

Title:

Defining the Components Of Local Signaling Networks That Regulate Cell Morphology Using Quantitative Morphological Signatures.

Abstract:

Classical genetic and biochemical approaches have identified hundreds of unique proteins that play roles in the dynamic remodeling of cell shape, but there is little understanding of how these proteins are physically organized into networks in subcellular space, and how information flows through this sophisticated molecular circuitry in real-time. In order to model the signaling networks that regulate cell shape, we have developed technology in order to quantify single cell morphology in a fast, robust, and cost-efficient manner. We are using this technology in tandem with systematic high-throughput RNAi screening to develop quantitative morphological signatures for every gene in the Drosophila genome. This compendium of signatures represents a novel dataset that can be used to determine relationships between genes, predict gene function and protein localization, or that can be integrated using computational methods with publicly available datasets to generate a comprehensive model of a signaling network that controls cell shape.