1 Introduction

Behavioural, physiological and connectionist models of paired associates learning (PAL) and serial learning (SL) are primarily concerned with measures of accuracy, errors and response latencies. However, the correlation between forward and backward cued recall provides an important constraint to models of PAL [1] and this correlation is nearly perfect [2]. One study measured the correlation in SL [3]. Participants learned a serial list to a perfect recall criterion and then answered cued recall questions about nearest-neighbour pairs derived from the list. The correlation between forward and backward probe directions was moderate, substantially lower than the correlation between test/re-test in the same direction and substantially greater than a control for list-to-list variability.

While this could be used to suggest that PAL and SL are subserved by distinct systems with different dynamics, we argue that one can still treat SL and PAL within a single theoretical framework. In this view, the PAL and SL paradigms represent ends of a continuum spanned by a single parameter controlling the degree to which neighbouring pairs of items are isolated from the rest of the list. In previous work we showed analytically how this Isolation Principle may be straight-forwardly integrated into the two main classes of models of SL, positional and chaining models [3]. We derived analytical expressions for the correlation between forward and backward probes in a simplified chaining model and a simplified positional coding model and showed that differences in a parameter that controls the degree of isolation can account for the behavioural dissociations between PAL and SL. Here we simulate a chaining model for simulated lists containing both pairs of and triples of items. We show how the Isolation Principle predicts a dissociation in the correlation between probe directions when moving from pairs of items even to the next smallest number of items: three.

2 The Model

The model is a an associative chain, which was the first structure proposed to link memory for associative and order information [4, 5]. It is a Hebbian matrix model (e.g., [6, 7, 8, 9]).

Study trial In a study trial, the model stores a list of L words indexed by l by summing the outer products between pairs of items, storing forward and backward associations in separate memory matrices, W_f and W_b, respectively:

$$W_f = \sum_{l=1}^{L-1} \sum_{k>l} S_{lk} \gamma_{lk} \mathbf{f}_k \mathbf{f}'_l \tag{1}$$

$$W_b = \sum_{l=2}^{L} \sum_{k<l} S_{lk} \gamma_{lk} \mathbf{f}_k \mathbf{f}'_l \tag{2}$$

where $\mathbf{f}_l$ are N-dimensional vectors whose elements are i.i.d., Gaussian random variables with mean=0 and variance=$1/N$. S_{lk} are scalars that determine the mean strength of an association and γ_{lk} are independent random variables such that $\mathrm{E}[\gamma_{lk}] = 1$ and $\mathrm{var}[\gamma_{lk}] = \sigma_\gamma^2$. For all simulations, we set $S_{lk} = S_{kl}$, that is, the stored forward and backward associative terms are perfectly correlated. According to the Isolation Principle, we set $S_{l,l+1} = 1$ when $\{l, l+1\}$ are within a pair or a triple, and $S_{l,k} = 0$ when $\{l, k\}$ are in different pairs or triples. To manipulate the effect of remote associations, $S_{l,l+2} = S_{remote}$, where l and $l+2$ were the A and C items of a triple, respectively. For the first simulation, we only include nearest-neighbour associations, so $S_{remote} = 0$; for the second simulation, remote associations are strong, $S_{remote} = 0.8$.

Cued recall To probe the model, we multiply the memory matrices by the probe word, $\mathbf{f}_x$. We assume that the model probes not only the matrix in the correct direction, but also to some degree, the matrix in the opposite direction, to retrieve an item vector, $\mathbf{f}_r$; this was a necessary condition for obtaining a near-perfect correlation between forward and backward cued recall in simulated [9] and analytically derived [3, 2] chaining models. Probing in the forward or backward directions:

$$(W_f + rW_b)\mathbf{f}_x = \mathbf{f}_r \tag{3}$$
$$(rW_f + W_b)\mathbf{f}_x = \mathbf{f}_r \tag{4}$$

where r weights the degree of associative ambiguity. Then, the response item is selected using a competitive retrieval rule based on the match between $\mathbf{f}_r$ and all the items in the word pool. Similarity, ξ_{ir} is computed as

Parameter	Value (Sim 1)	Value (Sim 2)
N	500	500
N_{pool}	500	500
θ	0.4	0.4
σ_γ	0.5	0.5
r	0.6	0.6
$N_{samples}$	20	20
S_{remote} (within triple)	0	0.8

Table 1: Parameter values for both simulations.

$$\xi_{ir} = \mathbf{f}_i \cdot \mathbf{f}_r \tag{5}$$

and negative similarities ξ_{ir} are set to 0. Items are sampled with replacement, with probability equal to $\frac{\xi_{jr}}{\sum_i \xi_{ir}}$. If $\xi_{jr} > \theta$, where θ is a strength threshold, item j is output; otherwise, sampling continues to a maximum of $N_{samples}$.

3   Simulations

Each simulation learned 2000 lists containing 5 triples and 5 pairs each, in randomized order. Words were selected at random from a word pool. Each pair and each AB and BC sub-pairs from each triple, was probed twice successively. The discrete correlation, Yule's Q, was computed for all pairs of probe directions on probes 1 and 2. Yule's Q for the control was computed by selecting probes from different pairs on tests 1 and 2, where the shuffling was done within lists and within pair types (AB, AB_ and _BC).

4   Results and Discussion

Figure 1a shows mean accuracy for forward and backward probes. Probes of pair blocks show an advantage, due to the fact that they are isolated from the rest of the list, and thus experience the least amount of interference. When probing with the middle item of a triple, B, mean performance suffers. This is a consequence of *target ambiguity* [10].
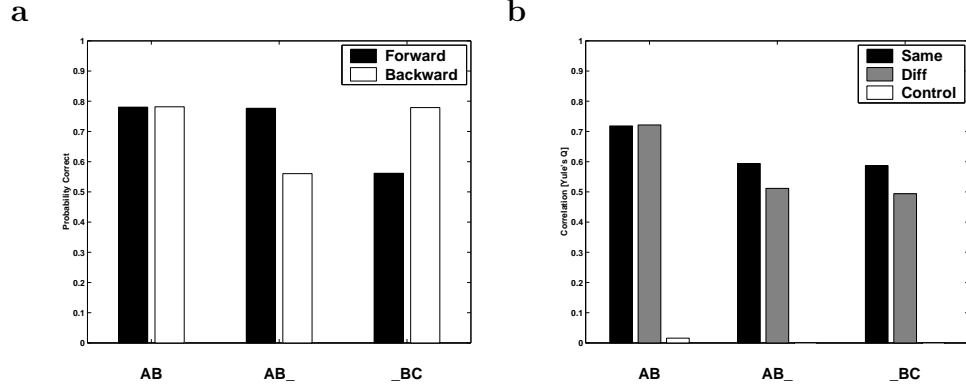
Figure 1: Results for simulation #1, without remote associations. **a**, Mean accuracy for forward and backward probes, for sub-pairs taken from pair blocks (**AB**), the first sub-pairs of triple blocks (**AB_**) and the second sub-pairs of triple blocks (**_BC**). **b**, Correlations (Yule's Q) between successive tests 1 and 2 where the probe direction was the same on both tests ("same") or opposite ("diff"), or else taken from different sub-pairs within the same list ("control").
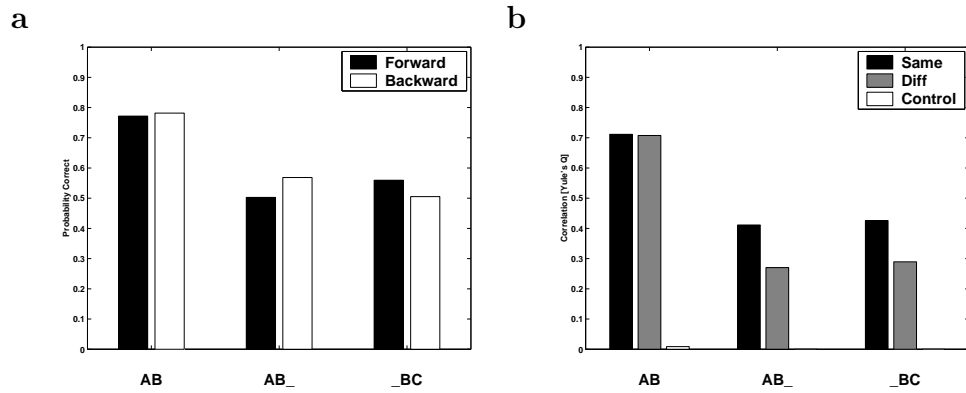

Figure 2: Results for simulation #2, with remote associations (see caption for Figure 1)

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Turning now to the correlation, Figure 1b shows that, as expected based on previous data on pairs, triples and long serial lists [3, 10], performance on forward and backward probes ("diff" condition) are correlated as highly as the are two probes in the same direction ("same" condition). However, for sub-pairs of the triples, the correlation between different probe directions is substantially lower than that for the same probe conditions, but is much more positive than the control for the correlation due to list-to-list variability.

The target ambiguity effects in Simulation 1 have not been detectable empirically [10]. We propose that they were present but obscured by the effect of remote associations, which would tend to equalize accuracy for different probe types within a triple. We added remote associations to the second simulation. Figure 2a shows this indeed removes the evidence for target ambiguity from the mean performance measures. Figure 2b shows that it does so without reversing the pattern of correlations. Also note that the correlations for triples are lower than in the first simulation, because the additional influence of the remote association differentially affects forward and backward probes. In contrast, because pairs are isolated, the addition of remote associations leaves the correlation for pairs unchanged.

These simulations confirm our prior analytic arguments that the Isolation Principle can account for apparent dissociations between PAL and SL [3], and further, question the notion that associative chaining models are challenged by failures to find empirical evidence for associative interference such as target ambiguity effects.

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