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Addressing very short stimulus encoding times in modeling schizophrenia cognitive deficit

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HIGHLIGHTS

- A modified mathematical model for describing the encoding process is introduced.
- This model permits very short encoding times while prohibiting instantaneous encoding.
- The model is consistent with data obtained from controls and schizophrenia patients.
- This model introduces a task parameter α.
- A method for estimating α is developed.

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ABSTRACT

It is well known that encoding times in persons with paranoid schizophrenia are longer than those of normal controls. Neufeld and others have argued that this is the consequence of additional subprocesses being executed during the encoding process in the case of schizophrenia. In general they expressed an encoding time as the sum of k' independent exponentially-distributed subprocesses, each executed with rate v. A troubling consequence of their application of this model to real data was that some individuals appeared to encode instantaneously (i.e., $k' = 0$ was observed). This was accommodated in Neufeld et al. (2010) by placing a Poisson distribution on k'. In this paper the view is taken that $k' = 0$ is not realistic and an alternative model is developed in which k' is restricted to positive integers. This is made compatible with very short encoding times by introducing a task parameter α into the model. The problem of estimating α is addressed at length.

1. Introduction

Of considerable interest in cognitive science are the earmarks of psychopathology, in particular the key elements which might distinguish one disorder from another. One concept which has received considerable attention is that of *encoding* in the case of paranoid schizophrenia (for a review see Neufeld, 2007a). Encoding is the process by which an object or event is transformed mentally into a form which facilitates carrying out the task at hand. For example, consider a basic memory search task (Sternberg, 1975) where the participant is first presented with a collection of alphanumeric items (memory set) then later is presented with an item (probe item) which may or may not have been in the set. The total reaction time is the amount of time required for the participant to indicate whether or not the probe item belonged to the memory set. In order to accomplish this, the participant must first encode the probe item, i.e., extract its salient physical features (curves, lines, intersections, etc.) in order to facilitate comparison with members of the memory set. The total reaction time z can then be decomposed into a sum

$$z = t + y + w \tag{1}$$

where t represents the encoding time, y consists of the additional time required to complete mental processes such as making comparisons with members of the memory set and rendering a decision, and w is the remaining time required to complete the physical reaction indicating a yes–no response.

Converging evidence suggests that persons with schizophrenia display prolonged reaction times and that this prolongation is due specifically to a protracted encoding time t (significantly, the other terms y and w are spared; e.g., Neufeld, Vollick, & Highgate, 1993; Neufeld, 2007a). This elongation of encoding times is particularly apparent in persons with paranoid schizophrenia (Neufeld & Williamson, 1996). One goal of Neufeld, Vollick, Carter, Boksman, Levy, George, et al. (2007) and Neufeld, Boksman, Vollick,

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George, and Carter (2010) was to explore mathematical models that adequately capture the encoding process. The expression "the encoding process" is used because evidence suggests that the same model architecture holds for persons in general. In the case of paranoid schizophrenic illness, a slippage in a parameter occurs, not a change in model architecture (Neufeld, 2007a; Neufeld et al., 2010). Germane to the models of encoding times is the idea that successful encoding requires completion of a certain number k' of subprocesses (which may vary from individual to individual). Apparently in the case of paranoid schizophrenia the average number of executed subprocesses is increased as compared to healthy persons (Neufeld et al., 2010, 2007). Recently, Taylor, Théberge, Williamson, Densmore, and Neufeld (2016, 2017) observed a similar effect when conducting the Stroop test on schizophrenia patients.

The tendered mathematical models discussed herein were based on the analysis of reaction time data from an experiment of George and Neufeld (1987) which is also described in detail in Neufeld et al. (2010, 2007). Participants viewed a four-letter word in the central visual field for 1.5 s. This was immediately followed by the presentation of a probe item for 20 ms; this probe item consisted of two words, one in the left visual field and one in the right visual field. Participants were instructed to press the "yes" key as quickly as possible if either of the probe words matched the first word; otherwise they were to press "no" as quickly as possible. In the case of a match, there was considered to be a differential encoding load (low vs. high) depending on the visual field in which the matching probe word was presented. A word presented in the right visual field should be processed more quickly (left hemispheric superiority for verbal stimuli) than one presented in the left visual field. For the purposes of this investigation only positive trials (i.e., trials on which a probe word matched the original word) were considered. In this way a 2×2 factorial design with four cells was created, where the first cell consisted of reaction times from normal controls under low encoding load (NL), the second cell consisted of reaction times from normal controls under high encoding load (NH), the third was comprised of reaction times from paranoid schizophrenia patients under low encoding load (SL), and the fourth was comprised of reaction times from paranoid schizophrenia patients under high encoding load (SH). There were 14 participants in each cell, each subject to 32 trials. If z_{ij} denotes the reaction time on the jth trial of the ith participant in one of the four cells, then

$$z_{ij} = t_{ij} + y_{ij} + w_{ij} \tag{2}$$

where the components on the right hand side of (2) take the meaning of those in (1). Data analysis proceeded by first calculating the sample mean and the sample variance of the reaction times for each participant within a cell. Those values were then averaged over all the participants within the cell (see the sampling schematic in Appendix A where there are M participants per cell, each subject to N reaction time trials). The effect was to produce two statistics from each cell, an average mean $\bar{\bar{z}}$ and an average variance $\bar{u}^2$. These quantities were the basic units of analysis and had the advantage of canceling out much of the noise in the individual trials so that differences between cells could be observed. The basic results were as expected: reaction times were longer when the encoding load was higher or when the participants had paranoid schizophrenia. A particularly interesting and important result, however, was that means and variances were *additive* over the four cells (i.e., there was no interaction between health status and encoding load). Mean reaction times for both normal and schizophrenia individuals increased by the same amount as the encoding load moved from low to high; similarly for mean variances. This observation is important as it restricts the possible valid mathematical models for encoding, a topic which has been addressed at length by Neufeld et al. (2010) and Taylor et al. (2016, 2017).[1]

Since, as noted earlier, the reaction time components y and w seem to be spared in paranoid schizophrenia, it is not unreasonable to assume that over all participants the y_{ij} variables are independently and identically distributed with some mean $E(Y)$ and variance $\mathrm{Var}(Y)$, and similarly that the w_{ij} are independently and identically distributed with mean $E(W)$ and variance $\mathrm{Var}(W)$. However it is expected that the distribution of the t_{ij} variables will depend on the cell to which the participant belongs, since encoding is affected by encoding load and health status. Computing expectations over a particular cell (*) it follows from (1) we then have

$$E(\bar{\bar{z}})^* = E(T)^* + E(Y) + E(W) \tag{3}$$

where only the first term on the right hand side depends on the cell (*). Note also that if we consider participant i in the cell then, using statistical independence of the summands, we obtain

$$E(u_i^2) = \mathrm{Var}(Z_i) = \mathrm{Var}(T_i) + \mathrm{Var}(Y) + \mathrm{Var}(W) \tag{4}$$

where only the first term on the right hand side depends on the participant. Then averaging over all participants in the cell, we obtain

$$E(\bar{u}^2)^* = E(\mathrm{Var}(T))^* + \mathrm{Var}(Y) + \mathrm{Var}(W) \tag{5}$$

where only the first term on the right hand side of (5) depends on the cell (*). Additivity is clearly unaffected in both (3) and (5) by the "nuisance variables" Y and W; the initial work of Neufeld et al. (2010, 2007) was to propose models of encoding times T that could support additivity in (3) and (5) with few enough free parameters that they could be estimated from the eight available statistics $\bar{\bar{z}}_1, \bar{\bar{z}}_2, \bar{\bar{z}}_3, \bar{\bar{z}}_4$, and $\bar{u}_1^2, \bar{u}_2^2, \bar{u}_3^2, \bar{u}_4^2$. The model of choice (to be described fully in the next section) featured a parameter m which can be described as the expected number $E(k')$ of subprocesses required for a normal individual to successfully encode under the low encoding load. The impetus for the present paper was the fact that m was estimated to be considerably less than one, thereby implying that some individuals must be able to encode instantaneously without executing any subprocesses. This was a point of both conceptual and mathematical difficulty. In this paper we modify the original model (see Section 3) in such a way as to force the number of encoded subprocesses to be at least one, yet accommodate the possibility of very short encoding times as suggested by the data. This is done by introducing an additional parameter $\alpha > 0$ (called a *task parameter*). In Section 4 a method for estimating α is obtained for noise-free data. In Section 5 this method is extended to noisy data and applied to the case where the number of subprocesses is distributed according to a geometric distribution.

[1] Essentially, the family of eligible model structures and parameter changes has comprised combinations whose properties of predicted summary statistics (e.g., means) conform to those of the empirical observations (specifically, experimental-factor additivity of encoding times). Example structures include the Erlang distribution (gamma distribution with a discrete shape parameter k') where k' denotes the number of constituent subprocesses of the modeled process. Additivity occurs when k' is incremented by the same amount across diagnostic groups when encoding load is changed, and is incremented by the same amount across encoding loads when health status is changed. Mathematical specifics, and consideration of additional structures, are reviewed in Neufeld et al. (2010) and Taylor et al. (2016, 2017), with computational proofs dating back to the initial work on stochastic modeling of schizophrenia cognition (Neufeld et al., 1993; Neufeld & Williamson, 1996). In paradigms where the above additivity has not come into play, releasing the scale parameter (subprocess-wise "rate", or "capacity" v), in addition to, or instead of, the shape parameter k', has not led to improved empirical fit of encoding-model predictions among schizophrenia and control participants (Carter & Neufeld, 1999). The present paper develops a related gamma model where additivity also holds.