Supplemental Materials

Signal Detection Theory (SDT)

SDT has been used to analyze data from a wide variety of decision contexts, such as clinical diagnosis, detection of a plane on a radar screen, and eye-witness testimony. In this chapter, I only discuss the use of SDT to analyze the results of recognition memory studies, but the results are easily generalizable to other decision contexts. When applied to the results of a "yes"-"no" recognition memory experiment, SDT estimates latent parameters representing memory sensitivity and response bias from observed data. This section of Supplemental Materials shows how to derive the equations needed to estimate a measure of memory sensitivity, d', and a measure of response bias, *c-centered*, from hit and false alarm rates for the equal-variance, Gaussian model. On a recognition test, hits occur when participants say they recognize a test item that they did study (targets); false alarms occur when participants say they recognize a test item that they did not study (foils). For general discussions of SDT sensitivity and bias measures see Macmillan & Creelman (2005) and Wickens (2002).

The estimation process requires a model that relates the observed hits and false alarms to the unobserved measures of memory sensitivity and response bias. Neuropsychologists commonly use the equal-variance Gaussian model to estimate $d'$and *c-centered* respectively, which is the model discussed here. Assume participants study 100 abstract pictures for which their memory is immediately tested by a mixture of 100 pictures studied (targets) and 100 pictures not studied (foils). During the test phase of the task, participants see one test picture at a time and are instructed to respond "yes" if they believe the test picture was one they previously studied and "no" otherwise. The SDT model assumes that when a test picture is presented it elicits an episodic-memory familiarity experience. It is further assumed that there exists a

function that maps these familiarity experiences onto quantitative familiarity values, X_f for foils and X_t for targets. When distributions of X_f and X_t overlap, recognition memory is less than perfect.

The equal-variance SDT model described below makes these additional assumptions:

1. The familiarity values, X_f and X_t vary along a single familiarity dimension.
2. Variations in the unobserved values X_f and X_t are normally distributed.
3. The noise distribution has a mean = 0 and a standard deviation = 1.
4. Variance for the target distribution equals the variance for the foil distribution
5. A participant responds "yes" if the familiarity value for a test picture exceeds a criterion threshold (C).

Given the assumptions, the location of X_f and X_t along the familiarity axis can be mapped to z-score values.

Figure 1 presents a visual representation of this model. As can be seen, the memory sensitivity parameter, d', is the mean of the target distribution, as well as the distance between the foil mean and the target mean. The response criterion, *C*, is represented by the solid line. Familiarity values above *C* elicit a "yes" response, indicating that the participant believed the test item was a target; those below elicit a "no" response, indicating a foil. Foil values exceeding *C* are false alarms with a rate represented by the crossed hatched lines. Target values exceeding *C* are hits with a rate represented by the sum of the tilted and cross hatched lines. The dotted line, being centered half-way between the foil and target means, represents an unbiased threshold criterion because the two types of errors, false alarms and misses, are equal. The distance between *C* and the unbiased criterion line is the bias parameter, *c-centered*. When *c-centered* is greater than the unbiased criterion, the participant is responding conservatively. When *c*-

centered is below the unbiased criterion, the participant is responding liberally. The distance between the mean of the foil distribution and the mean of the target distribution can be divided into the distance from the mean of the foil distribution to *C* , i.e., d_1, and the distance from *C* to the mean of the target distribution, i.e., d_2, such that $d' = d_1 + d_2$.

A challenge to deriving the equations for $d'$and *c-centered* from the hit and false alarm rates is that the rates are defined as areas towards the right tail of the normal distribution, i.e., areas above the criterion *C*. However, typically, cumulative probability tables for the normal distribution use areas that accumulate from the left tail, giving areas below a particular z-value. Moreover, some statistics text books only provide z-values above a probability of .50 and rely on the symmetry of the normal distribution to convey z-values for probabilities below .50. The differences between the definition of hits and false alarms and standard cumulative normal probability tables complicate calculation of d' and *c-centered* from hits and false alarms.

To relate hit rates (HR) and false alarm rates (FA) to z-values from a standard cumulative normal probability table, we need to calculate z(1- FA), the area under the foil curve below the threshold *C*, and z(1-HR), the area under the target curve below *C* (See Figure 1). Moreover, because z(1-p) = -z(p), given the symmetry of the normal probability distribution, the transformations z(1-FA) = -z(FA) and z(1-HR) = -z(HR) will relate Hits and False Alarms to z-values from a standard cumulative normal probability table.

Consider the results from a single participant whose hit rate was 0.575 and a false alarm rate of 0.210. So, 21% of the foil distribution is above the criterion threshold, *C*, or equivalently 79% falls below *C*. In this case, what is the z-value of *C*? Examining Figure 2 will help answer this question. Figure 2A shows the false alarm rate represented by an area exceeding an unknown z-value representing the response criterion, C. Because of the symmetry of the normal

distribution, this area can be reflected into the left tail of the normal distribution. Using a standard software tool that converts p-values to z-values, such PlanetCalc's *Z-score from P-value* online calculator (https://planetcalc.com/7803/), we see that p = .210 corresponds to the z-value= -.81, as shown in Figure 2B. Thus, 21% of the normal distribution falls .81 standard deviations below the mean of the foil distribution. Recall that 79% of the normal distribution fell below *C* (Figure 2C). Given that z(1 – FA) = -z(FA), the unknown value of criterion *C* must be -(-.81) = .81 standard deviations from the mean of the foil distribution (Figure 2C). More simply, z(1.00 - .21) = -z(.21) = -(-.81) = .81, which equals d_1. In general, $|C - 0| = d_1$ and *C* = -z(FA).

Now consider the z-value of the criterion *C* in relation to the target distribution. By the argument described for the foil distribution, z(1-HR) = -z(HR). So, z(1.00 – 0.575) = -z(0.575) = -.19. The criterion threshold *C* is .19 units from the mean of the target distribution, i.e. $|C - d'| = d_2$. Now we can estimate d':

$$d' = d_1 + d_2 = .81 + .19 = 1.00.$$

Notice in the discussion above, z(1-HR) = -z(HR) = $C - d'$. Multiplying both sides of the second equality by -1 yields $d' - C$ = z(HR). Recall $C = -$ z(FA), so d' + z(FA) = z(HR), implying

$$d' = z(HR) - z(FA).$$

Using the above formula to calculate d'in our example and taking the z-values from a standard cumulative normal probability table:

z(.575) = .19 and z(.210) = -.81. So, $d' = .19 - (-.81) = 1.00$.

See Macmillan & Creelman (2005) and Wickens (2002) for further comments and examples.

As shown in Figure 1, *c_centered* is the distance between the response criterion *C* and the half way point between the foil and target distributions: *c_centered* = $C - \frac{d'}{2}$. Substituting -z(FA)

for C and z(HR) – z(FA) for d' yields *c_centere*d = -Z(FA) – 0.5[z(HR) – Z(FA)] = -0.5z(FA) - 0.5z(HR).

$$c\_centered = -0.5[(z(FA) + z(HR)].$$

As with the derivation of d', see Macmillan & Creelman (2005) and Wickens (2002) for further comments and examples.

The equations for d' and *c_centered* presented above assume the z-values for the hit rate and false alarms are obtained from a cumulative normal probability table, where the area under the curve accumulates from the left-hand tail of the normal curve towards a z-value on the right. Because the hit rate and false alarm rate correspond to areas of the normal probability distribution above the criterion threshold *C,* some authors provide equations for d' and *c_centered* based on the assumption that the z-values in their equations refer to areas of the normal curve that accumulate from the right-hand tail of the normal distribution towards the criterion threshold *C* (e. g. Snodgrass & Corwin, 1988). When right tailed normal values are used, the formulas for d' and *c_centered* provided above must be multiplied by -1 to give the correct values. The PlanetCalc calculator provides left-tailed and right-tailed z-values for the cumulative normal distribution. It can be used to show that the two different sets of equations used to define d' and *c_centered* yield the same values.

Diffusion Model

Ratcliff's diffusion model (DM) is a popular approach to model accuracy and response time jointly (Ratcliff, Smith, Brown, & McKoon, 2016). The two-choice diffusion model assumes that people accumulate noisy information about perception or memory from a starting point until one of two threshold boundaries is reached – leading to a two-choice decision (Metin, et al., 2003; Ratcliff & Tuerlinck, 2002). As shown in Figure 3, the model assumes that the total

response time from the presentation of a stimulus to a response unfolds in a series of three stages, representing the time needed to encode the stimulus, the time to reach a decision and the time to make a response. The DM models Non-decision Time separately from Decision Time, with T_{er} typically interpreted as the mean Non-decision time summed over the encoding and response times (Figure 4). The parameter st_{er} is the range of T_{er}, which determines its trial to trial variability.

Figure 5 displays the working of the decision stage. The model assumes that information accumulates at a particular rate until one of two decision boundaries is reached. Accumulation rates for different trials are represented by the arrows in Figure 5. The trial by trial variation in evidence accumulation slope is assumed to follow a normal distribution with a mean slope, v, and its variance, s_v^2. The decision boundaries are abstract and may represent any clear binary choice, such as the decision "word" or "non-word" in a lexical decision task, "tone present" or "tone absent" in a tone detection task, or "yes" or "no" when recognizing a suspect in a police lineup. If the lower boundary is assumed to be 0, the distance between the two boundaries on the accumulated evidence axis is a. The boundary width, a, is constant across trials.

Notice in Figure 5, all arrows start at the same point on the accumulated evidence axis as indicated by parameter Z. However, Z may vary from trial to trial over the range s_z. When Z $=\frac{a}{2}$, the decision process is not biased towards either of the decision boundaries. When, as in Figure 6, Z is either 0 ater than or less th ∞ , the decision process is biased towards one or the other decision boundary. When the evidence drives the decision towards the upper boundary, Z values greater than $\frac{a}{2}$ will speed the decision, whereas values less than $\frac{a}{2}$ will slow the decision, given a constant slope as indicated in Figure 6.

The variability parameters described so far, st_{er}, s_v, and s_z, all account for trial-to-trial

variation. The final parameter, *s*, governs moment to moment variation in the slope within a trial (Figure 7). Prior to fitting a DM to data, an investigator must give the intra-trial variability parameter, *s*, a specific value in order to scale the other DM parameters (Farrell & Lewandowsky, 2018; Ratcliff & Tuerlinck, 2002). Typical values for *s* are 0.1 and 1.0. Given within trial variation, smaller values of the boundary separation parameter, *a*, could lead to fast but incorrect responses. Figure 7A shows a diffusion path operating over a wide boundary separation range and leading to a correct response. Figure 7B shows that by narrowing the boundary separation, the same diffusion path reaches a quick but inaccurate decision. On other trials, DM may predict quick and accurate decisions.

Notice in Figure 5, as the evidence accumulation slopes increase in absolute value, they come closer to converging with the accumulated evidence axis, while their projection onto the decision time line becomes closer to but never goes below zero. On the other hand, there is no upper limit to how slow the decision time might be. This DM property implies that response times produced by DM should be positively skewed. Figure 8 shows the response time distribution over trials for a diffusion model of recognition memory. Response times were simulated using the diffusion parameter values and R code available in Farrell & Lewandowsky (2018). A circle represents a single response time for each of 1000 simulated trials. The prediction of positive skew can be seen in the figure, especially in the histogram, which displays frequency counts for the 50 response time bins. That DM predicts the positive skew often seen in empirical response times supports DM's representational construct validity.

Software for Computational Models of Cognition and Behavior

The software listed below was available as of May, 2020. Some sites update their software to increase the scope or efficiency of application or to fix bugs. Because software bugs

are common, those sites that have an explicit process to update software when bugs are found are likely to have the more trustworthy software.

Signal Detection Theory(SDT)

MatLab function for SDT analyses: dprime.m

https://www.mathworks.com/matlabcentral/fileexchange/65377-sensitivity-index-d

The dprime.m function calculates d' and c (i.e., *c-centered*) for an equal variance SDT model (Böckmann-Barthel, 2020).

R packages for SDT analyses and much more: psycho.R and neuropsychology.R

https://cran.r-project.org/package=psycho

Also see:

https://github.com/neuropsychology/neuropsychology.R

Both packages are designed for neuropsychological research. The dprime routine included in these packages computes SDT indices: d', c, β, A', and B''. The package *psycho.R* also provides data from various projects, several methods for managing single subject data, routines to generate combinations of predictors from a formula, power analysis, and various other transformations and routines (Makowski, 2018). The package *neuropsychology.R* includes the dprime routine but also routines to prepare tables and graphs for output and to aid the interpretation of the Akaike Information Criterion and the Bayesian Information Criterion, as well as various transformations and R utilities (Makowski, 2016).

Multinomial Processing Tree Modeling

R package for multinomial processing tree modeling: MPTinR

https://cran.r-project.org/web/packages/MPTinR/index.html

MPTinR calculates the Fisher information approximation measure of model complexity for MPT

models, fits models for categorical data outside the MPT model class and provides a function for model selection for either nested or non-nested models (Singmann & Kellen, 2013)

Diffusion modeling

R package: rtdists

https://cran.r-project.org/package=rtdists

The R package *rtdists* calculates response time distributions for diffusion models and for linear ballistic accumulator models (maintained by Henrik Singmann <singmann@gmail.com>). In the *rtdists* package, the parameterization of st_{er} is different from what is typically found in the literature (Package 'rtdists', March 6, 2020). Consult Farrell & Lewandowski (2018) for examples of *rtdists* applications.

References for Supplemental Materials

Böckmann-Barthel, M. (2020). Sensitivity index d'.MATLAB Central File Exchange. Retrieved May 12, 2020.

Farrell, S., & Lewandowsky, S. (2018). *Computational modeling of cognition and behavior*. Cambridge University Press. http://link.springer.com/article/10.3758/s13428-012-0259-0

Macmillan, N.A., & Creelman, C. D. (2005). *Detection theory: A users guide* (2nd Ed.). Lawrence Erlbaum Associates.

Makowski, D. (2016). Package 'neuropsychology': An R toolbox for psychologists, neuropsychologists and neuroscientists. Available from https://github.com/neuropsychology/neuropsychology.R

Makowski, D. (2018). The Psycho Package: An efficient and publishing-oriented workflow for psychological science. *Journal of Open Source Software*, 3(22), 470. https://doi.org/10.21105/joss.00470

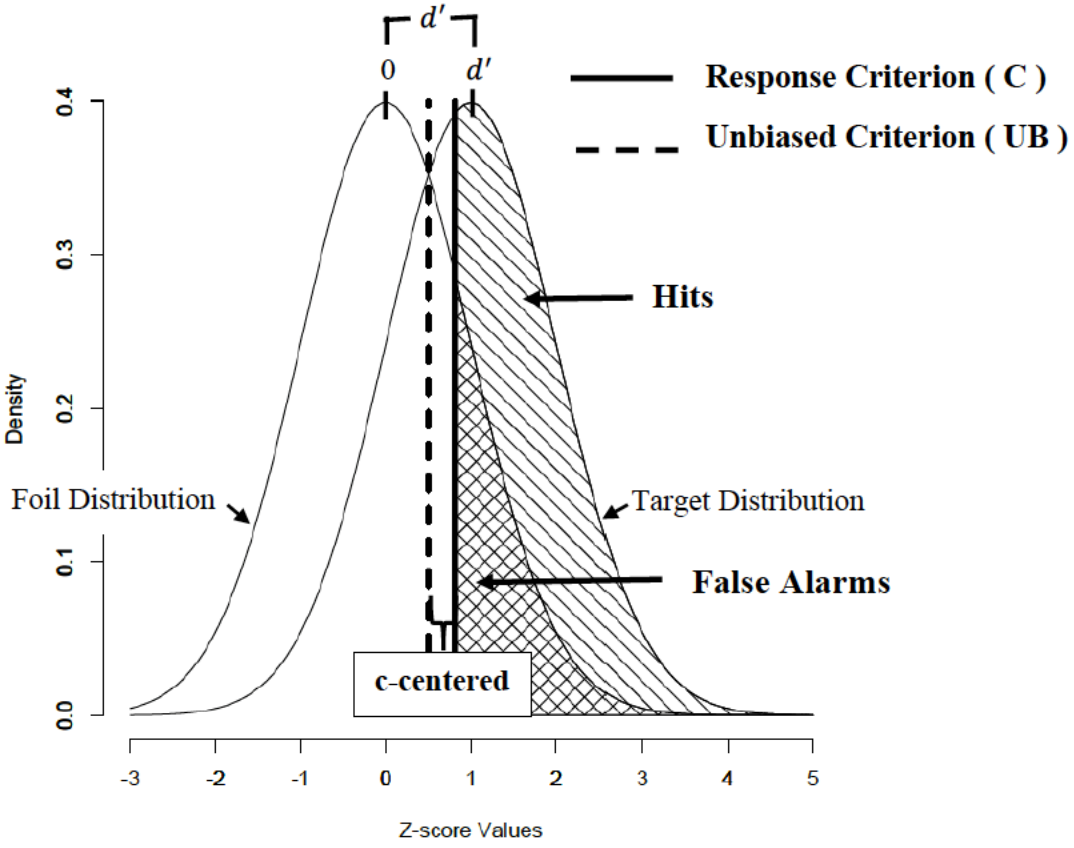
Ratcliff, R., Smith, P. L., Brown, S. D., McKoon, G. (2016). Diffusion decision model: Current issues and history. *Trends in Cognitive Sciences*, 20(4), 260-281. https://doi.org/10.1016/j.tics.2016.01.007.

Singmann, H. & Kellen, D> (2013). MPTinR: Analysis of multinomial processing tree models in R. *Behavior Research Methods*, 45(2), 560–575. https://doi.org/10.3758/s13428-012-0259-0

Snodgrass, J. G., & Corwin, J. (1988). Pragmatics of measuring recognition memory: Applications to dementia and amnesia. *Journal of Experimental Psychology: General*, 117(1), 34-50.

Wickens, T. D. (2002). *Elementary signal detection theory.* Oxford University Press.

Figure 1



The UB line is located at $\frac{d'}{2}$, i.e., half-way between the target and foil distributions.

Figure 2

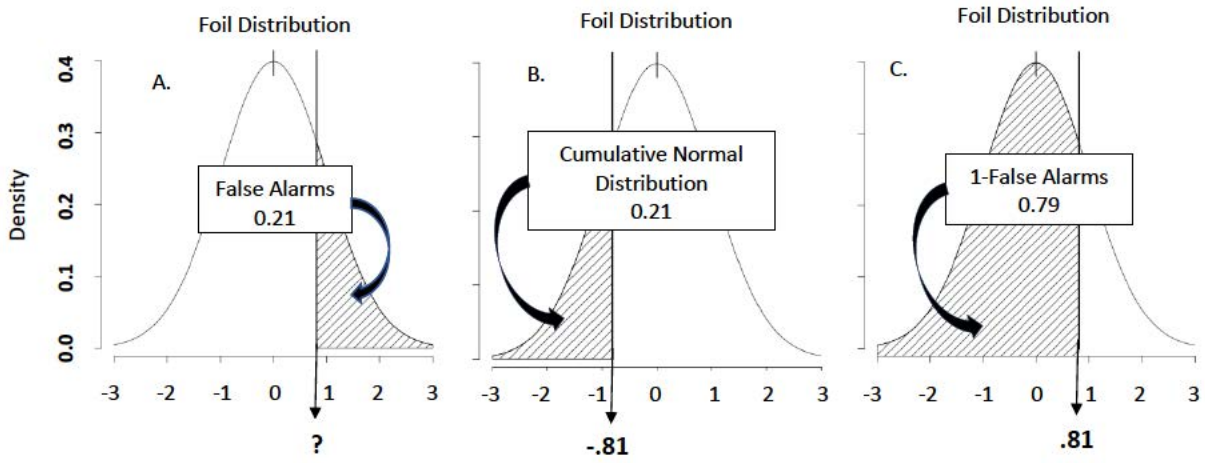

Foil Distribution
A.
Density
0.0
0.1
0.2
0.3
0.4
False Alarms
0.21
-3 -2 -1 0 1 2 3
?
Foil Distribution
B.
Cumulative Normal
Distribution
0.21
-3 -2 -1 0 1 2 3
-.81
Foil Distribution
C.
1-False Alarms
0.79
-3 -2 -1 0 1 2 3
.81

Figure 3

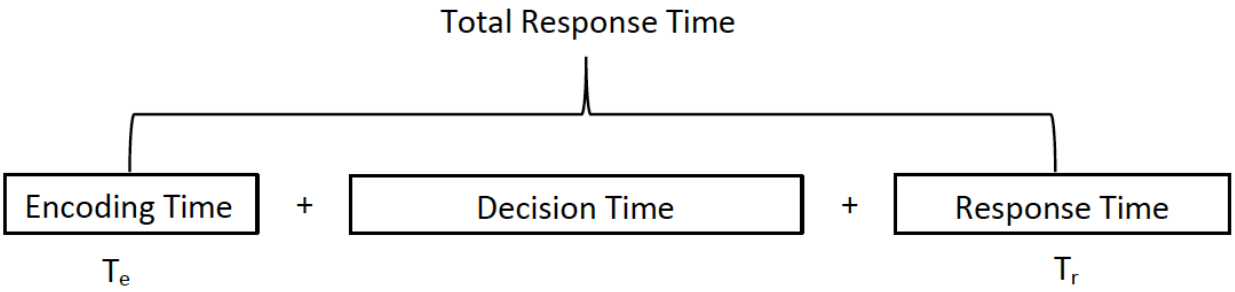

Total Response Time
Encoding Time
+
Decision Time
+
Response Time
T_e
T_r

Figure 4

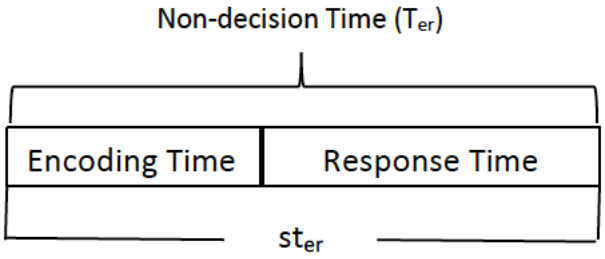


Figure 5

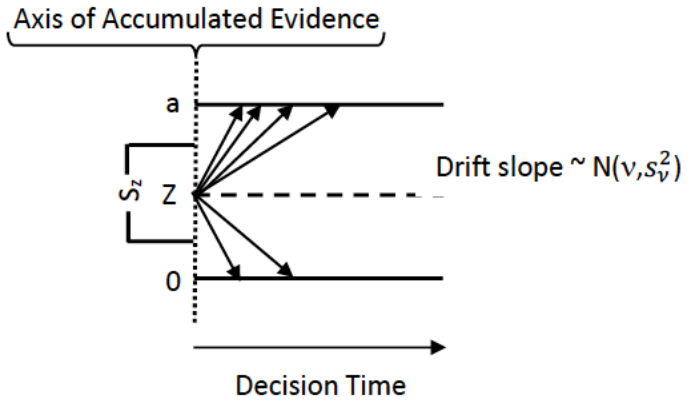

Axis of Accumulated Evidence
a
Z
0
S_z
Drift slope ~ N(ν,s_ν^2)
Decision Time

Figure 6

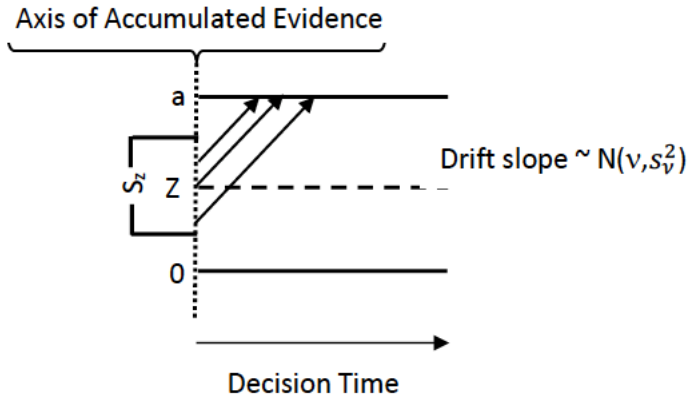

Axis of Accumulated Evidence
a
Drift slope ~ N(ν,$s_ν^2$)
S_z
Z
0
Decision Time

Figure 7A and 7B

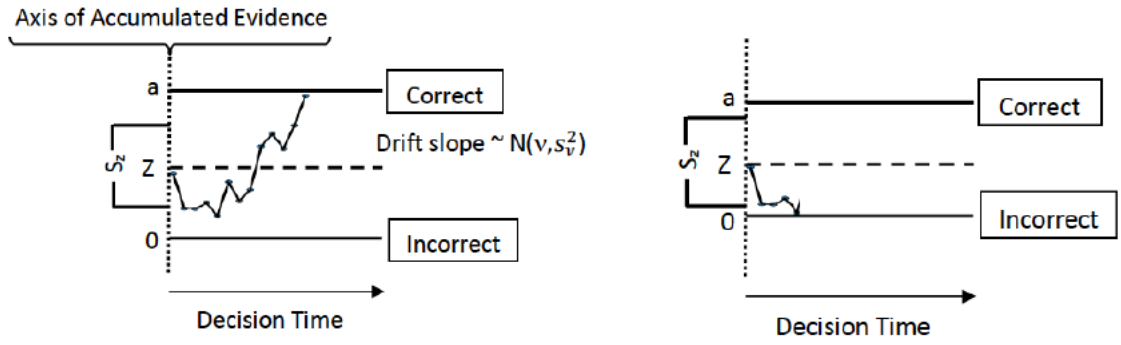
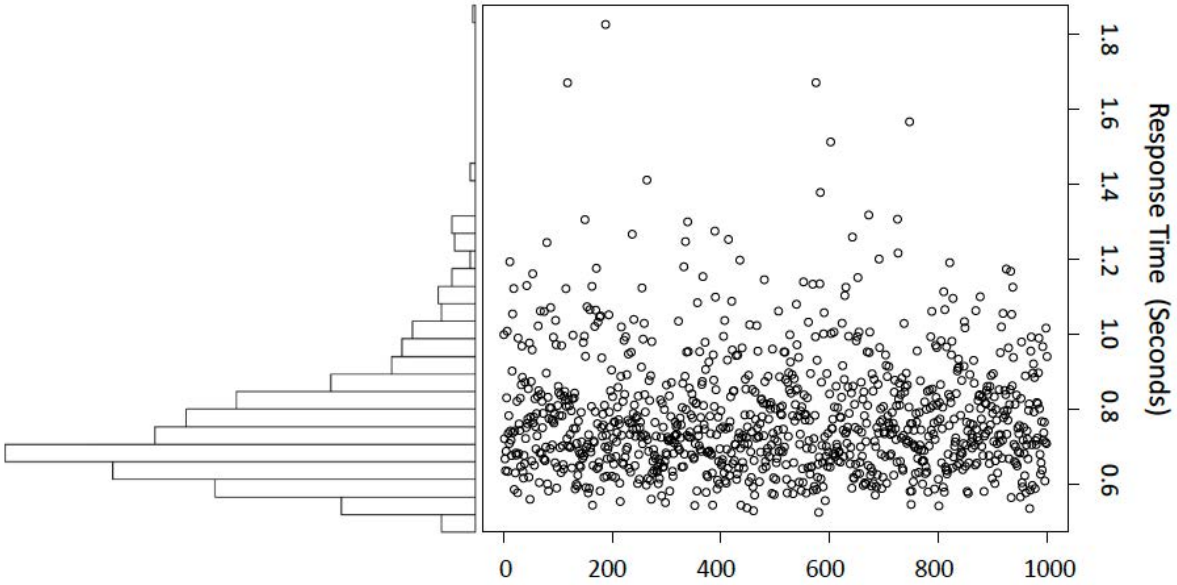


Figure 8



Note. The diffusion plot presents simulated response time values for 1000 trials. The simulated values were derived from the rdiffusion function in the rtdist R library with DM parameters: a =.1, v=.2, Z=.05, t_{er} =.5, s_z=.05, st_{er} =.2, s_v=.05, s=.1) https://cran.r-project.org/package=rtdists.