

Construction of a Machine Learning tool based on partial differential equations, intending livestock data assimilation.

The realistic modeling intended to quantify precisely some biological mechanisms is a costly task, generally leading to heavy mathematical models. The in-silico experimentations allowed by these models are valuable to describe and explain specific biological processes. However the complex implementation of these models limits their flexibility and adaptation. On the other hand, the classical Machine Learning algorithms are in most cases insufficient to describe the links existing between the biological processes. In fact, most of the biological reactions are governed by multiple underlying phenomena - fluxes, fixation, accumulation, delay - difficult to take into account within the framework of the relatively simple mathematical models involved in those algorithms. Their structure and functioning make these two types of approaches unsuitable either to assimilate various biological data or to predict a reaction induced by complex biological reactions.

The aim of the thesis is to reach a compromise between precision, parsimony and flexibility to design an efficient biomimetic predictive tool extracting knowledge from livestock data. To achieve this, we build a mathematical model based on partial differential equations embarking the mathematical expression of various biological-like phenomena (convection, diffusion, saturation, *etc*).

The evolution of biological variables result of numerous complex physical fluxes and chemical reactions. All these processes can be summarized by the evolution of a global information. This evolution synthesizes the processes of convection, diffusion and accumulation that occur since the injection or the ingestion of molecules until their action in the body of the animal. Therefore the algorithm comes out of the discretization of a system of partial differential equations. This system describes the evolution and the action of this information circulating in an avatar of the real animal. This avatar outlines the dynamic of the biological reactions of the animal body in the context of a specific problem. Each differential equation contains parameters corresponding to biological-like factors : The convection and the diffusion speeds, some saturation levels, the fixation speed, *etc*. And, these parameters are learnt by the developed Machine Learning tool.