A tutorial on Bayesian and Frequentist Event History Analyses for psychological

time-to-event data

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13   Abstract

14 Time-to-event data such as response times, saccade latencies, and fixation durations are

15 ubiquitous in experimental psychology. To move beyond mean performance measures,

16 various distributional analyses have been proposed. Here we focus on one particular

17 distributional analysis known as discrete-time event history analysis, a.k.a. hazard

18 analysis, duration analysis, failure-time analysis, survival analysis, and transition analysis.

19 Across four tutorials that we make publicly available on Github and OSF, we illustrate how

20 to calculate and interpret descriptive statistics, and how to implement Bayesian and

21 frequentist regression models, using the R packages tidyverse, brms, and lme4. Along the

22 way, we discuss how to manage inter-individual differences, implications for experimental

23 design, and how to select among various options when analysing time-to-event data using

24 discrete-time survival analysis.

25   *Keywords:* response times, event history analysis, Bayesian regression models

26   Word count: X

27   A tutorial on Bayesian and Frequentist Event History Analyses for psychological

28   time-to-event data

Introduction

30   In experimental psychology, it is still standard practice to analyse response times

31 (RTs), saccade latencies, and fixation durations using analysis-of-variance. However,

32 differences in means conceal when an experimental effect starts, how long it lasts, and

33 whether its onset is time-locked to other events. Such information is useful not only for

34 interpretation, but also for cognitive psychophysiology and computational model selection

35 (Panis, Schmidt, Wolkersdorfer, & Schmidt, 2020). In this tutorial we focus on a

36 distributional method for analyzing time-to-event data that is known as discrete-time event

37 history analysis (EHA), a.k.a. survival, hazard, duration, failure-time, and transition

38 analysis (Allison, 1982, 2010; Singer & Willett, 2003). Across four tutorials that we make

39 publicly available on Github and OSF, we illustrate how to calculate and interpret

40 descriptive statistics, and how to implement Bayesian and frequentist regression models,

41 using the R packages tidyverse, brms, and lme4.

42   To apply EHA, one must be able to define the event of interest (any qualitative

43 change that can be situated in time, e.g., a button press, saccade onset, fixation offset),

44 time point zero (e.g., target stimulus onset, fixation onset), and measure the passage of

45 time between time point zero and event occurrence in discrete or continuous time units.

46   The shape of a distribution of waiting times can be described in multiple ways (Luce,

47 1991). Let RT be a continous random variable denoting a particular person's response time

48 in a particular experimental condition. Because waiting times can only increase,

49 continuous-time EHA does not focus on the cumulative distribution function $F(t) = P(RT$

50 $\leq t)$ and its derivative, the probability density function $f(t) = F(t)'$, but on the survivor

51 function $S(t) = P(RT > t)$ and the hazard rate function $\lambda(t) = f(t)/S(t)$. The hazard rate

52 function gives you the instantaneous rate of event occurrence at time point t, given that

53 the event has not occurred yet.

54   Similarly, after dividing time in discrete, contiguous time bins indexed by t, let RT be

55 a discrete random variable denoting the rank of the time bin in which a particular person's

56 response occurs in a particular experimental condition. Discrete-time EHA focuses on the

57 discrete-time survivor function $S(t) = P(RT > t)$ and the discrete-time hazard function

58 $h(t) = P(RT = t| RT \geq t)$, and not on the probability mass function and the cumulative

59 distribution function. The discrete-time hazard probability function gives you the

60 probability that the event occurs (sometime) in bin t, given that the event has not

61 occurred yet in previous bins. For two-choice RT data, the discrete-time hazard function

62 can be extended with the conditional accuracy function $ca(t) = P(correct \mid RT = t)$, which

63 gives you the probability that a response is correct given that it has been emitted in time

64 bin t (Allison, 2010; Kantowitz & Pachella, 2021; Wickelgren, 1977). This latter function is

65 also known as the micro-level speed-accuracy tradeoff function.

66   Statisticians and mathematical psychologists recommend focusing on the hazard

67 function when analyzing time-to-event data for various reasons. First, as discussed by

68 Holden, Van Orden, and Turvey (2009), "probability density functions can appear nearly

69 identical, both statistically and to the naked eye, and yet are clearly different on the basis

70 of their hazard functions (but not vice versa). Hazard functions are thus more diagnostic

71 than density functions" (p. 331). Second, because RT distributions may differ from one

72 another in multiple ways, Townsend (1990) developed a dominance hierarchy of statistical

73 differences between two arbitrary distributions A and B. For example, if $F_A(t) > F_B(t)$ for

74 all t, then both cumulative distribution functions are said to show a complete ordering.

75 Townsend (1990) showed that a complete ordering on the hazard functions —$\lambda_A(t) > \lambda_B(t)$

76 for all t— implies a complete ordering on both the cumulative distribution and survivor

77 functions —$F_A(t) > F_B(t)$ and $S_A(t) < S_B(t)$— which in turn implies an ordering on the

78 mean latencies —mean A < mean B. In contrast, an ordering on two means does not imply

79 a complete ordering on the corresponding $F(t)$ and $S(t)$ functions, and a complete ordering

on these latter functions does not imply a complete ordering on the corresponding hazard functions. This means that stronger conclusions can be drawn from data when comparing the hazard functions using EHA. For example, when mean A < mean B, the hazard functions might show a complete ordering (i.e., for all t), a partial ordering (e.g., only for t > 300 ms, or only for t < 500 ms), or they may cross each other one or more times. Third, EHA does not discard right-censored observations when estimating hazard functions, that is, trials for which we do not observe a response during the data collection period so that we only know that the RT must be larger than some value. This is important because although a few right-censored observations are inevitable in most RT tasks, a lot of right-censored observations are expected in experiments on masking, the attentional blink, and so forth. Fourth, hazard modeling allows incorporating time-varying explanatory covariates such as heart rate, electroencephalogram (EEG) signal amplitude, gaze location, etc. (Allison, 2010) which is useful for cognitive psychophysiology (Meyer, Osman, Irwin, & Yantis, 1988). Finally, as explained by Kelso, Dumas, and Tognoli (2013), it is crucial to first have a precise description of the macroscopic behavior of a system (here: h(t) and ca(t) functions) in order to know what to derive on the microscopic level. For example, fitting parametric functions or computational models to data without studying the shape of the h(t) and ca(t) functions can miss important features in the data (Panis, Moran, Wolkersdorfer, & Schmidt, 2020; Panis & Schmidt, 2016).

We focus on factorial within-subject designs in which a large number of observations are made on a relatively small number of participants (small-N designs). This approach emphasizes the precision and reproducibility of data patterns at the individual participant level to increase the inferential validity of the design (Baker et al., 2021; Smith & Little, 2018). In contrast to the large-N design that averages across many participants without being able to scrutinize individual data patterns, small-N designs retain crucial information about the data patterns of individual observers. This is of great advantage whenever participants differ systematically in their strategies or in the time-courses of their

effects, so that blindly averaging them would lead to misleading data patterns. Indeed,

Smith and Little (2018) argue that, "if psychology is to be a mature quantitative science,

then its primary theoretical aim should be to investigate systematic functional

relationships as they are manifested at the individual participant level" (p. 2083). Note

that because statistical power derives both from the number of participants and from the

number of repeated measures per participant and condition, small-N designs can have

excellent power (Baker et al., 2021; Smith & Little, 2018).

We used R (Version 4.4.0; R Core Team, 2024)[1] for all reported analyses. Web links

are printed in bold.

Tutorial 1: Calculating descriptive statistics using a life table

To illustrate how to quickly set up life tables for calculating the descriptive statistics

(functions of discrete time), we use a published data set on masked response priming from

Panis and Schmidt (2016), available on **ResearchGate**. In their first experiment, Panis

and Schmidt (2016) presented a double arrow for 94 ms that pointed left or right as the

target stimulus with an onset at time point zero in each trial. Participants had to indicate

the direction in which the double arrow pointed using their corresponding index finger,

within 800 ms after target onset. Response time and accuracy were recorded on each trial.

Prime type (blank, congruent, incongruent) and mask type were manipulated. Here we

focus on the subset of trials in which no mask was presented. The 13-ms prime stimulus

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[1] We, furthermore, used the R-packages *citr* (Version 0.3.2; Aust, 2019), *dplyr* (Version 1.1.4; Wickham, François, Henry, Müller, & Vaughan, 2023), *forcats* (Version 1.0.0; Wickham, 2023a), *ggplot2* (Version 3.5.1; Wickham, 2016), *lubridate* (Version 1.9.3; Grolemund & Wickham, 2011), *papaja* (Version 0.1.2.9000; Aust & Barth, 2023), *patchwork* (Version 1.2.0; Pedersen, 2024), *purrr* (Version 1.0.2; Wickham & Henry, 2023), *RColorBrewer* (Version 1.1.3; Neuwirth, 2022), *readr* (Version 2.1.5; Wickham, Hester, & Bryan, 2024), *stringr* (Version 1.5.1; Wickham, 2023b), *tibble* (Version 3.2.1; Müller & Wickham, 2023), *tidyr* (Version 1.3.1; Wickham, Vaughan, & Girlich, 2024), *tidyverse* (Version 2.0.0; Wickham et al., 2019), and *tinylabels* (Version 0.2.4; Barth, 2023).

was a double arrow with onset at -187 ms for the congruent (same direction as target) and incongruent (opposite direction as target) prime conditions.

After loading in the data file, one has to (a) supply required column names, and (b) specify the factor condition with the correct levels and labels. The required column names are as follows:

- "pid", indicating unique participant IDs;

- "trial", indicating each unique trial per participant;

- "condition", a factor indicating the levels of the independent variable (1, 2, . . .) and the corresponding labels;

- "rt", indicating the response times in ms;

- "acc", inicating the accuracies (1/0).

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

```r
data_wr <- read_csv("../Tutorial_1_descriptive_stats/data/DataExp1_6subjects_wrangled.csv")
colnames(data_wr) <- c("pid","bl","tr","condition","resp","acc","rt","trial")
data_wr <- data_wr %>%
  mutate(condition = condition + 1, # original levels were 0, 1, 2.
         condition = factor(condition, levels=c(1,2,3), labels=c("blank","congruent","incongruent")))
```

To set up the life tables and plots of the discrete-time functions h(t), S(t) and ca(t) using functional programming, one has to nest the data within participants using the group_nest() function, and supply a user-defined censoring time and bin width to our function "censor()", as follows.

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

142 Note that the censoring time should be a multiple of the bin width (both in ms). The

143 censoring time should be a time point after which no informative responses are expected

144 anymore. In experiments that implement a response deadline in each trial the censoring

145 time can equal that deadline time point. Trials with a RT larger than the censoring time,

146 or trials in which no response is emitted during the data collection period, are treated as

147 right-censored observations in EHA. In other words, these trials are not discarded, because

148 they contain the information that the event did not occur before the censoring time.

149 Removing such trials before calculating the mean event time can introduce a sampling bias.

150 The person-trial-bin oriented dataset has one row for each time bin of each trial that is at

151 risk for event occurrence. The variable "event" in the person-trial-bin oriented data set

152 indicates whether a response occurs (1) or not (0) for each bin. When plotting the data,

153 some warning messages will be generated, like these:

154 - Removed 2 rows containing missing values or values outside the scale range
155   (`geom_line()`).
156 - Removed 2 rows containing missing values or values outside the scale range
157   (`geom_point()`).
158 - Removed 2 rows containing missing values or values outside the scale range
159   (`geom_segment()`).

160 The warning messages are generated because some bins have no hazard and ca(t)

161 estimates, and no error bars. They can thus safely be ignored. One can now inspect

162 different aspects, including the life table for a particular condition of a particular subject,

163 and a plot of the different functions for a particular participant.

164 Table 1 shows the life table for condition "blank" (no prime stimulus presented) -

165 compare to Figure 1. A life table includes for each time bin, the risk set (number of trials

166 that are event-free at the start of the bin), the number of observed events, and the

167 estimates of h(t), S(t), ca(t) and their estimated standard errors (se). At time point zero,

168 no events can occur and therefore h(t) and ca(t) are undefined.

169 Figure 1 displays the discrete-time hazard, survivor, and conditional accuracy

170 functions for each prime condition for participant 6. By using discrete-time h(t) functions

171 of event occurrence - in combination with ca(t) functions for two-choice tasks - one can

172 provide an unbiased, time-varying, and probabilistic description of the latency and

173 accuracy of responses based on all trials of any data set.

174 For example, for participant 6, the estimated hazard values in bin (240,280] are 0.03,

175 0.17, and 0.22 for the blank, congruent, and incongruent prime conditions, respectively. In

176 other words, when the waiting time has increased until *240 ms* after target onset, then the

177 conditional probability of response occurrence in the next 40 ms is more than five times

178 larger for both prime-present conditions, compared to the blank prime condition.

179 Furthermore, the estimated conditional accuracy values in bin (240,280] are 0.29, 1,

180 and 0 for the blank, congruent, and incongruent prime conditions, respectively. In other

181 words, if a response is emitted in bin (240,280], then the probability that it is correct is

182 estimated to be 0.29, 1, and 0 for the blank, congruent, and incongruent prime conditions,

183 respectively.

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

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

186 0.36, 0.25, and 0.07 for the blank, congruent, and incongruent prime conditions,

187 respectively. And when a response does occur in bin (400,440], then the probability that it

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

189 conditions, respectively.

Table 1

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

bin	risk_set	events	hazard	se_haz	survival	se_surv	ca	se_ca
0.00	219.00	NA	NA	NA	1.00	0.00	NA	NA
40.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
80.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
120.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
160.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
200.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
240.00	219.00	0.00	0.00	0.00	1.00	0.00	NA	NA
280.00	219.00	7.00	0.03	0.01	0.97	0.01	0.29	0.17
320.00	212.00	13.00	0.06	0.02	0.91	0.02	0.77	0.12
360.00	199.00	26.00	0.13	0.02	0.79	0.03	0.92	0.05
400.00	173.00	40.00	0.23	0.03	0.61	0.03	1.00	0.00
440.00	133.00	48.00	0.36	0.04	0.39	0.03	0.98	0.02
480.00	85.00	37.00	0.44	0.05	0.22	0.03	1.00	0.00
520.00	48.00	32.00	0.67	0.07	0.07	0.02	1.00	0.00
560.00	16.00	9.00	0.56	0.12	0.03	0.01	1.00	0.00
600.00	7.00	4.00	0.57	0.19	0.01	0.01	1.00	0.00

Note. The column named "bin" indicates the endpoint of each time bin (in ms), and includes time point zero. For example the first bin is (0,40] with the starting point excluded and the endpoint included. se = standard error. ca = conditional accuracy.
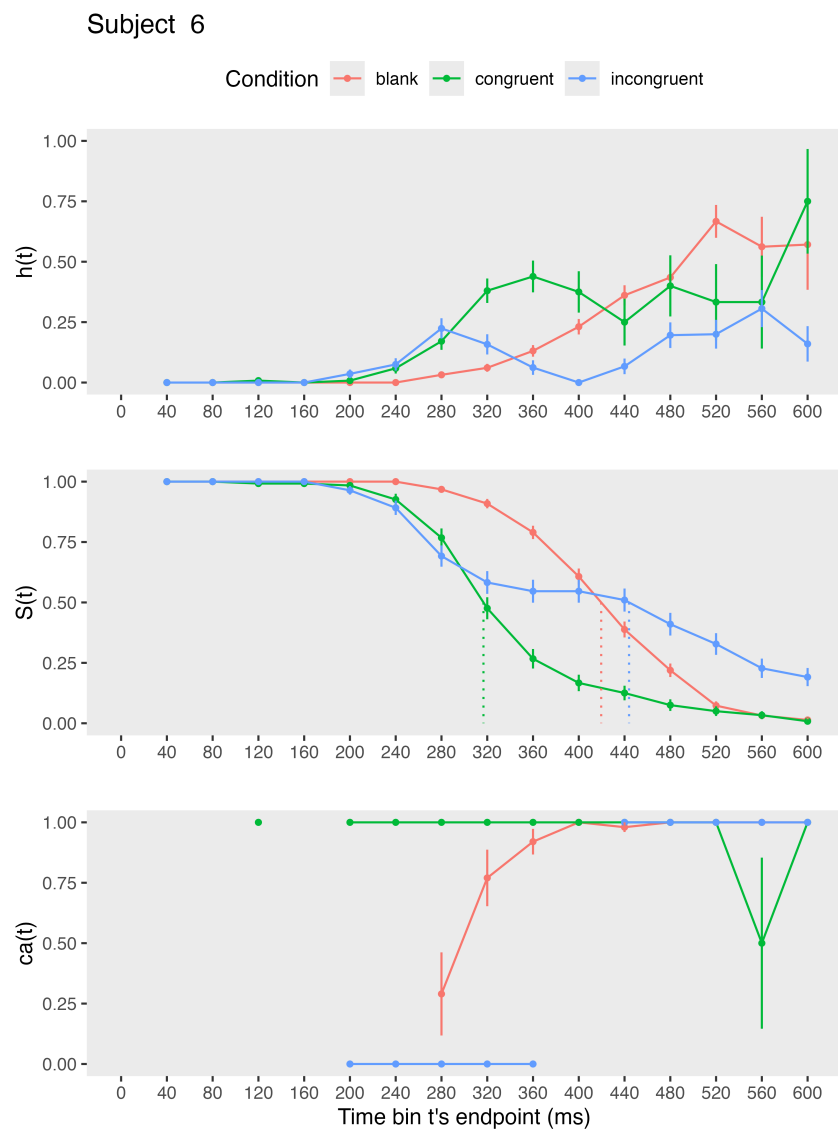
Figure 1. Estimated discrete-time hazard, survivor, and conditional accuracy functions for participant 6, as a function of the passage of discrete waiting time.

These results show that this participant is initially responding to the prime even though (s)he was instructed to only respond to the target, that response competition emerges in the incongruent prime condition around 300 ms, and that only later response are fully controlled by the target stimulus. Qualitatively similar results were obtained for the other five participants. Also, in their second Experiment, Panis and Schmidt (2016)

195 showed that the negative compatibility effect in the mask-present conditions is time-locked

196 to mask onset. This example shows that a simple difference between two means fails to

197 reveal the dynamic behavior people display in many experimental paradigms (Panis, 2020;

198 Panis, Moran, et al., 2020; Panis & Schmidt, 2022; Panis, Torfs, Gillebert, Wagemans, &

199 Humphreys, 2017; Panis & Wagemans, 2009; Schmidt, Panis, Wolkersdorfer, & Vorberg,

200 2022). In other words, statistically controlling for the passage of time during data analysis

201 is equally important as experimental control during the design of an experiment, to better

202 understand human behavior in experimental paradigms. As we will show in Tutorials 2 and

203 3, statistical models for h(t) and ca(t) can each be implemented as generalized linear mixed

204 regression models predicting event occurrence (1/0) and response accuracy (1/0) in each

205 bin of a selected time range, respectively.

Tutorial 2: Fitting Bayesian hazard models

207 In this second tutorial we illustrate how to fit a Bayesian hazard regression model for

208 the data set used in the first tutorial.

Tutorial 3: Fitting Frequentist hazard models

210 In this third tutorial we illustrate how to fit a frequentist hazard regression model for

211 the data set used in the first tutorial.

Tutorial 4: Calculating descriptive statistics when there are two independent variables

214 In this final tutorial we illustrate how to calculate and plot the descriptive statistics

215 for the full data set of Experiment 1 of Panis and Schmidt (2016).

216   **Discussion**

217   **Individual differences**

218   • role of response deadlines, low-level vs. higher-level processes,

219   • clustering algorithms based on h(t) and ca(t) data

220   •

221   **Cognitive psychophysiology and computational model selection**

222   **Power analysis**

223   • example repo on github

224   **Preregistration**

225   • example preregistration for knot data

226   **Conclusions**

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