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MAI.  
2008

🕒 de 16h30 à 17h30

## SÉMINAIRE

# Phenotypic Transitions in a multi-trait landscape

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A central question in molecular evolution concerns the nature of phenotypic transitions, in particular if neutral mutations hamper or somehow facilitate adaptability of proteins or RNAs to new requirements. Proteins and RNA have been found to accomplish different task by fluctuate between different phenotypes (structures), with frequencies and thus intensity of the associated trait being proportional to their stability. Therefore, functional promiscuity may correspond to different structures with energies close to the ground state which then represent multiple selectable traits. We here postulate that these near-ground state structures facilitate smooth transitions between phenotypes. Using biophysical model systems with exhaustive mappings of genotypes (sequences) onto phenotypes (structures), we demonstrate that this is indeed possible because of a smooth gradient of stability along which any phenotype can be optimised and also because of mutational proximity of similar phenotypes in genotype space. Our model provides a rationalisation of the intriguing, and otherwise puzzling experimental observation that adaptation to new requirements, e.g. latent function of a promiscuous enzyme, can proceed while the "old", phenotypically dominant function is maintained along a series of seemingly neutral mutations. Thus pleiotropy may facilitate adaptation of latent traits BEFORE gene duplications and increase the effective adaptability of proteins