

Medicompills Architecture: A Mathematical Precise Tool to Reduce the Risk of Diagnosis Errors on Precise Medicine

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Abstract : Powered by Machine Learning, Precise medicine is tailored by now to use genetic and molecular profiling, with the aim of optimizing the therapeutic benefits for cohorts of patients. As the majority of Machine Language algorithms come from heuristics, the outputs have contextual validity. This is not very restrictive in the sense that medicine itself is not an exact science. Meanwhile, the progress made in Molecular Biology, Bioinformatics, Computational Biology, and Precise Medicine, correlated with the huge amount of human biology data and the increase in computational power, opens new healthcare challenges. A more accurate diagnosis is needed along with real-time treatments by processing as much as possible from the available information. The purpose of this paper is to present a deeper vision for the future of Artificial Intelligence in Precise medicine. In fact, actual Machine Learning algorithms use standard mathematical knowledge, mostly Euclidian metrics and standard computation rules. The loss of information arising from the classical methods prevents obtaining 100% evidence on the diagnosis process. To overcome these problems, we introduce MEDICOMPILLS, a new architectural concept tool of information processing in Precise medicine that delivers diagnosis and therapy advice. This tool processes poly-field digital resources: global knowledge related to biomedicine in a direct or indirect manner but also technical databases, Natural Language Processing algorithms, and strong class optimization functions. As the name suggests, the heart of this tool is a compiler. The approach is completely new, tailored for omics and clinical data. Firstly, the intrinsic biological intuition is different from the well-known "a needle in a haystack" approach usually used when Machine Learning algorithms have to process differential genomic or molecular data to find biomarkers. Also, even if the input is seized from various types of data, the working engine inside the MEDICOMPILLS does not search for patterns as an integrative tool. This approach deciphers the biological meaning of input data up to the metabolic and physiologic mechanisms, based on a compiler with grammars issued from bio-algebra-inspired mathematics. It translates input data into bio-semantic units with the help of contextual information iteratively until Bio-Logical operations can be performed on the base of the "common denominator" rule. The rigorousness of MEDICOMPILLS comes from the structure of the contextual information on functions, built to be analogous to mathematical "proofs". The major impact of this architecture is expressed by the high accuracy of the diagnosis. Detected as a multiple conditions diagnostic, constituted by some main diseases along with unhealthy biological states, this format is highly suitable for therapy proposal and disease prevention. The use of MEDICOMPILLS architecture is highly beneficial for the healthcare industry. The expectation is to generate a strategic trend in Precise medicine, making medicine more like an exact science and reducing the considerable risk of errors in diagnostics and therapies. The tool can be used by pharmaceutical laboratories for the discovery of new cures. It will also contribute to better design of clinical trials and speed them up.

Keywords : bio-semantic units, multiple conditions diagnosis, NLP, omics

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