Lectins and lectomes: from structural glycobiology to glycoinformatics

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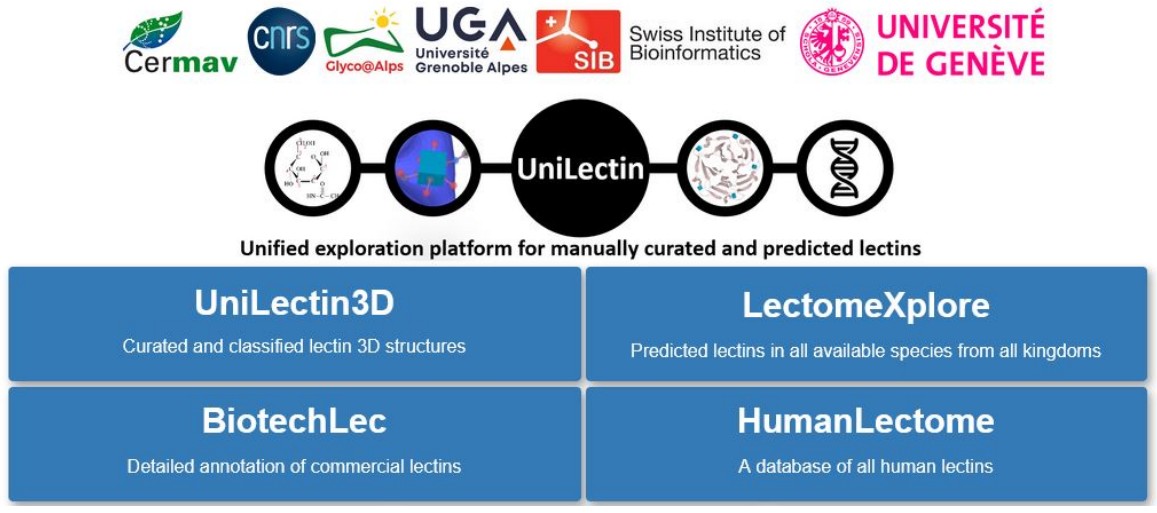
The ability of lectins for deciphering the structural message embedded in complex glycans is a remarkable source of protein fold diversity. Thousands of 3D-structures of lectin-glycan ligand complexes are available from X-ray crystallography and NMR and since 2019, stored in UniLectin3D, a searchable database providing binding information linked to protein sequence and structure as well as glycoscience databases [1]. Despite the interest of identifying new lectins in a larger range of organisms, the poor quality of sequence annotation in databases hinders lectin detection in newly sequenced organisms.

The limited size of functional domains and the low level of sequence similarity challenge usual bioinformatics tools. To meet this type of challenges, our two groups co-develop the UniLectin portal. We first built upon UniLectin3D to define a new structure-based classification, and used the latter to design a sequence-based lectin prediction software.

The result of screening millions of sequences of the NBCI-nr and UniProt databases can be found in LectomeXplore, a database proved invaluable for detecting lectins in fungal or microbial communities (3) or identifying lectins with new functional properties (4). Recently, we launched the HumanLectome database gathering almost 200 curated or putative human lectins, with information of specificity, expression and structure and the BiotechLec guide describing commercial lectins classically used as carbohydrate-recognition tools.



UniLectin portal: logo and modules on homepage (unilectin.unige.ch)

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Bibliographic references:

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