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Molecular order in concurrent response sequences

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Abstract

We studied the order of emission of concurrently reinforced free-operant two-response sequences such as left–left (LL) and left–right (LR). The end of each sequence was demarcated by stimulus change. The use of demarcated sequences of responses, as opposed to individual responses, provides an expanded set of distinct, temporally ordered behaviour pairings to investigate (e.g., LL followed by LL, LL followed by LR, etc.); it is as well a real-life analogue. A sequential analysis of new and existing rat and pigeon data revealed patterns in both overall and post-reinforcer-only sequence emission order. These patterns were consistent across species and individuals, and they followed higher-order organising principles. We describe sequence non-repetition, last-response repetition, and the proportion and post-reinforcer effects, and relate them to existing molar and molecular behaviour principles. Beyond their immediate implications, our results illustrate the value of sequential analysis as a tool for the investigation of molar-molecular behavioural relations.

Keywords: Response sequences; Sequential analysis; Molar-molecular; Probability; Concurrent schedules; Pigeons; Rats

1. Introduction

Researchers have identified many orderly behaviour–environment relations, many of which apply over relatively longer-term ("molar") aggregation scales such as single or multiple sessions. An example is the generalised matching law, which describes the steady-state relation between obtained response and reinforcer ratios in the concurrent schedules used to study choice. (In a concurrent schedule, two or more schedules of reinforcement operate simultaneously, and the behaver can alternate freely between them.) A continuing research question concerns the degree to which molar relations like this one result from shorter-term "molecular"-level causal control (e.g., that found on a minute-to-minute basis). Heyman (1979), for example, found no evidence for sequential dependencies in response emission order in a standard concurrent variable-interval (VI) VI schedule, but others have (e.g., Silberberg et al., 1978, both with and without changeover delays). Silberberg et al. suggested that molecular control was primary. Williams (1991) countered that the literature offered sufficient data to support the existence of direct molar control producing matching to the molar reinforcer probabilities.

In recent years, molar choice theorising has continued to develop (e.g., Davison and Nevin, 1999), but at the same time research demonstrating molecular order in concurrent schedules has become progressively more convincing. For example, Davison and Baum (2000) and Landon and Davison (2001) reported molecular order in concurrent schedules with reinforcement probability ratios that changed up to seven times a session: individual reinforcers produced predictable, repeatable effects. Increasingly, it appears that molar matching may after all be explicable from more molecular mechanisms of control: Baron and Perone (2001) considered that "the balance has tipped in favor of [this] interpretation" (p. 359). Molecular order remains insufficiently understood, however.

The concurrent-schedules paradigm using two individual-response behavioural units such as left and right keypecks has dominated the study of choice, and has been locally analysed using the various forms of conditional probability for changeovers (e.g., MacDonall, 2000) and Markov models (e.g., Cleaveland, 1999; also see Silberberg et al., 1978). However, studying more than two behavioural units creates more temporally ordered behavioural possibilities, and thus the basis for more comprehensive analyses. The basic procedure entails dif-

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ferentially reinforcing the concurrent production of the four possible two-response sequences: left–left (LL), left–right (LR), right–left (RL), and right–right (RR).

In a seminal study, Stubbs et al. (1987) utilised this procedure with pigeons on dependently arranged VI schedules, with a 1-s blackout after unreinforced sequences to demarcate them. Sequence emissions increased or decreased following the contingencies, and could be approximated by the strict matching law (see Schneider and Davison, 2005, for a reanalysis using the generalised matching law). At a molecular level, Stubbs et al. performed a conditional probability analysis on data from two experimental conditions and found indications of sequential dependencies. They did not, however, compare their probabilities with those expected based on chance concatenation of the actual sequence distributions.

A sequential analysis method that is based on the actual sequence distributions is described in Bakeman and Gottman (1986); it is frequently employed in applied and comparative psychology (e.g., Justice et al., 2002; Walker and Fell, 2001), though seldom in the present context (but see Richardson and Clark, 1976). In a Lag-1 analysis, the behavioural emission order is examined. The observed frequencies of each possible ordered behaviour pairing (e.g., LL sequence followed by LR sequence) are compared with the frequencies expected by chance, based on the actual behaviour distributions—a straightforward application of probability theory. The differences can then be converted to z-scores and analysed statistically. Any Lag-1 sequential dependencies may themselves depend upon their positions in longer sequences (e.g., Cleaveland, 1999; Iversen, 1986, 1991), which can also be analysed using this method. The temporal intervals between the events are irrelevant in this particular analysis.

To take a simplified example: in a 100-sequence sample, suppose there are 25 emissions each of the four sequences (LL, LR, RL, and RR). Suppose also that each sequence type is emitted as a block, with the 25 LLs followed by the 25 LRs, etc. A random distribution of sequences would predict that each sequence would precede and follow itself and all the other sequences equally often: roughly 6 times each. That is, looking at the 25 instances of LL in the sample, LL would be followed by LL about 6 times; LR 6 times; RL 6 times; and RR 6 times. Obviously, the example data are far otherwise, with 24 LL–LL ordered sequence pairings, 1 LL–LR, and no LL–RLs or LL–RRs. What we shall call the sequential probability ratios are the (observed − expected)/expected frequency ratios for the 16 sequence pairings. Given random sequence-emission order, the observed − expected difference should be close to 0, and so therefore should the ratio. Instead, the values for this example are 3.0 for LL–LL, −0.83 for LL–LR, and −1.0 for LL–RL and LL–RR. In the analysis of the actual data, each observed frequency was also converted into a z-score, based on the expected frequency (see Appendix A).

The same analysis can be performed for the reinforced sequences only and those sequences that immediately followed them. Because these post-reinforcer sequential probability patterns turned out markedly different from the overall patterns in the present data set, the overall sequential probability ratios were then recalculated for all data sets with the reinforced sequences removed as leading sequences in the sequence pairings (but still remaining as following sequences). All overall sequential probability data exclude the post-reinforcer data.

Schneider and Morris (1992) were the first to utilise this sequential analysis method on concurrent-schedule sequence data. Rats were the subjects, and the required minimum interresponse time (IRT) was substantially longer (4–7 s) than that used by Stubbs et al. Delays this long make sequences less likely to function as coherent units, and indeed, responding was intermediate between matching of sequences as units and matching only of the final responses in the sequences to relative reinforcers (standard response matching). For the sequential analysis, as described above, probability theory allowed determination of the expected-from-chance number of occurrences of a sequence followed by any other sequence (e.g., LL followed by LR). If the sequences were emitted in random order, the differences between the observed and expected-from-chance frequencies would be small. Alternatively, sequential dependencies might occur: some sequences might follow others at higher-than-chance or lower-than-chance frequencies, showing that the emission of sequences was under sequential control. Schneider and Morris (1992) found nonrandom patterns of this type for their two-response sequences; moreover, these patterns were consistent across individuals. However, a post-reinforcer sequential analysis of the sort described above was not performed, and the overall sequential probability analysis included the post-reinforcer data.

In the current study, we reanalysed the rat data of Schneider and Morris (1992) and the pigeon data of Schneider and Davison (2005), which shared the same basic concurrent-sequence procedure; Schneider and Davison (2005) performed a molar analysis only. We augmented these studies by running and analysing additional conditions with rats, with different overall reinforcer rates and different minimum IRTs. We looked for sequential patterns and higher-level sequential-order principles, and we made cross-species comparisons to test for generality.

2. Materials and methods

2.1. Subjects

The new data were acquired in three phases (see Table 1). Subjects for each phase were four individually housed, experimentally naive Sprague–Dawley rats, designated 1A through 1D (Phase 1), 2A through 2D (Phase 2), and 3A through 3D (Phase 3). They were maintained at about 85% of their free-feeding weights, with water available in their home cages. In Phase 1, rats were males 3–4 months old at the beginning of the experiment. Phase 2 rats were 2-month-old females; Phase 3, 5-month-old males.

2.2. Apparatus

Two standard Lafayette two-lever operant chambers with houselights were used. Fans in the outer sound-attenuating shells provided both ventilation and masking noise. Food pel-