

# Qlife

# Quantitative Biology Winter School Series

## THE GENOMICS OF TRANSPOSABLE ELEMENTS

UNMASKING THEIR COMPLEX CONTRIBUTION TO GENOME FUNCTION AND EVOLUTION

FEBRUARY 6<sup>TH</sup> - 10<sup>TH</sup>, 2023 - PARIS

### LECTURERS & SPEAKERS

Chloé Agathe AZENCOTT, Paris  
Rebecca BERRENS, Cambridge  
Deborah BOURC'HIS, Paris  
Vincent COLOT, Paris  
Sandra DUHARCOURT, Paris  
Richard DURBIN, Cambridge  
Josefa GONZALEZ, Barcelona  
Gaël CRISTOFARI, Nice  
Michael IMBEAULT, Cambridge  
Jan KORBEL, Heidelberg  
Leandro QUADRANA, Saclay  
Helen ROWE, London  
Felipe KARAM TEIXEIRA, Cambridge  
Jose TUBIO, Santiago de Compostela

### SCIENTIFIC COMMITTEE CHAIR

Vincent COLOT, Paris

### COORDINATOR

Patrick CHARNAY, Paris

Genomics has revealed beyond any doubt that transposable element (TE) activity has significantly shaped the structure and function of extant genomes, ranging from bacteria to humans. Indeed, TE sequences are the main constituent of genomic DNA in many eukaryotic species and they have been co-opted at the macroevolutionary timescale to provide new protein functions as well as sequence motifs involved in the rewiring of gene regulatory networks. Ongoing TE mobilization is also an important generator of genetic diversity, with broad implications for health, disease and adaptation. Moreover, thanks to the epigenetic mechanisms that target them, TE sequences can influence the expression of genes in their vicinity in ways that are distinct from the effects of SNPs and other small size sequence polymorphisms. However, because TE sequences are typically present in large number of copies, which complicate their analysis, we still lack a comprehensive understanding and quantitative assessment of their multiple possible impacts in extant genomes.

The course will assemble world-leading experts from diverse fields to present recent advances in genomics and computational science that make it now possible to study at scale TE sequences and their varied effects. It will constitute a venue for cross-disciplinary discussions, with the goal of catalysing collaborations and of offering a novel conceptual basis for addressing questions on the contribution of TE sequences to organismal biology, disease, adaptation and evolution. The computational workshops will illustrate how robust and quantitative methods based on recently developed computational toolkits can be implemented to unmask and interrogate TE sequences in genomes.

Common lunches and dinners with the speakers and instructors will foster informal discussions. The winter school is limited to 24 participants. It is open to Master 2 and PhD students, as well as postdocs, engineers and junior scientists with backgrounds in life science, chemistry, physics, computer science or mathematics.

Basic experience in data handling under Unix/Linux and in Python or R programming is required.

Additional information is available at:

<https://www.enseignement.biologie.ens.fr/spip.php?article261>

**APPLICATION DEADLINE DECEMBER 4<sup>TH</sup>, 2022**

REGISTRATION FEES: 150 €\*

- Registration link: <https://forms.office.com/r/fBVAMyLV52>
- In addition, provide a CV, a 1 page motivation letter (including justification for travel grant if requested) and a supporting letter from a supervisor with "Qlife TE Genomics WS 2023\_LASTNAME" as subject header to [qlife.events@psl.eu](mailto:qlife.events@psl.eu)

\* Fees cover food and lodging from Monday morning to Friday afternoon. Some travel grants will be available.

