Topological Proteomics

a report on joint work with W. Schubert, P. Serocka, and A. Barysenka
and some relevant references

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Abstract

One of the most important aspects of cellular protein networks is the spatial distribution of the proteins across cell compartments and organelles (membranes, nucleus, mitochondria, etc.). That means that for some cellular function (like cell migration) to be exerted by its proteins, a cell has not only to synthesize the necessary amounts of the required proteins, but also to distribute them within the cell in the specific way that is also required for the cell function in question. Conventional proteomics profiling tools that are based on *homogenizing* cell samples do, almost by definition, not provide any information on this important aspect of molecular processes taking place in a cell — an aspect, however, that appears to be closely related to normal and abnormal functioning of the cell.

To provide such information, a new multi-parameter fluorescence-microscopy technique called MELK[1] was developed at Magdeburg University by Walter Schubert and his coworkers; it is discussed in [1] (see also [2, 3, 4, 11, 12]). Details regarding this technology and the tasks associated with the data obtained by using it are discussed in [5, 6]; for biological applications of MELK Technology, see [7, 8, 9,

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[1] *Multi-Epitop Liganden Kartographie*

10, 13]. This technique produces a whole stack of intensity images of one and the same biological object (for example, a slice of nervous tissue), each image in that stack corresponding to one particular protein (or any other biologically relevant molecule of interest). Two typical gray-level images are shown in Fig.1.

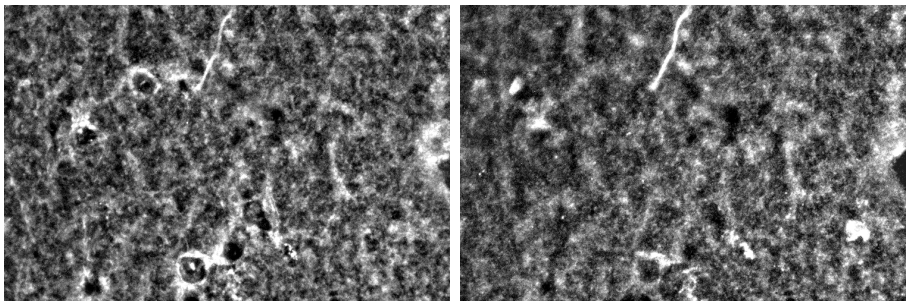

Figure 1: Two fluorescence images displaying the spatial distribution of two different proteins across a slice of nervous tissue.

This new technology poses, of course, many new challenges to data and medical image analysis. In the lecture, I will mainly deal with the particular important aspect of "correlated thresholding" for separating signal and noise in a stack of toponome images.

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