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Optimization of wind turbine placement using a viral based optimization algorithm

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Abstract

In the present research, a new viral based optimization algorithm is used to find the optimal solution to wind turbine placement problems considering constant wind speed and unidirectional uniform wind. In this study, a MATLAB based program is developed to search the optimal number and position of wind turbines in large wind farms with the objective of minimizing the total cost per unit of power produced from the wind park. The results obtained by the proposed algorithm are compared with results from previous studies.

Keywords Wind power, optimization, wind farm

1. Introduction

The uneven heating of the earth's surface produces areas of high and low pressures, this imbalance causes displacement of the air surrounding the earth resulting in the wind. The wind produces energy because it is always moving. This energy can become trapped by leaves or blades of large size and stored as electricity. Nowadays the modern versions of the windmills, called wind turbines, are used to generate electricity. Wind turbines equipped with long, thin blades of metal or plastic that resemble airplane propellers on top of slender towers are often grouped together to form wind farms. A wind power plant consists of a group of wind turbines at a specific location and is also called wind farm. This group of wind turbines shares various costs, such as the cost of maintenance and installation, which can yield competitive advantage against other energy sources when the wind is sufficiently strong

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and there is enough space available. But, the use of wind farms implies losses regarding the ability of taking advantage of the entire wind available in the area due to the introduction of wind-wakes, which are caused by the wind-turbines, reducing the total power generation and increasing maintenance costs due to turbulent winds. That's why a major task when installing this type of wind farms is the assessment of wind speed at each location and each point on the ground as this speed is modified by factors such as elevation, surface, temperature, turbulence, etc. The process of energy transformation that occurs in the wind turbine, wind turbine loses leaves a portion of the energy because this is converted into kinetic energy in the rotor of the turbine, so the wind comes turbine rotor speed is reduced and can be considered as turbulent.

Usually this wind that is generated behind the rotor of the turbine is called wake. The wake and the wind flow around it are mixed and the mixing region expands toward the center of the wake and to the edge of it which makes the wind speed increases, so the lack of speed the wake is consumed and it becomes more widespread but with less effect until the wind flow is recovered downstream. In a wind turbine as the wind power is removed leaving a wake is marked by reduced wind speeds and increased turbulence. If a wind turbine is working within the region of the wake of another turbine, or at a point within the wind farm which is affected by several of these wakes, then the turbine will produce less energy than those turbines that interact directly with the natural wind flow. Therefore the layout of wind farms is very important, since it has impact in the economic, safety and reliability evaluations of the system. Several factors must be taken into account to achieve an efficient arrangement of wind turbines. It must take into account the installed capacity, problems related to noise, aesthetics, budget, site constraints, among others.

This research focuses on minimizing the cost per unit of energy, or as it was calculated by maximizing the total energy production while reducing the total summation of all the costs associated with the wind farm. The viral systems algorithm is employed for optimizing this objective function, using an analytical wake formulation to model the impact of this factor on the wind farm performance.

2. Literature Review

During the last decades, the effects of wind turbine wake have been studied by a large number of researchers, each using different models for analysis and different methods to optimize the results. Typically, these methods to model the wake are divided into two main categories, (i) Analytical models which are characterized by their use of sets of analytical expressions, these models are known for their simplicity, and their various applications not only to the field of wind turbine placement, but also to a number of other purposes. The first analytical models used for Wake modeling are presented in the work of Betz [1] and Lanchester [2] in the early 1920's, their work laid the foundation for future research on the analysis of wind farms. Other research which may be categorized by the use of analytical models is presented by Frandsen [3], in his work the Betz model is used, but taking into account the interaction of multiple wakes considering an equidistant space between each one of the possible wind turbine arrays. Some researchers [4] used a model that takes in account the effect of turbulence in the performance of the downstream turbines. Honorable mention must be made to the model developed by Jensen [5] which treats wake as the turbulence which exists behind the wind turbine, which causes that the vortex shedding is neglected and from where the model can be reduced to the calculation of the momentum downstream of the turbine. The second category (ii) are computational models like the ones presented by Crasto et al. [6] and Crespo [7]. Typically, researchers have focused on the use of analytical models for optimizing the layout of wind turbines in wind farms because of its simplicity, flexibility to solve a large number of problems and that computer models typically consume large amount of computational resources due to the lack of flexibility of the applications to different problems. An example of this is the work of Mossetti 1994 [8] which used the model proposed by Jensen to solve a wake modeling problem for the placement of wind turbines on a wind farm. He defined its objective function as the minimization of two goals, to which weights were given, the total cost first and secondly the total production, these goals were combined in an evaluation function defined as the minimization of the weighted cost per unit power. To test his model he used three different scenarios. Grady et al. [9] tried the same problem as Mosetti et al. in this work the authors used the same approach as by Mosetti et al. Marmidis et al. [10] and also approached the same problem as Mosetti and Grady, the difference being that Marmidis et al. analyzed only the simplest case in which wind comes from a fixed direction at a constant speed.

3. Wake and cost modeling

The model used in this work is very similar to the wake decay model developed in 1986 by Jensen. This model is based on the idea of the global momentum conservation in the wake downstream of the wind turbine and assumes that the wake is turbulent and the contribution of the tip vortices is neglected. So this wake model is only applicable in the remote wake region. It is also assumed by this model that the wake expands in a linear way with downstream distance. From where assuming that the momentum is conserved inside the wake, allows the wind speed u for downstream distance x in the turbine to be expressed by equation 1:

$$u = u_0 \left[1 - \left(2a / (1 + \alpha (x/r_1))^2 \right) \right] \qquad (1)$$

Where u_0 is the mean wind speed, a represents the axial induction factor, x is the distance downstream of the between wind turbines, r_r is the downstream rotor radius and α is defined as the entrainment constant. The downstream radius, r_1, is associated to the rotor radius, r_r, by using the following expression (equation 2):

$$r_1 = r_r \sqrt{(1 - a) / (1 / 2a)} \qquad (2)$$

The turbine thrust coefficient or CT, is related to the axial induction factor through the Betz relation, which is the ratio at which wind speed is reduced when it approaches the wind turbine, and a is called the axial induction factor, and this relation is presented in the equation 3:

$$CT = 4a(1 - a) \qquad (3)$$

The entrainment constant can be defined as how fast or slow the wake increases or expands and is empirically given by equation 4, where z is the hub height of the wind turbine and z_0 is the surface roughness.

$$\alpha - 0.5 / \ln(z / z_0) \qquad (4)$$

In some cases a wind turbine could encounter multiple wakes, so, in this case is possible to assume that the total kinetic energy of the mixed wakes is equal to the summation of the individual kinetic energy deficits and the resulting velocity downstream of N turbines is given by the following equation.

$$u_i - u_0 \left[1 - \sqrt{\sum_{i-1}^{N} (1 - (u/u_0))^2} \right] \qquad (5)$$

The equation presented in Mosetti et al. for calculating the power output for the turbine is shown in equation 6:

$$P_{total} = \sum_{i-1}^{N} 0.3 u_i^3 \qquad (6)$$

Equation 7 refers to the total cost of the turbines, this cost is only dependent on the number of wind turbines installed in the wind farm as presented by Mittal [11]. This equation represents a non-dimensional cost that is a function only of the number of wind turbines placed and is based on the discounts of purchasing a large number of wind turbines. Based on this assumption, a reduction in cost of 1/3 is likely when a large number of wind turbines are purchased.

$$\cos t = N\left(\frac{2}{3} + \frac{1}{3}\exp^{-0.00174 N^2}\right)$$

(7)

The objective function for this research is the minimization of the cost per unit power which is our is given by:

$$\text{Objective function} = \text{cost} / P_{total}$$

(8)

4. Optimization method

The word virus comes from Latin and means poison. Previously, biologists and epidemiologists did not know exactly what a virus was, but they knew that certain molecules contained something that caused disease in the host. Although viruses are compared with bacteria, they differ in that viruses are not composed of cells, which are much smaller than these, having a size similar to a large molecule.

A virus generally consists of a nucleic acid, which is covered by a protein called capsid, nucleic acid binding and capsid forms a nucleus-capsid. In this they resemble the chromosomes of a cell, for what some see them as loose chromosomes. Chromosomes are known to control the chemistry inside the cell, so that when a virus is introduced into a host cell, establish a control on their own. Usually are skilled in the submission of the chemistry of the cell to its own purposes, putting all the cellular apparatus at the service of the formation of new virus. In most cases, the cell dies in the process. Viruses need a host to survive, so they are not independent as bacteria, and can only multiply inside living cells.

Two systems of virus replication exist, the lytic cycle and lysogenic cycle. The explanation of these cycles is referred to the virus occurring in bacteriophages. The lytic reproduction cycle has this name because the infected cell dies due to rupture by releasing the new virus copies. The cycle begins with the absorption phase in which the virus binds the host cell, followed by the stage known as injection, which nuclieco acid from the virus enters the cell through a hole in the bacterial wall. Once this happens, the eclipse phase begins copies of the capsid proteins are produced as well as the synthesis of RNA. Once the capsid and RNA are complete, the assembly of the same and the production of virus starts. The viruses leave the cell by enzymatic breakdown of the bacterial wall. These new viruses are in a position to infect a new cell

The first two phases of this cycle are the same as those described in the previous cycle. In the eclipse phase viral nucleic acid recombines with the bacterial DNA, introduced into this cell as a further gene. This viral form is called prophage, or attenuated virus. In this state, the prophage can be maintained for an indefinite period and may even reproduce with the cell, producing new lysogenic daughter cells. The prophage will remain dormant until a change in the cellular environment that causes a cellular change, for example, sudden changes in temperature or desiccation, or decreased oxygen concentration. This modification leads to the liberation of the prophage, becoming an active virus infection cycle continues to produce cell death and release of new virus.

The following steps illustrate the working mechanisms of the proposed viral system based-algorithm to solve the wind turbine placement problem:
- Create *n* number of initial viruses to form the initial population of solutions.
- Ensure feasibility for these solutions.
- Arrange the solutions based on the calculated objective value.
- Divide the solutions depending on the form of replication. The solutions in the first positions follow lytic replication, because they usually offer the best solutions. The residual solutions follow a lysogenic replication because they do not offer the best solutions; they need to change in order to produce better solutions.
- In case of Lytic replication:
  - Calculate the limit number of nucleus-capsids replication *(LNRx)*. The infected cells with better solutions are going to the evolution process more quickly.

$$LNR_x = LNR_0\left(\frac{f(x) \quad f\widehat{(x)}}{f\widehat{(x)}}\right)$$

(9)

  - Calculate the number of nucleus replicated *(NR)* that occurs in this interaction, this is calculated by

multiplying the Limit nucleus-capsid, *LNRx* by the single probability of one replication, *pr*.

$$NR(x) = LNR_x \quad pr \tag{10}$$

○   Compare the total number of nucleus replicated against the limit. If the total number of nucleus replicated is greater than limit number of nucleus-capsids replication the cell is considered active and starts expansion process.

$$\sum_{i\,1}^{n} NR \geq LNR_x \tag{11}$$

○   The active viruses search in their neighborhood for the local optima.
○   Check the neighborhoods, to see the antigenic response to the infection.
○   Calculate the probability of creating antibodies of each neighbor (*pan*), taking in consideration *q* the probability for the worst individual.

$$pan(x) \quad q \quad (1 \quad q)^i \tag{12}$$

○   If the probability of creating antibodies is larger or equal to that the antibodies probability this cell follow the lysogenic replication.
• In case of Lysogenic replication:
  ○   Calculate the limit number of interaction (LIT) that each cell is following a lysogenic cycle.

$$LIT_x = LIT_0 \left(\frac{f(x) \quad \hat{f}(x)}{\hat{f}(x)} \right) \tag{13}$$

○   Mutate the cell when wakes up.
○   Return the recently mutated cell to the original process.
• Stop, at the time that *N* interactions had happened.

5. Numerical Example

The number of wind turbines and their placement is to be determined so that the cost per unit power for the entire wind farm is minimized. Constant wind speed and unidirectional uniform wind: are considered. The wind direction is unidirectional and the wind speed is constant at 12 m/s. For this example a square grid partitioned into one hundred potential locations was used as the area for placing the turbines. Each of this partitions have a width of 5 rotor diameters or, as calculated for this example 200m based on the utilized wind turbine type. Each of these wind turbines is going to be placed in the center of each of their segments, giving the area the dimensions of 50 by 50 diameters. It is assumed that area is flat with a surface roughness height of 0.3 m which is characteristic of a land site. In addition, the 5 diameter square segment size already suits the rule of thumb spacing in both vertical and horizontal directions. Other important parameters for this study are shown on Table 1. The following Viral system's parameters where used during the simulation based on previews research performed by viral system algorithm: Population size of 100, number of iterations of 1000, a probability of infection 30%, probability of generating antigens of 0.6%, probability of Lytic replication of 60%, and a probability of lysogenic replication of 40%.

Table. 1 Wind turbine properties

Hub height (z)	60 m
Rotor radius (rr)	40 m
Thrust coefficient (Ct)	0.88
Ground roughness (Z0)	0.3m

After the optimization was performed, a configuration of thirty wind turbines is presented as the optimum combination, in sets of 10 wind turbines placed in rows 1, 6 and 10. The figure below shows a graphical representation of the described configuration, and also replicates the solution configuration presented in Mosseti's work.
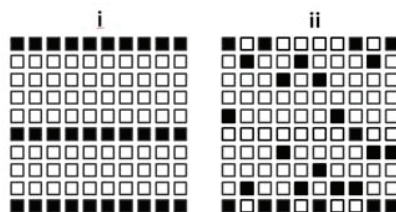

Fig. 1 Optimal configuration (i) present study, (ii) Mosetti et al.'s study.

The proceeding table is an evaluation of the objective function, total power output, efficiency of power output, cost and number of turbines for each of the designs.

Table 2. Comparison of solutions – Case 1, (i) present study, (ii) Mosetti et al.'s study

	i	ii
Number of turbines	30	26
Total Power (kW)	14814	12352
Cost	22.08	19.99
Efficiency	0 953	0.916
Objective Function	0.0015	0.00161

Comparing the results shown by Mosetti et al against those obtained using the model of Jensen and Viral system algorithm to search for an optimal result, can be observed that the value of the objective function in case (i) is smaller, therefore it can be concluded that a better result for this specific case has been found.

6. Conclusions

In the present study, a new meta-heuristic method was applied for optimizing the placement of wind turbines in wind farms. The results obtained by this meta-heuristic method were compared with results from previews studies and important enhancements in the results are shown. Further development for this methodology is needed, in order to solve more complicated cases, considering multidirectional winds and variable wind speeds. Also the consideration of other important factors into the model is needed, factors like the effect of ambient turbulence in the wake recovery, the effect of ground, variable hub height of the wind turbines and different terrains.

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