Electronic enzyme with reconfigurable active site for recognizing a digital input signal and processing it into another output signal

Brief description

Digital electronic circuit that emulates the function and configuration of the active site of a biological catalyst or enzyme, which is set up by a genetic algorithm, searching for the proper logic gates and states of the sliding switches modelling the active site. This solves the design of a device inspired by biochemistry, whose function is like a lock and key mechanism that can be set up by an optimization algorithm. In summary, an electronic enzyme is a bio-inspired electronic circuit that can be set up using evolutionary methods.

How does it work?

The transformation of an input signal (S_{nm}) into an output signal (P_{nm}), both previously set by the device user (Figure 1), requires the configuration of the enzyme's active site (C_{nm} and O_{nm}) that simulates the electronic circuit. The configuration is performed by applying a non-conventional genetic algorithm or SDS procedure, short for “simulated DNA shuffling”, a method that eliminates the drawbacks characteristic of conventional genetic algorithms in the design of electronic circuits and other devices.

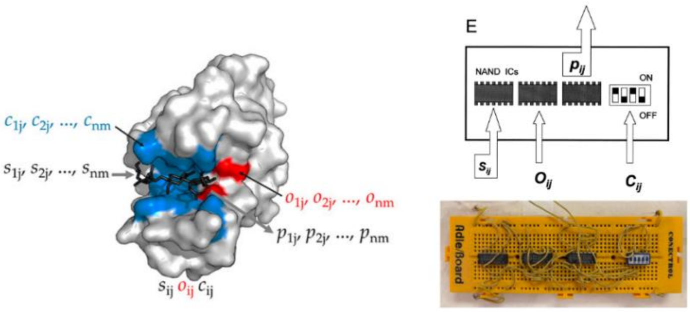

Figure 1. (Left). *Organization of an enzyme E, lysozyme, showing the active site: in blue, the binding site (C_{nm}) of the substrate S_{nm}, a peptidoglycan, and in red, the catalytic site (O_{nm}). The product P_{nm} of the reaction S + E → P is the result of performing the Boolean operation S_{ij} O_{ij} C_{ij} in the active site.*
(Right). *Circuit and outline of the electronic enzyme showing its components. The figure on the left is modified from Thomas Shafee, 2015. (https://commons.wikimedia.org/wiki/File:Enzyme_structure.svg).*

What problem does it solve?

The device and configuration procedure are characterized by the economy of the components, the efficiency of the input signal recognition system, and the reconfigurable nature of the device through the SDS algorithm, emulating an enzyme whose active site evolves according to the input/output signals.

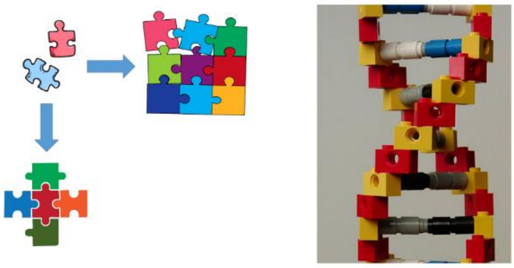

Figure 2. (Left). *Assembly of units using a lock-and-key model, with the binding mediated by electronic enzymes.*

(Right). *DNA model with LEGO, taken from https://commons.wikimedia.org/wiki/File:Lego_DNA.jpg.*

Medicine Faculty. Entrepabellones building 7 y 8.
C/ Doctor Severo Ochoa, 7. 28040 Madrid.
comercia@ucm.es

Digital signal recognition based on the use of electronic enzymes is useful in the intelligent recognition between units, e.g. machines or their parts, which must recognize each other in a similar way to a key and lock (Figure 2). The units are assembled according to a specific program or assembly protocol.

What future products will it develop?

An 'electronic enzyme' can be used for industrial purposes or in biotechnology. In industry, a compound machine is made up of several simple machines joined together in series. For instance, a crane, car or a clock. Sometimes, beyond this definition, it is necessary to assemble different units with a common purpose in a similar way to a compound machine. For example, the machinery in an assembly line, the coupling between train cars, or the pieces in a construction set. In these cases, it is possible to include the appropriate electronic enzyme in the units to be assembled, thus achieving a pre-programmed coupling between units. The result of a key-lock recognition between the units to be assembled can be linear or ring-shaped, allowing for other possible couplings or assemblies.

Another application is in biotechnology, where the evolution of metabolic pathways in organisms can be simulated by computer, for example in fermentations of industrial relevance.

Competitive advantages compared to other research

The electronic enzyme described here is an example of bio-inspired hardware whose cost is well below that of other commercial platforms. Its configuration with an SDS genetic algorithm is performed with a Python routine that does not require a high-performance computer.

Where has it been developed?

The research group 971006 - MADMIB - MODELING, DATA ANALYSIS, AND COMPUTATIONAL METHODS IN BIOLOGY has accumulated extensive experience in applying finite and molecular automata theory to the modelling of molecules relevant to biology, today called biomolecules.

The line of research described in this file was recovered and updated in 2023. On this occasion, a novel method was introduced that combines graph theory with automata theory to simulate the evolution of metabolic pathways in organisms. Its usefulness was illustrated with the simulation of the evolution of glycolysis and the Krebs cycle (https://doi.org/10.3390/computation11060107), including, due to its industrial interest, alcoholic fermentation.

And moreover...

This research group can provide the following services:

- Advice and consulting on specific problems requiring a metaheuristic methodology.
- Collaboration, study, design, and development of possible technological applications of electronic enzymes or other technologies whose development and application require bio-inspired solutions.

Researcher in charge

Rafael Lahoz-Beltra, lahozraf@ucm.es
Department: B**iodiversity, Ecology, and Evolution (Biomathematics)**
Faculty: **Biology**