MRI Gastric Images Processing using a Multiobjective Fly Algorithm

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MRI Gastric Images Processing using a Multiobjective Fly Algorithm *

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Abstract. When dealing with rare and sparse data, like the ones collected during a long and expensive experimental process, machine learning is used in a different perspective. In this context, optimisation-based approaches combined with user visualisation and interactions are sometimes the best way to cope with modelling issues. We present here an example related to an experimental project aiming at understanding the kinetics of gastric emptying using MRI images of the stomach of healthy volunteers. We show how a cooperation/co-evolution algorithm, the "Fly Algorithm", can be made multi-objective, and its output, a complex Pareto Front, analysed using interactive Information Visualisation (InfoVis) and clustering.

Keywords: Machine Learning · Cooperative-co-evolution · Multi-objective optimisation · Pareto Front analysis · Visualisation

1 Introduction

The work presented here is part of a large project focused on the understanding of the influence of food structure on digestion. Advanced imaging techniques allow observing the digestion process at different scales. Small scale measurements were performed *in vitro* on large facilities (small-angle neutron scattering (SANS), small-angle X-ray scattering (SAXS), and X-ray imaging) [2,3] while magnetic resonance imaging (MRI) of the gastrointestinal tract (GIT) provides *in vivo* information at large scale (stomach and duodenum of healthy human volunteers).

We focus here on MRI observations of the kinetics of gastric emptying for two species of ingested food: i) progressively and partially digested cooked pasta, and ii) frozen garden peas, which keep their shape in early gastric stages (Fig. 1).

We show how a "Fly Algorithm" [4] can be efficiently adapted to detect peas in these MRI images (around 20 peas in one stomach for the current experimental data). Being able to follow peas in these images is important as it reveals how the food bolus is stirred inside the stomach to favour the action

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of the gastric juice. The Fly Algorithm has been turned into a multi-objective cooperative-coevolution algorithm, and expert knowledge has been integrated through simple Information Visualisation (InfoVis) techniques: a multi-objective scheme provides Pareto front data which needs to be understood and explored by the end-user.

2 The multi-objectives Fly Algorithm

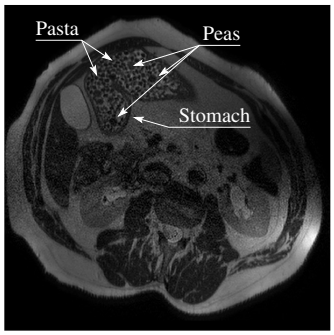


Fig. 1. MRI slice of a human stomach containing peas and pasta.

Peas (not cooked nor chewed) keep their shape and size in early gastric stages. A pea thus appear in a MRI slices as a circle of a fixed radius of about 4mm ($R = 8$ pixels). It is darker and more homogeneous than the background. These properties are featured thanks to 7 objective functions. Objectives 1, 2 and 3 are based on homogeneity measurements (inside a circle or a ring centred on the potential pea position), while Objectives 4, 5, 6 measure the isotropy. Finally Objective 7 ensures the pea area is darker than its background.

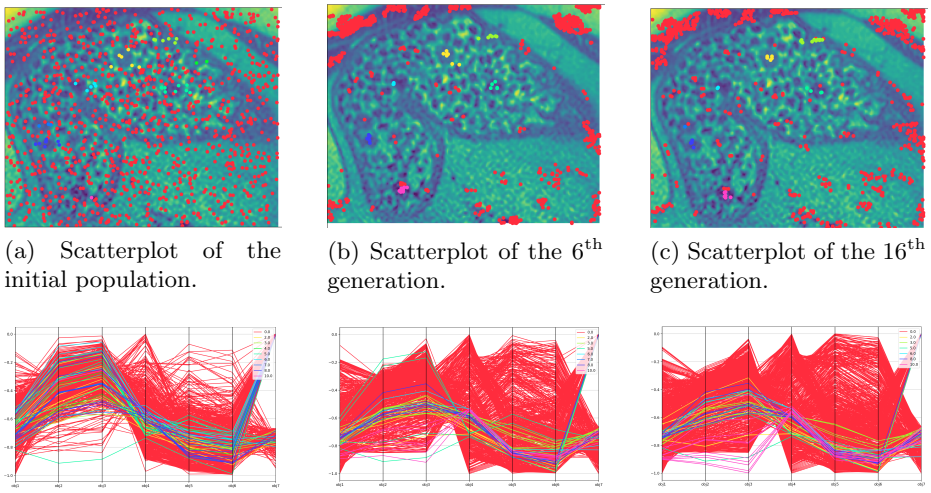
The Fly Algorithm maintains a population of potential pea locations, and evolves it to optimise the previous 7 objectives using a multi-objective scheme (inspired from NSGA-II, [1]). The evolved population then stabilises on a Pareto front.

3 Visualisation and interactive decision making

Each point of the Pareto front not only corresponds to a possible pea location, but also to a different objective priority trade-off. Automatically extracting the points that really correspond to peas is not trivial. This can be done efficiently thanks to interactive visualisation.

A scatterplot displays the position of the individuals over the MRI image (see Fig. 2), while a parallel coordinates plot[5] shows the values of the seven objective functions for each individual. The user can interactively select areas of points in the scatterplot that correspond to peas. Each selected area gets a unique colour, the same in both plots. 7 validity ranges (two thresholds per objective) are defined for filtering out the 25,000 individuals generated during the evolutionary process. The scatterplots are then clustered using a Gaussian Mixture Model (GMM) (see Fig. 3a). Clusters that are close to each other (e.g.

[5] This plot represents a point in a n-dimensional space as a broken line with $n-1$ segments, joining its n coordinates located on n vertical axes.



(a) Scatterplot of the initial population.

(b) Scatterplot of the 6^{th} generation.

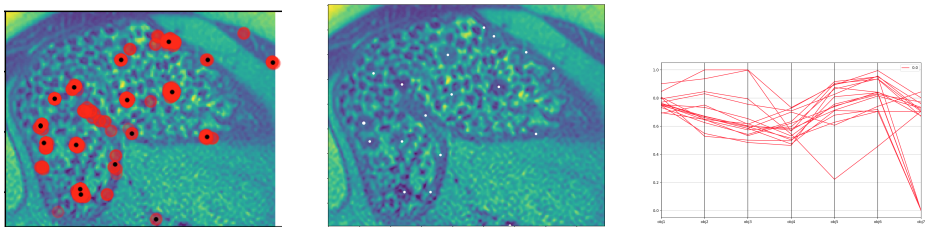
(c) Scatterplot of the 16^{th} generation.

(d) Parallel coordinates plot corresponding to (a).

(e) Parallel coordinates plot corresponding to (b).

(f) Parallel coordinates plot corresponding to (c).

Fig. 2. Scatterplots and parallel coordinates plots of successive generations. All solutions (flies) are plotted in red by default. When the user selects an area in the scatterplot, a specific colour is assigned to this area and linked to the corresponding lines in the parallel coordinates plot.



(a) Clusters.

(b) Cluster centres.

(c) Parallel coordinates plot.

Fig. 3. Candidate solution clusters.

within a pea diameter) are then merged. All clusters centres are extracted (see Fig. 3b). In total, 19 points were selected. Thanks to another parallel coordinates plot a new set of thresholds is defined (see Fig. 3c) to further refine the results and limit the number of false positive (i.e. points that do not actually correspond to peas). The last set of thresholds is used to highlight stronger candidates (7 purple dots in Fig. 4).

4 Conclusions and future work

We present here some preliminary results based on the first multi-objective version of the Fly Algorithm. We have also shown that an interactive process, combining image display, scatterplot and parallel coordinates plots, facilitates the analysis of the output of this Fly Algorithm.

This interactive scheme will be used to produce training data for a deep neural network, for a further robust and more automatic processing of the whole dataset (all MRI slices of 3D volumes and sequences of 3D volumes, at different digestion duration, for all volunteers). The next step will be to follow the peas as a set of particles, to reconstruct their movements inside stomach and their progressive ejection through the pylorus along digestion.

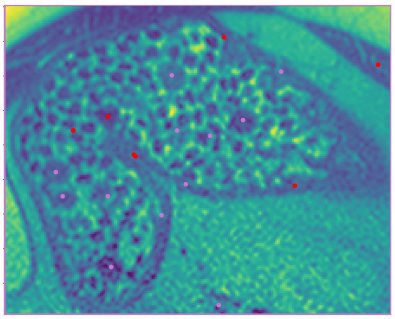


Fig. 4. Final result.

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