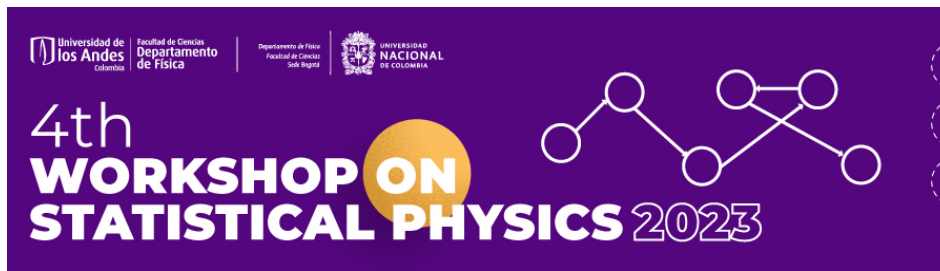


4th Workshop on Statistical Physics



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Tipo: **Poster**

A generalised model for noise propagation in transcriptional genetic cascades.

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Cellular processes are inherently stochastic, leading to protein level variations and gene expression fluctuations known as noise. Accurately understanding how noise spreads within gene networks is vital for creating gene circuits capable of withstanding noise and for comprehending signal reliability in biological networks. However, current models focusing on noise propagation are often limited to specific systems or short gene cascades. In response, we developed a novel model for noise propagation in gene expression using Langevin approach, applicable to networks comprising numerous genes, while considering the impact of the intracellular environment on gene expression. Our model offers a more comprehensive depiction of gene networks and proves valuable in the design of synthetic biological circuits in bacteria; moreover, it may shed light on how evolutionary processes shape circuit sizes to achieve both signal fidelity and cellular functionality.

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