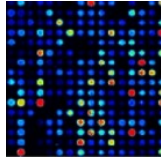


# SÉMINAIRE – MATH FOR GENOMICS

SÉANCE DU MERCREDI 7 MARS 2018. 10H30.  
EVRY. IBGBI. LAMME.

## Méthodes phylogénétiques comparatives



Laboratoire de  
Mathématiques  
et Modélisation  
LaMME d'Évry



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**Hélène CHIAPELLO & Mahendra MARIADASSOU (INRA)**

(joint presentation)

**Title: A survey of Phylogenetic Comparative Methods (PCM) with an application to the detection of coevolution in *Listeria* sRNA and coding genes.**

In this presentation we will introduce the problem of comparing two traits sampled on related organisms. We will first motivate this question with several examples taken from microbiology, notably a motivating example of detection of coevolution between sRNAs and coding genes in *Listeria*. We will in particular explain how and why naive comparison methods fail. We will then present the mathematical framework of Phylogenetic Comparative Methods (PCM) and discuss the biological assumptions and statistical tools it relies on. We will spend some time on recent developments made to model complex traits. We will finally return to our motivating example and present some results obtained by applying PCM to a *Listeria* phylogenomic dataset.