Sunil Template

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Chapter 1

Multi objective evolutionary algorithms applied to Protein Structure Prediction Problem

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1.1 Introduction

1.2 Protein folding

We will briefly recall some of the main biological concepts related to the protein folding problem that are relevant to our discussion.

Proteins are macromolecules made out of twenty different amino acids, also referred to as residues. An amino acid has a peptide backbone and a

distinctive side chain group. The peptide bond is defined by an amino group and a carboxyl group connected to an alpha carbon to which a hydrogen and side chain group are attached.

Amino acids are combined to form sequences which are considered the primary structure of the peptides or proteins. The secondary structure is the locally ordered structure brought about via hydrogen bounding mainly within the peptide backbone. The most common secondary structure elements in proteins are the alpha helix and the beta sheet. The tertiary structure is the global folding of a single polypeptide chain.

Under specific conditions, the protein sequence folds into a unique native 3-d structure. Each possible protein fold has associated energy. The *thermodynamic hypothesis* states that the native structure of a protein is the one for which the free energy achieves the global minimum. Based on this hypothesis, many methods that search for the protein native structure define an approximation of the protein energy and use optimization algorithms that look for the protein fold that minimizes this energy. These approaches mainly differ in the type of energy approximation employed and in the characteristics of the protein modeling.

The achievement of the protein native structure is the result of the so-called protein folding process. The laws that govern protein folding are unknown. Therefore a number of ideas have emerged that try to answer this question: how do amino acid sequences specify proteins 3-d structure?

There are two main approaches to protein folding, commonly referred as the "classical" and "new" views. The "classical" view considers folding as a defined sequence of states leading from the unfolded to the native state. This sequence is called the pathway [9]. In the "new" view approach, folding is seen as the progressive organization of an ensemble of partially folded structures through which the protein passes on its way to the folded structure [7]. This approach emphasizes the idea of each state being an ensemble of rapidly interconverting conformations. One of the main differences between both approaches is that the "new" view allows for a more heterogeneous transition state than the "classical" view, which concentrates on a single, well-defined folding pathway [1].

Figure 1.2 shows one schematic representation of the "classical" (left) and "new" (right) views of protein folding. In the figure, each possible protein configuration is represented as a circle, and arrows represent possible transitions between configurations. In both approaches, the native state (filled circle) is achieved when the energy is minimized.

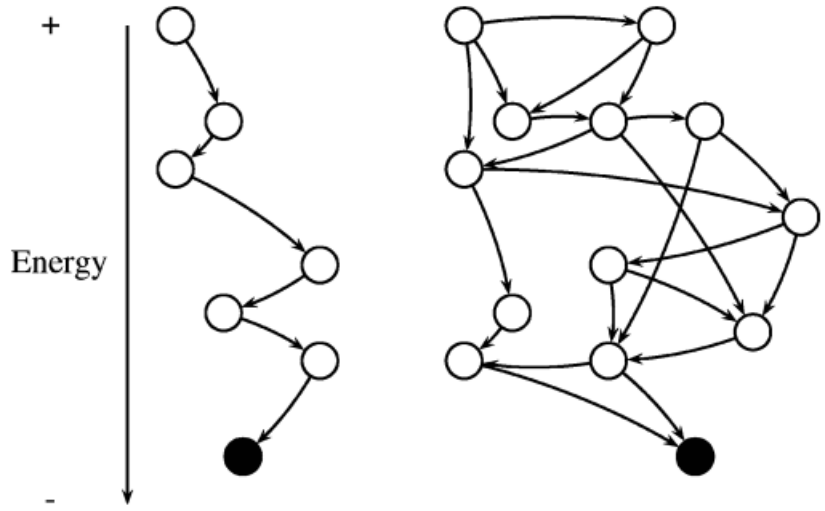

FIGURE 1.1: Schematic representation of the classical (left) and new (right) views of protein folding.

1.3 Multi-objective Optimization

Evolutionary Algorithm (EA) is a optimization and search technique, highly parallel, inspired by the Darwinian principle of natural selection and genetic reproduction. The nature principles that inspire the EAs are simple. According to the theory of C, Darwin, the principle of natural selection favors individuals with high fitness, therefore, with high probability of reproduction. Individuals with more descendants have more chance to perpetuate their genetic code in future generations. The genetic codes is what gives the identity of each individual and are represented in the chromosomes. These principles are used in the construction of computational algorithms, that searches for better solutions given a specific problem by the evolution of a population of solutions coded in artificial chromosomes – data structures used to represent a feasible solution for a given problem in the algorithm execution [8].

Real world problems commonly have multiple objectives to minimized/maximized and are present in most knowledge areas. To optimize multi objective problems, are considered two or more objectives witch usually are conflicting. To these problems is impossible to find one unique solution. A set of solutions is reached evaluating the Pareto dominance relation [2] between the solutions. The main objective is to find the solutions that are non-dominated by any other. A solution dominates other, if and only if, it was

better in at least one of the objectives, without being worst in any of the objectives. The set of non-dominated solutions constitutes the Pareto Front. Finding the the real Pareto Front is a NP-hard problem [5], this way, the objective is to find a good approximation of this front.

Multi-Objective Evolutionary Algorithms (MOEAS) are extensions of EAs to multi objective problems that applies the concepts of Pareto dominance to create different strategies to evolve and diversify the solutions. In this work were used two MOEAs: NSGAII [3] and IBEA [11].

1.3.1 Non-dominated sorting Genetic Algorithm II

The main characteristic of this algorithm is a strong elitism mechanism, classifying at each generation every solution in different fronts according with the non-dominance relation (line 15 of Algorithm 1). After the classification, solutions from the first front, are non-dominated by any other solution. Solutions from the second front are dominated only by the solutions of the first front, and so on. For solutions of the same front, the algorithm uses a Crowding Distance operator to calculate how distant are the neighbors of a given solution (line 19 of Algorithm 1). Solutions with high values of Crowding Distance have priority, because they will contribute more to the population's diversity. The binary tournament selects solutions from the small front with the higher values of Crowding Distance. A new population is generated using the crossover and mutation operators (line 25 of Algorithm 1).

1.3.2 IBEA (Indicator-Based Evolutionary Algorithm)

In the multi-objective optimization context, optimizing consists in find a front with a good approximation to the true Pareto front. However, there is no general definition about what is the true Pareto front. This way, indicators have been used to evaluate the quality of a approximation front. The *hypervolume* is a example of indicator to the evaluation and comparison of fronts.

The IBEA is an algorithm that considers the optimization by the use of quality indicators. The indicator is the way used to evaluate the non-dominated set of solutions [4]. To use the IBEA it is necessary define which indicator will be used to associate each ordered pair of solutions to a scalar value. One of the most used indicators is the *hypervolume* due to its capacity of evaluate the convergence and diversity at the same time of the search process [6].

$$F(x_i) = \sum_{x_j \in (P - x_i)} -e^{\frac{-I_{Hy}(x_j, x_i)}{k}} \tag{1.1}$$

For the IBEA fitness calculation (Equation 1.1), k is a parameter commonly used with a value of 0.05. The value for $F(x_i)$ corresponds to a quality

Algorithm 1 NSGAII

```
1: N ← Population Size
2: T ← Max evaluations
3: P_0 ← CreatePopulation(N);
4: CalculateFitness(P_0);
5: FastNonDominatedSort(P_0);
6: Q_0 ← 0
7: while Q_0 < N do
8:     Parents ← BinaryTournament(P_0);
9:     Children ← CrossoverMutation(Parents);
10:    Q_0 ← Children
11: end while
12: CalculateFitness(Q_0);
13: t ← 0
14: while t < T do
15:    R_t ← P_t ∪ Q_t;
16:    Fronts ← FastNonDominatedSort(R_t);
17:    P_{t+1} ← 0
18:    i ← 0
19:    while P_{t+1} + Front_i < N do
20:        CrowdingDistanceAssignment(Front_i);
21:        P_{t+1} ← P_{t+1} ∪ Front_i
22:        i ← i + 1
23:    end while
24:    CrowdingDistanceSort(Front_i);
25:    P_{t+1} ← P_{t+1} ∪ Front_i[1 : (N − P_{t+1})]
26:    Parents ← BinaryTournament(P_{t+1});
27:    Q_{t+1} ← CrossoverMutation(Parents);
28:    t ← t + 1
29: end while
30: return P ← Set of non-dominated solutions.
```

loss measure of the approximation to the Pareto front if the solution x_i was removed of the population [4], based on the value of the quality indicator I_{Hy}, in this case, the *hypervolume*. Based on the fitness calculation described above, the basic IBEA algorithm consists in iteratively do the selection (line 10 of Algorithm 2), crossover, mutation (line 11 of Algorithm 2) and environment selection, removing the worst individual from the population and updating the values of fitness of the remaining individuals (lines 4 to 8 of Algorithm 2).

[1] *Hypervolume*: Proposed quality indicators used in the study of [12], denoted as the "size of the covered search space". This indicator has two important advantages in relation to others [10]: 1 - Sensitive to any kind of improvement in the approximation set in relation to other set. 2 - As result of 1, the indicator guarantee that for any approximation set A that has high values of hypervolume, also has all the solutions of the true Pareto front.

Algorithm 2 IBEA

1: $N \leftarrow$ Population Size
2: $T \leftarrow$ Max Evaluations
3: $k \leftarrow$ Scale factor of Fitness
4: $P \leftarrow$ CreatePopulation(N);
5: $m \leftarrow 0$
6: CalculateFitness(P);
7: **while** $m \geq T$ or other stop criterion is reached **do**
8: $\overline{P} \leftarrow$ BinaryTournament(P);
9: $P \leftarrow$ CrossoverMutation($\overline{P}$);
10: $m \leftarrow m + 1$
11: **while** Size(P) $> N$ **do**
12: $x^* \leftarrow$ WorstIndividualByFitness();
13: RemoveFromPopulation(x^*, P);
14: CalculateFitness(P);
15: **end while**
16: **end while**
17: **return** $P \leftarrow$ Set of non-dominated solutions

1.4 Proposed method

1.5 Experiments

1.6 Conclusion

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