INFOGENESE EN BIOLOGIE VEGETALE

G. Hunault (1), F. Beaujard (2), H.B. Lück (3), J.Lück (3)

(1) Lab. d’Informatique et de Mathématiques appliquées, Université d’Angers
(2) Station d’Agronomie, INRA - Centre d’Angers
(3) Lab. de Botanique analytique et Structuralisme Végétal, Faculté des Sciences et Techniques St Jérome Marseille

ABSTRACT

The construction of theoretical models in biology, situated at the cross-roads of biology, mathematics and computer science, often leads to a tool as final product. Its genesis can be named ‘Infogenesis’. The procedure of the resolution of theoretical problems is analyzed on examples of practical purposes taken from plant biology.

The first example deals with mineral plant nutrition, explaining a way to go from theoretical ionic balances to the experimental realization of nutritional solutions with macro-element components.

The balanced concentrations of ions are expressed in terms of concentrations of electrical charges (milli-equivalent per litre). The neutral combination of anions and cations results from salts, acids or bases introduced in water. To achieve this combination, a table lines up concentrations in cations in the last column and concentrations of anions in the bottom line, their sums being equal. The obtained quantities of salts appear at the intersections of lines and columns. An expected ionic equilibrium is equivalent to the filling up of the table considered as a mathematical matrix. The algorithm constructing the table permits e.g. to use fewer salts or some salts preferentially. The procedure minimizing the values of elements corresponding to non-desired salts is presented. A prior order, which is the reverse to the use of preferential anion/cation pairs, is required for the successive treatments of the elements.

An algorithm of "successive splittings" respects the weights of sums in lines and columns. It mainly looks for the maximal quantity that can be taken from a chosen box in the table i.e. from the salts, and carries out its splitting. The repetition of this operation takes into account the impossibility to add a positive value to a minimized term. Therefore, during the operation, some lines and columns have to be "frozen", i.e. their values are considered as unchangeable. The number of rewritings of the table by the splitting method depends on the order of treatment of the elements, their number and the weight of lines and columns.

The method gives a global approach of the mineral nutrition in terms of ion concentrations. An initial chemical definition of the problem leads to the constructions of algorithm on the basis of the successive splitting method. It is resolved mathematically and computerized via a dynamic arrangement of elements in the table. The determination of salts formulas from the known ionic concentrations is the practical objective and the filling up of the table is the computerized means. Initial data is the sums in lines and columns. The resolution is accomplished by the weighted redistribution of the values taken from each box in the table. The realization is done within a loop of calculations, rewriting the terms of the grid according to a predefined preferential order.

In a second example, a procedure opening the way to the construction of the form for a plant from empirical data is discussed. The study of the vegetative development of woody ornamental plants is necessary to manage the production of commercial varieties during the plants breeding process. The aspect of the plant, regularly recorded, can be reconstructed by image synthesis. Additionally, knowledge about the underlying biological mechanisms becomes accessible if the synthesis images are ordered by the algorithmic formulation of hypotheses on the development.
Non-destructive recording of data during the growth of the aerial living branching system is based on elementary units of construction, each unit including a leaf, an axillary bud, a node and an internode. Each elementary unit is referred to by a unique address describing the way from the plant root up to the considered node. The coding of the address is the AF type which is compared to the lexicographical type. Coding, ordering the constituents of the plant and the spatial links (dimensions, orientations in space) together constitute a numerical memory of the development (NMD). The visualization of the enhanced shape is given by a graphical representation.

The modelization of plant growth by an algorithm approach uses a set of production rules that contains the complete topological structure. The construction of the associated drawings allows a comparative study of the morphological structure. Branching systems generated by L-Systems or the proposed PL-System, are discussed. The NMD is a possible interface for the comparison of a measured tree structure and a generated tree structure. In the PL-System a segment is characterized by indexes indicating the potentiality of the total branch length and the effective rank of the segment on the axis. A system of linear equations (in matrix form) calculates the indexes of the axes produced by a bifurcation. Where a corresponding L-System would be more concise, the PL-System opens a theoretical way to study relationships between plant forms. As it produces automatically the addresses of the NMD, comparisons with experimental data are easy, especially if highlighted by computerized graphical representations of the branching systems.

Biology contributes to the detailed description of the development of woody plants, both by data records and growth models. Computer science structures the NMD and produces the associated shape and volume. The resolution is based on a drawing algorithm managing the multiplication of the elementary units. The realization is a stepwise animation of related graphical blocks. A second biological objective is the comparison of the observed shape and the shape generated by PL-Systems. It is realized by a comparison between observed and theoretical NMDs generated by grammars.

Biology, mathematics and computer science fuse in a same objective of modelization. An accurate definition of the biological objectives, separating data from the resolution scheme, is necessary, distinguishing between items that relate to the resolution algorithm or to the mathematical formulation and those which refer to the implementation on a computer.

1. INTRODUCTION

En biologie, la construction de modèles théoriques prend une place de plus en plus vaste car ils permettent une approche fine et globale de phénomènes complexes. Les objectifs qui leurs sont assignés sont multiples. Explicatifs, prévisionnels, plus simplement descriptifs ou construits pour des expérimentations élaborées, ils posent à chaque fois le problème de l'intervention de disciplines variées faisant appel parfois à des domaines éloignés, tels la biologie, les mathématiques, l'informatique. Dès lors, la conception d'un modèle, avoir en avoir défini l'objectif, exige une véritable fusion de diverses compétences dont le produit, avec la vulgarisation de techniques mathématiques et informatiques évoluées, est bien souvent la construction d'un logiciel. La genèse de ces outils pourrait être regroupée sous la notion d'Infogenèse.

A l'aide d'exemples pris dans nos travaux respectifs, nous présentons une façon de structurer la pensée pour un objectif plus général de modélisation. Les exemples concernent la biologie végétale ; ils ont des finalités pratiques mais chacun pose la question de la démarche et la résolution de problèmes théoriques sur lesquels nous insisterons.

Un premier exemple venant de la nutrition minérale présente une méthode qui rend aisé le passage du raisonnement en termes d'équilibres ioniques à la réalisation expérimentale. Un second exemple montre l'organisation générale d'une démarche qui ouvre la