Fourier transform-based fast characterization of cell shapes as a tool for intelligent classification of cells In intravital microscopy

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In numerous tissue types, the kinetic behavior of cells as well as the complexity and the aspect ratio of their shapes adjust to short- and long-term changes in the actual physiological and pathological conditions of the tissue. Generally, the kinetic behavior of cells is characterized by the so called “cell tracks”, i.e. the time course of the 3-D location of the centroids of the cells, as well as by various parameters characterizing the volume of the tissue occupied by the cell and those describing the surface corresponding to the outer membrane of the cell. Cells are then often classified based on a number of these parameters, often guided by *a priori* knowledge provided by expert biologists or medical professionals. Whilst such approach will provide an excellent starting point for analyzing complex intravital image data, ultimately we will need faster methods for automated characterization and more intelligent tools for unbiased analysis that may also reveal hidden correlations amongst the track- and shape-describing parameters.
Here we propose the use of Discrete Fourier Transform (DFT) applied on multiple---angle cross sections of cells prepared automatically by a set of ImageJ/Fiji macros.
We find that the first 10 DFT parameters (F0–F9) are sufficient to describe even the complex shape of microglia in the healthy or cancerous tissue of the mouse brain, or that of the macrophages in the mouse gut under physiological or pathological conditions, imaged via two-photon intravital microscopy. After normalizing the DFT components (using the amplitude *Fi*=SQRT{Re(Fi)2+Im(Fi)2}) so that they are independent of the cell size (by dividing *Fi* (i={2..9}) by *F1*), we were able to find clusters in the Fourier parameter space by using methods of Artificial Intelligence (AI), e.g. Self-Organizing Maps (SOM).
These AI methods have also been successfully applied here to identify correlated cell tracks by training SVMs as well as SOMs on a selected group of cell tracking parameters.
In more complex cases, a 3-D SOM was necessary in order to provide adequate separation of track groups; however, for visualization purposes the 2-D version may be preferred in order to make comprehension easier for the observer. We further propose that such automated and unbiased methods may be used as part of the design of intelligent microscopes, where the actual flow of experiments can be continually adjusted based on the instantaneous analysis of the recorded 3-D and 4-D image stacks.