According to the central dogma of molecular biology, the genetic information encoded in DNA (genes) flows to messenger RNA (mRNA) through the process of transcription, and then mRNA molecules are transported from the nucleus to cytoplasm and serve as templates for proteins synthesis. RNA is a fascinating biomolecule that not only carries genetic information from DNA to proteins but also directly regulates many processes in the cell through its ability to fold into complex secondary and tertiary structures. Studying RNA architecture and its interactions with other RNA or protein in the cell is fundamental to understanding the function of RNA in biological processes. For a long time, little was known about how RNA folding occurs *in vivo,* but the recent development of new, sophisticated methods for the measurement of RNA structures in living cells has revolutionized the field of RNA structural and functional studies. Coupling RNA chemical mapping with next-generation sequencing and advanced bioinformatics tools has shifted the perspective from single RNA studies *in vitro* to thousands of RNA molecules in complex cellular environments. These new approaches have revealed many novel insights into mRNA structure and showed important differences in the *in vivo* and *in vitro* mRNA folding. However, despite intensive studies, we are only beginning to understand the correlation between mRNA structure and function in the cell, and it still unclear how mRNA structure is regulated in the cell environment.

In this project, we will use recent technological advances to explore the structure of thousands of mRNA molecules in living cells. We aim to explain why mRNAs adopt a different structure *in vivo*, how mRNA structures change throughout the mRNA lifecycle, and how mRNA structures regulate the cellular processes. Our studies will be carried in yeast (*Saccharomyces cerevisiae),* an excellent model organism for studying the molecular basis of biological processes. Yeast cell organization is similar to that of higher organisms, and a significant fraction of fundamental functional pathways are evolutionarily conserved between yeast and human. To our knowledge, this project will be the first study of mRNA structure across yeast cell compartments (nucleus and cytoplasm) and in yeast inhibited for protein synthesis.

This project will increase the knowledge about the native mRNA structure in the cellular environment and the role of mRNA architecture in the cellular processes. Understanding how mRNA translation and stability are regulated by mRNA structure is also critical for developing mRNA vaccines and other mRNA therapeutics. We will also create and make available to the scientific community an online database containing thousands of experimentally-supported structures of *S. cerevisiae* mRNA. This rich source of information about yeast mRNA *in vivo, in vitro,* and in the cellular compartments will open new areas of investigation for many scientists.