High-Content Movement Analysis as a Diagnostic Tool in *C. elegans* PETER WINTER, ANDREA LANCICHINETTI, Department of Chemical and Biological Engineering, Northwestern University, LEAH KREVITT, Department of Biological Sciences, Northwestern University, LUIS AMARAL, Department of Chemical and Biological Engineering, Northwestern University, RICK MORIMOTO, Department of Molecular Biosciences, Rice Institute for Biomedical Sciences, Northwestern University — Many neurodegenerative diseases manifest themselves through a loss of motor control and give us information about the underlying disease. This loss of coordination is observed in humans and in the model organisms used to study neurodegeneration. In *Caenorhabditis elegans*, there is an extensive genetic library of strains that lack functional neuronal signaling pathways and expressing proteins associated with neurodegenerative diseases. While most of these strains have decrease motility or cause paralysis, relatively few have been screened to look for more subtle changes in motor control such as stiffness, twitching, or other changes in behavior. we use high-resolution position and posture data to automatically analyze the movement of worms from different genetic backgrounds and characterize 14 movement characteristics. By creating a quantitative mapping between the movement characterization and an online database of gene annotation, gene expression, and anatomy, we aim to predict a likely set of cellular and molecular disruptions. This work provides a proof of concept for the use of detailed movement analysis to uncover novel disruptions in certain motor control processes. Knowledge of the molecular origin of these disruptions provided by our understanding of *C. elegans* genetics and physiology could lead to new diagnostic and therapeutic targets for neurodegenerative disease.

Andrea Lancichinetti
Department of Chemical and Biological Engineering,
Northwestern University