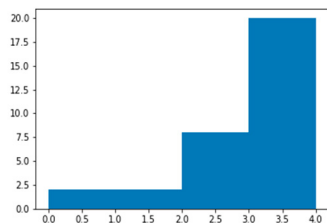
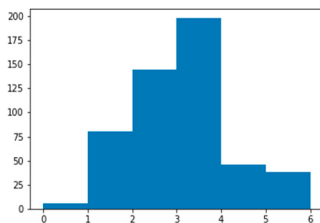


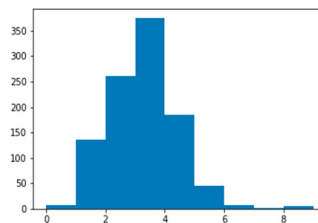
Supplementary Material



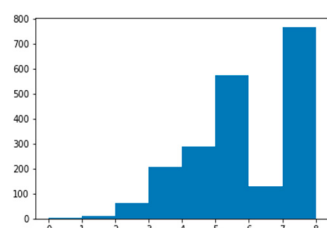
cortical



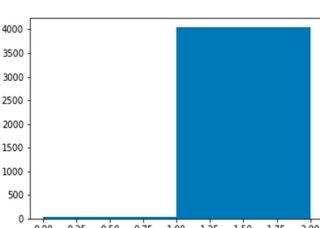
cycle-cdk



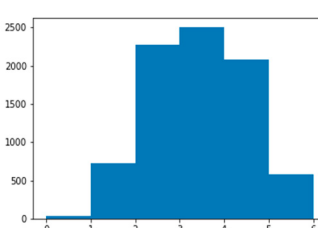
core-cell-cycle



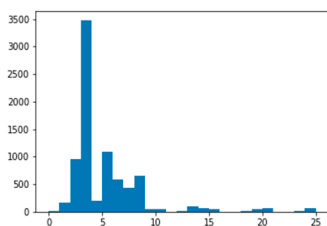
toll-drosophila



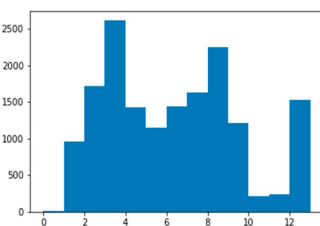
metabolic



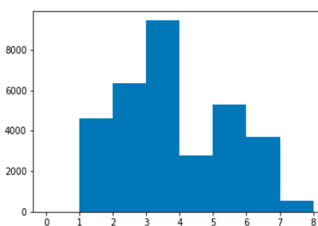
l-arabinose-operon



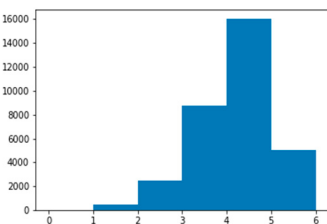
lac-operon-bistability



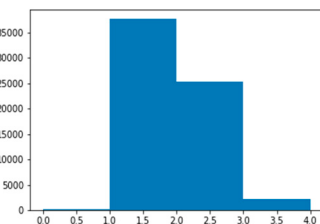
arabidopsis



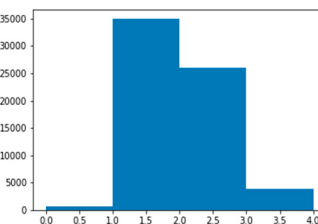
anemia



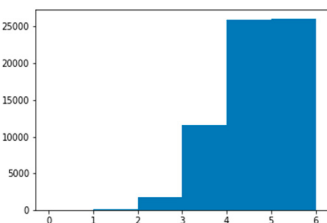
cardiac



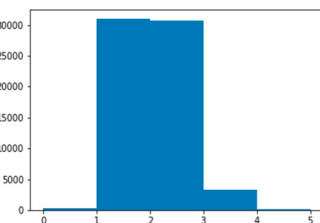
bt474-ErbB



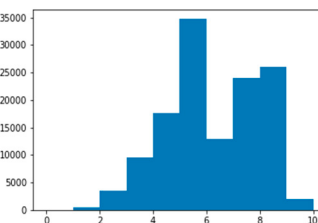
skbr3-short



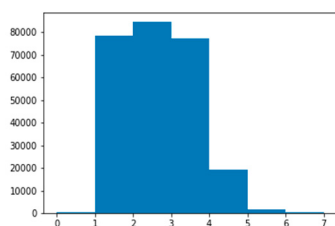
neurotransmitter



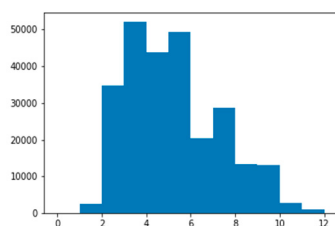
hcc1954-ErbB



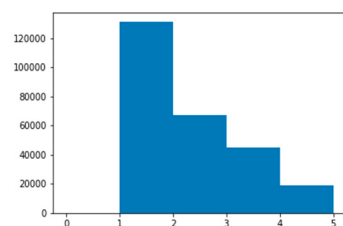
body-drosophila



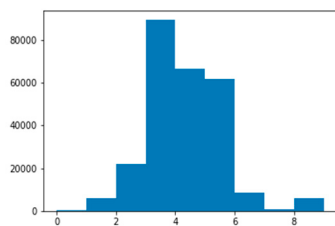
cd4



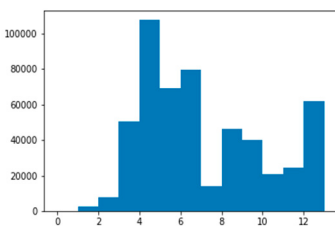
budding-yeast



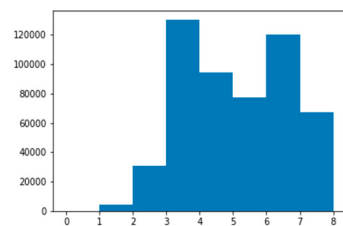
t-lgl-survival



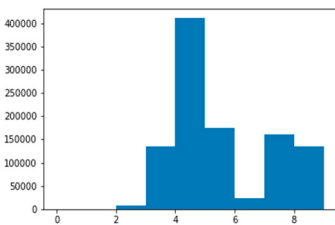
vegf-drosophila



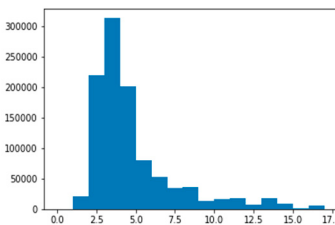
oxidative-stress



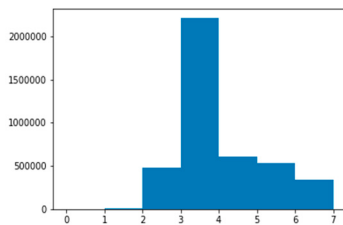
gonadal



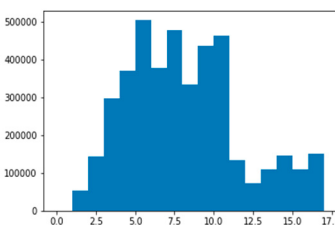
mammalian



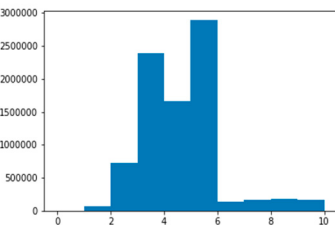
yeast-cycle



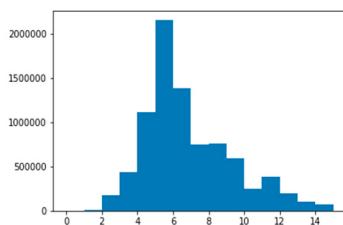
b-cell



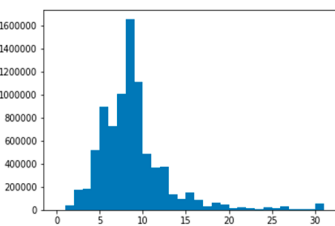
aspergillus-fumigatus



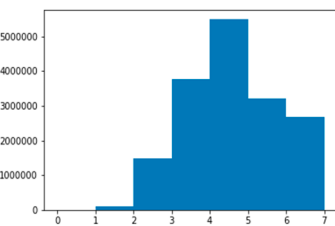
fgf-drosophila



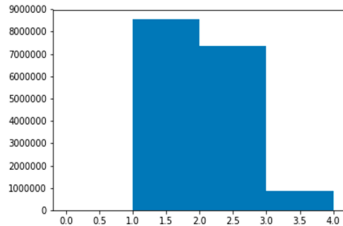
t-cell-differentiation



aurka



spz-drosophila



tol

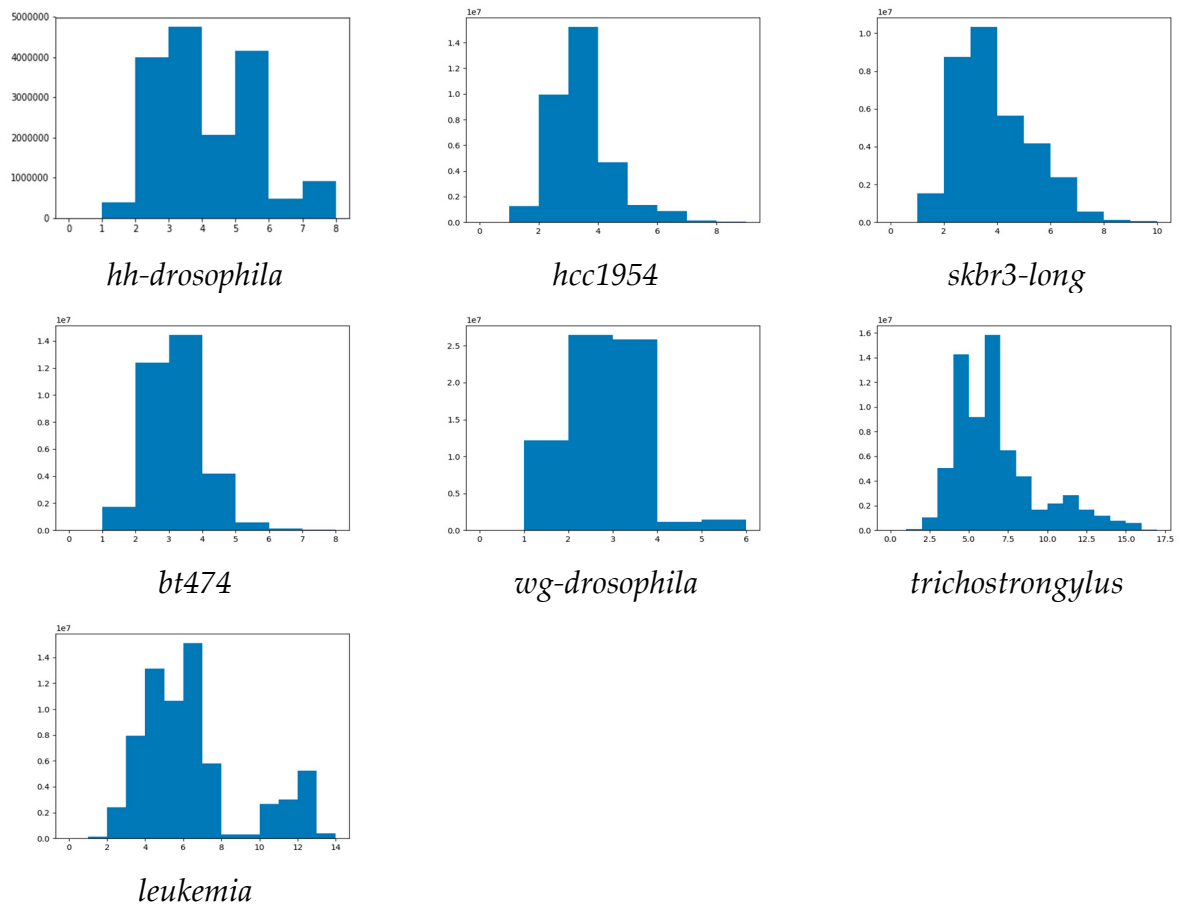


Figure S1. Histograms of transient lengths: how many state transitions all state configurations go through until they reach attractors. For the 37 biological networks, the maximum is 31 in *aurka*, which means that every state configuration of all biological networks converges to attractors within 32 state transitions. This implies that the basins of attraction of biological networks tend to be relatively shallow.

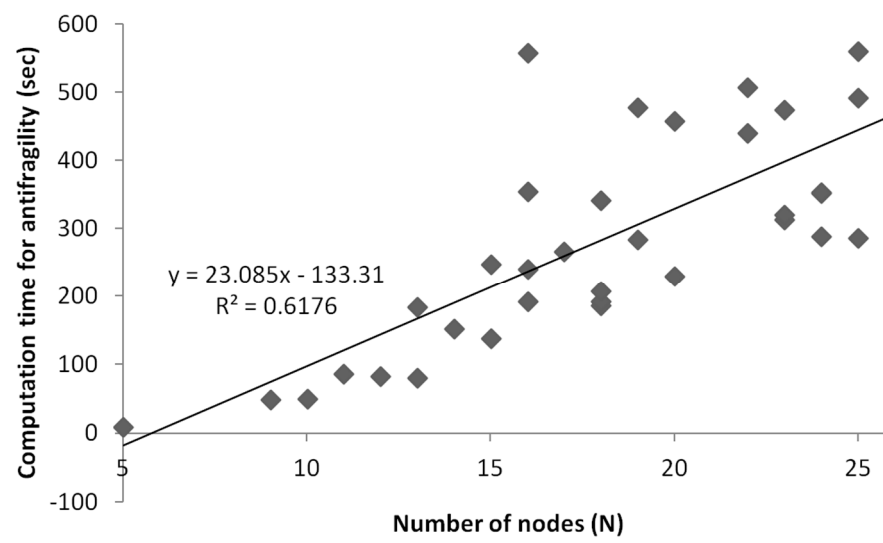


Figure S2. Time complexity of calculating antifragility. It linearly increases with the number of nodes (N).

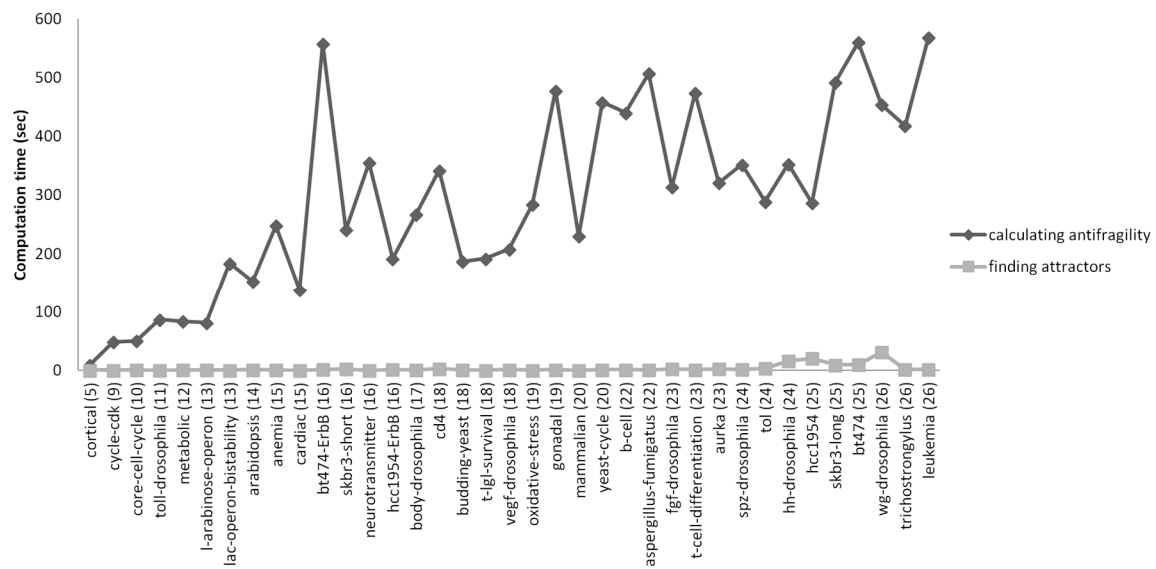


Figure S3. Comparison of computation time between calculating antifragility and finding attractors for the 37 biological networks.