# A COMPUTATIONAL APPROACH FOR CYTOSKELETAL ORGANIZATION CHARACTERIZATION

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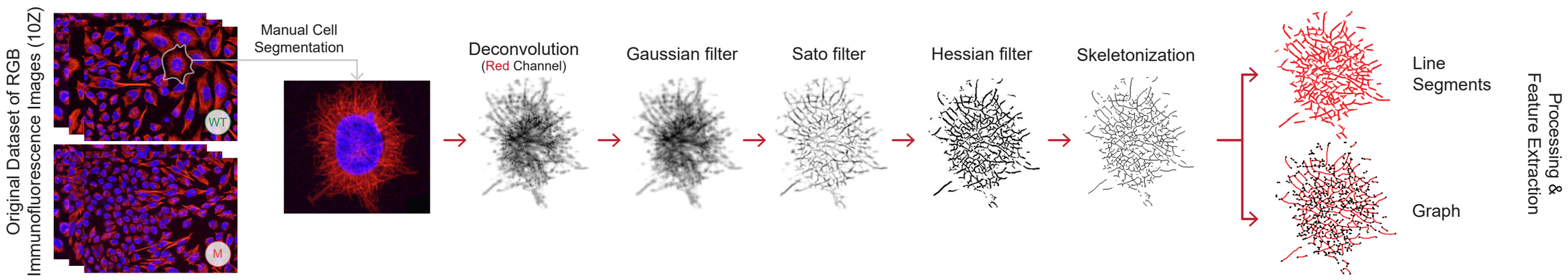
## INTRODUCTION & OBJECTIVES

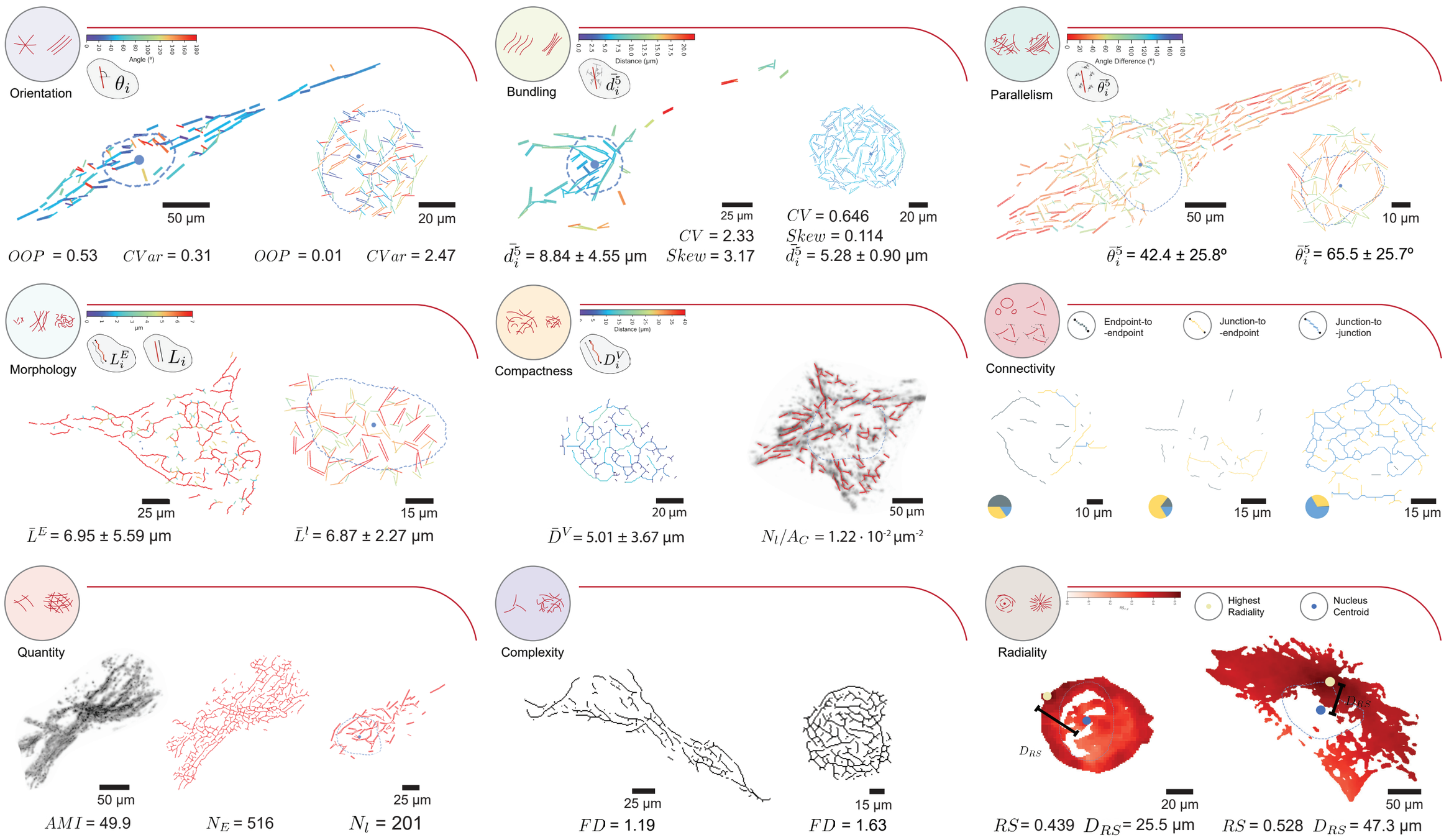
The **cytoskeleton** is a complex fibrous network spanning the whole cytoplasm [1, 2]. Composed of regulatory and structural proteins, it is pivotal in maintaining cellular architecture and in modulating various cellular processes such as migration and invasion [3,4]. It is well established that during **cancer** progression, cells undergo cytoskeleton reorganization through the dynamic interplay of its components, including **microtubules** [5].

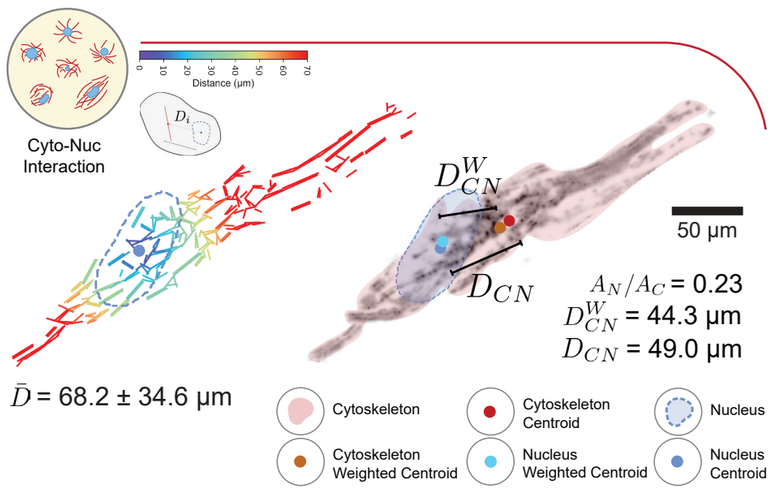
However, little is known on how cytoskeletal proteins are remodeled and how these modifications cooperate to mediate cell invasion. Thus, in this work, we have developed a novel computational approach, based on **image processing** and **feature extraction**, to asses and quantify **cytoskeleton organization**. Specifically, we have investigated immunofluorescence images of cells labelled for α-tubulin and expressing wild-type (**WT**) or mutant (**M**) forms of E-cadherin, as a model of **non-invasive** and **invasive** phenotypes, respectively [6].

## METHODS

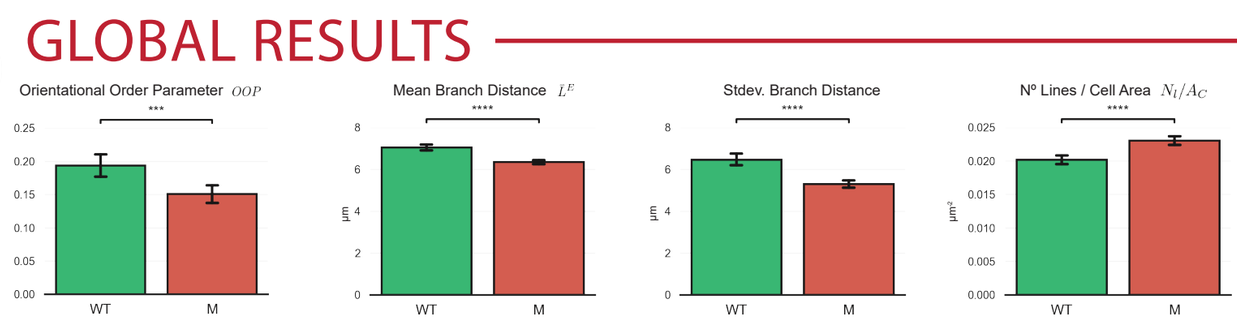



## CYTOSKELETON ORGANIZATION




## GLOBAL RESULTS




Microtubules of mutant cells (**M**) (invasive potential) were shown to have more **dispersed orientations**, to be **shorter**, to have **uniform length patterns** and to be more **compactly distributed**, compared to **WT** cells (without invasive potential).

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