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Evolutionary dynamics of populations with genotype-phenotype map

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There is a complex relationship between genotype and phenotype. One of the outstanding features of this map is that it is not a one-to-one map, because many genotypes are compatible with the same phenotype. Whereas genes are the entities passed on from one generation to the next and their frequencies measured over populations (the remit of population genetics), selection acts at the level of phenotypes. Thus, assigning fitness values to genes (mutant variants, different alleles, etc.) is not, in general, the valid approach. We are trying to put forward some of the new properties we may expect to emerge when the genotype-phenotype difference is taken into account, both in a general setting and in particular cases related to disease. We have been focused on formulating models of evolutionary dynamical processes with genotype-phenotype map, give a definition of phenotype based on the attractors of simple models of the dynamics gene regulatory networks, and simulate it in order to ascertain its dynamical properties. We have introduced a bipartite network to study genotype and phenotype together and their structural relationship. Also a way to understand their structure is to study their clustering coefficient, existence of communities, which are related to phenotypic robustness, or connectivity between communities (it means, innovation).