Hacking bioactive peptides one byte at the time

Dr. Fabien PLISSON

National Laboratory in Genomics for Biodiversity LANGEBIO-CINVESTAV IPN, Irapuato, Gto. 36821, Mexico
fabien.plisson@cinvestav.mx, http://www.langebio.cinvestav.mx/ & https://www.fabienplisson.com

Proteins are macromolecules that regulate different processes in our body. Some help us grow, others defend us against bacterial or viral infections. Most proteins that we find in nature must face numerous obstacles to allow their applications as drugs or vaccines against human diseases. Many peptides and proteins are limited from translating into clinics due to several obstacles including their low metabolic stability, poor oral bioavailability and high toxicity. Reducing hurdles to clinical trials without compromising the therapeutic promises of peptide candidates becomes an essential step in peptide-based drug design and protein engineering.

Protein engineering (or peptide design) is the process to convert them into their useful or valuable forms. One promising application of machine learning (ML) algorithms lies in protein engineering; the relationships between protein sequences and respective functional measurements (i.e. biological activities) enable the optimization of proteins functions. This talk will introduce briefly the applications of bioactive peptides as drugs before talking about the development of machine-learning models to facilitate their discovery and optimize their design.