In the post-genomic era, there is a growing need for new experimental paradigms for investigating the links between genomics and biology. While entire genome sequences of many model systems are now available, the task of deciphering the genetic code requires characterizing the phenome of these systems in order to establish the genotype-phenotype links. This need has led to the development of new quantitative phenotyping technologies across different levels of the biological hierarchy.

In this talk, I present new computational techniques to conduct image-driven in vivo phenotyping at the cellular level. The techniques have been developed in the context of investigating phenotypic variations of cells in cancer. Studies over the last decade have provided mounting evidence that the normal cells and molecules that surround tumor cells - collectively termed the tumor microenvironment - are involved in the initiation, growth, and spread of tumors. While examples of this phenomenon have been characterized in studies from a genetic standpoint, the lack of appropriate methodolo-