Titre du sujet : Automatic Classification of biomedical images

Mention de thèse : ATSI

HDR Directeur de thèse inscrit à l'ED STIC : Barlaud Michel

Co-encadrant de thèse éventuel :
Nom :
Prénom :
Email :
Téléphone :

Email de contact pour ce sujet : barlaud@i3s.unice.fr

Laboratoire d'accueil : I3S

Description du sujet :
Classification Supervisée d'images de cellules

L'objectif de cette thèse est
- D'améliorer et adapter des algorithmes de classification basés sur le Boosting à la classification des cellules
voir la description et les publications

http://www.i3s.unice.fr/~piro/

- Appliquer la méthode dans le cadre de classification des cellules dans le cadre de radiothérapies en collaboration avec Pr Thierry Pourcher and Pr Jacques Darcourt, Tiro Lab, de la Faculté de médecine
English version:

Supervised Classification of biomedical images

The project addresses automatic classification of cell imaging in fundamental biology and medical research. The aim is to develop tailor-made programmes for the analysis of subcellular protein localisation and/or cell shape. Images are obtained with a high content microscope (a new facility of the School of Medicine of Nice) and will allow statistical analysis on a large number of cells. In cancer gene therapy, TIRO partner studies the use of the sodium iodide symporter (NIS) gene as a therapeutic transgene in a metabolic radiotherapy strategy (collaborative work supported by the French Cancer Institute, INCa). Automatic classification will allow better understanding of the post-transcriptional regulation of NIS targeting, as well as identification of the essential amino acid motifs involved in correct and efficient processing. This work could provide important clues for the design of a gene therapy-tailored NIS transgene. Many other projects of TIRO or other teams will benefit of this new method.

The basic idea of our new classification algorithm is to learn prototypes for classification in a boosting framework. There are two approaches:

- One-versus-all learning method, which brings the boosting principle into prototype-based classification, by defining prototypes as weak classifiers to be induced via the minimization of a risk functional. An inherently multiclass MLNN algorithm, that relies on generic density estimation kernels. Our novel approach performs close to Bayes risk on benchmark synthetic data, outperforming both kernel SVM and kNN Classifiers.

Experiments on some well-known benchmark real-world image datasets, which contain from 8 to challenging categories show that although our low complexity method (log n) improves classical uniform kNN and performances close to state of the art Support Vector Machine.

The goal of the proposed Thesis is both:

- Improve UNN and MLNN taking into specific features for this biomedical application, see http://www.i3s.unice.fr/~piro/
- Compare (in term of precision and complexity) with classical methods (kNN, SVM) classification of biomedical images (5 classes) in cooperation with Pr Thierry Pourcher and Pr Jacques Darcourt, Tiro Lab, see http://www.biophytiro.unice.fr/tiro/
Contact
Professor Michel Barlaud
Membre de l’Institut Universitaire de France
barlaud@i3s.unice.fr

URL: http://www.i3s.unice.fr/~piro/