Statistical Analysis and Visual Exploration of Topological Proteomics Data (I,II)

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The new multiparameter fluorescence microscopy technique MELK (cf. http://www.meltec.de/frame01.htm) allows to produce a stack of intensity images of the same tissue sample, each image in the stack corresponding to one particular protein of interest. We present visualization and image processing tools for interactive visual exploration of the spatial distribution of protein patterns and for matching them with morphological data regarding the tissue sample in question.

In addition, considering such a stack of intensity images as a family of real-valued functions defined on the corresponding pixel set, we use Boltzmann statistics for identifying and quantifying positive and negative interaction in protein networks. More precisely, we determine *optimal* threshold values for these intensity functions that maximize the *mutual information content* of the resulting black & white images.

This will be illustrated using examples from current biomedical research projects.