Identifying Sub-Cellular Domains in PC3 cells by Analysing Caveolin-1 Proteins from Nanoscopy Super-Resolution Data

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1 The Biology

**Caveolae**
- Omega-shaped small (50-100 nm) invaginations of the plasma membrane
- Formed by the polymerization of caveolin-1 (Cav1) and Cavin-1/PTRF (Polymerase I and transcript release factor)
- Contain a subset of lipid-raft components

**Cav1 Scaffolds**
- Cav1 has been described to function outside of caveolae, in structures we term “Cav1 scaffolds”
- Caveolae and scaffold are responsible for many cell functions.

2 Image Acquisition

**Wide field - TIRF**
- Cav1 & PTRF proteins imaged using standard light microscopy

**GSD - TIRF**
- Cav1 & PTRF proteins imaged using super-resolution microscopy
- Below the diffraction limit of the standard light microscopy

3 Goals

- To study at nano-meter scale the Cav1 proteins in the two membrane domains: caveolae and non-caveolar Cav1 scaffolds
- To identify these two membrane domains, and study their distributions and structures

4 Methodology

**3D point cloud - PC3 cell**
- Network analysis: PC3 nuclei coloring based on degree at 7=159
- Filtering

**3D point cloud - PC3-PTRF cell**
- Network analysis: PTRF nuclei coloring based on degree at 7=208
- Filtering

- Scaffolds formed in the absence of PTRF protein in PC3 cells
- Caveolae and scaffolds formed in PC3-PTRF cells

5 Results

- Degree distribution at 7=208
- Distribution of points close to centroids: an indication of a hollow cluster

6 Conclusion

Using computational network analysis techniques and prior knowledge of size and shape properties, we were able to localize caveolae and scaffolds in super-resolution microscopy data

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