



CENTRE DE RECERCA MATEMÀTICA

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## Evolution on heterogeneous genotype networks causes phenotypic entrapment

### Abstract:

The relationship between genotype and phenotype is many-to-many. In particular, genotypes encoding a particular phenotype form vast, connected networks that often span the whole space of possible genotypes.

Regarding their topological properties, genotype networks are highly heterogeneous in degree and, in most known cases, assortative (as in RNA and proteins). These properties have important effects on the dynamics of populations evolving on genotype networks. As time elapses, the probability that a random walker on such networks visits nodes of increasingly higher degree augments. In evolutionary terms, this implies that the probability that a population changes phenotype depends in a non-trivial way on the time the population has maintained the current one.

We derive a mathematical framework that quantifies this phenotypic entrapment and explicitly shows the dependence on measurable quantities such as network assortativity, mutation rate, or fitness of the phenotype. These results have important implications in a reliable definition of a molecular clock, which in general has a non-constant ticking rate due to the heterogeneity of genotype networks.

**Date:** Thursday, November 21, 2013

**Place:** Room C1/028

**Time:** 12:00

