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Identifying Subregularies within a Case Series with Formal Models: Sequence Representations for Speech

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Fundamentally, speech involves producing sequences, a property shared with other cognitive capacities like writing, short-term memory and movement. We are interested in how sequences are represented for speech and ask if mechanisms are shared or specialised across language, memory and movement domains. We show how aphasic case series data and formal statistical modelling can be used together to test these questions. Statistical modelling compares alternative accounts by expressing theoretical claims in statistical form and then measuring both the fit between observed data and model and the number of parameters each model requires. Balancing fit and parameters is fundamental if models are to provide an adequate account but also generalise to new data. We have been using formal techniques based on Akaike's Information Criterion (Burnham & Anderson, 2002) to test theoretical accounts across case series data. A number of explicit sequence accounts exist, including oscillator coding (Brown, Preece, & Hulme, 2000), competitive queuing (Houghton, 1990), the start-end model (Henson, 1998), the primacy model (Page & Norris, 1998), compound chaining (Botvinick & Plaut, 2006) and the both edges model (Fischer-Baum, McCloskey, & Rapp, 2010). All of these can produce the frequently observed U-shaped serial position function where errors concentrate in the middle of a sequence. We report a new pattern in which the probability of error *decreases* with phoneme position in a word. This, along with strictly increasing patterns (e.g. Ward & Romani, 1998), also found in our series, limits compatible accounts to those that have a two dimensional representation based on the beginning and end of the sequence. We also show, however, that the fundamental factor seems to be the number of phonemes previously correct in the decreasing pattern and the number of previous errors in the increasing pattern. Moreover, the two distinct patterns are associated with distinct articulatory and phonological loci when patients from the series are assessed on independent grounds. These patterns challenge existing models of sequence production and highlight the strengths of using case-series data and statistical modelling.

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