Abstract Submitted
for the MAR14 Meeting of
The American Physical Society

A quantifiably complete repertoire of C. elegans locomotion ANDRE BROWN, MRC Clinical Sciences Centre, ROLAND SCHWARZ, European Bioinformatics Institute, ROBYN BRANICKY, WILLIAM SCHAFER, MRC Laboratory of Molecular Biology — Visible phenotypes have played a critical role in understanding the molecular basis of behaviour in model organisms. However, most current descriptions of behaviour are based on manually identified events or a limited set of quantitative parameters. Here we report an extension of the concept of behavioural motifs to exhaustively catalogue C. elegans locomotion and derive a repertoire that is quantifiably complete. A repertoire learned for spontaneous behaviour in wild-type worms can be used to fit data from mutants or worms in different environmental conditions and provides a sensitive measure of phenotypic similarity. Repertoire 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. Repertoire derivation is general, so that given a representation of posture, our approach will apply to other organisms.

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Date submitted: 27 Sep 2013 Electronic form version 1.4