GECO EVOLUTIONARY AND COMPUTATIONAL GENOMICS

BIOINFORMATICS, PHYLOGENY AND EVOLUTIONARY GENOMICS GROUP

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Research Interests: "Nothing in a genome makes sense, except in the light of molecular evolution"...

Genomes are the product of various evolutionary processes: certain genomic traits that we observe today reflect functional constraints that currently operate or that have operated in the past; others result from non-adaptive processes. **To identify the features of the genome that are important for its functioning, it is necessary to look for features whose mode of evolution deviates from the neutralist model**: this is the basic principle of the comparative analysis of genomes, which is at the heart of all my research activity. My work follows a double logic: **study the evolution of genomes to better understand how they work** - and *vice versa*, **take into account the molecular mechanisms of genome functioning in order to better interpret sequence evolution**. We explore genetic diversity at different level, both across species and within species (population genomics). My work is based on bioinformatic and statistical analysis of sequences, but also relies heavily on close collaborations with 'wet-lab' biologists.

These last years, my main focus has been on exploring the **consequences of homologous recombination on genome evolution**. In particular, we have discovered that in many species, recombination induces non-Mendelien inheritance, favoring the fixation of GC-alleles (gBGC – for GC-Biased Gene Conversion). This non-adaptive process has a major impact on the evolution of genomic landscapes and also on gene expression processes. We are now trying to understand how and why does gBGC evolve, and how and why do recombination rates vary in space (along chromosomes) and in time (across species).

I am also interested in **understanding how the constraints imposed by the cost of gene expression shape genome evolution**. We have shown that gene expression level is an important determinant of selective pressures acting on numerous features: on protein sequences, on gene dosage, on splicing accuracy, and on translation efficiency. We are now exploring how variation in the efficacy of selection contributes to the evolution of the complexity of gene expression patterns across species.

I am also working, in collaboration with researchers from Paris and Gif, on the genomics of *Paramecia*. This unicellular eukaryote displays many very peculiar features that make it a fantastic model to explore various topics (whole genome duplications, proliferation of selfish genetic elements, alternative splicing, transgenerational inheritance of epigenetic modifications, ...).