Institut de Minéralogie et de Physique des Milieux Condensés
Unité Mixte de Recherche 7590
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SÉMINAIRE
Lundi 11 février, 10h30

Salle de Conférence, 4ème étage, Tour 22-23, Salle 1
IMPMC, Université P. et M. Curie, 4, Place Jussieu, 75005 Paris

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BIOINFORMATICS TOOLS FOR TRANSCRIPTOME ANALYSES IN YEASTS

The characterization of gene regulatory networks (GRN) raises challenging questions regarding both the choice of the experimental datasets and the bioinformatics methodologies to examine these data.
In this context, transcriptome analyses give valuable information. Strategies to optimize simultaneously (i) the discovery and (ii) the cross species comparisons of GRNs will be presented and illustrated with the analysis of the transcriptional programs that drive the chemical stress response in three yeast species: the model yeast *Saccharomyces cerevisiae* and two pathogenic species *Candida glabrata* and *Candida albicans*.

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