finding an appropriate bin width in a given user case before  
236 fitting models will require testing a number of options, when calculating and plotting the  
237 descriptive statistics (see section 3.1). The goal is to find the smallest bin width that is  
238 supported by the amount of data available. Based on our experience, a bin width of 50 ms  
239 is a good starting value when the number of repeated measures is 100 or less. Overly small  
240 bin widths will result in erratic hazard functions as many bins will have no events, and  
241 thus hazard estimates of zero. Of note, however, is that time bins do not need to have the  
242 same width. For example, Panis (2020) used larger bins towards the end of the observation  
243 period, as fewer events occurred there.

244

### 3. Tutorials

245        Tutorials 1a and 1b show how to calculate and plot the descriptive statistics of  
 246        EHA/SAT when there are one or two independent variables, respectively. Tutorials 2a and  
 247        2b illustrate how to use Bayesian multilevel modeling to fit hazard and conditional  
 248        accuracy models, respectively. Tutorials 3a and 3b show how to implement, respectively,  
 249        multilevel models for hazard and conditional accuracy in the frequentist framework.  
 250        Tutorial 4 shows how to use simulation and power analysis for planning experiments.  
 251        Additionally, to further simplify the process for other users, the first two tutorials rely on a  
 252        set of our own custom functions that make sub-processes easier to automate, such as data  
 253        wrangling and plotting functions (see section C of the Supplemental Material for a list of  
 254        the custom functions).

255        The content of the tutorials, in terms of EHA and multilevel regression modelling, is  
 256        mainly based on Allison (2010), Singer and Willett (2003), McElreath (2020), Heiss (2021),  
 257        Kurz (2023a), and Kurz (2023b). We used R (Version 4.5.1; R Core Team, 2024)<sup>1</sup>,  
 258        for all reported analyses.

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<sup>1</sup> We, furthermore, used the R-packages *bayesplot* (Version 1.13.0; Gabry, Simpson, Vehtari, Betancourt, & Gelman, 2019), *brms* (Version 2.22.0; Bürkner, 2017, 2018, 2021), *citr* (Version 0.3.2; Aust, 2019), *cmdstanr* (Version 0.9.0.9000; Gabry, Češnovar, Johnson, & Brondum, 2024), *dplyr* (Version 1.1.4; Wickham, François, Henry, Müller, & Vaughan, 2023), *forcats* (Version 1.0.0; Wickham, 2023a), *futures* (Bengtsson, 2021), *ggplot2* (Version 3.5.2; Wickham, 2016), *lme4* (Version 1.1.37; Bates, Mächler, Bolker, & Walker, 2015), *lubridate* (Version 1.9.4; Grolemund & Wickham, 2011), *Matrix* (Version 1.7.3; Bates, Maechler, & Jagan, 2024), *nlme* (Version 3.1.168; Pinheiro & Bates, 2000), *papaja* (Version 0.1.3; Aust & Barth, 2024), *patchwork* (Version 1.3.0; Pedersen, 2024), *purrr* (Version 1.0.4; Wickham & Henry, 2023), *RColorBrewer* (Version 1.1.3; Neuwirth, 2022), *Rcpp* (Eddelbuettel & Balamuta, 2018; Version 1.0.14; Eddelbuettel & François, 2011), *readr* (Version 2.1.5; Wickham, Hester, & Bryan, 2024), *rstan* (Version 2.32.7; Stan Development Team, 2024), *standist* (Version 0.0.0.9000; Girard, 2024), *StanHeaders* (Version 2.32.10; Stan Development Team, 2020), *stringr* (Version 1.5.1; Wickham, 2023b), *tibble* (Version 3.3.0; Müller & Wickham, 2023), *tidybayes* (Version 3.0.7; Kay, 2024), *tidyverse* (Version 1.3.1; Wickham, Vaughan, & Girlich, 2024), *tidyverse* (Version 2.0.0; Wickham et al., 2019) and *tinylabels* (Version 0.2.5; Barth, 2023).

259 **3.1 Tutorial 1a: Calculating descriptive statistics using a life table**

260 **3.1.1 Data wrangling aims.** Our data wrangling procedures serve two related  
261 purposes. First, we want to calculate descriptive statistics for each condition in each  
262 individual using a life table. A life table (see Table 3) includes for each time bin, the risk  
263 set (i.e., the number of trials that are event-free at the start of the bin), the number of  
264 observed events, and the estimates of the discrete-time hazard probability  $h(t)$ , survival  
265 probability  $S(t)$ , probability mass  $P(t)$ , possibly the conditional accuracy  $ca(t)$ , and their  
266 estimated standard errors (se). The definitions of these quantities are provided in section B  
267 of the Supplemental Material.

268 Second, we want to produce two different data sets that can each be submitted to  
269 different types of inferential modelling approaches. The two types of data structure we  
270 label as ‘person-trial’ data and ‘person-trial-bin’ data. The ‘person-trial’ data (Table 1)  
271 will be familiar to most researchers who record behavioural responses from participants, as  
272 it represents the measured RT and accuracy per trial within an experiment. This data set  
273 is used when fitting conditional accuracy models (Tutorials 2b and 3b).

Table 1  
*Data structure for ‘person-trial’ data*

pid	trial	condition	rt	accuracy
1	1	congruent	373.49	1
1	2	incongruent	431.31	1
1	3	congruent	455.43	0
1	4	incongruent	622.41	1
1	5	incongruent	535.98	1
1	6	incongruent	540.08	1
1	7	congruent	511.07	1
1	8	incongruent	444.42	1
1	9	congruent	678.69	1
1	10	congruent	549.79	1

*Note.* The first 10 trials for participant 1 are shown. These data are simulated and for illustrative purposes only.

274 In contrast, the ‘person-trial-bin’ data (Table 2) has a different, more extended  
 275 structure, which indicates in which bin a response occurred, if at all, in each trial.  
 276 Therefore, the ‘person-trial-bin’ data generates a 0 in each bin until an event occurs and  
 277 then it generates a 1 to signal an event has occurred in that bin. This data set is used  
 278 when fitting discrete-time hazard models (Tutorials 2a and 3a). It is worth pointing out  
 279 that there is no requirement for an event to occur at all (in any bin), as maybe there was  
 280 no response on that trial or the event occurred after the time window of interest. Likewise,  
 281 when the event occurs in bin 1 there would only be one row of data for that trial in the  
 282 person-trial-bin data set.

Table 2  
*Data structure for ‘person-trial-bin’ data*

pid	trial	condition	timebin	event
1	1	congruent	1	0
1	1	congruent	2	0
1	1	congruent	3	0
1	1	congruent	4	1
1	2	incongruent	1	0
1	2	incongruent	2	0
1	2	incongruent	3	0
1	2	incongruent	4	0
1	2	incongruent	5	1

*Note.* The first 2 trials for participant 1 from Table 1 are shown. The width of the time bins is 100 ms. These data are simulated and for illustrative purposes only.

283 **3.1.2 A real data wrangling example.** To illustrate how to quickly set up life  
 284 tables for calculating the descriptive statistics (functions of discrete time), we use a  
 285 published data set on masked response priming from Panis and Schmidt (2016), who were  
 286 interested in the temporal dynamics of the effect of prime-target congruency in RT and  
 287 accuracy data. In their first experiment, Panis and Schmidt (2016) presented a double  
 288 arrow for 94 ms that pointed left or right as the target stimulus with an onset at time

289 point zero in each trial. Participants had to indicate the direction in which the double  
 290 arrow pointed using their corresponding index finger, within 800 ms after target onset.  
 291 Response time and accuracy were recorded on each trial. Prime type (blank, congruent,  
 292 incongruent) and mask type were manipulated across trials (i.e., repeated measures of  
 293 time-to-response). Here we focus for each participant on the subset of 220 trials in which  
 294 no mask was presented. The 13-ms prime stimulus was a double arrow presented 187 ms  
 295 before target onset in the congruent (same direction as target) and incongruent (opposite  
 296 direction as target) prime conditions.

297 There are several data wrangling steps to be taken. First, we need to load the data  
 298 before we (a) supply required column names, and (b) specify the factor condition with the  
 299 correct levels and labels.

300 The required column names are as follows:

- 301 • “pid”, indicating unique participant IDs;
- 302 • “trial”, indicating each unique trial per participant;
- 303 • “condition”, a factor indicating the levels of the independent variable (1, 2, ...) and  
     the corresponding labels;
- 304 • “rt”, indicating the response times in ms;
- 305 • “acc”, indicating the accuracies (1/0).

307 In the code of Tutorial 1a, this is accomplished as follows.

```
data_wr<-read_csv("../Tutorial_1_descriptive_stats/data/DataExp1_6subjects_wrangled.csv")
data_wr <- data_wr %>%
  rename(pid = vp, condition = prime_type, acc = respac, trial = TrialNr) %>%
  mutate(condition = condition + 1, # original levels were 0, 1, 2.
        condition = factor(condition,
                            levels=c(1,2,3),
                            labels=c("blank","congruent","incongruent")))
```

308        Next, we can set up the life tables and plot for each condition the discrete-time hazard  
 309      function  $h(t)$ , survivor function  $S(t)$ , probability mass function  $P(t)$ , and conditional  
 310      accuracy function  $ca(t)$ . To do so using a functional programming approach, one has to  
 311      nest the person-trial data within participants using the `group_nest()` function, and supply  
 312      a user-defined censoring time and bin width to our custom function “`censor()`”, as follows.

```
data_nested <- data_wr %>% group_nest(pid)

data_final <- data_nested %>%
  # ! user input: censoring time, and bin width in milliseconds
  mutate(censored = map(data, censor, 600, 40)) %>%
  # create person-trial-bin data set
  mutate(ptb_data = map(censored, ptb)) %>%
  # create life tables without conditional accuracies
  mutate(lifetable = map(ptb_data, setup_lt)) %>%
  # calculate conditional accuracies
  mutate(condacc = map(censored, calc_ca)) %>%
  # create life tables with conditional accuracies
  mutate(lifetable_ca = map2(lifetable, condacc, join_lt_ca)) %>%
  # create plots
  mutate(plot = map2(.x = lifetable_ca, .y = pid, plot_eha,1))
```

313       Note that the censoring time (here: 600 ms) should be a multiple of the bin width  
 314      (here: 40 ms). The censoring time should be a time point after which no informative  
 315      responses are expected anymore, in case one waits for a response in each trial. In  
 316      experiments that implement a response deadline in each trial the censoring time can equal  
 317      that deadline time point. Trials with a RT larger than the censoring time, or trials in  
 318      which no response is emitted during the data observation period, are treated as  
 319      right-censored observations in EHA. In other words, these trials are not discarded, because  
 320      they contain the information that the event did not occur before the censoring time.  
 321      Removing such trials before calculating the mean event time would result in  
 322      underestimation of the true mean.

323        The person-trial-bin oriented data set is created by our custom function ptb(), and it

324        has one row for each time bin (of each trial) that is at risk for event occurrence. The

325        variable “event” in the person-trial-bin oriented data set indicates whether a response

326        occurs (1) or not (0) for each bin. The next steps are to set up the life table using our

327        custom function setup\_lt(), calculate the conditional accuracies using our custom function

328        calc\_ca(), add the ca(t) estimates to the life table using our custom function join\_lt\_ca(),

329        and then plot the descriptive statistics using our custom function plot\_eha(). One can now

330        inspect different aspects, including the life table for a particular condition of a particular

331        subject, and a plot of the different functions for a particular participant.

332        In general, it is important to visually inspect the functions first for each participant,

333        in order to identify individuals that may not be following task instructions (e.g., a flat

334        conditional accuracy function at .5 indicates that someone is just guessing), outlying

335        individuals, and/or different groups with qualitatively different behavior. Also, to select a

336        suited bin width for model fitting, one can test and compare various bin widths in the

337        censor function, and select the smallest one that is supported by the data.

338        Table 3 shows the life table for condition “blank” (no prime stimulus presented) for

339        participant 6.

Table 3

*The life table for the blank prime condition of participant 6.*

bin	index t	RS	#events	h(t)	se[h(t)]	S(t)	se[S(t)]	ca(t)	se[ca(t)]	P(t)	se[P(t)]
0	0	220	NA	NA	NA	1.00	0.00	NA	NA	0.00	0.00
40	1	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
80	2	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
120	3	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
160	4	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
200	5	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
240	6	220	0	0.00	0.00	1.00	0.00	NA	NA	0.00	0.00
280	7	220	7	0.03	0.01	0.97	0.01	0.29	0.17	0.03	0.01
320	8	213	13	0.06	0.02	0.91	0.02	0.77	0.12	0.06	0.02
360	9	200	26	0.13	0.02	0.79	0.03	0.92	0.05	0.12	0.02
400	10	174	40	0.23	0.03	0.61	0.03	1.00	0.00	0.18	0.03
440	11	134	48	0.36	0.04	0.39	0.03	0.98	0.02	0.22	0.03
480	12	86	37	0.43	0.05	0.22	0.03	1.00	0.00	0.17	0.03
520	13	49	32	0.65	0.07	0.08	0.02	1.00	0.00	0.15	0.02
560	14	17	9	0.53	0.12	0.04	0.01	1.00	0.00	0.04	0.01
600	15	8	4	0.50	0.18	0.02	0.01	1.00	0.00	0.02	0.01

*Note.* The column named “bin” indicates the upper bound of each time bin (in ms), and includes time point zero. At time point zero, no events can occur and therefore both the discrete-time hazard  $h(t=0)$  and the conditional accuracy  $ca(t=0)$  are undefined. RS = risk set; se = standard error; NA = undefined.

Figure 2 displays the discrete-time hazard, survivor, conditional accuracy, and

probability mass functions for each prime condition for participant 6. By using

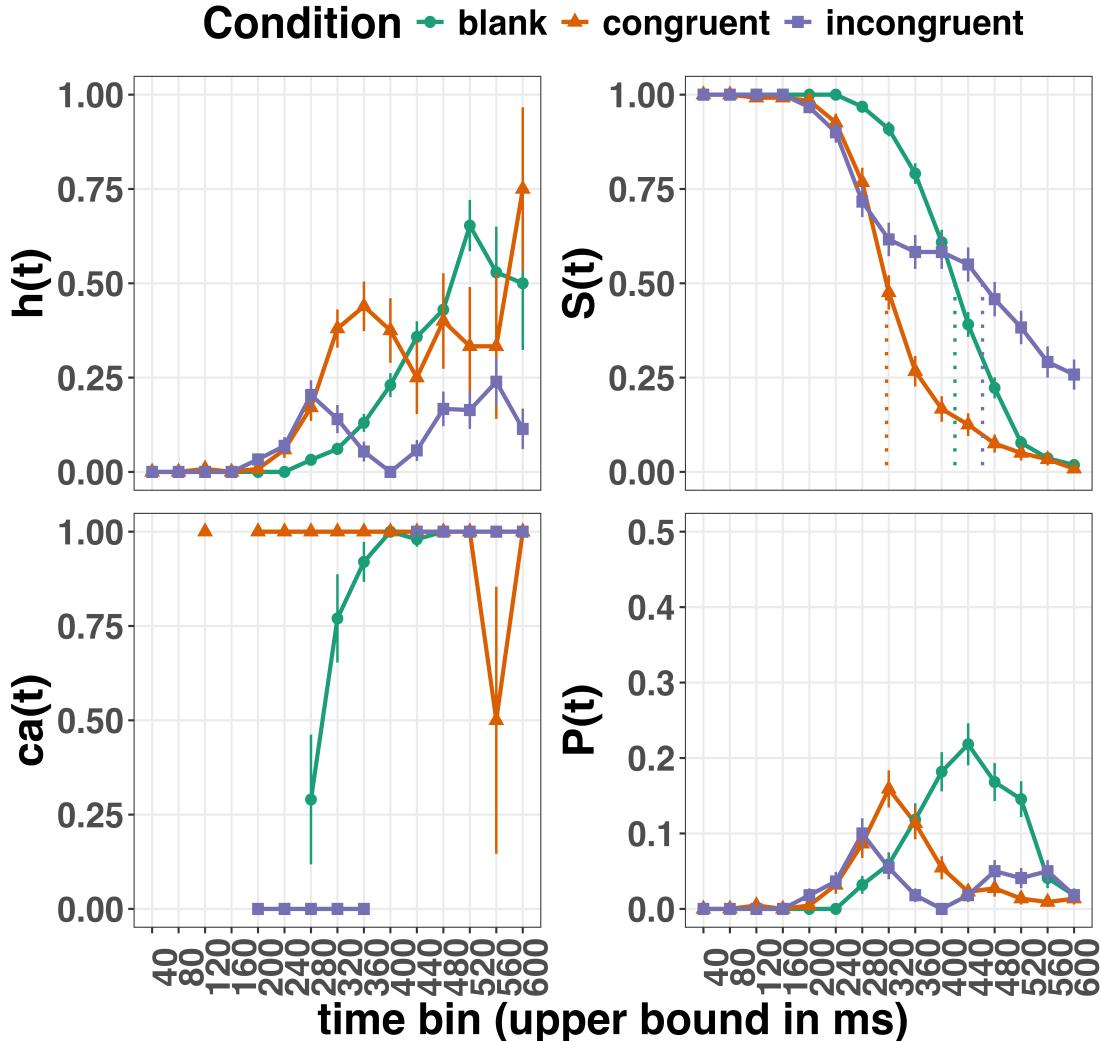
discrete-time hazard functions of event occurrence – in combination with conditional

accuracy functions for two-choice tasks – one can provide an unbiased, time-varying, and

probabilistic description of the latency and accuracy of responses based on all trials of any

RT data set.

## Descriptive stats for subject 6



*Figure 2.* Estimated sample-based discrete-time hazard ( $h$ ), survivor ( $S$ ), conditional accuracy (ca) and probability mass ( $P$ ) functions for participant 6. Vertical dotted lines indicate the estimated median RTs. Error bars represent  $\pm 1$  standard error of the respective proportion.

346 For example, for participant 6, the estimated hazard values in bin 280 are 0.03, 0.17,  
 347 and 0.20 for the blank, congruent, and incongruent prime conditions, respectively. In other  
 348 words, when the waiting time has increased until 240 ms after target onset, then the  
 349 conditional probability of response occurrence in the next 40 ms is more than five times  
 350 larger for both prime-present conditions, compared to the blank prime condition.

351 Furthermore, the estimated conditional accuracy values in bin 280 are 0.29, 1, and 0

352 for the blank, congruent, and incongruent prime conditions, respectively. In other words, if

353 a response is emitted in bin 280, then the probability that it is correct is estimated to be

354 0.29, 1, and 0 for the blank, congruent, and incongruent prime conditions, respectively.

355 However, when the waiting time has increased until *400 ms* after target onset, then

356 the conditional probability of response occurrence in the next 40 ms is estimated to be

357 0.36, 0.25, and 0.06 for the blank, congruent, and incongruent prime conditions,

358 respectively. And when a response does occur in bin 440, then the probability that it is

359 correct is estimated to be 0.98, 1, and 1 for the blank, congruent, and incongruent prime

360 conditions, respectively.

361 These distributional results suggest that participant 6 is initially responding to the

362 prime even though (s)he was instructed to only respond to the target, that response

363 competition emerges in the incongruent prime condition around 300 ms, and that only

364 slower responses are fully controlled by the target stimulus. Qualitatively similar results

365 were obtained for the other five participants. When participants show qualitatively similar

366 distributional patterns, one might consider aggregating their data and plotting the

367 group-average distribution per condition (see Tutorial\_1a.Rmd). More generally, these

368 results go against the (often implicit) assumption in research on priming that all observed

369 responses are primed responses to the target stimulus. Instead, the distributional data

370 show that fast responses are triggered exclusively by the prime stimulus, while only the

371 slower responses reflect primed responses to the target stimulus.

372 At this point, we have calculated and plotted the descriptive statistics for each type

373 of prime stimulus. As we will show in later Tutorials, statistical models for hazard and

374 conditional accuracy functions can be implemented as generalized linear mixed regression

375 models predicting event occurrence (1/0) and conditional accuracy (1/0) in each bin of a

376 selected time window for analysis. But first we consider calculating the descriptive

377 statistics for within-subject designs with two independent variables.

378 **3.2 Tutorial 1b: Generalising to a more complex design**

379 So far in this paper, we have used a simple experimental design, which involved one  
380 condition with three levels. But psychological experiments are often more complex, with  
381 crossed factorial designs and/or conditions with more than three levels. The purpose of  
382 Tutorial 1b, therefore, is to provide a generalisation of the basic approach, which extends  
383 to a more complicated design. We feel that this might be useful for researchers in  
384 experimental psychology that typically use crossed factorial designs.

385 To this end, Tutorial 1b illustrates how to calculate and plot the descriptive statistics  
386 for the full data set of Experiment 1 of Panis and Schmidt (2016), which includes two  
387 independent variables: mask type and prime type. As we use the same functional  
388 programming approach as in Tutorial 1a, we simply refer the reader to Tutorial\_1b.Rmd.

389 **3.3 Tutorial 2a: Fitting Bayesian hazard models to interval-censored RT data**

390 In this third tutorial, we illustrate how to fit Bayesian multilevel regression models to  
391 the RT data of the masked response priming data used in Tutorial 1a. Fitting (Bayesian or  
392 non-Bayesian) regression models to time-to-event data is important when you want to  
393 study how the shape of the hazard function depends on various predictors (Singer &  
394 Willett, 2003).

395 In general, when fitting regression models, our lab adopts an estimation approach to  
396 multilevel regression (Kruschke & Liddell, 2018; Winter, 2019), which is heavily influenced  
397 by the Bayesian framework as suggested by Richard McElreath (Kurz, 2023b; McElreath,  
398 2020). We also use a “keep it maximal” approach by specifying a full varying (or random)  
399 effects structure (Barr, Levy, Scheepers, & Tily, 2013). This means that wherever possible  
400 we include varying intercepts and slopes per participant. To make inferences, we use two

401 main approaches. We compare models of different complexity using information criteria  
402 and cross-validation, to evaluate out-of-sample predictive accuracy (McElreath, 2020). We  
403 also take the most complex model and evaluate key parameters of interest using point and  
404 interval estimates.

405       **3.3.1 Hazard model considerations.** There are several analytic decisions one  
406 has to make when fitting a discrete-time hazard model. First, because the first few bins  
407 often contain no responses, one has to select an analysis time window, i.e., a contiguous set  
408 of bins for which there is data for each participant. Second, given that the dependent  
409 variable (event occurrence) is binary, one has to select a link function (see section D of the  
410 Supplemental Material). The cloglog link is preferred over the logit link when events can  
411 occur in principle at any time point within a bin, which is the case for RT data (Singer &  
412 Willett, 2003). Third, one has to choose whether to treat TIME (i.e., the time bin index  $t$ )  
413 as a categorical or continuous predictor (see also section E of the Supplemental Material).  
414 For example, when you want to know if cloglog-hazard is changing linearly or quadratically  
415 over time, you should treat TIME as a continuous predictor. When you are only interested  
416 in the effect of covariates on hazard, you can treat TIME as a categorical predictor (i.e., fit  
417 an intercept for each bin), in which case you can choose between reference coding and  
418 index coding. With reference coding, one defines the variable as a factor and selects one of  
419 the  $k$  categories as the reference level. Brm() will then construct  $k-1$  indicator variables  
420 (see model M1d in Tutorial\_2a.Rmd for an example). With index coding, one constructs  
421 an index variable that contains integers that correspond to different categories (see models  
422 M0i and M1i below). As explained by McElreath (2020), the advantage of index coding is  
423 that the same prior can be assigned to each level of the index variable, so that each  
424 category has the same prior uncertainty.

425       In the case of a large- $N$  design without repeated measurements, the parameters of a  
426 discrete-time hazard model can be estimated using standard logistic regression software  
427 after expanding the typical person-trial data set into a person-trial-bin data set (Allison,

428 2010). When there is clustering in the data, as in the case of a small- $N$  design with  
 429 repeated measurements, the parameters of a discrete-time hazard model can be estimated  
 430 using population-averaged methods (e.g., Generalized Estimating Equations), and Bayesian  
 431 or frequentist generalized linear mixed models (Allison, 2010).

432 In general, there are three assumptions one can make or relax when adding  
 433 experimental predictor variables and other covariates: The linearity assumption for  
 434 continuous predictors (the effect of a 1 unit change is the same anywhere on the scale), the  
 435 additivity assumption (predictors do not interact), and the proportionality assumption  
 436 (predictors do not interact with TIME).

437 In tutorial\_2a.Rmd we fit several Bayesian multilevel models (i.e., generalized linear  
 438 mixed models) that differ in complexity to the person-trial-bin oriented data set that we  
 439 created in Tutorial 1a. We decided to select the 200-600 ms analysis time window, and the  
 440 cloglog link. Below, we shortly discuss two of these models. The person-trial-bin data set is  
 441 prepared as follows.

```
# read in the file we saved in tutorial 1a
ptb_data <- read_csv("Tutorial_1_descriptive_stats/data/inputfile_hazard_modeling.csv")

ptb_data <- ptb_data %>%
  # select analysis time range: 200-600 ms, with 10 bins (time bin ranks 6 to 15)
  filter(period > 5) %>%
  # define categorical predictor TIME as index variable named timebin
  mutate(timebin = factor(period, levels = c(6:15)),
  # factor "condition" using reference coding, with "blank" as the reference level
  condition = factor(condition, labels = c("blank", "congruent", "incongruent")),
  # categorical predictor "prime" with index coding
  prime = ifelse(condition=="blank", 1, ifelse(condition=="congruent", 2, 3)),
  prime = factor(prime, levels = c(1,2,3)))
```

442        **3.3.2 Prior distributions.** To get the posterior distribution of each model

443 parameter given the data, we need to specify prior distributions for the model parameters  
 444 which reflect our prior beliefs. In Tutorial\_2a.Rmd we perform a few prior predictive  
 445 checks to make sure our selected prior distributions reflect our prior beliefs (Gelman,  
 446 Vehtari, et al., 2020).

447        The middle column of Supplementary Figure 3 (section F of the Supplemental

448 Material) shows six examples of prior distributions for an intercept on the logit and/or  
 449 cloglog scales. While a normal distribution with relatively large variance is often used as a  
 450 weakly informative prior for continuous dependent variables, rows A and B of  
 451 Supplementary Figure 3 show that specifying such distributions on the logit and cloglog  
 452 scales actually leads to rather informative distributions on the original probability scale, as  
 453 most mass is pushed to probabilities of 0 and 1. As such, we modify the prior formulation  
 454 in order to make sure that it remains consistent with a weakly informative approach (see  
 455 section F of the Supplemental Material).

456        **3.3.3 Model M0i: A null model with index coding.** When you do not want to

457 make assumptions about the shape of the hazard function, or its shape is not smooth but  
 458 irregular, then you can use a general specification of TIME, i.e., fit one grand intercept per  
 459 time bin. In this first baseline or reference model, we use a general specification of TIME  
 460 using index coding, and do not include experimental predictors. We call this model “M0i”.

461        The other model (see section 3.3.4) extends model M0i by including our experimental  
 462 predictor prime type.

463        Before we fit model M0i, we select the necessary columns from the data, and specify

464 our priors. In the code of Tutorial 2a, model M0i is specified as follows.

```
model_M0i <-
  brm(data = data_M0i,
       family = bernoulli(link="cloglog"),
```

```

formula = event ~ 0 + timebin + (0 + timebin | pid),
prior = priors_M0i,
chains = 4, cores = 4,
iter = 3000, warmup = 1000,
control = list(adapt_delta = 0.999,
                step_size = 0.04,
                max_treedepth = 12),
seed = 12, init = "0",
file = "Tutorial_2_Bayesian/models/model_M0i")

```

465 After selecting the bernoulli family and the cloglog link, the model formula is  
 466 specified. The specification “0 + …” removes the default intercept in brm(). The fixed  
 467 effects include an intercept for each level of timebin. Each of these intercepts is allowed to  
 468 vary across individuals (variable pid). We request 2000 samples from the posterior  
 469 distribution for each of four chains. Estimating model M0i took about 30 minutes on a  
 470 MacBook Pro (Sonoma 14.6.1 OS, 18GB Memory, M3 Pro Chip).

471 **3.3.4 Model M1i: Adding the effects of prime-target congruency.** Previous  
 472 research has shown that psychological effects typically change over time (Panis, 2020;  
 473 Panis, Moran, et al., 2020; Panis & Schmidt, 2022; Panis et al., 2017; Panis & Wagemans,  
 474 2009). In the next model, therefore, we use index coding for both TIME (variable  
 475 “timebin”) and the categorical predictor prime-target-congruency (variable “prime”), so  
 476 that we get 30 grand intercepts, one for each combination of timebin level and prime level.  
 477 Here is the model formula of this model that we call “M1i”.

```
event ~ 0 + timebin:prime + (0 + timebin:prime | pid)
```

478 Estimating model M1i took about 124 minutes using the same MacBook Pro.

479       **3.3.5 Compare the models.** There are two popular strategies to evaluate how

480 well models will perform in predicting new data on average: Leave-One-Out (LOO)  
 481 cross-validation and the Widely Applicable Information Criterion or WAIC (McElreath,  
 482 2020). LOO-weights represent the optimal linear combination of models for predictive  
 483 performance, with higher weights for models with better out-of-sample predictive  
 484 performance. WAIC-weights represent the relative evidence for each model, with higher  
 485 weights for models with a better fit while accounting for model complexity (Kurz, 2023a;  
 486 McElreath, 2020).

```
model_weights(model_M0i, model_M1i, weights = "loo") %>% round(digits = 2) %>% format(nsmall=2)
```

487 ## model\_M0i model\_M1i  
 488 ## "0.00" "1.00"

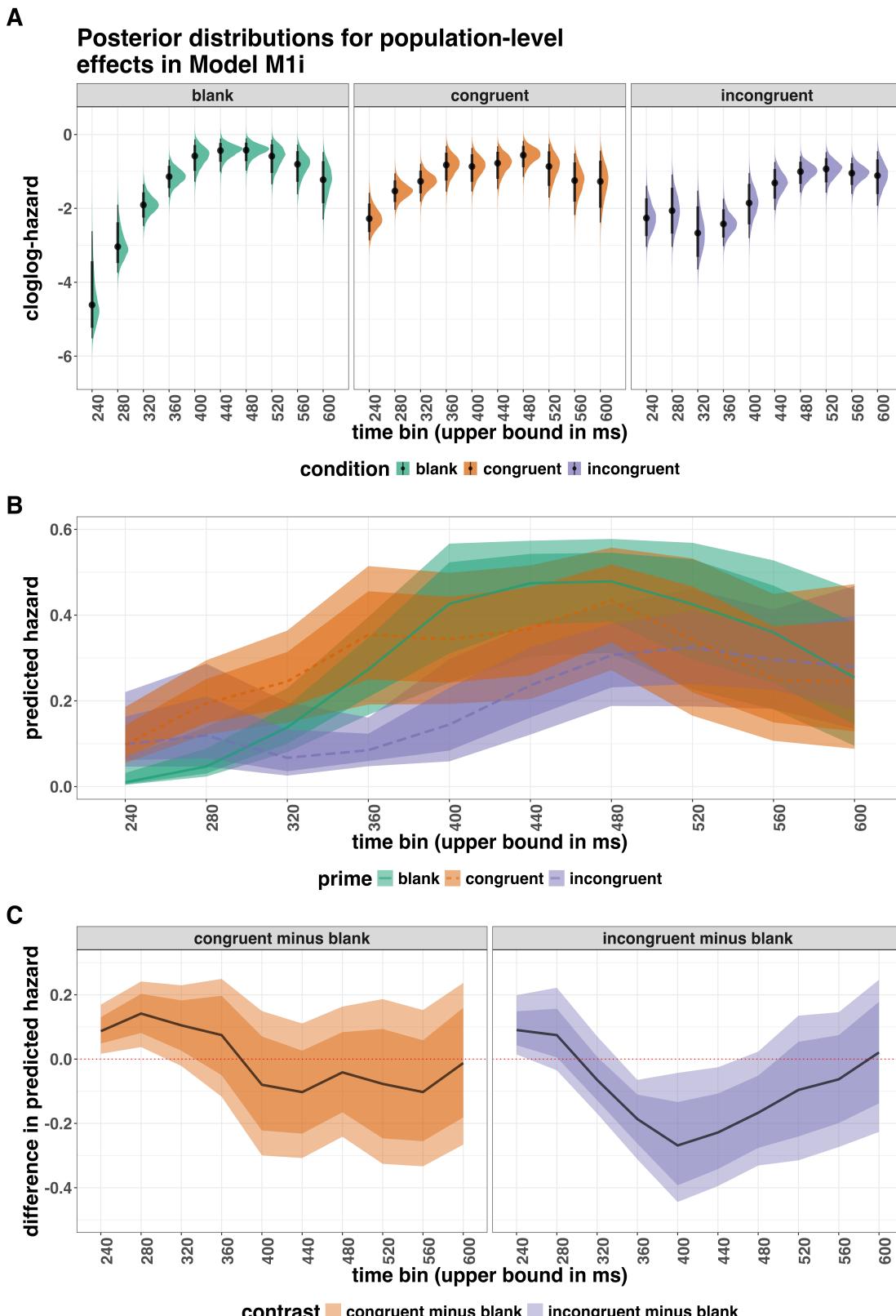
```
model_weights(model_M0i, model_M1i, weights = "waic") %>% round(digits = 1) %>% format(nsmall=2)
```

489 ## model\_M0i model\_M1i  
 490 ## "0.00" "1.00"

491       Clearly, both the loo and waic weighting schemes assign a weight of 1 to model M1i,  
 492 and a weight of 0 to model M0i.

493       **3.3.6 Evaluating parameter estimates in model M1i.** To make causal

494 inferences from the parameter estimates in model M1i (Frank et al., 2025), we first plot the  
 495 densities of the draws from the posterior distributions of its population-level parameters in  
 496 Figure 3A, together with point (median) and interval estimates (80% and 95% credible  
 497 intervals). A credible interval is a range of values that contains a parameter's true value  
 498 with a specified probability, given the observed data and model.



*Figure 3.* Discrete-time hazard modeling results at the population level. (A) Medians and 80/95% credible intervals of the posterior distributions of the population-level parameters of model M1i. (B) Point (median) and 80/95% credible interval summaries of the hazard estimates (expected values of the draws from the posterior predictive distributions) in each time bin. (C) Point (mean) and 80/95% credible interval summaries of estimated differences in hazard in each time bin.

499 Because the parameter estimates are on the cloglog-hazard scale, we can ease our  
500 interpretation by plotting the expected value of the posterior predictive distribution – the  
501 predicted hazard values – at the population level (Figure 3B). As we are actually interested  
502 in the effects of congruent and incongruent primes, relative to the blank prime condition,  
503 we can construct two contrasts (congruent-blank, incongruent-blank), and plot the  
504 posterior distributions of these contrast effects at the population level (Figure 3C). The  
505 point estimates and quantile intervals can also be reported in a table (see Tutorial\_2a.Rmd  
506 for details).

507 ***Example conclusions for M1i.*** What can we conclude from model M1i about  
508 our research question, i.e., the temporal dynamics of the effect of prime-target congruency  
509 on RT? In other words, in which of the 40-ms time bins between 200 and 600 ms after  
510 target onset does changing the prime from blank to congruent or incongruent affect the  
511 hazard of response occurrence (for a prime-target stimulus-onset-asynchrony of 187 ms)?

512 If we want to estimate the population-level effect of prime type on hazard, we can  
513 base our conclusion on the credible Intervals (CrIs) in Figure 3C. The contrast “congruent  
514 minus blank” was estimated to be 0.09 hazard units in bin 240 (95% CrI = [0.02, 0.17]),  
515 and 0.14 hazard units in bin 280 (95% CrI = [0.04, 0.25]). For the other bins, the 95%  
516 credible interval contained zero. The contrast “incongruent minus blank” was estimated to  
517 be 0.09 hazard units in bin 240 (95% CrI = [0.01, 0.21]), -0.19 hazard units in bin 360  
518 (95% CrI = [-0.31, -0.06]), -0.27 hazard units in bin 400 (95% CrI = [-0.45, -0.04]), and  
519 -0.23 hazard units in bin 440 (95% CrI = [-0.40, -0.03]). For the other bins, the 95%  
520 credible interval contained zero.

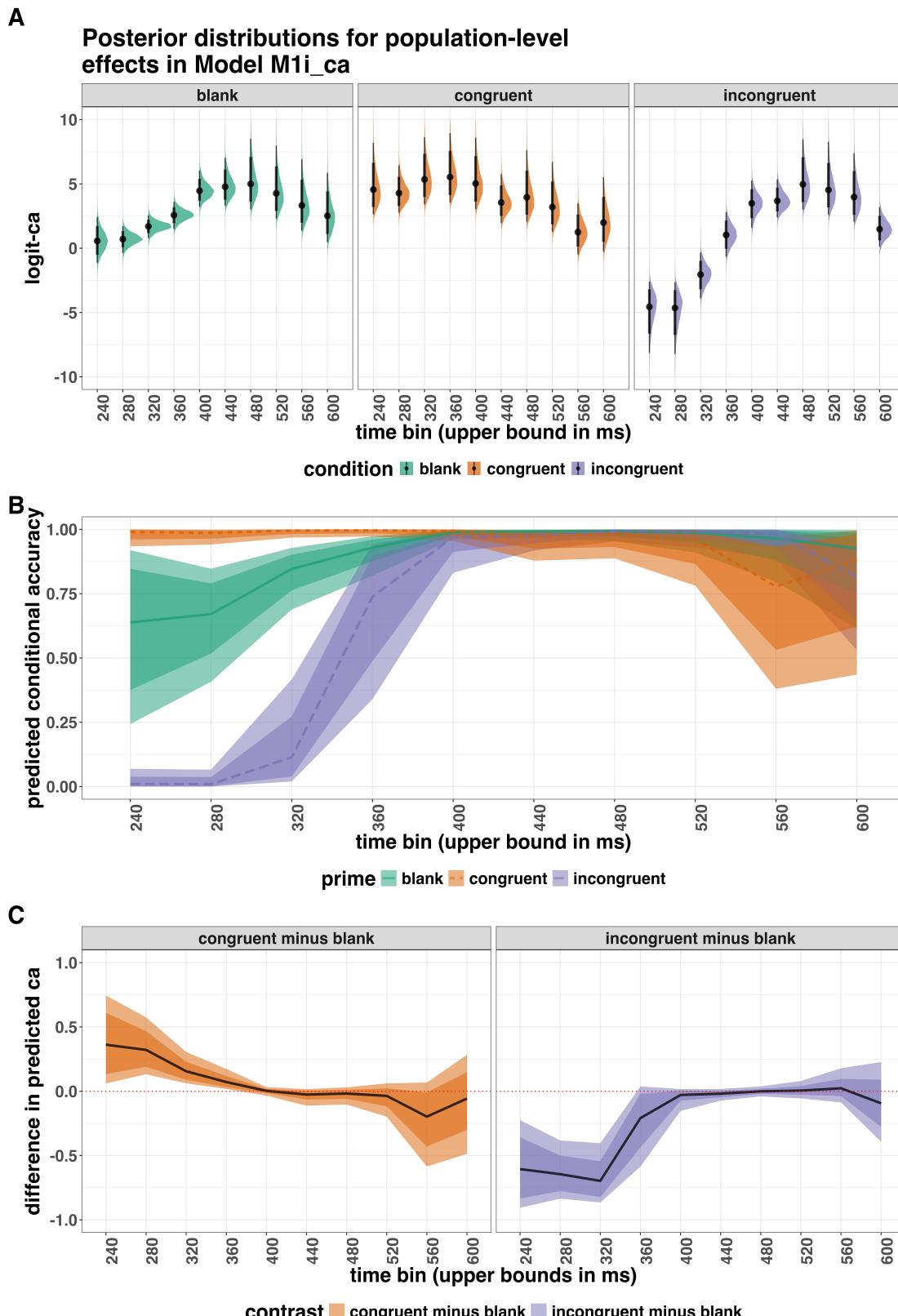
521 There are thus two phases of performance for the average person between 200 and  
522 600 ms after target onset. In the first phase, the addition of a congruent or incongruent  
523 prime stimulus increases the hazard of response occurrence compared to blank prime trials  
524 in time bin 240. In the second phase, only the incongruent prime decreases the hazard of  
525 response occurrence compared to blank primes, in the time period 320-440 ms. The sign of

526 the effect of incongruent primes on the hazard of response occurrence thus depends on  
527 how much waiting time has passed since target onset. Future modeling efforts could  
528 incorporate the trial number into the model formula, in order to also study how the effects  
529 of prime type on hazard change on the long experiment-wide time scale, next to the short  
530 trial-wide time scale. In Tutorial\_2a.Rmd we provide a number of model formulae that  
531 should get you going.

532 **3.4 Tutorial 2b: Fitting Bayesian conditional accuracy models**

533 In this fourth tutorial, we illustrate how to fit a Bayesian multilevel regression model  
534 to the timed accuracy data from the masked response priming data used in Tutorial 1a.  
535 The general process is similar to Tutorial 2a, except that (a) we use the person-trial data,  
536 (b) we use the symmetric logit link function, and (c) we change the priors (our prior belief  
537 is that conditional accuracy values between 0 and 1 are equally likely). To keep the tutorial  
538 short, we only fit one conditional accuracy model, which was based on model M1i from  
539 Tutorial 2a and labelled M1i\_ca.

540 To make inferences from the parameter estimates in model M1i\_ca, we first plot the  
541 densities of the draws from the posterior distributions of its population-level parameters in  
542 Figure 4A, together with point (median) and interval estimates (80% and 95% credible  
543 intervals).



*Figure 4.* Conditional accuracy modeling results at the population level. (A) Medians and 80/95% credible intervals of the posterior distributions of the population-level parameters of model M1i\_ca. (B) Point (median) and 80/95% credible interval summaries of the conditional accuracy (ca) estimates (expected values of the draws from the posterior predictive distributions) in each time bin. (C) Point (mean) and 80/95% credible interval summaries of estimated differences in conditional accuracy in each time bin.

544 Because the parameter estimates are on the logit-ca scale, we can ease our  
545 interpretation by plotting the expected value of the posterior predictive distribution – the  
546 predicted conditional accurcies – at the population level (Figure 4B). As we are actually  
547 interested in the effects of congruent and incongruent primes, relative to the blank prime  
548 condition, we can construct two contrasts (congruent-blank, incongruent-blank), and plot  
549 the posterior distributions of these contrast effects at the population level (Figure 4C).

550 Based on Figure 4C we see that on the population level congruent primes have a positive  
551 effect on the conditional accuracy of emitted responses in time bins 240, 280, 320, and 360,  
552 relative to the estimates in the baseline condition (blank prime; red dashed lines in Figure  
553 4C). Incongruent primes have a negative effect on the conditional accuracy of emitted  
554 responses in the first three time bins, relative to blank primes.

555 Finally, because many researchers will be more familiar with frequentist statistics, we  
556 also provide code to fit hazard and conditional accuracy models in the frequentist  
557 framework in Tutorial\_3a.Rmd and Tutorial\_3b.Rmd, using the R package lme4() (Bates  
558 et al., 2015).

### 559 3.5 Tutorial 4: Planning

560 In the final tutorial, we look at planning a future experiment, which uses EHA.

561 **3.5.1 Background.** The general approach to planning that we adopt here involves  
562 simulating reasonably structured data to help guide what you might be able to expect from  
563 your data once you collect it (Gelman, Vehtari, et al., 2020). The basic structure and code  
564 follows the examples outlined by Solomon Kurz in his ‘power’ blog posts  
565 (<https://solomonkurz.netlify.app/blog/bayesian-power-analysis-part-i/>) and Lisa  
566 Debruine’s R package faux{} (<https://debruine.github.io/faux/>), as well as these related  
567 papers (DeBruine & Barr, 2021; Pargent, Koch, Kleine, Lermer, & Gaube, 2024).

568 **3.5.2 Basic workflow.** The basic workflow is as follows:

- 569 1. Fit a regression model to existing data.
- 570 2. Use the regression model parameters to simulate new data.
- 571 3. Write a function to create 1000s of datasets and vary parameters of interest (e.g.,
- 572 sample size, trial count, effect size).
- 573 4. Summarise the simulated data to estimate likely power or precision of the research
- 574 design options.

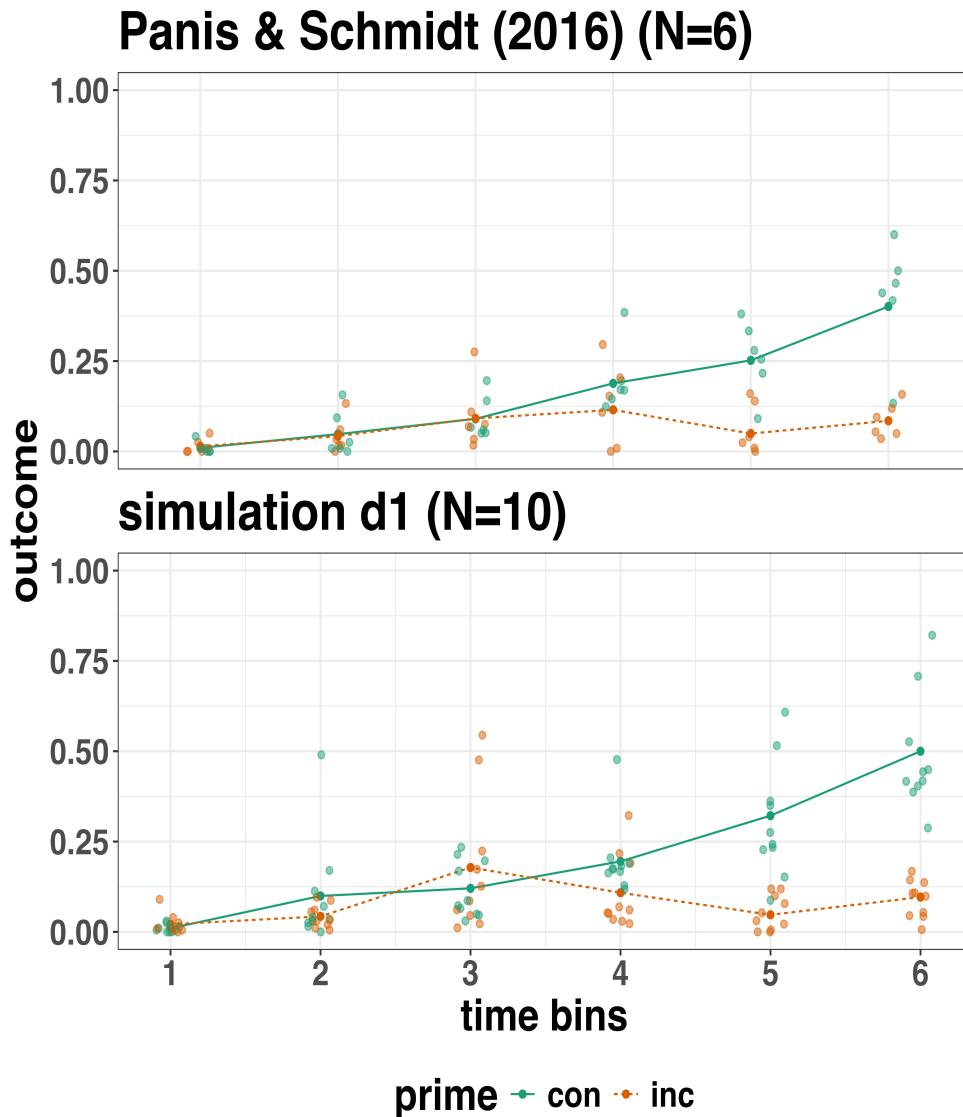
575 Ideally, in the above workflow, we would also fit a model to each dataset and  
 576 summarise the model output, rather than the raw data. However, when each model takes  
 577 several hours to build, and we may want to simulate many 1000s of datasets, it can be  
 578 computationally demanding for desktop machines. So, for ease, here we just use the raw  
 579 simulated datasets to guide future expectations.

580 In the below, we only provide a high-level summary of the process and let readers  
 581 dive into the details within the tutorial should they feel so inclined.

582 **3.5.3 Fit a regression model and simulate one dataset.** We again use the  
 583 data from Panis and Schmidt (2016) to provide a worked example. We fit an index coding  
 584 model on a subset of time bins (six time bins in total) and for two prime conditions  
 585 (congruent and incongruent). We chose to focus on a subsample of the data to ease the  
 586 computational burden. We also used a full varying effects structure, with the model  
 587 formula as follows:

```
event ~ 0 + timebin:prime + (0 + timebin:prime | pid)
```

588 We then took parameters from this model and used them to create a single dataset  
 589 with 200 trials per condition for 10 individual participants. The raw data and the  
 590 simulated data are plotted in Figure 5 and show quite close correspondence, which is  
 591 re-assuring. But, this is only one dataset. What we really want to do is simulate many  
 592 datasets and vary parameters of interest, which is what we turn to in the next section.



*Figure 5.* Raw data from Panis and Schmidt (2016) and simulated data from 10 participants.

### 593        3.5.4 Simulate and summarise data across a range of parameter values.

594        Here we use the same data simulation process as used above, but instead of simulating one  
 595        dataset, we simulate 1000 datasets per variation in parameter values. Specifically, in  
 596        Simulation 1, we vary the number of trials per condition (100, 200, and 400), as well as the  
 597        effect size in bin 6. We focus on bin 6 only, in terms of varying the effect size, just to make  
 598        things simpler and easier to understand. The effect size observed in bin 6 in this subsample  
 599        of data was a 79% reduction in hazard value from the congruent prime (0.401 hazard

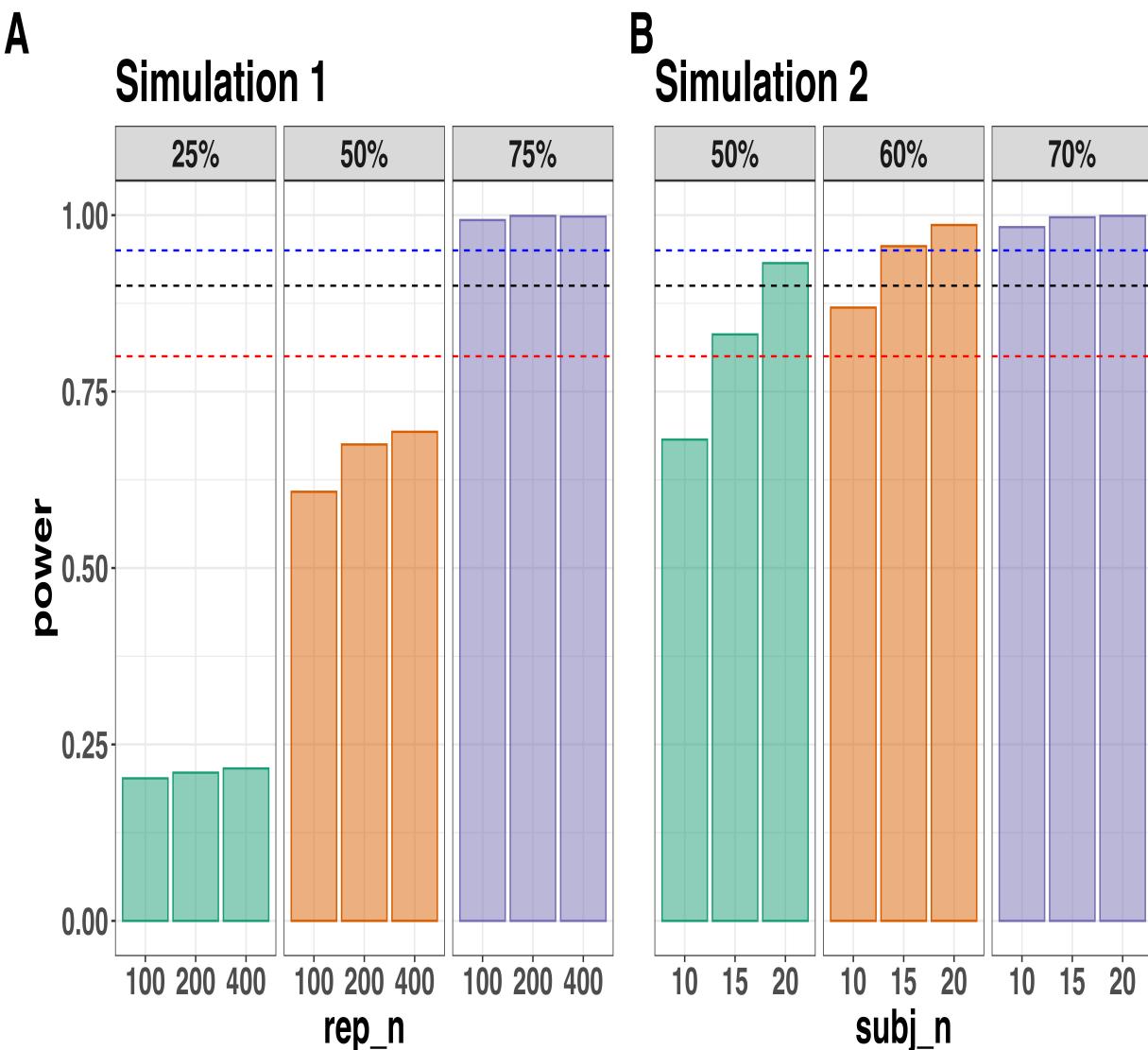
600 value) to the incongruent prime condition (0.085 hazard value). In other words, a hazard  
601 ratio of 0.21 (e.g.,  $0.085/0.401 = 0.21$ ). As a starting point, we chose three effect sizes,  
602 which covered a fairly broad range of hazard ratios (0.25, 0.5, 0.75), which correspond to a  
603 75%, 50% and 25% reduction in hazard value as a function of prime condition.

604 Summary results from Simulation 1 are shown in Figure 6A. Figure 6A depicts  
605 statistical “power” as calculated by the percentage of lower-bound 95% confidence intervals  
606 that exclude zero when the difference between prime condition is calculated (congruent -  
607 incongruent). In other words, we calculate the fraction of simulated datasets that  
608 generated an effect of prime that excludes the criterion mark of zero. We are aware that  
609 “power” is not part of a Bayesian analytical workflow, but we choose to include it here, as  
610 it is familiar to most researchers in experimental psychology.

611 The results of Simulation 1 show that if we were targeting an effect size similar to the  
612 one reported in the original study, then testing 10 participants and collecting 100 trials per  
613 condition would be enough to provide over 95% power. However, we could not be as  
614 confident about smaller effects, such as a hazard ratio of 50% or 25%. From this  
615 simulation, we can see that somewhere between an effect size of a 50% and 75% reduction  
616 in hazard value, power increases to a range that most researchers would consider  
617 acceptable (i.e., >95% power). To probe this space a little further, we decided to run a  
618 second simulation, which varied different parameters.

619 In Simulation 2, we varied the effect size between a different range of values (0.5, 0.4,  
620 0.3), which correspond to a 50%, 60% and 70% reduction in hazard value as a function of  
621 prime condition. In addition, we varied the number of participants per experiment between  
622 10, 15, and 20 participants. Given that trial count per condition made little difference to  
623 power in Simulation 1, we fixed trial count at 200 trials per condition in Simulation 2.  
624 Summary results from Simulation 2 are shown in Figure 6B. A summary of these power  
625 calculations might be as follows (trial count = 200 per condition in all cases):

- 626     • For a 70% reduction (0.3 hazard ratio), N=10 would give nearly 100% power.
- 627     • For a 60% reduction (0.4 hazard ratio), N=10 would give nearly 90% power.
- 628     • For a 50% reduction (0.5 hazard ratio), N=15 would give over 80% power.



*Figure 6.* Statistical power across data Simulation 1 (A) and Simulation 2 (B). Power was calculated as the percentage of lower-bound 95% confidence intervals that exclude zero when the difference between prime condition is calculated (congruent - incongruent). In Simulation 1, the effect size was varied between a 25%, 50% and 75% reduction in hazard value, whereas the trial count was varied between 100, 200 and 400 trials per condition (the number of participants was fixed at N=10). In Simulation 2, the effect size was varied between a 50%, 60% and 70% reduction in hazard value, whereas the number of participants was varied between N=10, 15 and 20 (the number of trials per condition was fixed at 200). The dashed lines represent 80% (red), 90% (black) and 95% (blue) power. Abbreviations: rep\_n = the number of trials per experimental condition; subj\_n = the number of participants per simulated experiment.

629       **3.5.5 Planning decisions.** Now that we have summarised our simulated data,

630 what planning decisions could we make about a future study? More concretely, how many

631 trials per condition should we collect and how many participants should we test? Like

632 almost always when planning future studies, the answer depends on your objectives, as well

633 as the available resources (Lakens, 2022). There is no straightforward and clear-cut answer.

634 Some considerations might be as follows:

- 635     • How much power or precision are you looking to obtain in this particular study?

- 636     • Are you running multiple studies that have some form of replication built in?

- 637     • What level of resources do you have at your disposal, such as time, money and

638 personnel?

- 639     • How easy or difficult is it to obtain the specific type of sample?

640       If we were running this kind of study in our lab, what would we do? We might pick a

641 hazard ratio of 0.4 or 0.5 as a target effect size since this is much smaller than that

642 observed previously (Panis & Schmidt, 2016). Then we might pick the corresponding

643 combination of trial count per condition (e.g., 200) and participant sample size (e.g., N=10

644 or N=15) that takes you over the 80% power mark. If we wanted to maximise power based

645 on these simulations, and we had the time and resources available, then we would test

646 N=20 participants, which would provide >90% power for an effect size of 0.5.

647       But, and this is an important caveat, unless there are unavoidable reasons, no matter

648 what kind of planning choices we made based on these data simulations, we would not

649 solely rely on data collected from one single study. Instead, we would run a follow-up

650 experiment that replicates and extends the initial result. By doing so, we would aim to

651 avoid the Cult of the Isolated Single Study (Nelder, 1999; Tong, 2019), and thus reduce the

652 reliance on any one type of planning tool, such as a power analysis. Then, we would look

653 for common patterns across two or more experiments, rather than trying to make the case

654 that a single study on its own has sufficient evidential value to hit some criterion mark.

655

#### 4. Discussion

656 This main motivation for writing this paper is the observation that EHA and SAT  
657 analysis remain under-used in psychological research. As a consequence, the field of  
658 psychological research is not taking full advantage of the many benefits EHA/SAT provides  
659 compared to more conventional analyses. By providing a freely available set of tutorials,  
660 which provide step-by-step guidelines and ready-to-use R code, we hope that researchers  
661 will feel more comfortable using EHA/SAT in the future. Indeed, we hope that our  
662 tutorials may help to overcome a barrier to entry with EHA/SAT, which is that such  
663 approaches require more analytical complexity compared to standard approaches. While  
664 we have focused here on within-subject, factorial, small- $N$  designs, it is important to realize  
665 that EHA/SAT can be applied to other designs as well (large- $N$  designs with only one  
666 measurement per subject, between-subject designs, etc.). As such, the general workflow  
667 and associated code can be modified and applied more broadly to other contexts and  
668 research questions. In the following, we discuss the main use-cases, issues relating to model  
669 complexity and interpretability, as well as limitations of the approach.

670 **4.1 What are the main use-cases of EHA for understanding cognition and brain  
671 function?**

672 For those researchers, like ourselves, who are primarily interested in understanding  
673 human cognitive and brain systems, we consider two broadly-defined, main use-cases of  
674 EHA. First, as we hope to have made clear by this point, EHA is one way to investigating  
675 a “temporal states” approach to cognitive processes, by tracking behavior as a function of  
676 step-wise increases in absolute waiting time. EHA thus provides a way to uncover the  
677 microgenesis of cognitive effects, by revealing when cognitive states may start and stop,  
678 how states are replaced with others, as well as what they may be tied to or interact with.  
679 Therefore, if your research questions concern **when psychological states occur, and**

680 **how they are temporally organized**, our EHA tutorials could be useful tools to use for  
681 basic knowledge development, as well as theory building.

682 Second, even if you are not primarily interested in studying the temporal organization  
683 of cognitive states, EHA could still be a useful tool to consider using, in order to qualify  
684 inferences that are being made based on comparisons between means. Given that distinctly  
685 different inferences can be made from the same data based on whether one computes a  
686 mean across trials or a RT distribution of events (Figure 1), it may be important for  
687 researchers to supplement comparisons between means with EHA. For instance, EHA  
688 might reveal that the conclusion of interest based on averaging across trials does not apply  
689 to all responses, but is instead restricted to certain periods of within-trial time.

## 690 4.2 Model complexity versus interpretability

691 Hazard and conditional accuracy models can quickly become very complex when  
692 adding more than one time scale, due to the many possible higher-order interactions. For  
693 example, some of the models discussed in Tutorial 2a, which we did not focus on in the  
694 main text, contain two time scales as covariates: the passage of time on the within-trial  
695 time scale, and the passage of time on the across-trial (or within-experiment) time scale.  
696 However, when trials are presented in blocks, and blocks of trials within sessions, and when  
697 the experiment comprises a number of sessions, then four time scales can be defined  
698 (within-trial, within-block, within-session, and within-experiment). From a theoretical  
699 perspective, adding more than one time scale – and their interactions – can be important  
700 to capture plasticity and other learning effects that may play out on such longer time  
701 scales, and that are probably present in each experiment in general (Schöner & Spencer,  
702 2016). From a practical perspective, therefore, some choices need to be made to balance  
703 the amount of data that is being collected per participant, condition and across the varying  
704 timescales. As one example, if there are several timescales of relevance, then it might be  
705 prudent for interpretational purposes to limit the number of experimental predictor

706 variables (conditions). This is of course where planning and data simulation efforts would  
707 be important to provide a guide to experimental design choices (see Tutorial 4 and section  
708 2.3).

709 **4.3 Limitations**

710 Compared to the orthodox method – comparing means between conditions – the  
711 most important limitation of multilevel hazard and conditional accuracy modeling is that it  
712 might take a long time to estimate the parameters using Bayesian methods or the model  
713 might have to be simplified significantly to use frequentist methods. Relatedly, as these  
714 models can be quite complex in terms of the number of possible parameters, more thought  
715 is required at the model specification and model building stages.

716 Another issue is that you need a relatively large number of trials per condition to  
717 estimate the discrete-time hazard function with relatively high temporal resolution (e.g., 20  
718 ms), which is required when testing predictions of process models of cognition. Indeed, in  
719 general, there is a trade-off between the number of trials per condition and the temporal  
720 resolution (i.e., bin width) of the discrete-time hazard function. Therefore, we recommend  
721 researchers to collect as many trials as possible per experimental condition, given the  
722 available resources and considering the participant experience (e.g., fatigue and boredom).  
723 For instance, if the maximum session length deemed reasonable is between 1 and 2 hours,  
724 what is the maximum number of trials per condition that you could reasonably collect?  
725 After consideration, it might be worth conducting multiple testing sessions per participant  
726 and/or reducing the number of experimental conditions. There is a user-friendly online tool  
727 for calculating statistical power as a function of the number of trials as well as the number  
728 of participants, and this might be worth consulting to guide the research design process  
729 (Baker et al., 2021). Finally, if you have a lot of repeated measurements per condition per  
730 participant, you can of course also try continuous-time methods (Allison, 2010; Elmer et  
731 al., 2023).

732

## 5. Conclusions

733       Estimating the temporal distributions of RT and accuracy provide a rich source of  
734      information on the time course of cognitive processing, which have been largely  
735      undervalued in the history of experimental psychology and cognitive neuroscience. We  
736      hope that by providing a set of hands-on, step-by-step tutorials, which come with  
737      custom-built and freely available code, researchers will feel more comfortable embracing  
738      EHA and investigating the shape of empirical hazard functions and the temporal profile of  
739      cognitive states. On a broader level, we think that wider adoption of such approaches will  
740      have a meaningful impact on the inferences drawn from data, as well as the development of  
741      theories regarding the structure of cognition.

742

**Author contributions**

743       Conceptualization: S. Panis and R. Ramsey; Software: S. Panis and R. Ramsey;  
744      Writing - Original Draft Preparation: S. Panis; Writing - Review & Editing: S. Panis and  
745      R. Ramsey; Supervision: R. Ramsey.

746

**Conflicts of Interest**

747       The author(s) declare that there were no conflicts of interest with respect to the  
748      authorship or the publication of this article.

749

**Prior versions**

750       All of the submitted manuscript and Supplemental Material was previously posted to  
751      a preprint archive: <https://doi.org/10.31234/osf.io/57bh6>

752

**Supplemental Material**

753

**Disclosures****754 Data, materials, and online resources**

755       Link to public archive:  
756      [https://github.com/sven-panis/Tutorial\\_Event\\_History\\_Analysis](https://github.com/sven-panis/Tutorial_Event_History_Analysis)  
757       Supplemental Material: Panis\_Ramsey\_suppl\_material.pdf

**758 Ethical approval**

759       Ethical approval was not required for this tutorial in which we reanalyze existing  
760      data sets.

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