MAR17-2016-020301

Abstract for an Invited Paper
for the MAR17 Meeting of
the American Physical Society

Representation matters: quantitative behavioral variation in wild worm strains

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Natural genetic variation in populations is the basis of genome-wide association studies, an approach that has been applied in large studies of humans to study the genetic architecture of complex traits including disease risk. Of course, the traits you choose to measure determine which associated genes you discover (or miss). In large-scale human studies, the measured traits are usually taken as a given during the association step because they are expensive to collect and standardize. Working with the nematode worm *C. elegans*, we do not have the same constraints. In this talk I will describe how large-scale imaging of worm behavior allows us to develop alternative representations of behavior that vary differently across wild populations. The alternative representations yield novel traits that can be used for genome-wide association studies and may reveal basic properties of the genotype-phenotype map that are obscured if only a small set of fixed traits are used.