## Abstract Submitted for the MAR13 Meeting of The American Physical Society

Characterization of genotype-phenotype mapping of biological networks reconciles robustness-evolvability paradox<sup>1</sup> CHENGHANG DU, HAO CHEN, CHEN ZENG, Department of Physics, The George Washington University — Typical biological system is both highly robust and highly evolvable. Yet robustness appears against changes whereas evolvability for changes. The concurrence of these two seemingly incompatible features is a central paradox for contemporary evolutionary biology. Using a Boolean model of yeast cell cycle networks, we quantitatively determine (1) the genotype-phenotype mapping. Here genotype stands for the network structure and phenotype for its dynamics; (2) the precise topology of neutral network, i.e. the interconnecting network of networks of different structures but the same dynamics; and (3) the number of new phenotypes in the vicinity of a neutral network. Our results demonstrate that both biological genotype and phenotype are atypical. We next show via sampling that all neutral networks exhibit a similar topology that is simply connected, fractal and sloppy (stiff in certain dimensions but diffusive otherwise). This percolating nature of neutral network leads to a positive correlation between robustness and evolvability and hence resolves the paradox. A likely explanation for such a correlation is that higher robustness results in a larger neutral network, measured by its designability and radius of gyration, which in turn accesses more new phenotypes.

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