Multi-objective model optimisation using genetic algorithms for pleurotus sp. cultivation

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Abstract. Malaysia is the largest exporter of Elaeis Guineensis (Palm oil) in the international market. Oil palm cultivation generates a significant amount of lignocellulosic biomass derived from empty fruit bunches (EFB) as waste product. This research focused on optimizing the mycelium growth in Pleurotus sp. cultivation by using EFB as a culture medium. The EFB was cut into the range of size of substrate (S) from 1.5 cm to 3.0 cm, soaked in water for overnight, applied steam treatment and incubated at the selected range of temperature (T) from 29 °C to 32 °C. The responses were mycelium extension rate (M) and nitrogen concentration in mycelium (N). The multi-objective optimisation of M and N requires the objective functions which represent both processes. For this type of problem, multi-objective genetic algorithm was chosen as the methodology, specifically using NSGA-II algorithm. Through the implementation of selected multi-objective genetic algorithm, it was able to produce the pareto front for optimising both nitrogen concentration and the extension rate of the mycelium. The highest nitrogen concentration and mycelium extension rate was from the result with crossover and mutation probability of 0.5 and 0.2. It produced 388.45 mg/L of nitrogen concentration and 0.370 cm/day of mycelium growth.

1. Introduction
In recent years, oyster mushroom (Pleurotus ostreatus) has become one of the most cultivated mushrooms in the world, mainly in Brazil. There are many factors involved in mushroom production such as type of substrate, pH of substrate, moisture content, temperature [1], size of substrates [2], mass ratio of spawns to substrates pre-treatment of substrate [3] etc. There are some mushroom grower uses EFB as their substrate for mushroom cultivation but still at the stage of trials. Looking forward to optimising the factors affecting of Pleurotus sp. cultivation, most of other research only focus on the factors of mushroom growth and there are only very few research practices the optimisation for the growth condition and substrate preparation [4].

Multi-objective optimisation had been used widely to solve multi-disciplinary field which used pareto to find the optimal solutions. Qu et al. [5] proposed a Self-organised Speciation based Multi-objective Particle Swarm Optimiser (SS-MOPSO) to solve the multimodal multi-objective optimisation problems. The proposed method was tested on fourteen test problems and produced superior performance when compared to other methods. A new method also being proposed by Wilding et al. [6] to optimise a nuclear power conversion system (PCS) and emergency cooling system. A new mixed-integer
optimization method (MI-NSGA) was developed and used on PCS problem. The PCS optima reached efficiency of 35.63% and cooling system performance was improved.

Researchers had been used multi-objective optimisation using Response Surface Methodology (RSM) and Non-dominated Sorting Genetic Algorithm (NSGA-II) to obtain the optimal performance. The pareto front for optimal solutions had been generated by NSGA-II to optimise corrugated tube inserted with multi-channel twisted tape [7]. Three regression response models represent numerical data had been used to find the optimised response. A study by Li et al. [8] had optimised warpage, volumetric shrinkage and residual stress using NSGA-II to optimise fibre-reinforced composite injection moulding process. NSGA-II also being applied by [9] to minimise NOx emission on a small single cylinder 4-stroke engine. The lowest NOx emissions while using the biodiesel and exhaust gas recirculation was 63.76% with B10 fuel blend and 30% exhaust gas recirculation rate.

2. Process description of optimization using response surface method

2.1. Statistical analysis

Levels of independent factors such as size of substrate (S) and temperature (T) were based on results obtained from previous study. A two-factor-two level face centred central composite design (CCRD) was applied where the values of the independent factors were coded as in the range of -2 and +2 as shown in table 1. The experimental set-up shown in table 2 was design and analysed by using Design Expert software version 7.0 to build and evaluate models and to plot the three-dimensional response surface curves. The responses were mycelium extension rate (M) and nitrogen concentration in mycelium (N). Thirteen experiments were performed which involved five replicates for centre point. The five replicates for the centre point were used to estimate the experimental error.

| Factors                  | Symbol | Coded | Actual level | Coded level |
|--------------------------|--------|-------|--------------|-------------|
| Size of substrates (cm)  | S      | A     | 1.5          | -2          |
|                          |        |       | 2.0          | -1          |
|                          |        |       | 2.5          | 0           |
|                          |        |       | 3.0          | 1           |
|                          |        |       | 3.5          | 2           |
| Temperature during spawn running (°C) | T | B | 28 | -2 |
|                          |        |       | 29           | -1          |
|                          |        |       | 30           | 0           |
|                          |        |       | 31           | 1           |
|                          |        |       | 32           | 2           |

2.2. Preparation of substrate

The substrate which were empty palm fruit bunch (EFB) were collected from palm oil plantation at Banting, Selangor. EBB substrate was cut into the range of size as in table 2, then soaked in water for overnight, filtered to drain excess water and weighed for 100 grams. Then, the substrates were pre-treated with steam treatment and inoculated with 1:14 mass ratio of spawn to substrate, by placing the spawn on the surface of substrate. The bottles were closed and incubated at temperature set in table 2 in the dark condition.

2.3. Sample analysis

Sample analysis was conducted after all run fully colonized with mycelium. There were two responses which were mycelium extension rate (M) and nitrogen concentration in mycelium (N).
2.3.1. Determination of mycelium growth. Spawn run (mycelium extension) was observed regularly until appears white colonization. Each experiment was determined the days for complete mycelium growth. Mycelium growth was measured in centimetres as the length of the mycelium spreading from the surface of substrates toward the bottom of bottles [10].

Table 2. Experimental setup that has been constructed by using RSM by Design Expert software.

| Run | Factor 1 | Factor 2 |
|-----|----------|----------|
|     | A: Size of substrates (S) (cm) | B: Temperature (T) (°C) |
| 12  | 2.0      | 29       |
| 11  | 3.0      | 29       |
| 4   | 2.0      | 31       |
| 13  | 3.0      | 31       |
| 10  | 1.5      | 30       |
| 5   | 3.5      | 30       |
| 2   | 2.5      | 28       |
| 7   | 2.5      | 32       |
| 6   | 2.5      | 30       |
| 3   | 2.5      | 30       |
| 8   | 2.5      | 30       |
| 9   | 2.5      | 30       |
| 1   | 2.5      | 30       |

2.3.2. Nitrogen concentration analysis by using HACH Spectrophotometer. N was determined by using Persulfate Digestion Method (Method 10072). The mycelium was collected from the substrates and diluted by using deionized water using 40 dilution factors. Then, N was analysed by using HACH Spectrophotometer.

3. Genetic algorithm optimisation methodology

3.1. Objective function

The objective functions were acquired from a study by [11] which did the modelling of mycelium growth in Pleurotus sp. cultivation by using agricultural wastes. Equation (1) shows the objective function for mycelium extension rate (M). The objective function M represented the mycelium extension rate in cm/day which this rate was affected by five variables A, B, C, D and E.

\[ M = 0.60 - 0.023A + 0.019B - 0.029C + 0.029D - 0.14E + 0.041BD - 0.034BE - 0.044CE + 0.044DE \] (1)

Variables A represent the type of substrate and variables B represented size of substrate. The factor C was the value of mass ratio of spawn to substrate (SP/SS). While the variables D was the cultivation temperature and the variables E represent the types of substrate pre-treatment. The objective function for nitrogen concentration (N) is expressed by equation (2) which represented the volume of nitrogen concentration in mg/L which was also affected by the same five variables A, B, C, D and E. These two fitness functions will be used together for multi-objective optimisation to find the maximum extension rate and nitrogen concentration. The optimisation algorithm should be able to propose a pareto front of maximum value for both objectives functions.

\[ N = 352 + 241.5A + 43B - 0.50C + 50.50D + 21.50E + 59.50AB + 41.00AD - 35.50BC + 47.50BE - 33.00CD - 39.00CE + 32.00DE \] (2)
3.2. **Optimisation process**

The optimisation process from start to finish is shown in figure 1 to obtain the optimise mycelium rate and nitrogen concentration values. Firstly, the optimization problem will be loaded into the project. The problem contains the objectives and factors that will be used to create solutions. The next step was to initialize the parameter of the genetic algorithm such as the index and the probability for the genetic crossover and mutation. The crossover was set to simulate the interchange of genetic between two chromosomes and mutation was used to simulate the genetic alteration of a chromosome after crossover. Next, the parent population was generated based on loaded problem. The parent population was used to generate an offspring population through crossover and mutation. It also being used to create new population together with its offspring population. After crossover and mutation operators were applied to the population, it was combined between the parent population and offspring population.

![Flowchart](image)

**Figure 1.** Flowchart of the optimisation process.

After the population was combined into one, it being sorted, and each chromosome was ranked accordingly. Non-dominate sorting method was being used during the sorting process and best solution
was given higher ranking. The selection process was done next with the selection of the best solution. The selection process was based on the ranking given from previous step. If best solutions with similar rank exceed the population limit, then the solutions were selected using crowd distance to fit into the limit. The termination criteria checked was performed after the selection process. If the termination was not met, then the offspring will be generated again using crossover and mutation and selection process was applied next. The loop kept continued until the termination conditions had been satisfied. The final process was to generate the output for optimal $M$ and $N$ functions.

The optimisation process used the NSGA-II algorithm from jMetal [12] an object-oriented Java-based framework for multi-objective optimization with metaheuristics. NSGA-II is a very famous algorithm to use to solve multi-objective optimization problems [7-9]. The algorithm was slightly modified to ensure it met the requirement to implement the optimisation process.

4. Results and discussion

Referring to figure 2, for highest value of nitrogen concentration was at 563.50 mg/L with its lowest value of mycelium extension rate was 0.357 cm/day. For the highest mycelium extension rate was at 0.387 cm/day but it was the lowest nitrogen concentration at 334.05 mg/L. The optimal values for both results were 385.57 mg/L of nitrogen concentration and 0.371 cm/day of mycelium extension.

Figure 3 shows the pareto front for the multi-objective optimisation with crossover of 0.7 and mutation of 0.1. The highest value of nitrogen concentration was at 689.93 mg/L and the lowest value of mycelium extension rate at 0.347 cm/day. The highest mycelium extension rate was at 0.387 cm/day, with the lowest nitrogen concentration at 334.13 mg/L. The optimal condition was at 387.38 mg/L of nitrogen concentration and 0.371 cm/day of mycelium extension.

![Figure 2](image1.png)

**Figure 2.** Pareto front for multi-objective optimisation with crossover of 0.5 and mutation of 0.1.

![Figure 3](image2.png)

**Figure 3.** Pareto front for multi-objective optimisation with crossover of 0.7 and mutation of 0.1.
The results for optimisation with crossover of 0.5 and mutation of 0.2 is shown in figure 4. The highest value of nitrogen concentration was at 689.79 mg/L with the lowest value of mycelium extension rate 0.347 cm/day. The highest mycelium extension rate was 0.387 cm/day, with the lowest nitrogen concentration at 334.06 mg/L. The optimal values for both results were at 398.77 mg/L of nitrogen concentration and 0.369 cm/day of mycelium growth.

![Figure 4](image1.png)

**Figure 4.** Pareto front for multi-objective optimisation with crossover of 0.5 and mutation of 0.2.

Figure 5 shows the pareto front for the multi-objective optimisation with crossover of 0.7 and mutation of 0.2. The highest value of nitrogen concentration was at 496.87 mg/L and the lowest value of mycelium extension rate at 0.362 cm/day. The highest mycelium extension rate was at 0.387 cm/day, with the lowest nitrogen concentration at 334.02 mg/L. The optimal condition was at 388.45 mg/L of nitrogen concentration and 0.370 cm/day of mycelium extension.

![Figure 5](image2.png)

**Figure 5.** Pareto front for multi-objective optimisation with crossover of 0.7 and mutation of 0.2.

Referring to figure 6, for highest value of nitrogen concentration was at 689.98 mg/L with its lowest value of mycelium extension rate was 0.347 cm/day. For the highest mycelium extension rate was at 0.387 cm/day but it was the lowest nitrogen concentration at 334.05 mg/L. The optimal values for both results were 387.93 mg/L of nitrogen concentration and 0.370 cm/day of mycelium extension.
Figure 6. Pareto front for multi-objective optimisation with crossover of 0.7 and mutation of 0.3.

5. Conclusion
As observed on the plotted graphs, the distribution pattern looks quite similar, having a sharp curve in somewhere in middle. The maximum mycelium extension rate for all data set is similar, with the value of 0.387 cm/day. However, the maximum nitrogen concentration for all data set is different. The optimisation results with the parameters for crossover probability 0.7 and mutation probability 0.2 had produced the lowest maximum nitrogen concentration at 496.87 mg/L and the optimisation with crossover 0.7 and mutation 0.3 produced the highest nitrogen concentration at 689.98 mg/L compared to the other five optimisation results. The highest nitrogen concentration and mycelium extension rate was from the result with crossover and mutation probability of 0.5 and 0.2. It produced 388.45 mg/L of nitrogen concentration and 0.370 cm/day of mycelium growth.

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