Mots clés :

- Directeur de thèse : Thomas BOUDIER
- Co-encadrant(s) :
- Unité de recherche : Laboratoire inconnu!
- Ecole doctorale : École Doctorale Informatique, Télécommunications, Électronique de Paris
- Domaine scientifique principal: Divers

Résumé du projet de recherche (Langue 1)

Image segmentation, being the main challenge in image analysis that deals with extraction of quantitative information. Segmentation partitions an image into a number of separate regions which might correspond to objects in the image. The simplest technique is thresholding, by considering a threshold below which pixels/voxels are assumed as background. Finding optimal threshold is critical; if the threshold is very low, the observed nuclei in fluorescent image are touching and requires a post-processing, on the other hand, with very high threshold, nuclei with low intensities will be deleted. Afterwards, qualitative information can be extracted directly from segmented image. However, in order to give more meaning to detected objects, these objects can be assigned to predefined classes. This challenge is carried out in this thesis through an automatic method of segmentation and classification which was applied to the study of cell cycle of nuclei in 3D/4D embryo microscopy images. Our method ensures optimal threshold for each object. In this thesis, we present two new segmentation techniques which are based on supervised learning of predefined classes of objects. The first technique of supervised segmentation is realized by combining machine learning and iterative thresholding (bottom-up thresholding). For each threshold, the detected objects will be classified. At the end of thresholding, to find optimal threshold for each object, the threshold that gives the highest probability of belonging in the stabilized class is taken. This technique was tested on three different datasets and gave good results despite the presence of temporal and spatial variations of intensity. In the same perspective, another technique based on a region-growing (top-down thresholding) approach was developed to overcome overlapping and inhomogeneous cell nuclei problems. This technique is based on region-growth from the local maximum. Once the regions meet, combinations of regions are created and combination that gives the highest membership probability to predefined classes of object is retained. The originality of this work is that segmentation and classification are performed simultaneously. The program is also generic and applicable to wide biological datasets, without any parameter (parameter-free).