



May 18th, 5:00 PM - 7:00 PM

## Effects of local mutations in quadratic iterations

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# Effects of local mutations in quadratic iterations

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The study of copying mechanisms is of great importance to genetics. We study in a theoretical system how a mutation (replication error) affects the temporal evolution of the system, on both a local and global scale (from tumor formation to overall systemic unsustainability).

We introduce a new mathematical framework for studying replication mechanisms, in the form of discrete iterations of complex quadratic maps. This approach builds upon a century of existing knowledge of iterated maps towards obtaining results with potential impact on applications. More specifically, our modeling framework considers a “correct” function acting on the complex plane (representing the space of genes to be copied) and a “mutation,” acting at a specific focal point, of a given size  $r$ , and moves radially toward an outer radius  $R$ . We use the Julia set of the system to quantify simultaneously the long-term behavior of the entire space under such transformations. We analyze how the position, timing and size of the mutation can alter the topology of the Julia set, hence the system’s long-term evolution, its progression into disease, but also its ability to recover or heal.

In the context of genetics, such results may help shed some light on aspects such as the importance of location, size and type of mutation when evaluating a system’s prognosis, and of customizing timing of treatment to address each specific situation. Our current work is a proof of principle. Once these aspects are understood theoretically, they can be further applied to empirically driven genetic models, validated with data and used for predictions.