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OPTIMAL SYNTHESIS OF REVERSE OSMOSIS SYSTEMS USING GENETICS ALGORITHMS

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Abstract
In this paper we present a method for optimal synthesis of reverse osmosis networks that take in account the operational foundations as well as economics aspect including operational and preliminary plant costs. The network structure is coded as a superstructure, which represents all reverse osmosis networks configurations. Cost equations relating the capital and operating cost to the design variables, as well as the structural variables of the designed network have been introduced in the objective function. This problem was solved using genetics algorithms taking in advantage the direct relation among GA chromosome binary strings and the physical connection present in each possible structure.

Keywords: Reverse osmosis, Genetics Algorithms, Optimal design

1 Introduction

The optimal design of systems composes by several unit process such as a network of reverse osmosis modules is a very complex task involved nonlinear models and mixed continuous and discrete variables. The classical design technique is based on formulating the problem as a mixed-integer nonlinear programming (MINLP) problem, whose objective is to minimize the total annualized cost, while incorporating thermodynamic, technical and flexibility constraints (El-Halwagi et al.,1997; Qi and Henson ,2000). As an alternative method for solution this problem, we proposed the use of genetics algorithms. The main reasons to use this method are the direct relation among GA chromosome binary strings and the physical connection present in each possible structure.

2 Genetics Algorithms

GA’s are meta-heuristics optimization methods based on the biological principles of natural selection and are specially suitable for multimodal objective functions, as well as, complex systems difficult to model. In GA, the decision variables are encoded into bit strings in order to be able to use crossover and mutation mechanism based on the evolutionary theory. The reproduction is determined by a fitness function associate with the capability of survival of an individual. The main characteristics of GA’s are: Search from a population. The fitness functions (the objective) is evaluated as a black box, then no additional knowledge are necessary. The efficiency of a GA is closely linked with the objective function and set-up parameters as: encoded strings, bits resolution, initial and final population, generation number, and operator probabilities. In this work, we take in advantage the direct relation among chromosome binary strings and the physical connection present in each possible structure. This issue was explored by Gerrard and Fraga (2000) for the optimal design of process networks with mass transfer mechanisms.

3 Problem Statements

One of the key for a successfully optimal design is the accuracy of the process model. Specifically, our approach incorporates a rigorous first principles model for the prediction of the reverse osmosis modules, known as “solution-diffusion model”. Considering a spiral type modules, we use an implicit formulation to evaluate permeate condition, and given by (Vyhmeister,2003):

$$\frac{P \cdot e^{U\left(\frac{1}{273+T^{o}}-\frac{1}{298}\right)}}{A \cdot Ar} - \Delta P + C_F \cdot RT\xi\left(1+\frac{F}{F-\xi P}\right) \cdot e^{\left(\frac{P \cdot 2e}{1.86 \cdot \mathrm{Re} \cdot Sc)^{1/3} \cdot Ar}\right)} = 0 \qquad (1)$$

The superstructure is a full connected flowchart which represents all reverse osmosis networks configurations, considering the inlet flows, outputs, pumps, mixers and splitters, as is shown in figure 1. The problem is to find the best connections among process units and modules operation conditions (pressures, flows and concentrations) that minimize a cost function relating the capital and operating cost of the design variables, satisfying the product specifications. To solve the problem, it is necessary to determine the mass balances considering all possible combinations. The superstructure balances can be resumed as:

Fresh feed

$$\sum_{1}^{N_m} X_i - \frac{F \cdot V_i}{T_1} \qquad (2)$$

$$\sum_{N_m+1}^{2N_m} X_i - C_F \cdot V_i \qquad (3)$$

Membrane feeds (mixers)

$$\sum_{1}^{N_m} X_{i+2N_m} - \left(X_i + \sum_{1(j)}^{2N_m} X_{(7+j)\cdot N_m + j+i-1}\right) \qquad (4)$$

$$\sum_{1}^{N_m} X_{1+3N_m} - \left(X_i \cdot X_{i+N_m} + \sum_{1(j)}^{2N_m} \frac{X_{(7+j)\cdot N_m + j+i-1+2N_m(1+N_m)} \cdot X_{(7+j)\cdot N_m + j+i-1}}{X_{i+2N_m}}\right) \qquad (5)$$

Membrane products (permeates and concentrates)

$$\mathop{/}\limits_{1}^{N_m} X_{i+4N_m} - Fc(X_{i+2N_m}, X_{i+3N_n}, \Delta P) \quad (6)$$

$$\mathop{/}\limits_{1}^{N_m} X_{i+5N_m} - Fp(X_{i+2N_m}, X_{i+3N_n}, \Delta P) \quad (7)$$

$$\mathop{/}\limits_{1}^{N_m} X_{i+6N_m} - Cc(X_{i+2N_m}, X_{i+3N_n}, \Delta P) \quad (8)$$

$$\mathop{/}\limits_{1}^{N_m} X_{i+7N_m} - Cp(X_{i+2N_m}, X_{i+3N_n}, \Delta P) \quad (9)$$

Splitter outs

$$\mathop{/}\limits_{1(i)}^{2N_m} \mathop{/}\limits_{1(j)}^{1+N_m} X_{(7+i)\cdot N_m + j + i - 1} - \frac{X_{i+4N_m} \cdot V_{1+N_m}}{T_{i+1}} \quad (10)$$

$$\mathop{/}\limits_{1(i)}^{2N_m} \mathop{/}\limits_{1(j)}^{1+N_m} X_{(7+j)N_m + j + i - 1 + 2N_m(1+N_m)} - X_{i+6N_m} \cdot V_{1+N_m} \quad (11)$$

System products (Permeates and concentrates)

$$X_{(8+N_m)N_m + 3N_m + 1 + 2N_m(1+N_m)} - \sum_{1(j)}^{N_m} X_{(8+j)N_m + j} \quad (12)$$

$$X_{(8+N_m)N_m + 3N_m + 2 + 2N_m(1+N_m)} - \sum_{1(j)}^{N_m} X_{(11+j)N_m + j} \quad (13)$$

$$X_{(8+N_m)N_m + 3N_m + 3 + 2N_m(1+N_m)} - \sum_{1(j)}^{N_m} \frac{X_{(14+j)N_m + j} \cdot X_{(8+j)N_m + j}}{X_{(8+N_m)N_m + 3N_m + 1 + 2N_m(1+N_m)}} \quad (14)$$

$$X_{(8+N_m)N_m + 3N_m + 4 + 2N_m(1+N_m)} - \sum_{1(j)}^{N_m} \frac{X_{(17+j)N_m + j} \cdot X_{(11+j)N_m + j}}{X_{(8+N_m)N_m + 3N_m + 2 + 2N_m(1+N_m)}} \quad (15)$$

Where $\mathop{/}\limits_{1}^{N_m}$ denote equal equations for i = 1 to N_m, (The module's number).

Give a super-structure, the scheme starts with a initial population of structures randomly generated, being evaluated each of them according his feasibility. In the next step, a NLP routine solve the mass balances, finally, with all states of the network known (flows, concentration, pressures) the fitness function, i.e. the economic objective function is evaluated. In each cycle, the GA is able to improve the initial population through evolutive mechanism until that the number of final generation is reached. When a non feasible structure is selected, a null value of NPV is assigned, minimizing their reproduction probability.

4 Results

We applied this approach to evaluate a optimal design of a desalinization plant containing 3 membrane modules (1020SS Fluid Systems) to process 3000 Lt/h of salt water (3000 ppm NaCl). The maximum salt concentration in the permeate system was set to 3 ppm. The cost function was the Net present value (NPV) over a 10 years horizon, considering the annual cost operation, plant investments, maintenance and equipment depressing. Details about system parameters and cost can be found in Vyhmeister (2003). The AG parameters were sets to an initial population of 30 individuals, 15 generations and 10% of mutation probability. The problem was solved using Matlab platform running on a standard P-IV PC. The best configuration given by the algorithm can be seem in figure 2 with a total permeate capacity of 9785 m3/d. This solution is the exact optimum when maximum production is the assigned.

A more complex problem involves 10 module, 21 nodes, 230 binary variables, 320 continuous variables, and 550 equations has also been solved, however the execution time was very big.

5 Conclusions

In this work an approach to solve the optimal design of reverse osmosis network based on genetics algorithms has been presented. Results show the flexibility of this approach being able to solve different systems (number and modules specification, reflux pattern) with minor programming tasks. Also, the GA brings a set of possible configurations near the optimum allowing better solutions analysis than if we had use a MINLP routine such as branch & bound algorithm where the specification of model constraints is often a very difficult task.

Notations

A = Solvent permeability parameter, (-)

A_r = effective membrane area, (m^2)

b = Membrane thickness , (mm)

C_p = Permeate concentration, (ppm)

C_c = Concentrate concentration, (ppm)

F = Feed flowrate, (Lt/h)

Fc= Concentrate flowrate, (Lt/h)

Fp = Permeate flowrate, (Lt/h)

P = Membrane pressure, (Atm)

R_e = Reynolds number, (-)

Sc = Schmidt number, (-)

T = Temperature, (ºC)

T_i = split flow factor, (-)

U = Temperature correction factor, (-)

V_i = binary connection variable, (0- 1)

X_i = Flowrate or concentration in network balance, (Lt/h or ppm)

ξ = Refuse factor, (-)

ΔP = Net pressure across module, (Atm)

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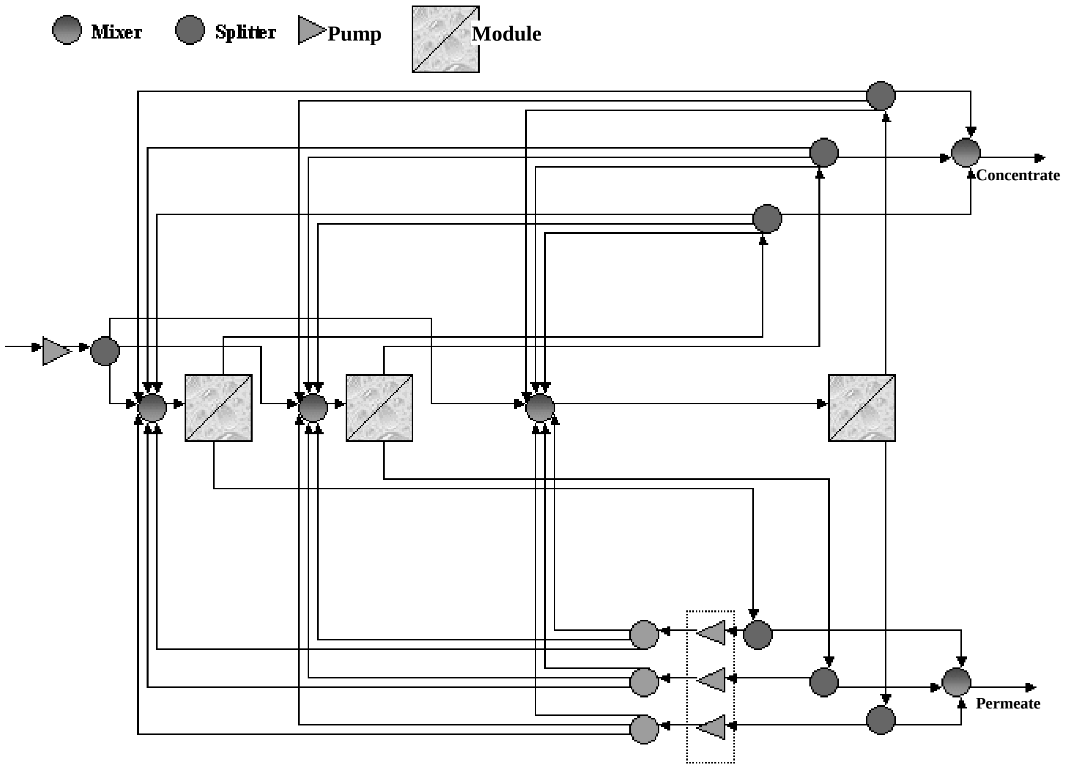

Figure 1 : The superstructure representation

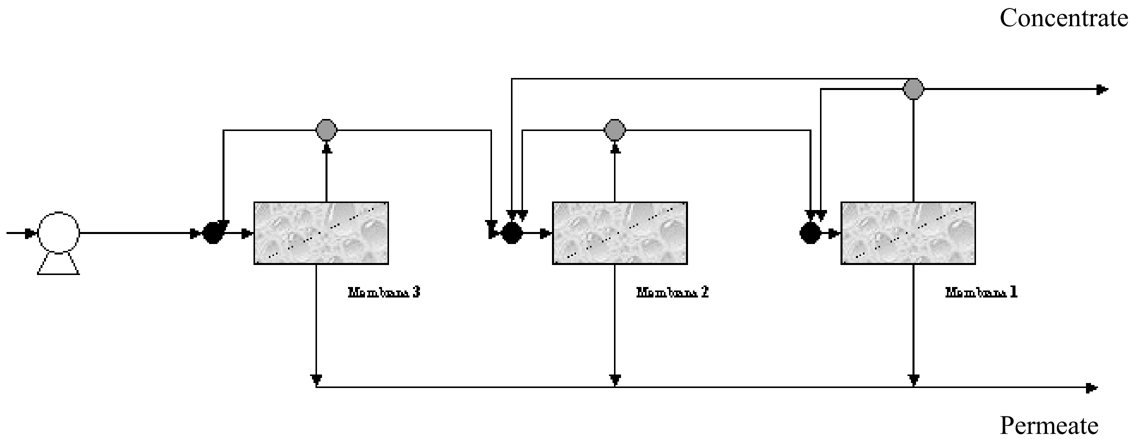

Figure 2: Optimal design for desalination plant with 3 modules