



Computational Systems Biology: Chapter 17. Developing a Systems Biology of Aging

Andres Kriete, Mathieu Cloutier

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What makes the study of aging particularly challenging is the wide spectrum of phenotypical changes that can be observed during its progression. While initial attention was paid to damage accumulation, dysfunction, and failure, it is now realized that aging, and associated diseases including dementias, are influenced by a multitude of interacting factors. Proximal mechanisms beyond passive accumulation of damage include regulatory mechanisms, stress responses, changes in networks, as well as genetic and stochastic effects. The application of computational systems biology in aging, which is in line with other attempts to overcome the study of isolated or compartmentalized mechanisms, has made initial progress allowing us to simulate partial aspects of the aging dynamics and to make new hypotheses about how these aging mechanism shape disease progression. Here we provide examples for analysis of networks, regulatory mechanisms, and spatiotemporal effects in the study of proximal mechanisms of aging and Parkinson's Disease. In addition, we introduce complexity theories that may contribute to explain the ultimate causes of aging with an evolutionary view.



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