



# Characterization of E-Cadherin Distribution from Fluorescence Images

J. Miguel Sanches<sup>1,2</sup>, Joana Figueiredo<sup>3</sup>, Isabel Rodrigues<sup>1,3</sup>, Raquel Seruca<sup>3</sup>

<sup>1</sup>Institute for Systems and Robotics, <sup>2</sup>Department of Bioengineering-Instituto Superior Técnico / Technical University of Lisbon, Portugal

<sup>3</sup>Instituto Superior de Engenharia de Lisboa (ISEL)

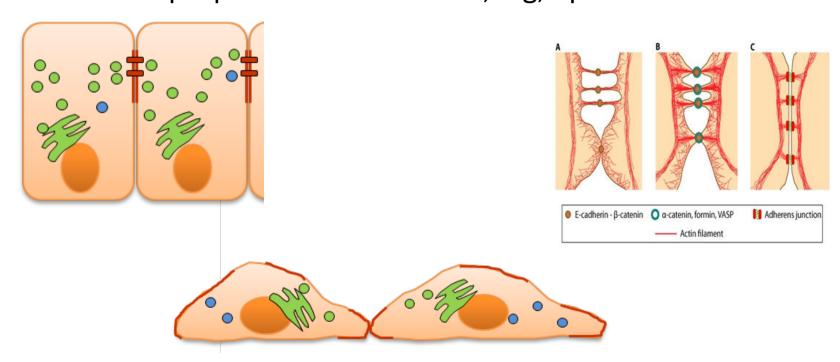
<sup>4</sup>IPATIMUP - Institute of Molecular Pathology and Immunology of the University of Porto, Portugal



#### Cell Adhesion



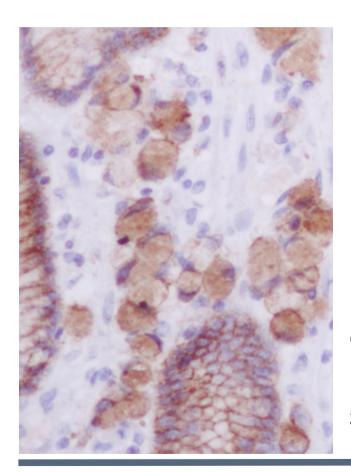
Physical linkage between cells is the basis of structural mechanical properties of the tissues, e.g, epithelial tissues

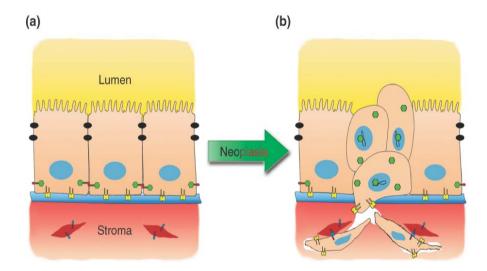




### Aberrant adhesion







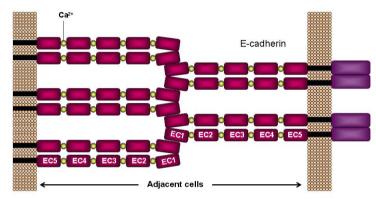
Cells become **non-adherent** and gain an increase ability to invade the surrounding tissue, e.g., cancer

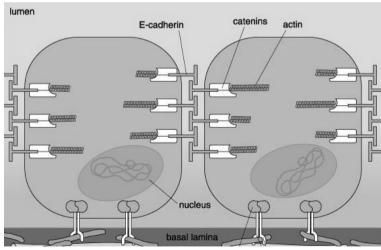


#### E-Cadherin



- E-cadherin is a central protein in cell-cell adhesion.
- Mutations on E-Cadherin gene (CDH1) lead to a dysfunctional molecule.
- These mutations are involved in epithelial cancer progression.







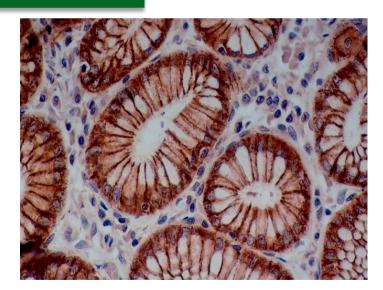
### E-Cadherin Distribution



The distribution of E-Cadherin molecule in normal cells is mainly observed at the membrane, where it plays its role in cell-cell adhesion.

#### Normal stomach tissue



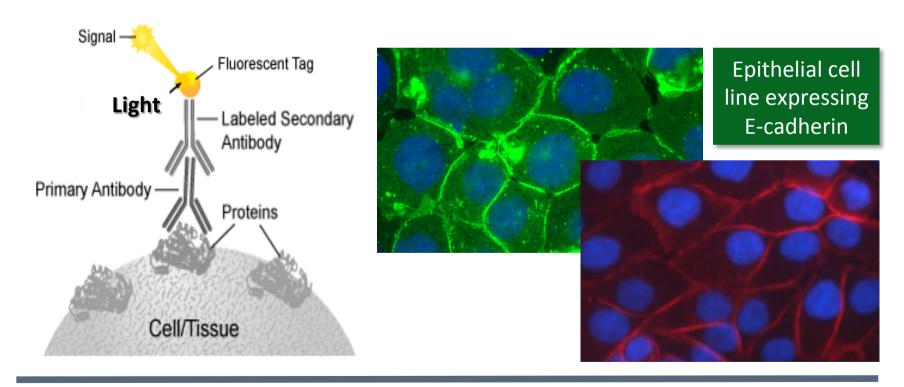




### Fluorescence Imaging



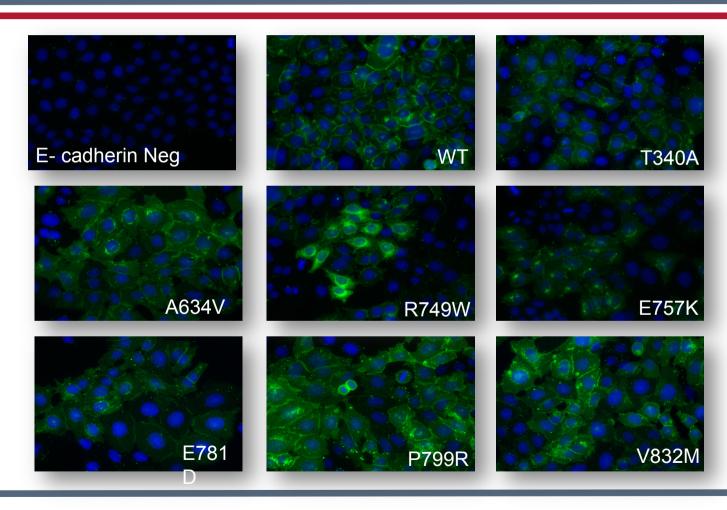
E-Cadherin distribution can be observer in epithelial cell line labeled with E-Cadherin tagged anti-body





# E-Cadherin Mutations Cell distribution

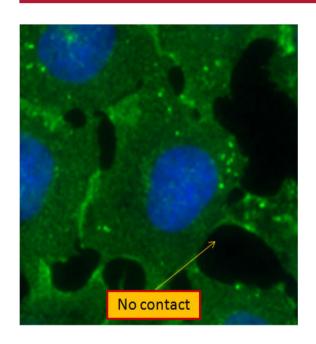


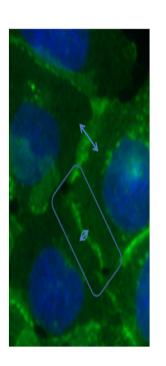


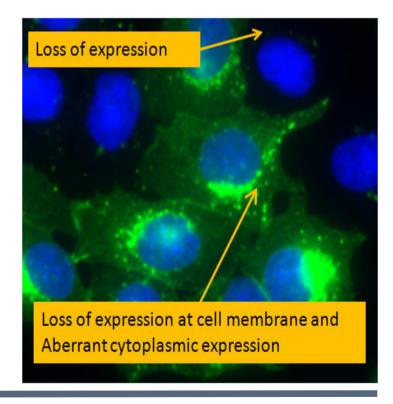


### Key features











# E-Cadherin distribution characterization

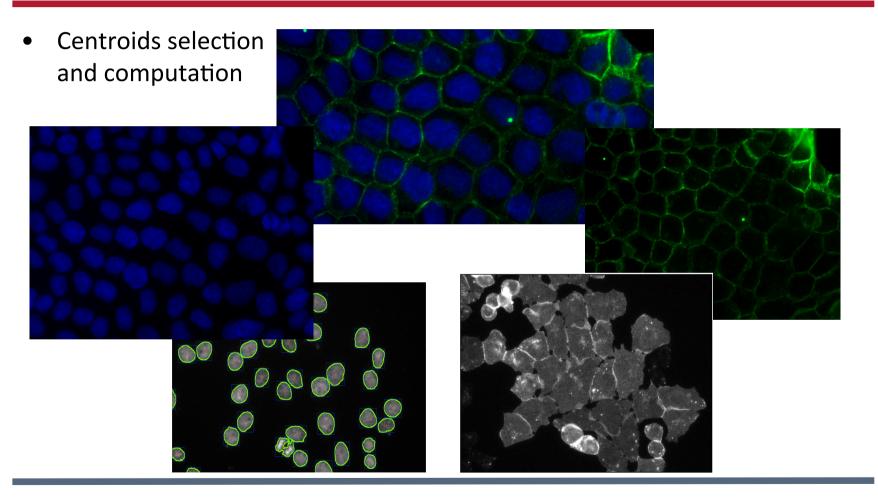


- Pre-processing and semi-automatic cell selection
- 2. Image radial profiles computation
- 3. Compensation for geometric distortions
- 4. Features extraction and distribution characterization



# Cell centroid estimation and semi-automatic selection

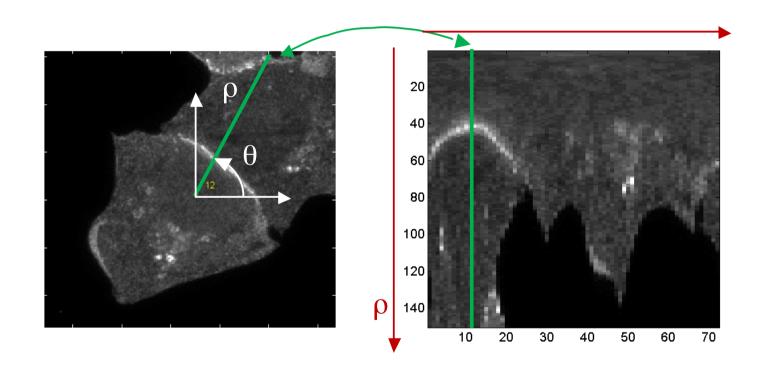






# Image of intensity profiles







### Geometric compensation



- Each profile (column) is modeled as a finite dimension 1D continuous function estimated by imposing similarity among columns
- The locations, x, of the original observations are adjusted in this continuous space according an energy function

$$f_{\theta}(\rho, \mathbf{x}_{\theta}, \mathbf{c}_{\theta}) = \sum_{k} c_{k,\theta}(\mathbf{x}_{\theta}) \phi_{k}(\rho)$$

$$\mathbf{c}_{\theta}^{t} = \underset{\mathbf{c}}{\operatorname{argmin}} \left\| f_{\theta}(\rho, \mathbf{x}_{\theta}^{t-1}, \mathbf{c}_{\theta}) - \mathbf{y}_{\theta} \right\|^{2} + \alpha \left\| D\mathbf{c}_{\theta} \right\| + \beta \left\| \mathbf{c}_{\theta} - \mathbf{c}_{\theta'} \right\|^{2}$$

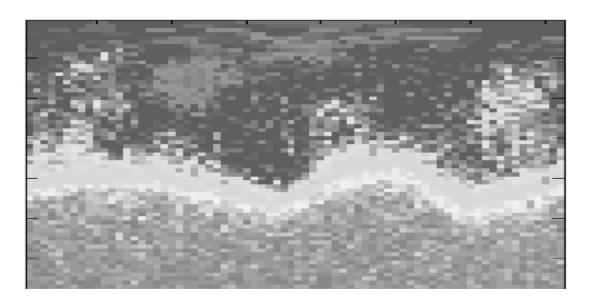
$$\mathbf{x}_{\theta}^{t} = \underset{\mathbf{x}}{\operatorname{argmin}} \left\| f_{\theta}(\rho, \mathbf{x}_{\theta}, \mathbf{c}_{\theta}^{t}) - \mathbf{y}_{\theta} \right\|^{2} + \gamma \left\| D\mathbf{x}_{\theta} \right\|^{2}$$



# Distribution characterization



- Image profiles 2D based characterization
- Prototype profile estimation1D based characterization





#### **Conclusions**



- Distribution of E-Cadherin protein across the cell from fluorescence images of microscopy
- Characterization metrics for discrimination for CDH1 gene mutations
- Radial E-Cadherin prototype distribution
  - Geometry invariant





# Thank you

J. Miguel Sanches

(jmrs@ist.utl.pt)