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Our group focuses on two main axes: **phylogenomics** (i.e. the inference of evolutionary history based on genomics data) and **evolutionary genomics** (understanding the molecular and population processes that drive genome evolution). We see genomes both as a subject of research (how do genomes evolve, why are they structured the way they are?), but also as a main source of empirical knowledge about the macroevolutionary patterns (what do they tell us about the history of life on Earth?), or about the phenotypes and life-history strategies of organisms. Our works heavily rely on methodological developments (bioinformatics, modeling and statistical inference).

Evolution of genome architecture and expression

Genomes are the result of a long-term evolutionary process, shaped by multiple evolutionary forces. Some genomic features are adaptive (i.e. are beneficial for the fitness of organisms), others result from non-adaptive processes (random drift and biased gene conversion – BGC) or are caused by conflicts between multiple levels of selection (e.g. meiotic drive or the spread of selfish genetic elements). We explore different aspects of genome architecture (base composition landscapes, genome structure and size, impact of transposable elements, ...) or functioning (gene expression, lncRNAs, epigenetic landscapes, ...), and try to disentangle the relative contribution of adaptive and non-adaptive processes to their evolution. For this purpose, we consider both the molecular mechanisms (mutation, repair, recombination) and the population processes (selection, drift, BGC, ...) that shape genetic variation.

Phylogenomics

We are interested in reconstructing the history of life on Earth. This research unfolds along several axes. First, we develop phylogenomic databases of aligned genetic sequences (e.g.

[BIBI](#) ↗

,

[RiboDB](#) ↗

or

[HOGENOM](#) ↗

). Second, we conduct methodological research on how to accurately reconstruct deep phylogenies, infer divergence times, reconstruct ancestral genetic sequences, gene repertoires and life-history traits. This methodological work is translated into publicly available software programs (e.g.

[SeaView](#) ↗

,

[PhyloBayes](#) ↗

,

[Coevol](#) ↗

). Finally, we apply these approaches to several important problems, among which: reconstructing the phylogeny of animals, of archaea, or the global tree of life; using phylogenies and ancestral gene repertoires to investigate the evolution of complex systems and the emergence of molecular and cellular functions in the three domains of life; reconstructing ancestral genetic sequences, a research activity that has industrial and biotechnological applications.

Teaching and outreach

We teach at University Lyon 1(

[Master Bioinfo@Lyon](#) 

), INSA, ENS Lyon, we organize bioinformatics internships. We regularly give conferences on evolution (tree of life, human evolution, genetic diversity, ...).

Prospective students and postdocs are invited to apply, as we often welcome visitors for internships or research projects.

Keywords: Molecular evolution and Population Genomics; Phylogenomics; Computational Genomics; Comparative genomics; Bioinformatics; Statistical inference.