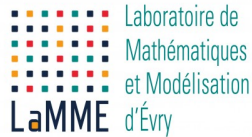
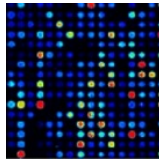


SÉMINAIRE – MATH FOR GENOMICS

SÉANCE DU MERCREDI 10 JANVIER 2018. 10H30.

EVRY. IBGBI. LAMME.

Problème d'assemblage de génomes



Véronique BRUNAUD (IPS2)

Title : Use case of an assembly with arabidopsis transcriptome, limits and views.

I will show an application of the most popular algorithm (based on de Bruijn graphs) to evaluate the assembly of RNA-Seq samples. I will present the biological context, problems and why biologist need these tools.

Briefly, one has to cope with

- the fact that the genome or transcriptome is unknown
- the millions of short sequences (or reads) to merge in one transcript
- the fact that a locus does not correspond to a unique transcript.

The main objective is to detect new objects :

- a reference
- new gene annotations
- new transcripts...

but there are many limits with complex genomes.

Michel KOSKAS (AgroParisTech)

Title : TBA