Inferring admixture in wild populations of yeast using admixture graphs

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Demographic history of populations and events of gene flow can be inferred from genomic data by explicitly modeling population parameters such as effective population sizes, migration rates and others. Another approach is to represent history of a population as a graph, where admixing populations are connected with each other by graph edges.

In this meeting I will talk about one method for constructing admixture graphs and explore its utility for inferring admixture history in wild populations of yeast.

CAFÉ et BEIGNES seront offerts GRATUITEMENT !

Hôte : Club Bioinfo IBIS

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