

Protein structure prediction as a hard optimization problem: the genetic algorithm approach

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Protein structure prediction can be shown to be an NP-hard problem; the number of conformations grows exponentially with the number of residues. The native conformations of proteins occupy a very small subset of these, hence an exploratory, robust search algorithm, such as a genetic algorithm (GA), is required. The dynamics of GAs tend to be complicated and problem-specific. However, their empirical success warrants their further study. In this paper, guidelines for the design of genetic algorithms for protein structure prediction are determined. To accomplish this, the performance of the *simplest* genetic algorithm is investigated for simple lattice-based protein structure prediction models (which is extendible to real-space), using energy minimization. The study has led us to two important conclusions for ‘protein-structure-prediction-genetic-algorithms’. Firstly, they require high resolution building blocks attainable by multi-point crossovers and secondly they require a local dynamics operator to ‘fine tune’ good conformations. Furthermore, we introduce a statistical mechanical approach to analyse the genetic algorithm dynamics and suggest a convergence criterion using a quantity analogous to the free energy of a population.

Short title: Genetic algorithm approach to structure prediction

Keywords: energy minimization; lattice models; simple exact models

Abbreviations: PSP protein structure prediction; GA genetic algorithm; PSP-GA protein-structure-prediction-genetic-algorithm; MC Monte Carlo; GA-MC genetic algorithm-Monte Carlo; HZ hydrophobic zipper; REM Random Energy Model

I. INTRODUCTION

Conceptually, proteins fold from their 1D polymer chain of amino acids (primary structure) to 3D stable, ‘unique’ conformations (tertiary structure). Anfinsen [1] showed that folding requires knowledge of the amino acid sequence alone; the determination of the native (biologically functioning) structure from its sequence is known as the *protein folding* problem. Much research has gone into elucidating the folding dynamics [2] but a practical theory is still beyond our understanding.

The folding problem attempts to understand the dynamics of the folding - *how* the sequence of amino acids arrive at the native state. It is clear that a full solution to this problem would be able to predict the tertiary structure of an amino acid sequence. Unfortunately, such a solution is beyond our understanding at present.

However, amino acid sequences are effectively being determined at a higher rate than that of their corresponding native structures. Since knowledge of the native structure is important to understanding the function of a protein, a potentially more practical problem is protein structure prediction. There is a possible confusion in terminology between the two terms, *protein folding* and *protein structure prediction*, as researchers use the terms loosely and interchangeably. The difference must be stressed as there are ‘folding simulations’, in the literature, which carry out a conformational search in a manner that is not attributable to the true folding dynamics of proteins (e.g. [3]).

Protein folding mainly concerns the dynamics of the problem which experimentalists study using hydrogen-exchange techniques, for example; theorists often use computer simulations of simple models, often on lattices, to elucidate the folding dynamics. Protein structure prediction, however, is only interested in the end result; experimentalists often use crystallisation techniques coupled with x-ray diffraction to determine the tertiary structure, whereas theorists tend to use computer-based optimization methods. This is the approach discussed in this paper. The problem involves two aspects: (1) the specification of the function to optimize and (2) the choice of a search algorithm.

The prediction of protein structures using optimization methods have been more successful using comparative modelling [4] techniques which include sequence alignment, threading [5] and the use of secondary structural propensities [6]. However, a physical approach based on energy minimization is used here. It is clear that the interactions between the residues and the solvent molecules drive the protein towards its native state. Determining the fundamental interactions is important, not only for protein structure prediction, but also for the protein folding problem. A further reason for the physical approach is that comparative modelling requires the known structure of one or more homologous proteins - these cannot always be guaranteed to exist.

The second aspect of the protein structure prediction problem is concerned with designing a search strategy for the energy minimization. It is clear that a blind search through the conformational space is impossible, as it would take a time greater than the age of the universe. A similar ‘paradox’ for real proteins, based on observed protein folding times ($\sim 10^{-3}s$), was first noted by Levinthal [7]. Furthermore, several authors have proved various models of protein structure prediction to be computationally NP-hard¹ [9–11]. This implies that no efficient algorithm can be designed to guarantee finding the native state amongst the exponentially many. A related idea to the complexity of the conformational search is the concept of ‘rugged’ energy landscapes [12]. Although optimal solutions are not guaranteed, robust, exploratory, non-deterministic search algorithms (e.g. simulated annealing [13] and genetic algorithms [14]) can locate good, near-optimal solutions, within a reasonable time. In the present paper, we focus on the design of a good conformational search strategy for the problem, leaving the discussion of the best choice of energy functions for protein structure prediction to a later paper.

Genetic algorithms were invented by John Holland [14] in his quest for a theory of adaptive processes. The concept was inspired by Darwin’s evolutionary theory (loosely ‘survival of the fittest’) and in particular ‘neo-Darwinism’ according to which genetic recombinations and mutations play a dominant role in the evolution of a species. It is generally believed that Nature evolves so that individuals that are the best adapted to their co-evolving environment survive, while the poor ones die off; this is an example of optimization, more commonly referred to as ‘adaptation’ in biology [15]. Due to their highly nonlinear nature, genetic algorithms are difficult to analyse. There is no asymptotic global optimum convergence proof, as there is in simulated annealing [16], nor are there any general rules to design a GA for a specific problem. However, their empirical success for the

solution of numerous NP problems ([17] and references therein) warrants their further study.

Previous applications of genetic algorithms to the protein structure prediction problem [18–20,3,21–23] have not considered the GA design issue. As in any problem, the simpler the algorithm is, the fewer the parameters it requires, the easier it is to understand and improve the performance. For this purpose we use a modified version of Goldberg’s [24] Simple Genetic Algorithm (SGA), written in C. Dandekar and Argos [18–20] also use a version of the SGA but their work differs to ours in that our objectives are different. Firstly, they optimize the structural features of proteins (such as α -helices and β -strands) rather than adopting an energy minimization approach. Secondly, little comparison was made with the performance of other algorithms. Schulze-Kremer [22] wrote an elaborate genetic algorithm to optimize real-space dihedral angles for a fully atomistic representation of proteins, based on CHARMM [25] energy minimization. Unfortunately, results were poor. Clearly, our principal research aim is to predict realistic structures as well, but only when a good method has been established. Unger and Moult [3,21] compared a Monte Carlo search with a ‘genetic algorithm’, using simple exact lattice models. However, their genetic algorithm is, strictly speaking, a hybrid GA. It incorporates several Monte Carlo conformers with the occasional crossover between structures. For this reason, we call their approach a ‘Genetic Algorithm-Monte Carlo’ (GAMC). They compared this method with a Monte Carlo search and concluded that the GAMC found lower energy solutions.

In this paper, we compare the Simple Genetic Algorithm with work by Unger and Moult [21]; Yue *et al.* [26] and Sali *et al.* [27] and determine guidelines for designing protein-structure-prediction-genetic-algorithms.

The paper is structured in the following way. Section II highlights the conformational search issue and the need for a genetic algorithm approach. Following that, section III provides a description of the method for determining guidelines for GA design. Section IV discusses the Simple Genetic Algorithm used for the lattice conformational search. The HP-model [28] and REM-model [29] are described in section V, as are the various methods used to minimize these potentials [26,3,21,27]. Lattice conformational search results from the SGA are compared with the other methods in section VI, while section VII provides a discussion of the ‘protein structure prediction-genetic algorithm’ (PSP-GA) design principles that have emerged from this work.

II. WHY GENETIC ALGORITHMS FOR PROTEIN STRUCTURE PREDICTION?

Protein structure prediction is analytically difficult to solve. The problem is thought to stem from the exponential nature of the conformational search space. The

¹A good introduction to the theory of NP-completeness and NP-hardness can be found in [8].

number of conformations of a protein with N amino acid residues grows exponentially as γ^N where γ is the average number of conformations per residue (typically ~ 10). This suggests that an algorithm would require an exponential time to search the whole conformational space for the native state.

However, problems with exponentially growing search spaces are not new in physics (e.g. ideal gases) but many are solvable due to the symmetries and conservation laws that can be exploited. With proteins there is an added difficulty that the interactions are complex - it is not clear whether there are enough symmetries to reduce the problem to a tractable solution. In addition to this, proteins, although macromolecular, do not contain $\sim 10^{23}$ atoms to guarantee a valid statistical mechanical and thermodynamic treatment.

Furthermore, work by Unger and Moulton [9]; Fraenkel [10]; Ngo and Marks [11] suggests that the protein structure prediction problem is NP-hard, that is computationally impossible to guarantee an exact solution. Bryngelson, Wolynes *et al.* [12], for example, advocate that the energy landscape of proteins must be ‘rugged’. This reflects the various energy barriers that have to be crossed and thus the hurdles that a conformational search algorithm must be able to deal with.

For these reasons ‘intelligent’ conformational search algorithms have become popular in structure prediction. Unlike gradient-based methods [30], which tend to terminate at local minima, genetic algorithms ‘hop’ around the conformational space independent of local derivatives. A selection process focuses the search in low energy areas, whereas a recombination stage maintains exploration of the search space.

III. DESIGNING GENETIC ALGORITHMS FOR PROTEIN STRUCTURE PREDICTION

A genetic algorithm is made up of 4 basic components: representation; selection; recombination and evaluation. Representation deals with formulating the specific problem as a digital string of parameters. This, combined with the evaluation function (in our case conformational energy) describes the optimization problem. The remaining two components, selection and recombination, provide the dynamics of the GA search, which drive the population of solutions towards the global optimum. Within each unit, there are several options leading to numerous variations of genetic algorithms; some examples and corresponding parameters are listed in table I. To determine guidelines for designing PSP-GAs, we used the following principles:

1. A first approach should always be the simplest approach. In order to analyse the GA dynamics, we used a GA with the simplest options and with the fewest parameters - a Simple Genetic Algorithm - to search lattice conformational space.

2. A systematic sample search of the parameter space was carried out to determine optimal parameter values for the SGA.
3. Having calibrated the SGA in step 2, we compared the SGA conformational search ability using several test energy functions.
4. Conformations, and their corresponding energies, generated by the SGA were compared with conformations predicted by other search methods.
5. The time evolution of conformations generated by the SGA were observed. Minimal requirements and improvements for PSP-GAs are proposed.

<i>GA Options and Parameters</i>
Population: static or variable size
Representation of solutions: bit string, reals, symbolic
Maximum number of generations or convergence criteria
Recombination operators: 1-pt crossover, uniform crossover, mutation, perturbation
Recombination probabilities: static, variable or dynamic
Selection methods: roulette, tournament, rank, elitism
Fitness scaling: linear with cut-off, quadratic, exponential

TABLE I. Examples of various options in designing a genetic algorithm.

The merit of simple exact lattice models [28] is the ability to test ideas easily and suggest extrapolations to real systems. Simple exact models are ‘simple’ since only a few parameters are required, and ‘exact’ since physical properties can be calculated exactly. Lattice models, although unrealistic in appearance, provide several advantages over real-space models. From a folding dynamics point of view, they can explore long time behaviour; while from a structure prediction/optimization point of view, as in our case, they provide a valuable test-bed for protein structure optimizers.

Runs with various initial conditions were carried out to ensure that the GA produced similar results each time.

IV. THE SIMPLE GENETIC ALGORITHM FOR LATTICE CONFORMATIONAL SEARCH

The Simple GA (SGA), as defined by Goldberg [24], is the simplest of all genetic algorithms. The original SGA manipulated binary strings which encode a trial solution of the problem at hand. However, a major modification for searching protein conformations on a cubic lattice is to use a more natural representation for this problem. Since a simple cubic lattice is spatially restricting, a string of bond directions represents a folded chain

of beads; each symbol corresponds to an increment or decrement in the appropriate Cartesian coordinate of the successive monomer beads (see table II). A conformation of the polymer is then translated to a set of monomer positions \mathbf{r}_i ($i = 1, \dots, N$) (where N is the number of monomer beads (residues)).

Direction	$\Delta\mathbf{r}$
(U)P	$r_z \mapsto r_z + 1$
(L)EFT	$r_x \mapsto r_x - 1$
(F)RONT	$r_y \mapsto r_y + 1$
(B)ACK	$r_y \mapsto r_y - 1$
(R)IGHT	$r_x \mapsto r_x + 1$
(D)OWN	$r_z \mapsto r_z - 1$

TABLE II. Bond directions describing lattice conformations. A bond direction corresponds to a change, $\Delta\mathbf{r}$, in one of the Cartesian coordinates of the successive monomer, keeping all other coordinates the same as the previous monomer.

This representation has access to *all* 6^N lattice conformations, including all the non-physical, non-self-avoiding conformations. Thus the search task is a formidable one. A random population of conformations is generated and manipulated according to the GA dynamics (selection and recombination). The population size, \mathcal{S} , is kept fixed. All individuals are replaced at each iteration, except for two copies of the current best conformation - this is known as ‘elitism’.

Selection is linearly proportional to fitness so that the probability, P_i , of selecting the i^{th} conformation, with a fitness value F_i , to propagate to the next time step is given by:

$$P_i = \frac{F_i}{\sum_{j=1}^{\mathcal{S}} F_j} \quad (1)$$

Probabilities must be positive so a linear mapping with a cut-off value is used to convert the energy (E) minimization problem to a fitness (F) maximization:

$$F_i = \begin{cases} -E_i & \text{if } E_i < 0; \\ 0 & \text{if } E_i \geq 0. \end{cases} \quad (2)$$

Selected individuals, strings, are modified in a recombination process, to generate new solutions. Figure 1 shows a schematic representation of the one-point crossover and gene-wise mutation operators used by the SGA. These operators act stochastically on the selected individuals with fixed probabilities. In one-point crossover, a random crossover point is chosen for a pair of selected individuals, and the bond directions (‘genes’) are swapped up to the crossover point. Mutations act on a single individual and randomly change the value of bond directions along the string. The workings of the SGA are summarised in figure 2.

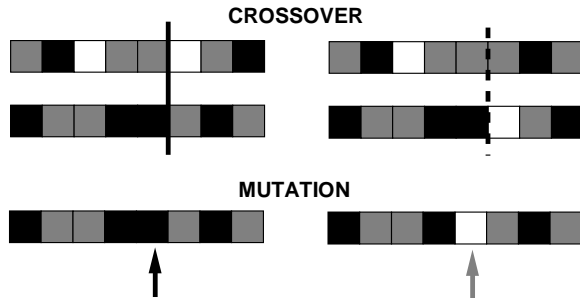


FIG. 1. The top half represents the action of a one-point crossover operator. Below is an illustration of a single gene-wise mutation. In both cases the left side represents the ‘before’ situation, and the right side, the ‘after’ state.

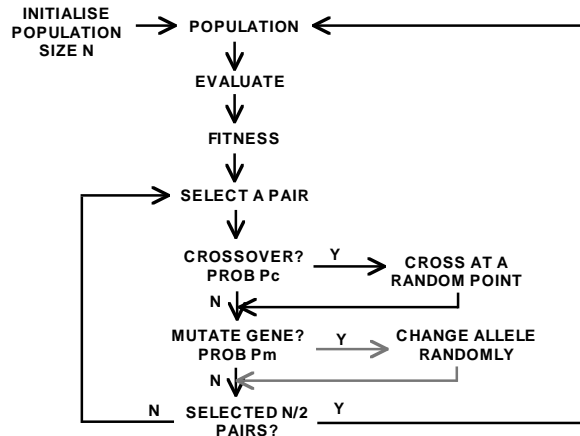


FIG. 2. The simple genetic algorithm. A population of N conformers is initialised. These trial conformations are evaluated and selected, based on their fitness. Pairs of selected conformers are crossed over with a probability, P_c . Each bond direction (‘gene’) is then randomly mutated with a probability, P_m . A new population is selected in this manner and repeated for many generations (typically 2000).

A. Random Energy Model

Originally used in spin glass theory, the Random Energy Model (REM) [31] was applied to protein folding by Bryngelson and Wolynes [32] and later formulated for lattice protein models by Shakhnovich and Gutin [29]. In the REM, a protein is described by a fixed sequence of random interaction energies. Although not discussed here, the random interaction model lends itself for analytical studies of the coil-globule transition in proteins [29]. Specifically, the conformational energy is calculated as:

$$E(\{\mathbf{r}_1.. \mathbf{r}_N\}) = \sum_{i,j=1;i < j}^N B_{ij} \Delta(\mathbf{r}_i - \mathbf{r}_j) + D_2 \sum_{i,j}^N \delta(\mathbf{r}_i - \mathbf{r}_j) + D_3 \sum_{i,j,k}^N \delta(\mathbf{r}_i - \mathbf{r}_j) \delta(\mathbf{r}_j - \mathbf{r}_k) \quad (3)$$

$$\Delta(\mathbf{r}_i - \mathbf{r}_j) = \begin{cases} 1 & \text{for } i \text{ \& } j \text{ nearest neighbours} \\ 0 & \text{otherwise} \end{cases}$$

$$\delta(\mathbf{r}_i - \mathbf{r}_j) = \begin{cases} 1 & \text{if monomers } i,j \text{ occupy same site} \\ 0 & \text{otherwise} \end{cases}$$

where,

$D_2 \equiv$ energetic penalty parameter for sites containing 2 or more monomers

$D_3 \equiv$ energetic penalty parameter for sites containing 3 or more monomers

$B_{ij} \equiv$ disorderly interaction energies

(energies are in units of $k_B T$ where k_B is Boltzmann's constant and T is the temperature in Kelvin)

The interaction matrix, B_{ij} , is symmetric but randomly generated with a Gaussian distribution:

$$P(B_{ij}) = (2\pi B^2)^{-\frac{1}{2}} \exp(-(B_{ij} - B_0)^2 / 2B^2) \quad (4)$$

The compactization observed in globule proteins is modelled in Eq.(3) using B_{ij} as a negative interaction potential with mean B_0 . B defines the spread, i.e. the standard deviation, of the compactization interactions. The greater the spread, the more heterogeneous the protein. A zero-spread corresponds to uniform interactions; this special case constitutes the Fixed Energy Model (FEM) which we have used for the larger polymers studied here (64mer, 125mer).

The last two terms in Eq.(3) represent excluded volume effects, that is they are energetic *penalties* for conformations with lattice sites occupied by more than two (D_2

term) or more than three (D_3 term) monomers. The objective of the genetic algorithm is to find conformations without multiple occupancies at a single site, by minimising this energy function.

B. HP-model

It is well known that correlations in the sequence of amino acid residues lead to sub-structures (secondary structures) common to all protein structures. These correlations can reduce the size of the 'alphabet' (code) from 20 symbols to a lesser number. The simplest and most interesting is the classification of residues into two types: H and P [33]. The energy function for this system favours interactions between HH monomer types and is indifferent to all other (PP and HP) interactions. This is known as the HP-model. It aims to highlight the importance of the hydrophobic effect in protein folding. In an aqueous medium, globular proteins tend to have a core of hydrophobic residues, surrounded by polar residues on the surface; in the HP-model, the H monomers correspond to hydrophobic residues that collapse to form a core surrounded by polar, P, monomers. Much work has been carried out by Dill and co-workers on this model [34,35,23,26,28].

The energy function for this model is:

$$E(\{\mathbf{r}_1.. \mathbf{r}_N\}) = -|\epsilon| \sum_{i,j=1;i < j}^N \Delta(\mathbf{r}_i - \mathbf{r}_j) + \epsilon_2 \sum_{i,j}^N \delta(\mathbf{r}_i - \mathbf{r}_j) + \epsilon_3 \sum_{i,j,k}^N \delta(\mathbf{r}_i - \mathbf{r}_j) \delta(\mathbf{r}_j - \mathbf{r}_k) \quad (5)$$

$$\Delta(\mathbf{r}_i - \mathbf{r}_j) = \begin{cases} 1 & \text{if } i,j \text{ both H-type \& nearest neigh.} \\ 0 & \text{otherwise} \end{cases}$$

$$\delta(\mathbf{r}_i - \mathbf{r}_j) = \begin{cases} 1 & \text{if monomers } i,j \text{ occupy same site} \\ 0 & \text{otherwise} \end{cases}$$

where,

$|\epsilon| \equiv$ strength of HH attraction (usually taken as 1)

$\epsilon_2 \equiv$ energetic penalty parameter for sites containing two or more monomers

$\epsilon_3 \equiv$ energetic penalty parameter for sites containing three or more monomers

Strictly speaking, the final two terms (ϵ_2, ϵ_3) in Eq.(5) are not included in the HP-model. We borrow these terms from the Random Energy Model to drive the conformational search towards self-avoiding conformations. This is necessary since *all* possible conformations are allowed; an energetic penalty is required to penalise conformations with multiple occupancies at a single site. For both models (REM and HP), the penalty terms reduce

to zero if the search is successful and a low energy self-avoiding conformation is found.

VI. RESULTS

The first test function used was that from the Random Energy Model, Eq.(3). Shakhnovich *et al.* [27] used a Metropolis Monte Carlo algorithm with this energy function to find the native states of 27mer heteropolymers. They interpreted the Monte Carlo ‘folding’ algorithm as modelling the folding dynamics of polymers. However, although Metropolis Monte Carlo methods asymptotically guarantee finding the thermal equilibrium state, it is unclear whether an interpretation beyond this has any validity. We view their procedure as a protein structure optimization approach. These authors enumerated all compact (cubic) self-avoiding conformations, which allow them to determine the global minimum of each random 27mer sequence generated. They reported [27] that three out of thirty sequences found the known global minimum; energies varied from -83.7 to -74.6 (in units of $k_B T$). Using the SGA, we found that three out of four sequences obtained compact, 100% cubic conformations (see fig. 3), with energies ranging from -78.1 to -69.9 (units in $k_B T$). We cannot determine whether they are the global energy-minimum structures without carrying out a full enumeration; this is computationally time consuming due to the NP-complete nature of the problem, and, more importantly, unnecessary for our design purposes. Furthermore, we were unsuccessful in our correspondence with the authors and were unable to obtain the random interaction matrices specifically used in their work ([27]).

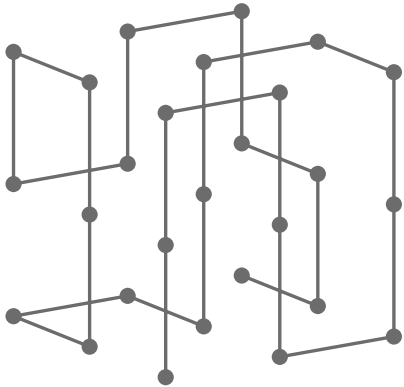


FIG. 3. Example of a 100% cubic 27mer conformation found by the SGA.

Longer polymers (64mer, 125mer) are more challenging since the conformational space grows exponentially with the polymer length. We continued to use the

REM with $B=0$. This corresponds to uniform interactions and thus guarantees that cubic conformations ($4 \times 4 \times 4$, $5 \times 5 \times 5$ respectively) occupy the multiply-degenerate ground states. The 64mer reached 91% cubicity and the 125mer runs found a conformation with 85% cubicity (fig. 4). Since we are restricting our discussion to cubic lattices, it is more accurate to describe structures according to how ‘cubic’ they are, rather than using the more general term ‘compactness’.

It is unfortunate that 100% cubic conformations were not found; however, we are using the simplest genetic algorithm. Nevertheless, this initial exercise was useful to establish optimal values for the GA parameters. The optimal GA parameters for short polymers were: a minimum population size of 400; a 20% probability of crossover and a 4% probability of mutating a bond direction. Longer polymers required a larger minimum population size of 1000; a 90% probability of crossover and a 2% probability of mutation. Having established a good set of GA parameters, the SGA was analysed using the second test function, the HP-model.

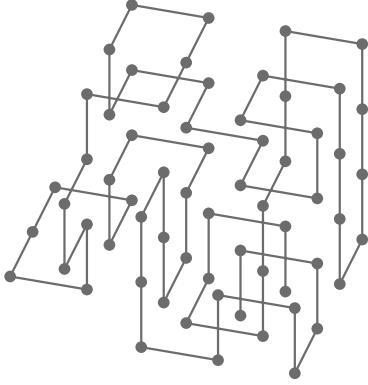
Unger and Moulton studied random HP-sequences of length 27 and 64 monomers [21]. They used two optimization methods: a Metropolis Monte Carlo (MC) method and a variation of the Monte Carlo method that incorporates a genetic algorithm (GAMC). The GAMC method corresponds to a population of Metropolis Monte Carlo conformers which ‘mix’ between themselves through a crossover operation. The comparisons between these methods and our SGA are shown in tables III and IV.

Our SGA beat Monte Carlo in 17 of the 20 test sequences and equalled it in finding low energy conformations for two sequences. On average, conformations generated by our SGA were 1.1 energy units lower than those found by the Monte Carlo method for the 27mers and 8.3 units lower for the 64mers.

When compared to the GAMC method, the SGA performed on average as well as the GAMC for the 27mers; SGA conformational energies were on average 0.5 unit higher. In the 64mer case, SGA conformations were on average 3.4 energy units higher than the conformational energies found by the GAMC. There was one 64mer sequence for which the SGA found a lower energy conformation than the GAMC. An important note is the speed at which the SGA found low energy conformations. Only a fraction of the total number of steps were required for the SGA when compared to the Monte Carlo and GA-Monte Carlo. For example, for the 27mer, to reach a solution of comparable quality, the number of steps required by the SGA was 3% of the number of steps required by the MC method, and 4% for the GAMC.

Further studies were carried out using HP-sequences taken from Yue *et al.* [26]. They designed ten 48mer sequences and determined the native conformational states using a constraint-based hydrophobic core construction method. This method determines the global minima of HP-sequences by constructing conformations with a

number of nearest neighbours=74



number of nearest neighbours=149

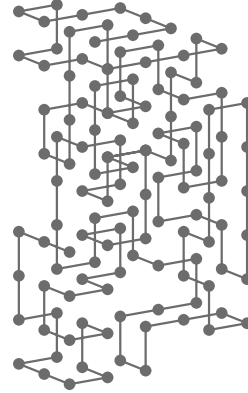


FIG. 4. Left: 91% cubic conformation for a 64mer homopolymer. Right: 85% cubic conformation for a 125mer homopolymer.

sequence	E_{SGA}	Num Steps	ΔE_{MC}	ΔE_{GAMC}
273d.1	-8	2.9E+04	-1	1
273d.2	-8	2.1E+04	1	1
273d.3	-8	1.1E+05	-2	0
273d.4	-15	2.7E+05	-4	0
273d.5	-7	9.6E+03	0	1
273d.6	-11	9.6E+04	-2	0
273d.7	-11	2.2E+04	-1	1
273d.8	-4	8.6E+04	0	0
273d.9	-7	6.0E+04	-1	0
273d.10	-10	5.6E+04	-1	1
AVERAGE	-8.9	7.6E+04	-1.1	0.5

TABLE III. SGA comparisons with Unger and Moul't's 27mer results. The sequence number corresponds to the number used by Unger and Moul't to label their HP sequences. E_{SGA} is the lowest energy found by the SGA. The 'num steps' column reports the number of energy evaluations carried out by the SGA to reach the lowest energy state. ΔE_{MC} is the energy difference between the lowest energies found by the SGA and Unger & Moul't's Monte Carlo procedure: $\Delta E_{MC} = E_{SGA} - E_{MC}$. Similarly, ΔE_{GAMC} is the energy difference between the SGA and Unger & Moul't's GAMC method.

sequence	E_{SGA}	Num Steps	ΔE_{MC}	ΔE_{GAMC}
643d.1	-21	6.4E+05	-9	6
643d.2	-26	1.5E+06	-9	3
643d.3	-36	1.7E+06	-12	-1
643d.4	-30	1.9E+06	-12	4
643d.5	-28	6.3E+05	-8	4
643d.6	-22	4.6E+05	-6	7
643d.7	-17	2.1E+05	-2	3
643d.8	-28	1.4E+06	-9	1
643d.9	-29	9.8E+05	-10	3
643d.10	-20	3.1E+05	-6	4
AVERAGE	-25.7	9.8E+05	-8.3	3.4

TABLE IV. SGA comparisons with Unger and Moul't's 64mer results. The sequence number corresponds to the number used by Unger and Moul't to label their HP sequences. E_{SGA} is the lowest energy found by the SGA. The 'num steps' column reports the number of energy evaluations carried out by the SGA to reach the lowest energy state. ΔE_{MC} is the energy difference between the lowest energies found by the SGA and Unger & Moul't's Monte Carlo procedure: $\Delta E_{MC} = E_{SGA} - E_{MC}$. Similarly, ΔE_{GAMC} is the energy difference between the SGA and Unger & Moul't's GAMC method.

core of H (hydrophobic) residues that also minimize the surface area of the conformation. The difference in the conformational energies found by the SGA and the native state energy is labelled as ΔE_N . Yue *et al.* also used a conformational search algorithm for HP-sequences called a ‘hydrophobic zipper’ (HZ). In this case, the H monomers attract nearby H monomers and bring them together in a process akin to nucleation. The energy difference between conformations found by this method and the SGA is denoted as ΔE_{HZ} . The comparisons are summarised in table V. Conformations found by the SGA were on average 6.0 energy units higher. An example of a compact conformation by the SGA is shown in figure 5. In no cases did the SGA equal or beat conformational energies obtained by the hydrophobic zipper method.

number of nearest neighbours=39

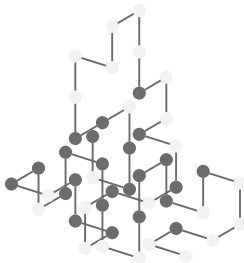


FIG. 5. Example of a compact HP conformation, with a hydrophobic core, found by the SGA.

Runs took from several minutes for short polymers (27mers, 48mers) to hours for longer cases (64mers, 125mers) on a DEC 3000 Alpha workstation.

VII. DISCUSSION

The conformations found by the SGA are not promising in themselves. However, the aim of the study is to analyse the simple genetic algorithm and determine what factors are important in designing PSP-GAs. What can we learn from these results about PSP-GAs?

It is clear from the 27mer studies that the SGA performs well for short polymers and tends to find compact,

sequence	E_{SGA}	#Steps	ΔE_{HZ}	ΔE_N
483d.81	-24	1.6E+06	7	8
483d.82	-24	4.7E+05	8	10
483d.83	-23	1.9E+05	7	10
483d.84	-24	8.6E+05	7	10
483d.85	-28	2.4E+05	2	4
483d.86	-25	5.5E+05	4	7
483d.87	-27	3.8E+05	2	5
483d.88	-26	4.2E+05	3	5
483d.89	-27	1.3E+05	4	7
483d.90	-26	7.0E+04	3	7
AVERAGE	-25.4	4.9E+05	9.4	7.3

TABLE V. SGA comparisons with Yue and Dill’s 48mer studies. Sequence number corresponds to the number used by Yue *et al.* to label their HP sequences. E_{SGA} is the lowest energy found by the SGA. The ‘num steps’ column reports the number of energy evaluations carried out by the SGA to reach the lowest energy state. ΔE_{HZ} is the energy difference between the lowest energies found by the SGA and Yue *et al.*’s hydrophobic zipper method: $\Delta E_{HZ} = E_{SGA} - E_{HZ}$. Similarly, ΔE_N is the energy difference between the SGA and the native state energy found by Yue *et al.* using the constraint-based hydrophobic core construction method.

low energy structures. However, as was evident in our initial investigation of 64mers and 125mers using the REM, the SGA performs below average. Although the SGA method was better than the Monte Carlo method, it did not perform as well as the GAMC and was even worse than the HZ algorithm. To some extent, it is not surprising that the hydrophobic zipper method performed better than the SGA. HZ is a specialised search algorithm for the HP-model and generates conformations by explicitly forming H-H contacts. It is not uncommon for specialised algorithms to solve certain cases of an NP-complete problem - however, a *general* solution remains difficult [36].

In general the SGA finds it hard to generate compact conformations for the longer polymers - why? We investigated this further using the HP-model. The best way to analyse the dynamics of the SGA is to observe its time evolution rather than merely the end result. Thus, the lowest energy conformations were observed at various time points. In several cases, the SGA produced two clusters of residues with hydrophobic (H) cores connected by a ‘thread’ - similar to loop regions in real proteins. It is promising that such conformations (see figure 6) are possible since proteins with sub-structures connected by loop regions are common in Nature. However, this is not the lowest energy conformation for the HP-model, so we conclude that the clustering is due to restrictions imposed by the GA dynamics, that is to selection and recombination. Selection is an important aspect of the GA dynamics but we do not think it is the reason for the occurrence of clustered solutions; if a lower energy globule existed in the population, the selection function would have assigned it a high probability and elitism would guarantee its selec-

tion into the next generation.

The problem must therefore lie in the recombination stage: it appears that the one-point crossover and mutation operations cannot inter-digitate the clusters successfully. We believe that these recombination operators would fold the clusters *into* each other creating many sites with multiple occupancies; these are penalised by the excluded volume terms in Eq.5 heavily reducing the ‘survival probability’ of such structures. The difficulty appears to be in the formation of only two large clusters, or ‘building blocks’; we think that more clusters but smaller in size would be easier to manipulate. How do we promote this in the GA dynamics?

Genetic algorithms manipulate partial solutions in their search for the overall optimal solution [14,24]. These partial solutions or ‘building blocks’ correspond to sub-strings of a trial solution - in our case local sub-structures within the overall conformation. Clearly, the level of crossover influences the size of the building blocks. A multi-point crossover would generate smaller building blocks (a higher ‘resolution’) and consequently smaller clusters that should facilitate their inter-digitation. In the case of the 27mer, the one-point crossover generates building blocks of 13.5 monomers, on average. Based on this argument, 48mers and 64mers require at least two to three point crossovers to reduce the size of the building blocks to ~ 10 . Furthermore, the local perturbation dynamics of the Monte Carlo methods aids the local ‘fine tuning’ of conformations as manifested by the GAMC method. It is believed that the two recombination operators of multi-point crossover and a local perturbation are required for any PSP-GA to be fully effective. Work is under way to design a PSP-GA to optimize real protein structures (rather than lattice models) which includes these requirements.

One further problem with genetic algorithms is ‘knowing when to stop’. Most optimization algorithms deal with a single solution at a time and decide to stop when there has been no change in the cost or energy function for a successive number of steps. Since GAs deal with an ensemble of solutions, a quantity analogous to the statistical mechanical free energy is used. The ‘population free energy’, F , is calculated from its ‘partition function’, Z :

$$Z = \sum_{i=1}^N e^{-E_i} \quad (6)$$

where the sum is over the total number of conformers in a population and E_i is the energy of the i^{th} conformer. Hence,

$$F = -\ln(Z) \quad (7)$$

This approach is advantageous over using the mean energy of the population in two ways. Firstly, the mean energy fluctuates around the equilibrium making it difficult to use as a stop criterion, and secondly, F contains more information on the shape of the energy distribution,

including, in particular, its ‘entropy’. F appears to play the role of a Lyapounov function in the GA dynamics - convergence is synonymous with its minimal value. Figure 7 plots the energy distributions of the population at various time steps. The plot shows very clearly that the GA dynamics converge the population of conformations to an equilibrium distribution. This is characterised by F as shown in figure 8.

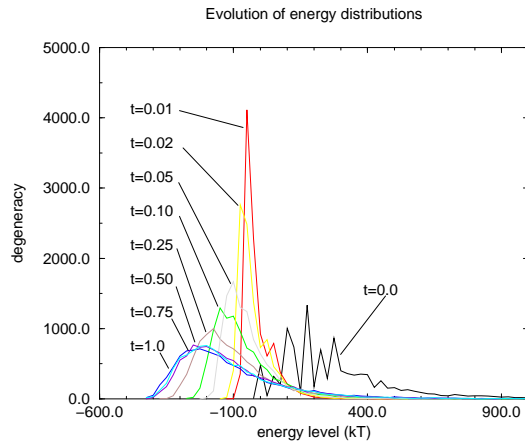


FIG. 7. Evolution of a population: plotting the energy distributions at various time steps. t is the percentage of the total run-time elapsed. The population converges within 50% of the run time.

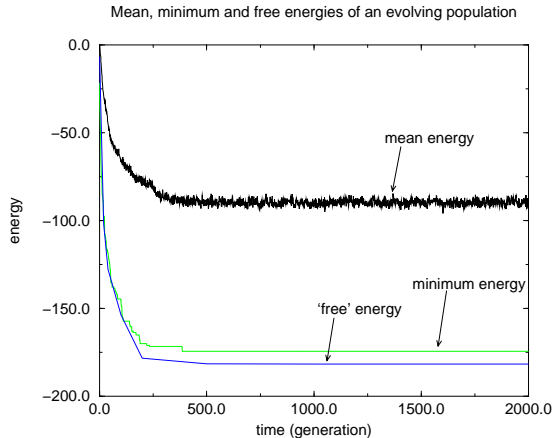


FIG. 8. Evolution of the energies of a population. The free energy, which characterises the energy distribution of a population, reaches a convergence, or equilibrium point.

In conclusion, the genetic algorithm approach to the protein structure prediction problem offers a promising potential method of solution. GAs are fast and efficient at searching the rugged conformational landscapes presented by protein molecules. We have established some guidelines for designing PSP-GAs in this paper and are currently implementing them in an improved GA to search for realistic protein structures.

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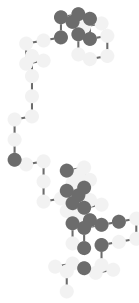
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3. nearest=27 energy=-16.000



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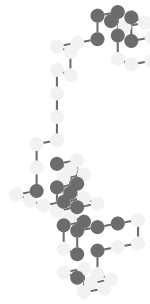


FIG. 6. Evolution of the best conformation per generation: formation of clusters in the Simple Genetic Algorithm. Dark=H=hydrophobic, Light=P=polar.