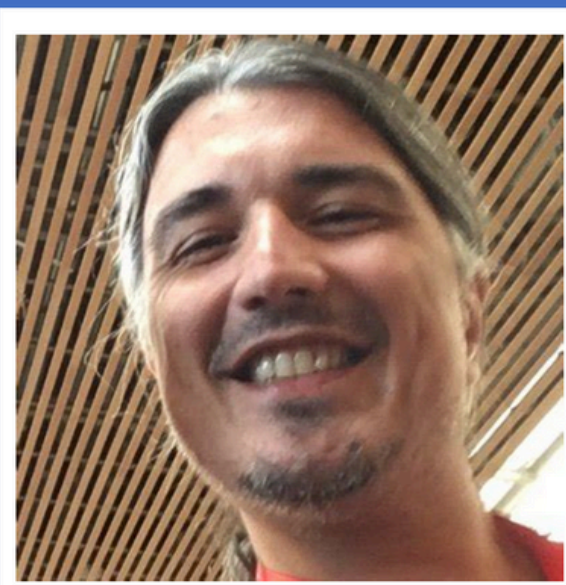




IBGC INVITED SEMINAR

MONDAY 7 JULY 2025
15H00

IBGC CONFERENCE ROOM



Thomas DERRIEN

Institut de Génétique et Développement de
Rennes, UMR6290

Invited by **Macha Nikolski** and
Daniel Garcia Ruano



EXPLORING THE NON-CODING GENOME THROUGH LONG-READ SEQUENCING

Long-read sequencing is opening new frontiers in transcriptome analyses by enabling the direct observation of full-length RNA molecules, thereby overcoming some limitations of short-read assembly. In this talk, I will present recent work from our group that combines long-read technologies with novel computational tools to uncover hidden layers of transcriptome complexity. I will introduce ANNEXA, a method we developed for context-specific annotation of long non-coding RNAs (lncRNAs) and will highlight our benchmark results on circular RNA (circRNAs) discovery with long-read RNASeq data. These approaches highlight how long-read technologies can deepen our understanding of the non-coding transcriptome, with accurate annotation as a necessary step toward functional exploration.