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Seminario Aleatorio

Sesión 355

A probabilistic view on the deterministic mutation-selection equation with pairwise interaction

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Abstract

We consider a classical deterministic model for the evolution of a haploid population with two allelic types which is subject to mutation, selection, and a special form frequency-dependent selection. The deterministic model arises (also) as the large population limit of the Moran model, in which neither parameters nor time are rescaled. Despite the deterministic nature of this limiting process, the ancestry of single individuals in the population is still stochastic. In the case with mutation and selection, the ancestral process is a random tree and a variant of the ancestral selection graph. To make the tree tractable, we prune branches upon mutations, thus reducing it to its informative parts. We connect the ancestral process to the deterministic model via duality; this leads to a stochastic representation of the deterministic solution. In particular, the stationary state obtains a nice probabilistic interpretation. We generalise the construction to the case with pairwise interaction.

Viernes 16 de octubre de 2020, 13:00 hrs. Hora de CDMX

<https://itam.zoom.us/j/95982068314?pwd=Z0pQZkJTYndxSzRHSTJyZk9HSUViUT09>

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El Seminario Aleatorio está destinado tanto a profesores como a estudiantes, por lo que el Departamento de Estadística agradece a los profesores que colaboren invitando a sus alumnos a estas sesiones.