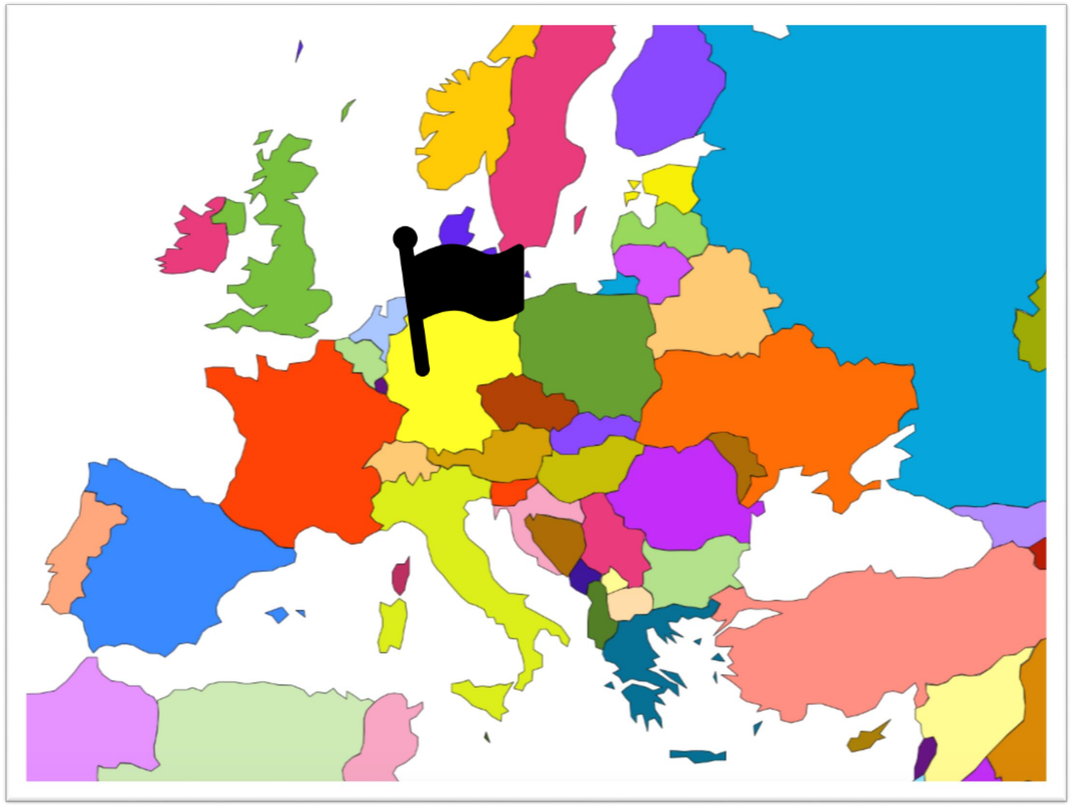
TESI @ UNIVERSITY OF MUNSTER (GERMANY)

Cells-in-Motion Cluster of Excellence (CiM) of the University of Munster actively work in the application of pattern recognition and machine learning techniques in biomedical applications.

Xiaoyi Jiang, the contact professor for the ERASMUS@University of Munster, is the head of the CiM.

Prof. Jiang in numbers: H-Index: 39; Citations: 7803



Required Skills for the thesis:

Machine Learning e Big Data Analytics, Artificial Vision

Give a look to the Lab Website

UNIVERSITÀ DEGLI STUDI DI SALERNO

Carmine Volpe

University of Munster

MOVING OBJECTS DETECTION AND TRACKING FROM VIDEO CAPTURED BY MOVING CAMERA

Abstract

The thesis aims to design, develop and testing an object detection algorithm based on the tracking of moving objects with a moving camera.
The most popular methods in the literature, in most of cases, constrain the environment in which the system is to be performed. The most common constraints are the following: (1) The system has to work in an environment already known a priori; (2) The movement of the camera must be constant or constrained; (3) The tracking is carried out on only one moving object. The system developed in this thesis has no restrictions: the input is any video with moving camera and, after a configuration phase, all the moving objects are detected and tracked and you can also view the same video with a bounding box around each moving object detected by the system.
To achieve the goal, the algorithm, for each frame, performs 5 phases. The first is the features extraction. To do this, two operations are carried out: the first is the use of the Sobel operator for the detection of all the edges of objects in the frame; the second is the use of Harris algorithm, which detects the corner of the objects (for each frame are extracted 5.000 features). In the second phase we extract, among all the features, those present in more consecutive frames, in order to compute the optical flow. For this purpose, we use the Lucas-Kanade algorithm. The third phase concerns the identification of the features belonging to moving objects (also called "dynamic" features), eliminating the remaining. To do so, we apply the principles of epipolar geometry: the distance is computed for each feature with the corresponding epipolar line and selecting the features with a distance greater than a threshold, predetermined during the training step. In the fourth phase, we implement a hierarchical clustering algorithm to detect moving objects. The algorithm creates a cluster (which is equivalent to an object) if it is composed of a minimum number of features. The rule for the aggregation of the features in one cluster is the maximum distance from the centre of the cloud. Finally, in the fifth phase, the tracking of the objects is carried out. Each object is associated with an ID in order to be identified. The tracking is performed using a linear weighted combination made up of two amounts: (1) A comparison of the color histograms of the frame portions in which the cluster is present; (2) The calculation of the orthogonal distance between the current centre of the cluster and the centre of the cluster detected in the previous frame.
The linear combination of the two amounts is called similarity: if this value exceeds a certain threshold, then the current cluster is associated with one already seen in the previous frame; otherwise, to this cluster a new ID is assigned. If, in some frame, the object is not detected or it is occluded (the object is in the ghost state), the Kalman filter is used for the prediction of its position in the next frame.

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UNIVERSITÀ DEGLI STUDI DI SALERNO

MIVIA

Dario De Rosa

University of Munster

GRAPH MATCHING PER LA RICERCA DI PATTERN IN DATABASE BIOLOGICI: STIMA DELLE PERFORMANCE ED OTTIMIZZAZIONI

Abstract

L’obiettivo della Tesi è di progettare un sistema che possa predire quale sia l’algoritmo di Graph Matching migliore che possa risolvere il problema di cercare tutti i possibili match di un grafo pattern all’interno di un grafo target.

Il sistema è calato in un contesto in cui i grafi modellano tipiche strutture biologiche come Molecole, Proteine e Contact Map di Proteine.
L’idea principale è quella di estrarre dai grafi particolari features strutturali così che sia possibile infine addestrare una Support Vector Machine.

Durante la fase di test, per rendere statisticamente significativi i risultati del sistema, si è scelto di ampliare il database di grafi “Bio” messo a disposizione dal laboratorio Mivia, creato in occasione del Contest “Graph Matching Algorithms for Pattern Search in Biological Databases” tenuto a Stoccolma nell’Agosto del 2014.