15 January 2018

Dear editors,

Please find attached our manuscript "Non-equilibrium rate heterogeneity explains fat-tailed fluctuations in Phanerozoic biodiversity" that we wish to submit for publication as a Research Article in *Science Advances*.

Our study is the first to demonstrate that complex, previously unexplained patterns in diversity fluctuations in the fossil record are the result of a simple underlying process emerging from non-equilibrium evolution on an adaptive landscape [1, 2]. Our theory provides a novel explanation for deep time diversity dynamics invoking emergence of lineage-level traits as the drivers of complexity via the same mechanisms by which complexity emerges in large physical [3] and social systems [4]. In the context of fossil diversity we show how this complexity arises naturally from the uniquely biological mechanisms of punctuated adaptive radiation [1, 2, 5] followed by long durations of niche conservatism [5–7] and thus identify these mechanisms as sufficient and necessary to produce observed patterns in the fossil record.

Using two seminal fossil datasets [8, 9] we show that fluctuations in marine biodiversity over the past 550 million years results from the superposition of many independently fluctuating subsystems whose fluctuations are Gaussian but give rise to non-Gaussian patterns when combined. These independent subsystems correspond to lineages of closely related animal taxa, implying that diversification within lineages is driven by random additive interactions with the environment. Our findings thus challenge the idea that changes in origination and extinction through deep geologic time are the result of complicated evolutionary interactions among organisms and between organisms and their environment [10–12]. However, we demonstrate that the evolutionary process responsible for generating new lineages varies slowly through time, possibly driven by non-random evolutionary innovations in the physiology and demography of new lineages. This slow change between lineages produces patterns of apparent complexity earlier ascribed to unnecessarily complicated mechanisms. We further show, using permutational null models, that our findings are not an artifact of how fossils are taxonomically classified but rather capture true underlying biological processes.

This work has not been published or accepted for publication, and is not under consideration for publication elsewhere. Thank you very much for your consideration.

Sincerely,

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