

Biological Functionality in Gene and Drug Networks

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Abstract

Complex biological functions are encoded by networks of interacting genetic components. Epistasis, describing the way multiple mutations in such networks affect each other's phenotypic consequences, provides essential information for elucidating the network functional architectures. I will describe a combined experimental-theoretical approach to quantify epistatic interactions in bacteria and yeast and to use epistasis information to identify functional gene and drug modules and their system-level organization.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth
Time: 1.00 - 2.00pm (followed by tea/coffee)
Travel directions are available at www.hamilton.ie

