From Regulatory Networks to Embryonic Architecture: a Computational Perspective into the Genomic Syntax of Developmental Programs

Director of Studies: Lorena Buono

Department Biology and Evolution of Marine Organisms

Seat: Naples

Abstract

Over the past two decades, Next Generation Sequencing (NGS) technology has revolutionized biology, providing an unprecedented opportunity to unravel intricate genetic landscapes governing development and evolution. Its high-throughput nature allows cost-effective sequencing of genomes, transcriptomes, and epigenomes, empowering researchers to explore genetic and regulatory mechanisms with unparalleled precision. NGS has facilitated comparative genomics, enabling comprehensive analyses of evolutionary relationships, unveiling conserved pathways, and identifying lineage-specific innovations crucial for understanding life form diversification. The onset of NGS techniques has not only propelled unprecedented advancements in genetic data generation but has also catalyzed a parallel revolution in computational biology and bioinformatics, leading to the development of sophisticated tools and algorithms for data analysis. These computational advancements streamlined genomic analyses and accelerated research through integrative approaches merging diverse omics data to unveil complex biological phenomena. The symbiotic relationship between NGS and bioinformatics constitutes the basis for this PhD project proposal. The present project aims to exploit a bioinformatics approach to delve deeper into the genomic syntax of deuterostome regulatory dynamics during the early stages of development, uncovering similarities and dissimilarities among three different organisms with a key role for evolutionary studies: the echinoderm *Strongylocentrotus purpuratus*, the cephalochordate *Branchiostoma lanceolatum* and the urochordate *Ciona intestinalis*.

We aim to combine RNA-seq, ATAC-seq, and Hi-C NGS data from distinct embryonic stages of the aforementioned marine organisms. This holistic approach involves the integration of differential gene expression, chromatin accessibility and 3D genome structure to build a comprehensive model of the genetic programs governing early developmental stages, with a special focus on gastrulation. Gastrulation is a key developmental process that establishes the germ layers and lays the foundation for the body plan formation. Given the remarkable conservation of gastrulation across species, our comparative study represents a crucial focal point for deciphering the evolutionary relationships of embryonic development across different species, contributing to our understanding of the shift from simpler organisms to more complex animals.

This investigation holds the potential to uncover shared ancestral elements and outline evolutionary divergence. This offers valuable insights into the driving forces behind selective pressures and adaptive processes that shape genetic dynamics, particularly in body plan formation. Through comparative analysis, it will highlight both shared and distinct features, deepening our understanding not only of conserved regulatory programs but also on how different species achieve similar outcomes through distinct genetic pathways. Furthermore, the implications span biomedical applications, potentially providing targets for studying human health and genetic diseases. Finally, yet importantly, the use of computational methods to analyze regulatory genomic syntax could lead to the development and fine-tuning of novel and more efficient bioinformatics tools and algorithms for comparative genomic analyses.