

Syntax in *C. elegans* locomotion

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Visible phenotypes have played a critical role in understanding the molecular basis of behaviour in model organisms. In previous work, we have shown that automated tracking and quantitative measurement of posture and motion parameters can sensitively identify new phenotypes in mutants of the nematode worm *C. elegans* [1]. However, it is not clear whether these parameters are in any way optimal nor whether they are useful for discovering new behaviours that we did not think to measure. As an alternative, we have also used unsupervised methods to automatically detect repeated behaviours in an unbiased way. A dictionary of such ‘behavioural motifs’ can be used to construct a phenotypic fingerprint for mutant strains and seems to be a promising way of predicting possible genetic associations [2].

Both of these approaches still leave several fundamental questions about behaviour unanswered. For example, how complex is worm behaviour? How long do we need to watch a worm before we have a good sample of its behavioural repertoire in a given condition? To address these kinds of questions, we have developed a simple method to capture the sequence of postural states of freely behaving worms and used it to derive a compact discrete representation of behaviour. Repetitive behavioural motifs are then identified in an unbiased way using a hierarchical dictionary-based compression algorithm to identify the syntax of worm behaviour (Figure 1). As opposed to the dictionary derived in our previous method, the compression-derived dictionary contains all of the repeated sequences the worm performed and is, in this sense, complete.

The dictionary learned for spontaneous behaviour in wild-type worms can be used to compress data from mutants or worms in different environmental conditions to measure phenotypic similarity. Dictionary comparison can also be used to assess inter-individual variation and the compositionality of behaviour, that is, the extent to which behavioural adaptation involves the creation of novel repertoire elements or the reuse of existing elements in novel sequences. Finally, the hierarchical nature of behaviour is built from the bottom up and may give insight into the evolution of behaviour: low-level behaviours that are used in many contexts may be evolutionarily more constrained than those controlling behavioural choices at higher levels.

References

- [1] Yemini, E., Jucikas, T., Grundy, L.J., Brown, A.E.X., Schafer, W.R. (2013). A database of *Caenorhabditis elegans* behavioral phenotypes. *Nature Methods*, **10**(9), 877-879.
- [2] Brown, A.E.X., Yemini, E., Grundy, L., Jucikas, T., Schafer, W.R. (2013) A dictionary of behavioral motifs reveals clusters of genes affecting *Caenorhabditis elegans* locomotion. *Proceedings National Academy of Sciences USA*, **110**(2), 791-796.

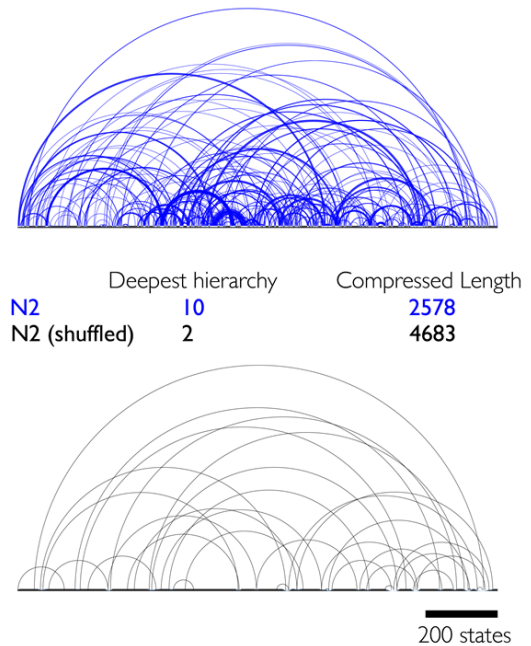


Figure 1. An arc diagram summarises the structure of worm locomotion by connecting segments of repeated behaviour identified in the compression-derived dictionary. Top: wild-type behaviour. Bottom: the same data after shuffling to destroy higher-order structure.