State of Art in Genetic Algorithms for Agricultural Systems

Sorana D. BOLBOACĂ[1], Lorentz JÄNTSCHI[2], Mugur C. BĂLAN[2],

Mircea V. DIUDEA[3], Radu E. SESTRAS[4]

[1] *"Iuliu Haţieganu" University of Medicine and Pharmacy Cluj-Napoca, 13 E. Isac, 400023 Cluj-Napoca, Romania; sorana@j.academicdirect.org.*

[2] *Technical University of Cluj-Napoca, 103-105 Muncii Bvd., 400641 Cluj-Napoca, Romania*

[3] *"Babeş-Bolyai" University, 11 Arany Janos, 400028 Cluj-Napoca, Romania*

[4] *University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Manastur
St., 400372 Cluj-Napoca, Romania; rsestras@notulaebotanicae.ro*

Abstract

Genetic algorithms are built as abstract populations of a number of candidate solutions, each of it being evaluated for accomplish a desired performance. Populations evolve from one generation to another through mutation, crossover and selection in order to obtain an acceptable solution. Genetic algorithms applications cover the subject of decision, classification, optimization and simulation of hard problems. The quality of a genetic algorithm is evaluated in terms of speed, accuracy and domain of applicability. The use of all genetic operators could assure the convergence towards the optimum solution for a specific hard problem. The approaches used to construct the search space and the objective function (survival of the fittest, natural selection) assure the diversity of genetic algorithms. Studies on the development and use of genetic algorithms in solving hard problems in the field of agricultural systems were identified, analyzed and are presented here.

Keywords: genetic algorithm, agricultural system, agro-economic system

Hard Problems and Meta-Heuristics

Daily life and scientific research require working with *problems*. In informatics and informatics-related fields (such as bioinformatics and chemoinformatics) a problem has precise meaning, close to that of an *algorithm*. An algorithm is a recipe that indicates what must be done in certain situations in order to meet a certain objective. Two resources are necessary in order to solve a problem: time (execution time, correlated with the number of basic instructions) and space (for storing entry data and variables).

Different problems have different *complexity*. Some problems for example have exponential complexity, which means that the best algorithm solves the problem over an execution time that increases exponentially with the size (volume, amount) of the entry data. These problems are known as *hard* since even the best algorithm (which exists or could exist) will probably be useless in the real world (Falkenauer, 1998). The following is an example of a hard problem (in which the exploration time of the search space is exponential): *A number of harvesting machines, a number or harvesting fields and a number of drivers (and even a number of storage spaces) are given. The best way to organize harvesting on a farm should be found when each harvesting machine implies a field and a driver.*

Searching for the *optimum* solution when the problem is hard exceeds the time available for existing applications. However, in practice several problems do not require an optimum and in most cases a *good solution* is enough for this kind of problems. Let us assume again that organizing harvesting on a farm is the hard problem. Thus, an algorithm that allows a reduction of harvesting costs from $40000 /week to $10000/ week is useful for the farm, although an optimal algorithm (that finds the global minimum) could reduce the costs to $8000 /week. Moreover, the algorithm that reduces the costs to $10000 /week is preferred over the one that reduces the costs to $8000 / week if the execution time of the latter is excessively high, for instance higher than the time available for harvesting.

In conclusion, the search for good approximation algorithms is perfectly legitimate: these algorithms do not ensure the global optimum for any instance with which they are fed, but they are able to produce solutions close to the optimum solution.

Because most hard problems have existed for many years, one or more heuristics had already been created for some hard problems. Heuristics are sets of rules designed

52

to solve a certain problem. They usually rely on common sense (as far as the expected solution is concerned) by avoiding obvious mistakes. However, they are frequently designed to produce a solution as close as possible to the optimum solution and since they are not able to produce a solution for any entry values they offer a solution just for the problem for which was been created. Although, most heuristics are ad-hoc and depend on the given problem, the development of informatics allowed researchers to formulate some general heuristics suitable to a large variety of hard problems. They have been called *meta-heuristics* due to their general nature. All three meta-heuristics: SA - Simulated Annealing (van Laarhoven and Aarts, 1987; Davis, 1987), TS - Tabu Search (Glover, 1977; Glover, 1986; Glover *et al.*, 1993) and GA- Genetic Algorithms have stochastic nature. Two of them (SA and GA) are based on the natural processes that have always been taking place around us.

Genetic Algorithms

Genetics and Genetic Algorithms

Observational studies, as well as the design and verification of model hypotheses, grounded the development of genetic algorithms until Fraser's papers (Fraser, 1957a; Fraser, 1957b). Thus, Lamarck (Lamarck, 1809), after striving to classify living organisms, supplied arguments that the classification of animals (especially invertebrates) and plants into species and varieties is more or less arbitrary. According to modern taxonomy, organisms are classified using a tree further divided into domains, kingdoms, phylums, classes, orders, families, genera, and species. Despite the fact that Lamarck's explanation, which was based on superstitions according to which the gaps in the species classification scheme were due to species disappearance, was later contradicted by Darwin's studies (Darwin, 1859). Even if, Lamarck's studies on species still are of utmost importance.

Even Darwin was influenced by Lamarck's conclusions, as Fisher noted in 1954 (Fisher, 1954). The main achievements in early genetics were completed by Mendel's studies on plant hybridization (Mendel, 1866), that led to what is currently known as Mendel's laws. The theory of hard inheritance (Weismann, 1893) completed past theories. Finally, Morgan's studies on the common fruit fly (Morgan *et al.*, 1915) led to the chromosome theory of inheritance that still constitutes that basis of modern genetics. Last but not least, Fisher's extremely valuable studies should be mentioned, since he supplied undeniable scientific arguments regarding the origin of species and the theory of evolution (Fisher, 1918; Fisher, 1922).

To sum up, the hard (Weismann, 1893) and the soft (Lamarck, 1809) inheritance, selection and survival (Darwin, 1859), character crossover (Mendel, 1866), genes and gene crossover (Morgan *et al.*, 1915), which were viv-

idly debated in the 19th century (Fisher, 1954), are all the pieces of a puzzle that is today's modern genetics (Ayala *et al.*, 1994). They are also inspiration sources for genetic algorithms.

The first simulations of evolution were found in the studies of Nils Aall Barricelli (Barricelli, 1954; Barricelli, 1957). Later, Alex Fraser published a series of papers on the simulated artificial selection of organisms with multiple loci that controlled a measurable trait (Fraser, 1957a; Fraser, 1957b; Fraser, 1957c; Fraser, 1960a; Fraser, 1960b; Fraser, 1960c; Fraser, 1962; Fraser and Hansche, 1965; Fraser *et al.*, 1966; Fraser and Burnell, 1967a; Fraser and Burnell, 1967b; Fraser and Burnell, 1970) that included all the essential elements of modern genetic algorithms.

Although the first studies that included genetic algorithm elements were published as early as 1954, comprehensive studies in this field were only published after 1970 (Bosworth *et al.*, 1972; Holland, 1975). Genetic algorithms were reinvented ten years later, after the introduction of the first Personal Computer (Davis, 1991, Holland, 1992).

Three criteria should be taken into account when the quality of a heuristic algorithm is evaluated:
▪ Speed: how fast the solution is obtained;
▪ Precision: how far from the global optimum the solution is;
▪ Aim: how large the entry data subset is compared with the set of all possible values for which the algorithm performs according to the previous two criteria;

The *No Free Lunch Theorem* (Wolpert and Macready, 1995; Wolpert and Macready, 1997) is connected with the *algorithmic complexity*. This theorem shows, by using the above-mentioned criteria, that all algorithms are strictly equivalent, which means that for Φ and Ψ (algorithms) and A input data, for which Φ is better than Ψ, there is B input data for which Ψ is better than Φ. To conclude that the effort to improve one's algorithms is useless, because they will perform just like any other algorithm, is a simple but wrong interpretation. What the theorem really states is that if performance is averaged on all possible data, then the algorithms will perform the same. The trick is not to attempt to feed all the algorithms with all possible data but rather to dedicate an algorithm to an *applicability domain* and to implement any special structure present in the data with which the algorithm is going to be fed. Therefore, the aim of the algorithm that performs well must be restricted to the data set that presents the special structures identified in the data set.

The following categories of problems may be solved by genetic algorithms:
▪ *Decision problems*
• A decision problem is defined for a closed question (that can be answered with yes/ no) on an infinite set of entry data. That is why decision problems are equal with obtaining the entry data set for which 'yes' is the answer to the problem. Decision problems are connected with op-

Bolboacă, S. D. et al. / Not. Bot. Hort. Agrobot. Cluj 38 (3) 2010, 51-63

53

timization problems as long as the best answer could be obtain.

▪ *Classification problems*

• A classification problem for objects from a given domain consists of dividing these objects into smaller classes and using determination criteria to establish if a certain object belongs or not to a certain class. One of the most famous classification problems is the one formulated by Carl LINNAEUS (23 May 1707 - 10 January 1778) regarding the classification of living organisms according to classes, orders, genera and species (Linnaei, 1735).

▪ *Optimization problems*

• An optimization problem deals with finding the best solution out of all possible solutions. Formally an optimization problem is a quadruple (I,f,m,g) where: I = set of instances; $f(\cdot)$ = set of feasible solutions defined on I; $m(\cdot,\cdot)$ = measure defined on the product of possible solutions and instances; g = min or max - goal function; and the goal is to find the optimum for x: $m(x,f(x))=g\{m(y,f(y), y \in I\}$.

• For each optimization problem there is an associated decision problem whose question is whether there is a possible solution for a certain measure m_0.

▪ *Simulation problems*

• Simulation imitates a real fact, state of fact or process. It implies the representation of certain key characteristics or behaviours of a physical or abstract system. It is used in many contexts including the modelling of natural systems and their functionality. The key elements in simulation include the acquisition of a valid information source on the studied subject, the selection of key characteristics and behaviours, the use of approximation and simplifying suppositions within the simulation and the evaluation of the accuracy and validity of the simulation results.

Genetic Algorithms and Genetic Operators

Genetic algorithms are adaptive heuristic search algorithms based on the theory of evolution. The concepts of natural and genetic selection are brought into mathematical simulation with the use of computers. The mimic of processes in the natural evolution of organic matter generally serves as instrument for genetic algorithms in order to solve decision, classification, optimization and simulation problems. The key elements of genetic algorithms are:

▪ The genetic model (genotype - phenotype dualism) as formulated and explained since the beginning of genetics (Morgan *et al.*, 1915; Fisher, 1918);

▪ Mapping (characters - gene dualism) as observed by the precursors of modern genetics (Lamarck, 1830; Mendel, 1866; Weismann, 1893);

▪ Mutation, as observed since the precursors of modern genetics:

• Random (De Veies, 1902);

• Deliberate by exposure to certain conditions (Patterson, 1928; Auerbach *et al.*, 1947);

• Under the pressure of environmental factors: (Cairns *et al.*, 1988);

▪ Natural selection or "survival of the fittest" (Darwin, 1859).

Genetic algorithms take the form of evolutionary programs and are computer simulations in which:

(search space)

▪ The operation is done on a population of abstract representations (Figure 1) named (according to the genetic elements based on which they were imagined) chromosomes or genotypes of a *genome*, in its turn each abstract representation of a *chromosome* is made of *genes*.
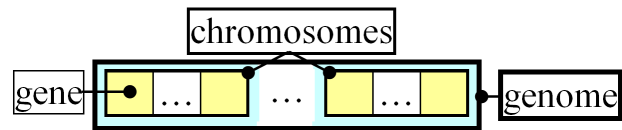

Fig. 1. Search space of a genetic algorithm

Each *generation* is made of a population of strings (or other abstract representations) analogous with DNA chromosomes. Each element of the population is a point in the search space and at the same time a possible solution.

Figure 1 represents the search space of a genetic algorithm. This may have several implementation variants. Three of these are presented below:

• If the genetic algorithm must solve a hard problem formulated in S-system formalism (Savageau, 1976), which is a type of formalism derived from the process model of stoichiometric reactions with preequilibrium ($\Sigma_i R_i \leftrightarrow \Sigma_j I_j \rightarrow \Sigma_k P_k$, where R_i reactants, I_j intermediaries, P_k products of a reaction in which the process constants: speed constants and partial reaction orders – are unknown and must be determined), then the following is a possible implementation:

▪ A gene: a constant (a partial order or a reaction speed constant) subject of the finding (optimization);

▪ A chromosome: a possible development of the reaction with specified partial orders and speed constants;

▪ Genome: all developments of a reaction presented in an iteration of the genetic algorithm.

• If the genetic algorithm must solve a hard problem of DNA, RNA or protein gene sequence alignment (Notredame *et al.*, 1996) in order to identify the similarity regions that may generate structural, functional or developmental relations among sequences, then the following is a possible implementation:

▪ A gene: two (or more) positions corresponding to two (or more) aligned sub-sequences (pseudo-aligned) and the length of their alignment;

▪ A chromosome: a possible alignment for the two (or more) sequences;

▪ Genome: all the possible alignments of sequences stored in an iteration of the genetic algorithm;

54

• If the genetic algorithm aims to solve a setting problem for maximizing the outcome of field productivity (Liu *et al.*, 2001), in which it is hard to set the controllable (or sometimes predictable) parameters for maximum productivity, then the following is a possible implementation:

▪ A gene: one of the following: soil pH, amount of N, P and K in fertilizers, amount of organic matter in the soil, degree of daily temperature increase (an average of highest and lowest temperatures), genetic potential (expressed in terms of the productivity obtained with optimum weather, soil and fertility), amount of precipitations for May, June, July and August, plantation density and the rotation factor;

▪ A chromosome: a state of fact that may occur in the working field;

▪ Genome: all states of fact stored in an iteration of the genetic algorithm.

(selection and survival)

▪ A *score* or survival chance of each solution is calculated (Figure 2) for each genotype using an *objective function*. The value of this function is associated with the ability of the individual to survive. Thus, it defines the *phenotype* associated with the genotype.

• Each generation matches its environment better (due to the elimination of individuals that fail to survive).

▪ The score associated with each phenotype (solution) represents the phenotype's ability to compete for environmental resources, therefore for *survival*. The aim of the genetic algorithm is to apply selective phenotype crossover and mutation (by decoding them into the genotypes they come from) in order to produce better offspring.

▪ The genetic algorithm maintains a cultivar (population sample) of a given (or sometimes variable) number of genotypes, which may be selected by applying the same operator. Thus, selection and survival are two associated concepts. Selection occurs in crossover and mutation, as well as in survival in populations limited by genotypes.

▪ During evolution, some part of the population individuals die and are replaced by others. In this way, better solutions will hopefully *arise* in the future while the weaker solutions will be eliminated. The passing from one generation to another will bring about increasingly better solutions as compared with previous generations.

▪ Table 1 presents the link between the score (expressed in the table by the Fitness (·) function) and the selection rule according to the method used (as known in the literature).

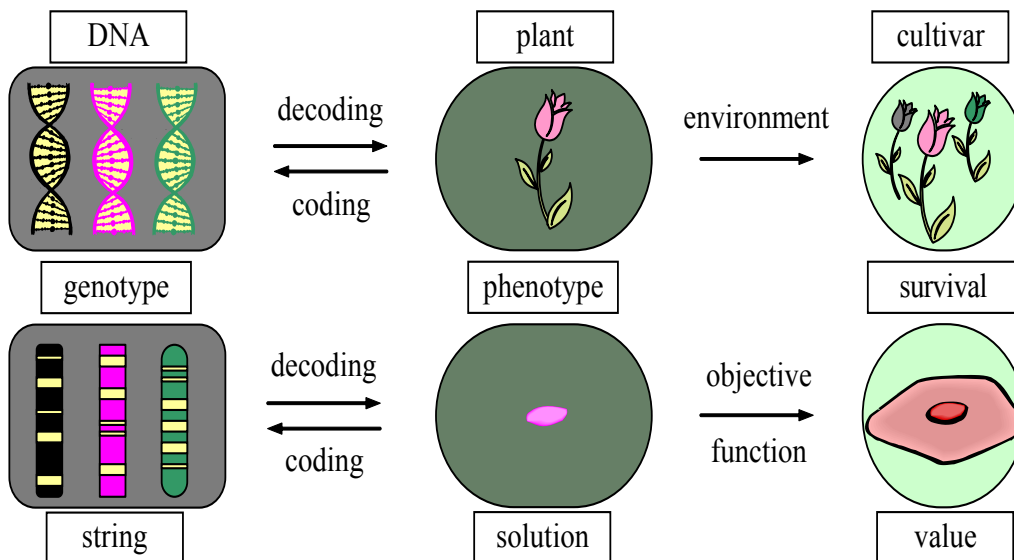▪ Figure 2 presents the selection and survival of pheno-

Fig. 2. Selection: genotype, phenotype and survival

▪ If each genotype represents a point in the search space and at the same time a possible solution, selection turns a genotype into a phenotype (operation that iterates the representation of possible solutions in the space of solutions and evaluates their value). The principle of natural selection is described as follows:

• The individuals (phenotypes) in the population compete for survival (selection).

• The genes of the selected individuals propagate from a generation to another (due to selection);

types, which could have several implementation options. Three of these options are presented below:

• If the genetic algorithm must solve a hard problem formulated in the S system (Savageau, 1976), then the following is a possible implementation:

▪ The row corresponding to a phenotype: a list of constant values that are subject to optimization and are associated with a virtual experiment;

▪ The solution corresponding to the genotype (and chromosome in Figure 1): time series of the virtual experiment elements (in a chemical reaction the solution repre-

Bolboacă, S. D. et al. / Not. Bot. Hort. Agrobot. Cluj 38 (3) 2010, 51-63

55

Tab. 1. Score and selection in genetic algorithms

Method	Score function expression	Selection	Comments/ observations
Proportional		$p_i=f_i/\Sigma_i f_i$	The selection chance is proportional to the score (the p_i probability is used in/ for selection)
Deterministic	$f_i=Fitness(Chromosome\_i)$	$i\,\|\,f_i=$ max. or min.	The strongest (or weakest) individual is selected (elitism)
Turnir		(f_i, f_j) max. or min.	Pairs of individuals compete for selection (again the fittest or the weakest)
Normalization	$g_i=(f_i-N_0)(f_{max.}-f_{min.})/(N_1-N_0)$	$p_i=g_i/\Sigma_i g_i$	A fixed scale $[N_0,N_1]$ normalizes the phenotype scores among different generations
Ranks	$h_i=Rank(f_i)(f_{max.}-f_{min.})/Size$	$p_i=h_i/\Sigma_i h_i$	The chance is proportional with the score rank where: Rank($\cdot$): rank; Size: genome volume

sents the time series of reactant concentrations, intermediaries and reaction products during the reaction);

▪ The value corresponding to the score: the squared sum of the differences between the observed values (as series or time series) and the estimated (by the phenotype) values of one (or more) observables (such as concentration or intermediary concentrations);

• If the genetic algorithm must solve a hard problem such as the alignment of amino acid sequences (Notredame *et al.*, 1996; Jäntschi *et al.*, 2009), then the following is a possible implementation:

▪ The row corresponding to a genotype: a list of pair positions of aligned subsequences followed by the length of each subsequence;

▪ The solution corresponding to the phenotype (and genotype in Figure 1): a series of values containing gap positions and shift lengths required to align the sequences;

▪ The value, corresponding to the score: a score function (usually in the form of a sum) that identifies the total cost for all gaps and shifts required to align the sequences, using predefined costs for a gap and shift of a unit in the sequence;

• If the genetic algorithm must set the parameters needed to obtain good field productivity (Liu et al, 2001), then the following is a possible implementation:

▪ The row corresponding to a genotype: a list of values that correspond to a virtual experiment and are subject to optimization. The values in the row may be: soil pH, amount of N, P and K in fertilizers, amount of organic matter in the soil, degree of daily temperature increase (an average of highest and lowest temperatures), genetic potential (expressed in terms of the productivity obtained with optimum weather, soil and fertility), amount of precipitations for May, June, July and August, plantation density and the rotation factor;

▪ The solution corresponding to the phenotype (and genotype in Figure 1): a row of values that characterize the solution, containing values obtained by applying functions that express: soil quality, weather conditions, cultivation management, genetic potential and the consequence of random events;

▪ The value corresponding to the score: the squared sum of the differences between the observed productivity

(in series of previous experiments) and the estimated (by the phenotype) productivity.

(crossover and mutation)

▪ Crossover represents the breeding of phenotypes. The phenotypes (usually two) are selected from the population using the selection operator; an area for crossover is selected (randomly or deterministically) across the gene row of the genotypes associated to the phenotypes and the values of the two areas of rows are exchanged (Figure 3). Thus two descendants are selected to be part of the new generation; the crossover is made in the hope that if two areas of genotypes are successfully recombined, this process is likely to produce better offspring.
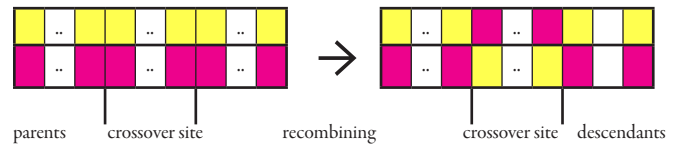

parents   crossover site   recombining   crossover site   descendants

Fig. 3. Double crossover involving the splitting and rejoining of parent chromosomes

▪ Mutation is the operator that introduces new changes (nonexistent in the population for a generation). The mutation, and its operator implicitly, has low probability of occurrence and is therefore applied with low probability (for instance a 1/8 probability in Figure 4). The mutation operator may implement a mutation which could be:

• Random: when part of a selected individual will have the values stored in its genes replaced with other values existing in the generic material of the population. Its role is to maintain diversity in the population in order to prevent the population from presenting premature convergence;

• Deliberate: when exposure to certain conditions turns into the use of a predetermined rule for changing gene values;

• Under the pressure of environmental factors: when gene values change in comparison with the phenotype score undergoing genetic change.
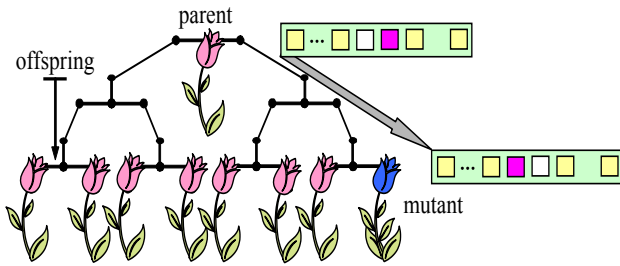
56

Fig. 4. Mutation

(evolution)

▪ By using only the selection, evolution will only be able to copy (clone) the best individual (phenotype) existing in the entire population;

▪ By using only the mutation, evolution will only manage to induce the random walking of the search space;

▪ By using crossover and selection, evolution will manage to converge towards a good solution that is however not suboptimal (close to optimal);

▪ Evolution through mutation and selection (without crossover) creates parallel algorithms, tolerant to disturbances in the search for hill-climbing

▪ The use of all operators (mutation, crossover and selection) ensure that the evolution has all the characteristics that define a genetic algorithm (Figure 5);

▪ Step 2: Crossover two parents and create their descendants (Figure 3) using a discrete probability function for choosing the section to be crossed over;

▪ Step 3: Mutate a genotype (Figure 4), maybe a crossover descendant from the previous step with low probability and using a discreet probability function for choosing the area to be mutated;

▪ Step 4: Initialize a new population with the new phenotypes (from steps 2 and 3);

▪ Step 5: Use the selection operator applied to the population of parents to complete the new population with phenotypes (at least until the initial number of members is restored);

▪ Step 6: Rebuild the values of the score function of the new population according to its new content;

• Until the best phenotype of the population meets an imposed condition (the end condition of the algorithm).

Approaches Derived from Genetic Algorithm Formalism

There are many variations and adaptations of genetic algorithms created to improve performance for a certain type of problems.

The following is a list of techniques derived and/or based on genetic algorithms: ▪ Ant colony optimization (Bouktir and Slimani, 2005); ▪ Bacteriologic algorithms
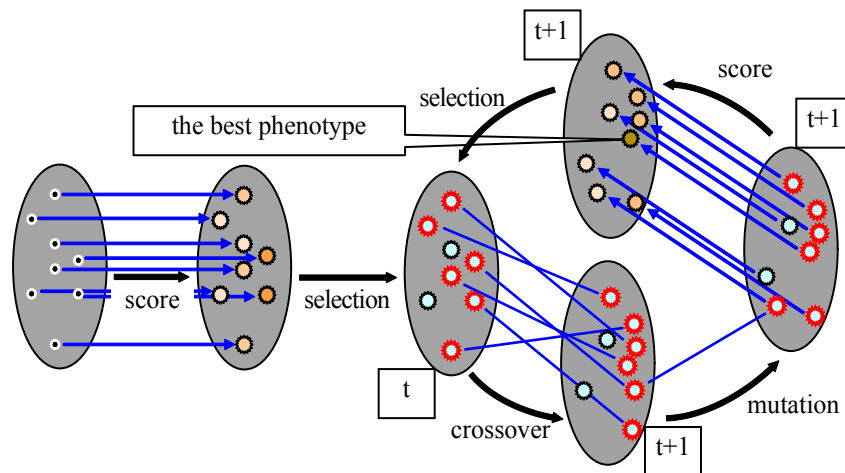

Fig. 5. Classical genetic algorithm workflow

▪ In a classical genetic algorithm (like the one in Figure 5), in order to solve a problem, a population of genotypes of a given size (Figure 1) is randomly generated or initiated with predefined values. The preliminary requirement of the genetic algorithm is the presence of the objective function that evaluates the score of a phenotype in the population; the genetic algorithm iterates as follows:

• Repeat:

▪ Step 1: Select two chromosomes using the selection operator (Figure 2);

(Benoit *et al.*, 2005); ▪ Cross-entropy method (de Boer *et al.*, 2005); ▪ Cultural algorithms (Kobti *et al.*, 2004); ▪Evolution strategies (Schwefel, 1993); ▪ Evolutionary programming (Fogel, 1999); ▪ Extremal optimization (Bak and Sneppen, 1993); ▪ Gaussian adaptation (Kjellström, 1991); ▪ Genetic programming (Banzhaf *et al.*, 1997); ▪ Memetic algorithm (Smith, 2007); ▪ Other variations collected in Davis (1991).

Other approaches conjugate genetic algorithms with other concepts. The following may be mentioned: ▪ Sup-

Bolboacă, S. D. et al. / Not. Bot. Hort. Agrobot. Cluj 38 (3) 2010, 51-63

57

port Vector Machines (Brown *et al.*, 2000); ▪ Structural pattern localization analysis by sequential histograms (SPLASH) (Splash, 2000); and ▪ Rough set (Hvidsten *et al.*, 2001).

Hard Problems of Evolution and Phylogenetic Trees

Genetic algorithms are used to find the answer to hard problems of evolution. Thus, the chloroplast genome in Manihot esculenta and the atpF evolution in the Malpighiales family are subject to research carried out by Daniell *et al.* (2008). The Taxus conifers and the evolution of the taxol biosynthesis genes TS and DBAT were discussed by Hao *et al.* (2009). The evolution of Chinese rose fragrances was tackled by Scalliet *et al.* (2008) while the evolution of the running plants Hemiptera and Psylloidea in association with Anacardiaceae were systematically studied by Burckhardt and Basset (2000).

The study of phylogenetic trees using a correspondence with the set of perfect matchings in complete graphs (Jäntschi and Diudea, 2009) was tackled by Diaconis and Holmes (1998). The authors showed that the analogy mentioned produces distance metrics between phylogenetic trees, thus allowing the enumeration of all trees in a minimum number of steps. The identification of the phylogenetic tree is a hard problem. Authors demonstrated that the Brauer algebra (Brauer, 1937) allows a simplest implementation of a genetic algorithm.

Problems related to large taxon samples in phylogenetic estimations were discussed in (Lemmon and Milinkovitch, 2002), where a meta-populational genetic algorithm (metaGA) involving several tree populations that are forced to cooperate in search of the perfect tree was found suitable. An important result was provided by (Lemmon and Milinkovitch, 2002) who found that the frequencies with which the trees and cliques collected by the meta GA algorithm may correspond to unbiased estimators of posterior probabilities (Huelsenbeck *et al.*, 2001).

A phylogenetic tree analysis in the major lines of Brachycera was carried out by Wiegmann *et al.* (2003), who indicated that Brachycera originated in the late Triassic or early Mesozoic and that all major inferior lines of Brachycera had contemporary origins in the middle Juassic before the origins of flowering plants (angiosperms). The authors obtained an increased phylogenesis resolution for Brachycera. Revised estimations on the fly age increased the temporal context of evolution interferences and the genomic comparisons between model flying organisms. Nucleotide sequences were manually aligned with an interactive alignment editor called Genetic Data Environment 2.2 (Smith *et al.*, 1994). Phylogenetic data included 2220 characters from 28S rDNA (including 608 variables and 294 parsimony informative3 corresponding to all data; 493 variables and 296 informative in Brachycera and 101 morphological characters (Yeates, 2002). The phylogenetic analysis of the combined data set was performed

with the parsimony option in the PAUP program (Fink, 1986).

An extended study of the early evolution and diversification of ants was reported by Brady *et al.* (2006). An important part of this study was the creation of the study methods used, which were described in the appendix of the above-mentioned paper. Thus, the authors used a series of programs operating with genetic algorithms:
▪ For sequence alignment: Clustal X (Larkin *et al.*, 2006);
▪ For divergence dating (estimation of ramification length) and the phylogenetic interference (parsimony analysis; maximum likelihood trees of inferences; comparison of alternate placements of the outgroups on the ingroup-only tree using the Shimodaira-Hasegawa test): PAUP* v4.0b10 (Fink, 1986);
▪ For models of nucleotide substitution: ModelTest v3.06 (Posada and Crandall, 1998);
▪ For nonparametric analysis of maximum likelihood load: GARLI v0.94 (Schultz *et al.*, 2006), derived from GAML (Lewis, 1998);
▪ For the Bayes analysis: MrBayes v3.1.2 (Ronquist and Huelsenbeck, 2003);
▪ For divergence dating (ramification length estimation) using the penalized likelihood approach: r8s v1.7 (Sanderson, 2002; Sanderson, 2003).

The results of Schultz and Brady study (2008) on ants showed that living relics of species of attine ants occupying transitional phylogenetic positions in agricultural systems were identified. The methodology used included phylogenetic analysis (parsimony, maximum likelihood and divergence dating), a nucleotide model of the Bayes type and a codon MCMC model plus a new approach - phylogenetic topography of agricultural systems:
▪ Terminal taxa were associated with states in a character with six states representing four agricultural systems of attines and leaf cutter agriculture (no, lower, medium, higher, leaf cutter, coral-fungus);
▪ Five species (*Myrmicocrypta n. sp. Brazil, Mycetagroicus triangularis, Cyphomyrmex n. sp., Cyphomyrmex morschi, Trachymyrmex irmgardae*, and *Pseudoatta n. sp.*) whose states were considered unknown and *Trachymyrmex papulatus* received a "lower agriculture" state, associations of states based on a garden collection from Agentina (a second collection from the same location cultivated a typical garden of high attines);
▪ The evolution of characters was optimized in a Bates codon-model consensus tree (with the length of branches) under the MacClade parsimony (Maddison and Maddison, 2000) and maximum likelihood (the StochChar module of the Mesquite program) (Maddison and Maddison, 2006);
▪ In parsimony, the optimizations of ancestral states were non-ambiguous. In the hypothesis of the Markov model with k states and 1 parameter (Lewis, 2001), the likelihood that each agricultural system arose from the

58

most recent ancestor of the corresponding ant clique was, as percentage from the total likelihood distributed among the six states of the character, of 0.9831 for the lower, 0.9995 for the median, 0.9905 for the higher, 0.9924 for the leaf-cutters and 0.9998 for coral-fungus.

Another phylogenetic analysis was carried out using genetic algorithms for development of a set of rules required to model the geographical populational distributions of web and wiping apes by characterizing ecological niches (Ortiz-Martınez *et al.*, 2008). Due to the random processes involved in the model, each model obtained with only one data set was different; in order to capture the variability the authors created 100 models for each species and then selected 10 models that gave the lowest mapping and omission error, following the procedure described in (Anderson *et al.*, 2003). The authors concluded that cobweb ants take up higher an area and a higher altitude difference than weeping apes. The model was validated for web apes due to the suitable amount of available data for this species. The validation of the model indicated that the predicted distribution of the species was statistically higher than the random one.

Hard Problems in Agro-Economic Systems

The applications of genetic algorithms in problems specific to agronomic systems were reviewed (Hashimoto, 1997; Mayer *et al.*, 1999). A series of important applications were reported in the literature of the time and new research perspectives were announced (Anisimova and Liberles, 2007).

Decision systems based on genetic algorithms may create models able of setting priorities (Smith, 2001), configuring production systems, and planning resource management (Kuo and Liu, 2003; Wardlaw and Bhaktikul, 2004).

Annevelink (1992) focused on fundamental aspects and presented a system able to assist decisions and management in horticultural systems. The system was implemented as a program run from a personal computer (PC). The following observation should be made: programs based on genetic algorithms generally use many memory and time resources; therefore, they have to undergo major adaptations for PC use. This system, named IMAG IPP, has a high level of tactical planning and an interactive environment for space planning in the operational planning level.

The creation of a decision system that may be used within optimal control methodology was studied by Seginer *et al.* (2007). The decision system was created for operating a system of humidity control in a solarium with ventilation where humidity was the prevailing control character.

Current research includes the theoretical grounds for a dynamic model for production control (Buwalda *et al.*, 2006) as well as the use of such a model for optimiz-

ing productivity and energy consumption for cultivating sweet peppers (*Capsicum annuum*).

The irrigation optimization (Montazar *et al.*, 2008) and the identification of optimum cultivation rules (Bozorg Haddad *et al.*, 2008) for wheat, barley, corn, beetroot, sunflower, cucumbers, onion, potatoes, tomatoes, beans, lentil, trefoil and pear trees in arid areas are the most recent results in the use of genetic algorithms.

Seginer and Ioslovich (1999) studied the optimization of production systems using a vegetation model with independent variables for production systems of lettuce in two development environments: quota- and area-limited production. The following conclusions were drawn:

▪ Plants of all ages (in various development stages) may grow together in only one climatic compartment;

▪ Spacing must be planned in order to maintain constant planting density;

▪ The optimum planting density is an ascending function of the light quantity and a descending function of the available temperature;

▪ If the production costs are high as compared with the costs of maintaining the cultivated area (rent) and the energy costs, then the optimum cultivation intensity is recorded for area-limited usage and not for quota-limited usage; the opposite is true when the rent is high;

▪ The cost difference for supplying extra light is low when natural light in more intense and lasts longer.

Cultivation models may be used as simulation instruments for quantitative estimation. Thus Rodkaew *et al.* (2004) reported a genetic algorithm that incorporated L-systems (Lindenmayer, 1968) for soybeans.

Based on previous results and experimental measurements carried out over two consecutive years a model for butterhead lettuce cultivation was created (Salomez and Hofman, 2007). The model expresses weight according to variations in ground temperature and small wave radiations.

Simulators based on genetic algorithms were successfully used to predict the production of peanuts contaminated with alpha toxins (Henderson *et al.*, 2000), to monitor growth using satellite data (Boken *et al.*, 2008), to evaluate the effect of hard metals and PCBs (polychlorinated biphenyls) on the picoplankton (fraction of plankton composed by cells between 0.2 and 2 µm that can be either photosynthetic or heterotrophic) (Caroppo *et al.*, 2006), the effect of military waste on marine organisms (Jäntschi and Bolboacă, 2008), the toxicity of para-substituted phenols on Tetrahymena pyriformis (Jäntschi *et al.*, 2008), as well as to analyze the complex associations between soil characteristics and abundant wild rice (Diaz *et al.*, 2005). Rare events such as extreme temperatures may be incorporated into models based on genetic algorithms that stimulate plant growth, as pointed out by (Kysely and Dubrovsky, 2005).

The relations between phenotypes and their characteristics have recently been researched in a few components

of table wines (Larsen *et al.*, 2007), the epistasis of self-pollinated plants (Cui and Wu, 2005), the hemagglutinating activity of Curcuma aromatic extracts in relation with the identity of the putative sequence (Tiptara *et al.*, 2008), as well as the *Ficus carica* L genotyping (de Masi *et al.*, 2005).

A recent approach (Letort *et al.*, 2008) predicted the phenotype characteristics in various environmental conditions in order to create strategies for multiplying and improving the desired characteristics.

Machines able of learning based on genetic algorithms may be useful for classifications. Systems were thus created for the automatic discrimination of seeds (Chtioui *et al.*, 1996; Chtioui *et al.*, 1997; Chtioui *et al.*, 1998), mushrooms (Hruschka *et al.*, 2003a; Hruschka *et al.*, 2003b) and plant images stored in data bases (Zhu *et al.*, 2008). Systems for differentiating sequences in the genomes of certain grass species and varieties were also reported (Saski *et al.*, 2007).

Finally yet importantly, genetic algorithms are used in decision, classification, optimization and simulation problems for natural resources as indicated by the following research. Decision hard problems were identified in the following: construction of strategic energy policies (Dagdeviren and Eraslan, 2008), classification of relief shapes (Moore *et al.*, 2003), and geological dating based on the uranium/lead ratio (Lundmark *et al.*, 2007). The optimization of systems for ensuring energy resources in horticulture was reported by (Husmann and Tantau, 2001) while Morimoto *et al.* (1997) studied the optimization of thermal treatment in fruit and (Chen, 1997) focused on the management of water resources. Simulation is used to predict solar potential (Bălan *et al.*, 2008; Sirdas and Sahin, 2008) and the potential of water resources (Anandhi *et al.*, 2008; Chen *et al.*, 2008).

Other current research areas include the identification of natural resource sets for maximizing regional diversity and maintaining long-term biodiversity (Cabeza and Moilanen, 2001) and the role of climate changes in modeling impact studies (Fowler *et al.*, 2007).

References

Anandhi, A., V. V. Srinivas, R. S. Nanjundiah and D. Nagesh Kumar (2008). Downscaling precipitation to river basin in India for IPCC SRES scenarios using support vector machine. International Journal of Climatology 28(3):401-420.

Anderson, R. P., D. Lew and A. T. Peterson (2003). Evaluating predictive models of species distributions: criteria for select optimal models. Ecological Modelling 162(3):211-232.

Anisimova, M. and D. A. Liberles (2007). The quest for natural selection in the age of comparative genomics. Heredity 99(6):567-579.

Annevelink, E. (1992), Operational planning in horticulture: Optimal space allocation in pot-plant nurseries using heuristic techniques. Journal of Agricultural Engineering Research 51(C):167-177.

Auerbach, C., J. M. Robson and J. G. Carr (1947). The chemical production of mutations. Science 105(2723):243-247.

Ayala, F. J., A. Escalante, C. O'hugin and J. Klein (1994). Molecular genetics of speciation and human origins. Proceedings of the National Academy of Sciences of the United States of America 91(15):6787-6794.

Bak, P. and K. Sneppen (1993). Punctuated equilibrium and criticality in a simple model of evolution. Physical Review Letters 71(24):4083-4086.

Bălan, M. C., M. Damian and L. Jäntschi (2008). Preliminary results on design and implementation of a solar radiation monitoring system. Sensors 8(2):963-978.

Banzhaf, W., P. Nordin, R. E. Keller and F. D. Francone (1997). Genetic Programming: An Introduction: On the Automatic Evolution of Computer Programs and Its Applications. M Kaufmann Publishers, San Francisco. 450 pp.

Barricelli, N. A. (1954). Esempi numerici di processi di evoluzione. Methodos 45-68.

Barricelli, N. A. (1957). Symbiogenetic evolution processes realized by artificial methods. Methodos 143-182.

Benoit, B., F. Fleurey, J.-M. Jézéquel and Y. Le Traon (2005). Automatic Test Case Optimization: A Bacteriologic Algorithm. IEEE Software 22(2):76-82.

Boken, V. K., G. Hoogenboom, J. H. Williams, B. Diarra, S. Dione and G. L. Easson (2008). Monitoring peanut contamination in Mali (Africa) using AVHRR satellite data and a crop simulation model. International Journal of Remote Sensing 29(1):117-129.

Bosworth, J., F. Norman and B. P. Zeigler (1972). Comparison of Genetic Algorithms with Conjugate Gradient Methods. NASA Contractor Reports, CR-2093.

Bouktir, T. and L. Slimani (2005). Optimal Power Flow of the Algerian Electrical Network using an Ant Colony Optimization Method. Leonardo Journal of Sciences 4(7):43-57.

Bozorg Haddad, O., M. Moradi-Jalal, M. Mirmomeni, M. Kholghi and M. A. Marino (2008). Optimal Cultivation Rules in Multi-Crop Irrigation Areas. Irrigation and Drainage 58(1):38-49.

Brady S. G., T. R. Schultz, B. L. Fisher and P. S. Ward (2006). Evaluating alternative hypotheses for the early evolution and diversification of ants. Proc Natl Acad Sci USA 103(48):18172-18177.

Brauer R. (1937). On algebras which are connected with the semisimple continuous groups. Annals of Mathematics 38(4):857-872.

Brown, M. P., W. N. Grundy, D. Lin, N. Cristianini, C. W. Sugnet, T. S. Furey, M. Jr. Ares and D. Haussler (2000). Knowledge-based analysis of microarray gene expression data by using support vector machines. Proceedings of

60

the National Academy of Sciences of the United States of America 97(1):262-267.

Burckhardt, D. and Y. Basset (2000). The jumping plant-lice (*Hemiptera, Psylloidea*) associated with *Schinus (Anacardiaceae)*: Systematics, biogeography and host plant relationships. Journal of Natural History 34(1):57-155.

Buwalda, F., E. J. Van Henten, A. De Gelder, J. Bontsema and J. Hemming (2006). Toward an Optimal Control Strategy for Sweet Pepper Cultivation - 1. A Dynamic Crop Model. ISHS Acta Horticulturae 718(III):367-374.

Cabeza, M. and A. Moilanen (2001). Design of reserve networks and the persistence of biodiversity. Trends in Ecology & Evolution 16(5):242-248.

Cairns, J., J. Overbaugh and S. Miller (1988). The origin of mutants. Nature 335(6186):142-145.

Caroppo, C., L. Stabili, M. Aresta, C. Corinaldesi and R. Danovaro (2006). Impact of heavy metals and PCBs on marine picoplankton. Environmental Toxicology 21(6):541-551.

Chen, Y.-M. (1997). Management of water resources using improved genetic algorithms. Computers and Electronics in Agriculture 18(2-3):117-127.

Chen, C.-S., C.-H. Liu and H.-C. Su (2008). A nonlinear time series analysis using two-stage genetic algorithms for streamflow forecasting. Hydrological Processes 22:3697-3711.

Chtioui, Y., D. Bertrand and D. Barba (1996). Reduction of the size of the learning data in a probabilistic neural network by hierarchical clustering. Application to the discrimination of seeds by artificial vision. Chemometrics and Intelligent Laboratory Systems 35(2):175-186.

Chtioui, Y., D. Bertrand, M.-F. Devaux and D. Barba (1997). Comparison of multilayer perceptron and probabilistic neural networks in artificial vision. Application to the discrimination of seeds. Journal of Chemometrics 11(2):111-129.

Chtioui, Y., B. Dominique and B. Dominique (1998). Feature Selection by a Genetic Algorithm. Application to Seed Discrimination by Artificial Vision. Journal of the Science of Food and Agriculture 76:77-86.

Cui, Y. and R. Wu (2005). Mapping genome-genome epistasis: A high-dimensional model. Bioinformatics 21(10):2447-2455.

Dagdeviren, M. and E. Eraslan (2008). Priority determination in strategic energy policies in Turkey using analytic network process (ANP) with group decision making. International Journal of Energy Research 32(11):1047-1057.

Daniell, H., K. J. Wurdack, A. Kanagaraj, S.-B. Lee, C. Saski and R. K. Jansen (2008). The complete nucleotide sequence of the cassava (*Manihot esculenta*) chloroplast genome and the evolution of atpF in *Malpighiales*: RNA editing and multiple losses of a group II intron. Theoretical and Applied Genetics 116(5):723-737.

Darwin, C. R. (1859). On the origin of species by means of natural selection. J Murray, London. 459 pp.

Davis, L. (1987). Genetic Algorithms and Simulated Annealing. Morgan Kaufmann, San Francisco. 216 pp.

Davis, L. (1991). Handbook of Genetic Algorithms. van Nostrand Reinhold, New York. 385 pp.

de Boer, P.-T., D. P. Kroese, S. Mannor and R. Y. Rubinstein (2005). A Tutorial on the Cross-Entropy Method. Annals of Operations Research 134(1):19-67.

de Masi, L., D. Castaldo, G. Galano, P. Minasi and B. Laratta (2005). Genotyping of fig (*Ficus carica* L) via RAPD markers. Journal of the Science of Food and Agriculture 85(13):2235-2242.

de Veies, H. (1902). The origin of species by mutation. Science 15(384):721-729.

Diaconis, P. W. and S. P. Holmes (1998). Matchings and phylogenetic trees. Proceedings of the National Academy of Sciences of the United States of America 95(25):14600-14602.

Diaz, B., A. Ribeiro, R. Bueno, D. Guinea, J. Barroso, D. Ruiz and C. Fernadez-Quintanilla (2005). Modelling Wild-Oat Density in Terms of Soil Factors: A Machine Learning Approach. Precision Agriculture 6:213-228.

Falkenauer, E. (1998). Genetic Algorithms and Grouping Problems. Wiley, New York. 220 pp.

Fink, W. L. (1986). Microcomputers and phylogenetic analysis. Science 234(4780):1135-1139.

Fisher, R. A. (1918). The Correlation between Relatives on the Supposition of Mendelian Inheritance. Philosophical Transactions of the Royal Society of Edinburgh 52:399-433.

Fisher, R. A. (1922). On the Dominance Ratio. Philosophical Transactions of the Royal Society of Edinburgh 42:321-341.

Fisher, R. A. (1954). Retrospect of the Criticisms of the Theory of Natural Selection, 84-98 pp. In: Huxley JS, Hardy AC, Ford EB (Eds.). Evolution as a Process. Allen and Unwin, London.

Fogel, L. J. (1999). Intelligence Through Simulated Evolution: Forty Years of Evolutionary Programming. Wiley Interscience, New York. 162 pp.

Fowler, H. J., S. Blenkinsop and C. Tebaldi (2007). Linking climate change modelling to impacts studies: Recent advances in downscaling techniques for hydrological modelling. International Journal of Climatology 27(12):1547-1578.

Fraser, A. S. (1957a). Simulation of genetic systems by automatic digital computers. I. Introduction. Australian Journal of Biological Sciences 10:484-491.

Fraser, A. S. (1957b). Simulation of genetic systems by automatic digital computers. II. Effects on linkage on rates of advance under selection. Australian Journal of Biological Sciences 10:492-499.

Fraser, A. S. (1957c). Simulation of genetic systems by automatic

digital computers. I. Introduction. Australian Journal of Biological Sciences 10:484-491.

Fraser, A. S. (1960a). Simulation of genetic systems by automatic digital computers. V. Linkage, dominance, and epistasis, 70-83 pp. In: Kempthorne O (Eds.). Biometrical Genetics. New York: Pergamon Press.

Fraser, A. S. (1960b). Simulation of genetic systems by automatic digital computers. VI. Epistasis. Australian Journal of Biological Sciences 13(2):150-162.

Fraser, A. S. (1960c). Simulation of genetic systems by automatic digital computers. VII. Effects of reproductive rate and intensity of selection on genetic structure. Australian Journal of Biological Sciences 13(3):344-350.

Fraser, A. S. (1962). Simulation of genetic systems VIII. Journal of Theoretical Biology 2(3):329-346.

Fraser, A. S. and D. Burnell (1967a). Simulation of genetic systems. XI. Inversion polymorphism. American Journal of Human Genetics 19:270-287.

Fraser, A. S. and D. Burnell (1967b). Simulation of genetic systems. XII. Models of inversion polymorphism. Genetics 57:267-282.

Fraser, A. S. and D. Burnell (1970). Computer Models in Genetics. McGraw-Hill, New York. 206 pp.

Fraser, A. S. and P. E. Hansche (1965). Simulation of genetic systems. IX. Major and minor loci, 507-516 pp. In: Geerts SJ (Eds.). Genetics Today, Proc. XI International Congress of Genetics, Oxford: Pergamon Press, 3.

Fraser, A. S., D. Burnell and D. Miller (1966). Simulation of genetic systems. X. Inversion polymorphism. Journal of Theoretical Biology 13:1-14.

Glover, F. (1977). Heuristics for Integer Programming Using Surrogate Constraints. Decision Sciences 8(1):156-166.

Glover, F. (1986). Future Paths for Integer Programming and Links to Artificial Intelligence. Computers & Operations Research 13(5):533-549.

Glover, F., E. Taillard and E. Taillard (1993). A user's guide to tabu search. Annals of Operations Research 41(1):1-28.

Hao, D. C., B. Huang and L. Yang (2009). Molecular evolution of paclitaxel biosynthetic genes TS and DBAT of Taxus species. Genetica 135(2):123-135.

Hashimoto, Y. (1997). Applications of artificial neural networks and genetic algorithms to agricultural systems. Computers and Electronics in Agriculture 18(2-3):71-224.

Henderson, C. E., W. D. Potter, R. W. Mcclendon and G. Hoogenboom (2000). Predicting aflatoxin contamination in peanuts: A genetic algorithm/neural network approach. Applied Intelligence 12(3):183-192.

Holland, J. H. (1975). Adaptation in Natural and Artificial Systems. University of Michigan Press., Michigan. 183 pp.

Holland, J. H. (1992). Adaptation in Natural and Artificial Systems: An Introductory Analysis with Applications to Biology, Control, and Artificial Intelligence. MIT Press, Cambridge. 228 pp.

Hruschka, Jr. E. R., E. R. Hruschka and N. F. F. Ebecken (2003a). A feature selection Bayesian approach for extracting classification rules with a clustering genetic algorithm. Applied Artificial Intelligence 17(5-6):489-506.

Hruschka, Jr. E. R., E. R. Hruschka and N. F. F. Ebecken (2003b). A feature selection Bayesian approach for a clustering genetic algorithm. In: Data Mining IV - Management Information Systems Series - vol. 7 ed. Southampton - WIT Press, UK, 7:181-192.

Huelsenbeck, J. P., F. R. Ronquist, R. Nielsen and J. P. Bollback (2001). Bayesian Inference of Phylogeny and Its Impact on Evolutionary Biology. Science 294(5550):2310-2314.

Husmann, H.-J. and H.-J. Tantau (2001). Integrated optimization of energy supply systems in horticulture using genetic algorithms. Computers and Electronics in Agriculture 31(1):47-59.

Hvidsten, T. R., J. Komorowski, A. K. Sandvik and A. Laegreid (2001). Predicting Gene Function from Gene Expressions and Ontologies. Pacific Symposium on Biocomputing 6:299-310.

Jäntschi, L. and M. V. Diudea (2009). Subgraphs of Pair Vertices. Journal of Mathematical Chemistry 45(2):364-371.

Jäntschi, L. and S. D. Bolboacă (2008). A structural modelling study on marine sediments toxicity. Marine Drugs 6(2):372-388.

Jäntschi, L., S. D. Bolboacă and R. E. Sestraş (2009). Hard Problems in Gene Sequence Analysis: Classical Approaches and Suitability of Genetic Algorithms. Biotechnology & Biotechnological Equipment 23(2):1275-1280.

Jäntschi, L., V. Popescu and S. D. Bolboacă (2008). Toxicity caused by para-substituted phenols on Tetrahymena pyriformis: The structure-activity relationships. Electronic Journal of Biotechnology 11(3):9(12), http://www.ejbiotechnology.info/content/vol11/issue3/full/9/9.pdf.

Kjellström, G. (1991). On the Efficiency of Gaussian Adaptation. Journal of Optimization Theory and Applications 71(3):589-597.

Kobti, Z., R. G. Reynolds and T. Kohler (2004). Agent-Based Modeling of Cultural Change in Swarm Using Cultural Algorithms. SwarmFest (online) 8:8p, http:// cscs.umich.edu/ swarmfest04/Program/PapersSlides/Kobti-SwarmFest04_kobti_reynolds_kohler.pdf.

Kuo, S.-F. and C.-W. Liu (2003). Simulation and optimization model for irrigation planning and management. Hydrological Processes 17(15):3141-3159.

Kysely, J. and M. Dubrovsky (2005). Simulation of extreme temperature events by a stochastic weather generator: Effects of interdiurnal and interannual variability reproduction. International Journal of Climatology 25(2):251-269.

Lamarck, J. B. P. A. (1809). An Exposition of Zoological Philosophy (..., in French). Dentu, Paris. 420 pp.

Larkin, M. A., G. Blackshields, N. P. Brown, R. Chenna, P. A. Mcgettigan, H. Mcwilliam, F. Valentin, I. M. Wallace,

62

A. Wilm, R. Lopez, J. D. Thompson, T. J. Gibson and D. G. Higgins (2006). Clustal W and Clustal X version 2.0. Bioinformatics 23(21):2947-2948.

Larsen, F. H., F. Van Den Berg and S. B. Engelsen (2007). An exploratory chemometric study of 1H-NMR spectra of table wines. Journal of Chemometrics 20(5):198-208.

Lemmon, A. R. and M. C. Milinkovitch (2002). The metapopulation genetic algorithm: An efficient solution for the problem of large phylogeny estimation. Proceedings of the National Academy of Sciences of the United States of America 99(16):10516-10521.

Letort, V., P. Mahe, P.-H. Cournède, P. De Reffye and B. Courtois (2008). Quantitative genetics and functional-structural plant growth models: Simulation of quantitative trait loci detection for model parameters and application to potential yield optimization. Annals of Botany 101(8):1243-1254.

Lewis, P. O. (1998). A genetic algorithm for maximum-likelihood phylogeny inference using nucleotide sequence data. Molecular Biology and Evolution 15(3):277-283.

Lewis, P. O. (2001). A likelihood approach to estimating phylogeny from discrete morphological character data. Systematic Biology 50(6):913-925.

Lindenmeyer, A. (1968). Mathematical models for cellular interaction in development. Journal of Theoretical Biology 18:280-315.

Linnaei, C. (1735). Systema Naturae. The Netherlands. 11 pp.

Liu, J., C. E. Goering and L. Tian (2001). A neural network for setting target corn yields. Transactions of the American Society of Agricultural Engineers 44(3):705-713.

Lundmark, A. M., F. Corfu, S. Spurgin and R. S. Selbekk (2007). Proterozoic evolution and provenance of the high-grade Jotun Nappe Complex, SW Norway: U-Pb geochronology. Precambrian Research 159(3-4):133-154.

Maddison, D. R. and W. P. Maddison (2000). MacClade v4.0. Sunderland: Sinauer (software)

Maddison, D. R. and W. P. Maddison (2006). Mesquite: A modular system for evolutionary analysis v1.1. Tucson: University of Arizona (software).

Mayer, D. G., J. A. Belward, H. Widell and K. Burrage (1999). Survival of the fittest - Genetic algorithms versus evolution strategies in the optimization of systems models. Agricultural Systems 60(2):113-122.

Mendel, J. G. (1866). Versuche über Plflanzenhybriden. Verhandlung Naturforsch Verein Brünn IV, 3-47. English translation: Druery C.T., Bateson W., 1901. Experiments in plant hybridization. J Roy Hortic Soc 26:1-32.

Montazar, A. and A. Rahimikob (2008). Optimal Water Productivity of Irrigation Networks in Arid and Semi-Arid Regions. Irrigation and Drainage 57(4):411-423.

Moore, A. B., K. P. Morris, G. K. Blackwell, A. R. Jones and P. C. Sim (2003). Using geomorphological rules to classify photogrammetrically-derived digital elevation models. International Journal of Remote Sensing 24(13):2613-

2626.

Morgan, T. H., A. H. Sturtevant, H. J. Muller and C. B. Bridges (1915). The Mechanism of Mendelian Heredity. H Holt & Co, New York. 262 pp.

Morimoto, T., W. Purwanto, J. Suzuki and Y. Hashimoto (1997). Optimization of heat treatment for fruit during storage using neural networks and genetic algorithms. Computers and Electronics in Agriculture 19(1):87-101.

Notredame, C., E. A. O'Brien and D. G. Higgins (1997). RAGA: RNA sequence alignment by genetic algorithm. Nucleic Acid Research 25(22):4570-4580.

Ortiz-Martinez, T., V. Rico-Gray and E. Martinez-Meyer (2008). Predicted and verified distributions of *Ateles geoffroyi* and *Alouatta palliat*a in Oaxaca, Mexico. Primates 49(3):186-194.

Patterson, J. T. (1928). The effects of X-rays in producing mutations in the somatic cells of *Drosophila melanogaster*. Science 68(1750):41-43.

Posada, D. and K. A. Crandall (1998). MODELTEST: Testing the model of DNA substitution. Bioinformatics 14(9):817-818.

Rodkaew, Y., S. Chuaiaree, S. Siripant, C. Lursinsap and P. Chongstitvatana (2004). Animating plant growth in L-system by parametric functional symbols. International Journal of Intelligent Systems 19(1-2):9-23.

Ronquist, F. and J. P. Huelsenbeck (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19(12):1572-1574.

Salomez, J. and G. Hofman (2007). A Soil Temperature/Short-Wave Radiation Growth Model for Butterhead Lettuce Under Protected Cultivation in Flanders. Journal of Plant Nutrition 30(3):397-410.

Sanderson, M. J. (2002). Estimating Absolute Rates of Molecular Evolution and Divergence Times: A Penalized Likelihood Approach. Molecular Biology and Evolution 19:101-109.

Sanderson, M. J. (2003). R8s: inferring absolute rates of molecular evolution and divergence times in the absence of a molecular clock. Bioinformatics 19:301-302.

Saski, C., S.-B. Lee, S. Fjellheim, C. Guda, R. K. Jansen, H. Luo, J. Tomkins, O. A. Rognli, H. Daniell and J. L. Clarke (2007). Complete chloroplast genome sequences of *Hordeum vulgare, Sorghum bicolor* and *Agrostis stolonifera*, and comparative analyses with other grass genomes. Theoretical and Applied Genetics 115(4):571-591.

Savageau, M. A. (1976). Biochemical System Analysis: a Study of Function and Design in Molecular Biology. Reading: Addison-Wesley. 199 pp.

Scalliet, G., F. Piola, C. J. Douady, S. Rety, O. Raymond, S. Baudino, K. Bordji, M. Bendahmane, C. Dumas, J. M. Cock and P. Hugueney (2008). Scent evolution in Chinese roses. Proceedings of the National Academy of Sciences of the United States of America 105(15):5927-5932.

Schultz, A.-K., M. Zhang, T. Leitner, C. Kuiken, B. Korber,

Bolboacă, S. D. et al. / Not. Bot. Hort. Agrobot. Cluj 38 (3) 2010, 51-63

63

B. Morgenstern and M. Stanke (2006). A jumping profile Hidden Markov Model and applications to recombination sites in HIV and HCV genomes. BMC Bioinformatics 7:265(15), http://www.biomedcentral.com/1471-2105/7/265.

Schultz, T. R. and S. G. Brady (2008). Major evolutionary transitions in ant agriculture. Proceedings of the National Academy of Sciences of the United States of America 105(14):5435-5440.

Schwefel, H.-P. (1993). Evolution and Optimum Seeking: The Sixth Generation. Wiley & Sons, New York. 456 pp.

Seginer, I. and I. Ioslovich (1999). Optimal spacing and cultivation intensity for an industrialized crop production system. Agricultural Systems 62(3):143-157.

Seginer, I., I. Ioslovich and M. Bux (2007). Optimal Control of Solar Sludge Dryers. Drying Technology 25(2):401-415.

Sirdas, S. and A. D. Sahin (2008). Relationship between drought and solar irradiation variables. Hydrological Processes 22(10):1460-1472.

Smith, S. W., R. Overbeek, C. R. Woese, W. Gilbert and P. M. Gillevet (1994). The genetic data environment and GUI for multiple sequence analysis. Computer Applications in the Biosciences 10(6):671-675.

Smith P. (2001). Priority setting in agricultural research: Beyond economic surplus methods. Public Admin Devel 21(5):419-428.

Smith, J. E. (2007). Coevolving Memetic Algorithms: A Review and Progress Report. IEEE Transactions on Systems, Man, and Cybernetics B: Cybernetics 37(1):6-17.

Splash, C. A. (2000). Structural pattern localization analysis by sequential histograms. Bioinformatics 16(4):341-357.

Tiptara, P., A. Petsom, S. Roengsumran and P. Sangvanich (2008). Hemagglutinating activity and corresponding putative sequence identity from *Curcuma aromatica* rhizome. Journal of the Science of Food and Agricultur 88(6):1025-1034.

van Laarhoven, P. J. M. and E. H. L. Aarts (1987). Simulated Annealing: Theory and Applications. D. Reidel, Dordrecht. 186 pp.

Wardlaw, R. and K. Bhaktikul (2004). Application of genetic algorithms for irrigation water scheduling. Irrigation and Drainage 53(4):397-414.

Weismann, A. (1893). The Germ-Plasm: A Theory of Heredity. C. Scribner's Sons, New York.

Wiegmann, B. M., D. K. Yeates, J. L. Thorne and H. Kishino (2003). Time Flies, a New Molecular Time-Scale for Brachyceran Fly Evolution Without a Clock. System Biology 52(6):745-756.

Wolpert, D. H. and W. G. Macready (1995). No Free Lunch Theorems for Search. The Santa Fe Institute: Technical Report, SFI-TR-95-02-010.

Wolpert, D. H. and W. G. Macready (1997). No Free Lunch Theorems for Optimization. IEEE T. Evolut Comput 1(1):67-82.

Yeates, D. K. (2002). Relationships of extant lower Brachycera: A quantitative synthesis of morphological characters. Zoologica Scripta 31(1):105-121.

Zhu, C., G. Yan, Z. Liu and L. Gao (2008). An Optimization Genetic Algorithm for Image Databases in Agriculture, II:1283-1289, 736(I)-744(II). In Li D (Eds.). Computer and Computing Technologies in Agriculture, Berlin: Springer-Verlag.