Depth-varying joint segmentation/deconvolution of vines' wood in fluorescence microscopy

Viticulture plays an import economic role in France. Esca is an ambiguous fungal disease that causes wood decays, a major threat for the grapevine industry and to which no treatment is presently available. Understanding the colonization process is a key factor in developing cures for a sustainable viticulture. Using fluorescence microscopy, we observed graftlings samples of vines inoculated with fungus suspected to cause esca. The images we obtained present a dark-green autofluorescent textured background, while filamentary fungus appears in light-green fluorescence. Our goals are to separate the pathogen from its environment, and then quantify it. The point spread function (PSF) describes the response of an imaging system to a point source or point object. The degree of spreading (blurring) of the point object is a measure for the quality of an imaging system. The PSF of our instrument (Wide Field microscope) is known. We want to include this information into our segmentation process to compensate its effect. The segmentation is based on Triplet Markov fields (TMF). We have no guarantee that the pathogen is on the focal plane, so the depth at which it is situated is unknown. It is therefore necessary to jointly deal with both problems of non-stationary deconvolution and segmentation. The TMF comprise both a representation of the class and the depth involved in the image formation. The image model we consider is $\boldsymbol{y}=\boldsymbol{H}(\boldsymbol{v})* \boldsymbol{x}+\boldsymbol{b}$, where $\boldsymbol{y}$ is the observed image, $\boldsymbol{x}$ represents the intensity classes convolved with $\boldsymbol{H}$, the PSF matrix, and $\boldsymbol{v}$ is a Gaussian field representing the depths. Finally, $\boldsymbol{b}$ is an independent Gaussian noise. Since there is no available database for this kind of images, we work in an unsupervised context using the iterative SEM method to alternate between simulations of $\boldsymbol{x}$ and $\boldsymbol{v}$ and the estimation of the different parameters. We tested the algorithm on simulated images first, then on real ones, to extract the pathogen. We also compared our model to Pairwise Markov Fields (PMF), where the depth is considered the same in all the image. Our method achieved segmentation with at least 5% less errors than when using the PMF approach.