Computer Algebra in Algebraic Topology and its Applications: Homological processing of biomedical digital images: automation and certification*

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Abstract

In this work a methodology to deal with digital images is presented. The main steps of our proposal are the following ones.

- Detect what kind of homological information is needed in a concrete problem of image processing.
- Manipulate the image to get an image where the topological information is as explicit as possible.
- Reduce the size of the data, ensuring that no relevant information is lost during the process.
- Apply some computer algebra program to compute the homological invariants.

The objectives of this kind of research are twofold:

- To automate some tasks made up to now manually (or semi-automatically) by biologists and other experimental scientists: tracing, marking, counting, and so on.
- To verify the correctness of the automated process.

Even if the second objective could be considered as excessive, in fields where the accuracy standards are not so high as in mathematics or theoretical computer science, it is necessary to stress that the simplifications done by experimental scientists are based on solid (even if heuristic) previous experience. If they must trust computer programs, it is convenient to produce them in a reliable manner, in such a way that scientists could be confident of the results mechanically obtained.

In the paper we will describe an instantiation of this methodology with the following features.

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- The images are related to the synaptical structure in neurons [1]; the topological invariant to be computed is the number of connected components (useful to determine the evolution of the density of the occurrence of synapses in neurons, under the effect of some drugs).
- The digital images obtained experimentally are handled by means of the *ImageJ* Java environment [9], producing a bitmap file where connected components should be counted.
- From the previous file an incidence matrix is constructed, which in processed through a Haskell program [8], to obtain a smaller matrix with the same homological information (we are using here Discrete Morse Theory, as explained in [10]).
- These Haskell programs are being analyzed by using the Coq proof assistant [3,2], and more specifically the *SSReflect* environment [5].
- The matrices obtained by means of the Haskell programs are given as input to the *fKenzo* system [6,7], a user interface for the *Kenzo* program [4], which actually computes the homological information.

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