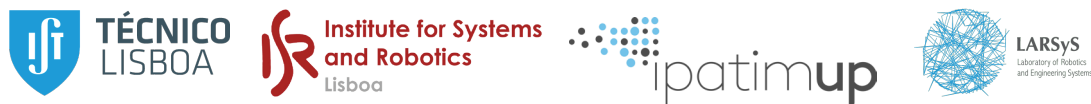


UNRAVELING THE CYTOSKELETAL ARCHITECTURE OF CANCER CELLS: DEVELOPMENT OF A NOVEL COMPUTATIONAL APPROACH

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LARSyS Annual Meeting | 17 & 18 July 2023

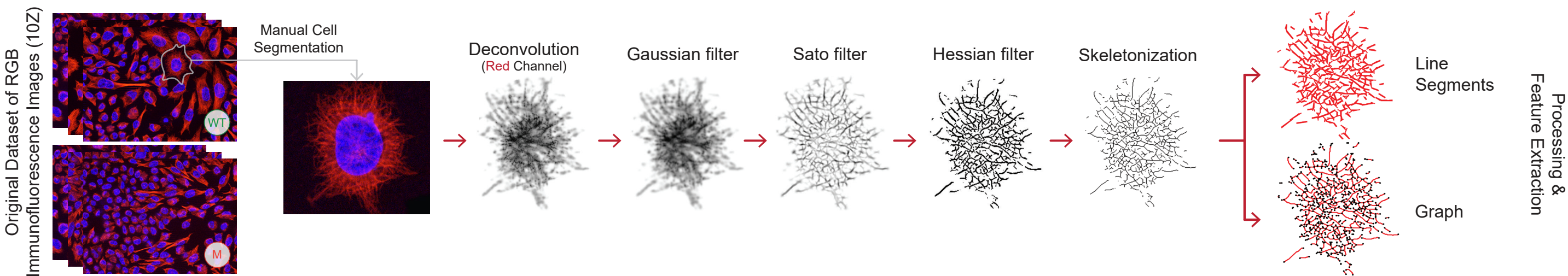


INTRODUCTION & OBJECTIVES

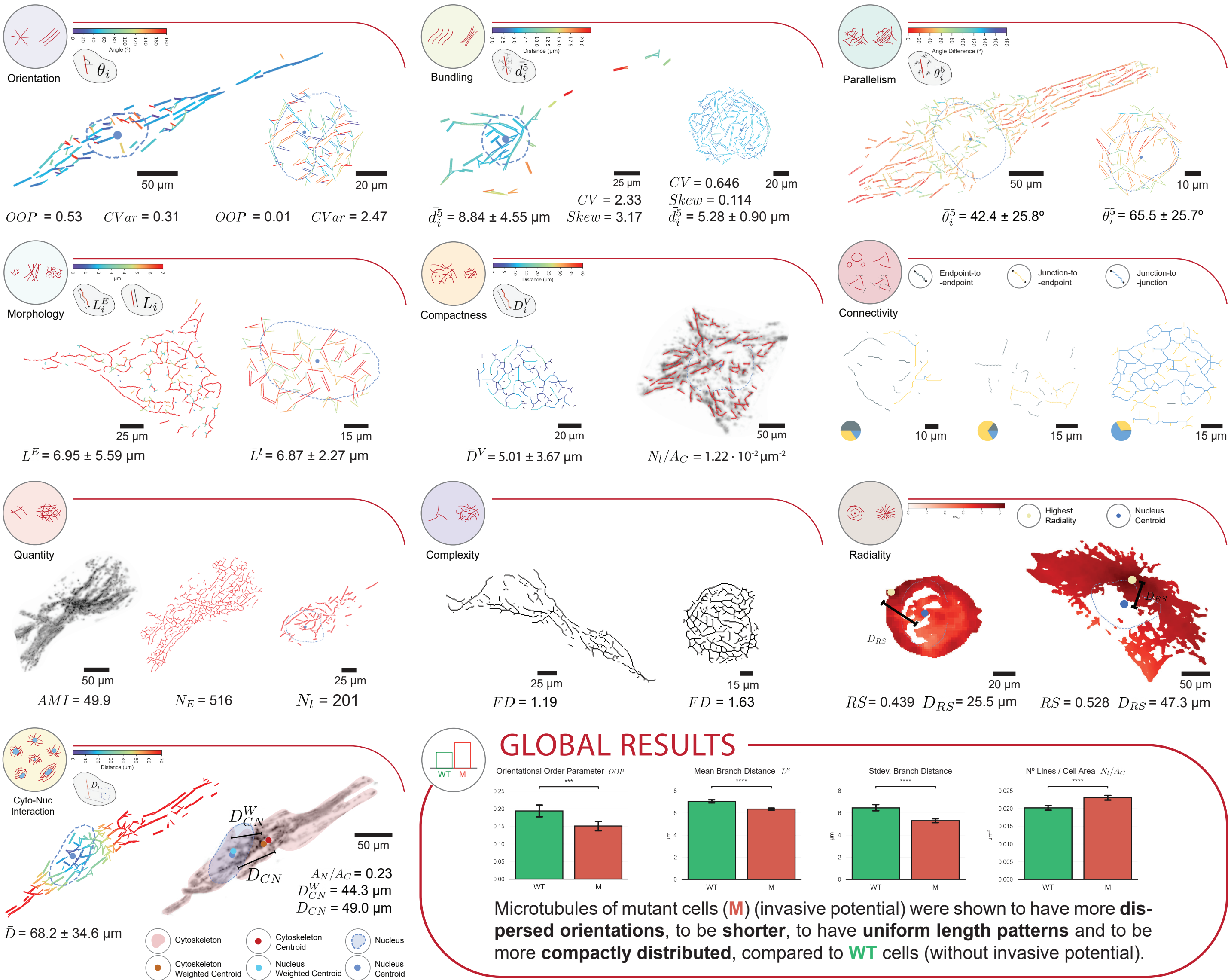
The **cytoskeleton** is a complex fibrous network spanning the whole cytoplasm [1, 2]. Composed of regulatory and structural proteins, it is pivotal in maintaining cellular architecture and in modulating various cellular processes such as migration and invasion [3,4]. It is well established that during **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 **cyto-skeleton 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



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ACKNOWLEDGEMENTS

Porto Comprehensive Cancer Center Raquel Seruca, Portuguese Foundation for Science and Technology (FCT), under the projects 2022.02665.PTDC, EXPL/MED-ONC/0386/2021, LARSyS-UIDB/EEA/50009/2020, NORTE-01-0145-FEDER-000029. The authors acknowledge "No Stomach for Cancer" for funding Seruca's research.