



**30**  
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## SÉMINAIRE

# Probabilistic approaches for detecting and locating whole genome duplications.

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Whole Genome Duplications (WGDs) can be difficult to detect when they are old and when synteny has been disrupted by genome rearrangements. To test the presence of WGDs on a species phylogeny, I will present two methods which do not require synteny information and build strength from the phylogenetic framework. They rely on a probability model for the evolution of gene families on a species tree with WGDs. Both methods use multiple gene families across multiple species. One method relies on aligned molecular sequences and the other simply uses information on gene counts. We assessed their performance with simulations and on a benchmark yeast dataset, where we recover strong evidence for a well-established WGD and a low retention rate of duplicated genes after this WGD.