A Geometric Quantification of the plant Endoplasmic Reticulum

One of the most difficult obstacles to make biological sciences more quantitative is the lack of understanding the interplay of form and function. Each cell is full of complex shaped objects which moreover change their form over time. To tackle this problem we suggest to use geometric invariants which are able to produce precise reference points to compare the cell's different functional elements like organelles under fixed and varying physiological conditions. Here we look at the topology of a static sample of the plant cortical ER under normal physiological conditions using a multidisciplinary approach combining image processing techniques, visualisation, computational geometry and graph theory. We represent the ER network by its skeleton which can mathematically be interpreted by graph (Edges and nodes). The graph serves as an abstract quantification of the ER and can be considered as a geometrical invariant, even and importantly in cases where the ER sample is moving. Moreover graph theoretic features are very robust against different kinds of small perturbations which should not change the ER function. We obtain a 3D reconstruction (an isosurface) of the ER network by thresholding the stack of images, obtained by confocal microscopy. Finally we associate to each edge in the graph its length (using its skeleton), and its surface area and volume (obtained from its isosurface). From different samples under similar experimental conditions and for a threshold of 10 we found that the average length of an edge is 3.78 μm, its average surface area is 18.46 μm2, and its average volume 8.69 μm3. The study also show that the average number of edges emerging from a node is 3, its average surface area is 12.91 μm2 and its average volume 7.19 μm3