Application and comparison of genetic and mathematical optimizers for freeze-drying of mushrooms

Ayon Tarafdar^{1,2} · Navin Chandra Shahi¹

Revised: 3 April 2018 / Accepted: 9 May 2018 / Published online: 21 May 2018
© Association of Food Scientists & Technologists (India) 2018

Abstract The suitability of genetic algorithm as an optimization tool for freeze drying of mushroom has been explored. The optimized solution set obtained from genetic algorithm was compared to a derivative based goal attainment algorithm (*fgoalattain*) to identify the better optimizer. Regression models for quality parameters of freeze dried button mushrooms were developed and models with $\geq 85\%$ correlation were selected and compiled into an objective function for optimization. Verified optimal solutions revealed that genetic algorithm was more proficient in optimizing physical quality parameters (rehydration and shrinkage ratio) as contrary to *fgoalattain* which optimized nutritional characteristics (ascorbic acid and protein) better. The ability of genetic algorithm for optimization from the perspective of a consumer was found to be better.

Keywords Freeze drying · Genetic algorithm · Modelling · Mushroom · Optimization

Introduction

Freeze-drying or lyophilisation is a process of drying by the principle of sublimation. It is used for drying bio-products which are heat sensitive or are otherwise degraded by conventional drying techniques involving heat

treatment. Despite its process complexity, it is widely used in the pharmaceutical (Pikal et al. 2005) and biotechnology industry (Ciurzyn'ska and Lenart 2011) for a large number of applications and its utilization is progressively growing in the food sector (Amine et al. 2014; Aykin and Erbas 2016; Fellows 2017; Tarafdar et al. 2017). The design considerations for pharmaceutical freeze drying processes are quite well defined (Goshima et al. 2016) but the same may not be adequate for food processing. Since biological materials do not follow a linear pattern during post harvest processes, a proper model with a robust optimization tool is required to determine the best conditions of process variables to obtain high quality end products in terms of physical and nutritional characteristics. Since the numbers of process variables and quality responses are more, it may be difficult to efficiently optimize a multiple input multiple output (MIMO) system such as freeze drying with traditional optimization techniques. Gradient based goal finding mathematical optimizers are more suited to single modal (one maxima or minima) functions and its application may not be adequate for complex multi-modal problems where local maxima or minima may be mistaken for global optimum. An optimization tool therefore, should ideally be complementary to processes where several multi-modal models will be generated. Genetic algorithm (GA) is one such technique which is based on Darwin's law of 'survival of the fittest'. It has numerous applications (Reed et al. 2000; Erenturk and Erenturk 2007) in a wide range of scientific fields and is often modified to produce hybrid optimizers which give results even superior to that of GA alone. GA is basically a search algorithm and not a calculus based algorithm. Hence, it is important to note that GA does not guarantee the 'best solution' but provides acceptable results for MIMO systems which avoid conflicts within the objectives under consideration (Konak et al.

✉ Ayon Tarafdar
ayontarafdar@gmail.com

¹ Department of Post Harvest Process and Food Engineering,
College of Technology, G.B. Pant University of Agriculture
and Technology, Pantnagar, Uttarakhand 263145, India

² Jodhpur, India

2006). The objective of this study is to exploit the characteristics of GA to solve a complex optimization problem relevant to the food sector and compare its results to a derivative based optimizer. The results of this study should serve other fellow researchers to identify suitable utility of GA in other food and industrial process applications.

Materials and methods

Material

Fresh button mushroom were obtained from the Mushroom Research Center (MRC) of G.B. Pant University of Agricultural and Technology, Pantnagar, Uttarakhand, India. The mushrooms were grown in a controlled environment and were procured on the day of harvest and stored under 4 °C until further use. Mushroom samples with head size diameter of 35–40 mm were chosen for the study. The initial moisture content of the mushrooms was recorded as 614.3 ± 0.2 to $1328.5 \pm 0.4\%$ on dry basis (d.b.) using standard hot air oven method.

Experimental procedure

Box–Behnken design (BBD) was chosen for the multi-objective optimization problem as recommended by Ferreria et al. (2007). The number of experiments was determined by Eq. (1):

$$N = 2k(k - 1) + C_0 \quad (1)$$

where N is the number of experiments, k is the number of factors and C_0 is the number of central points. The 3-level (−1, 0, +1), 4 factor (primary drying temperature, secondary drying temperature, pressure and sample thickness) experimental design matrix for BBD has been shown in Table 1.

Mushroom samples were cut into cuboids with defined cross sectional area of $1.5 \times 1.75 \text{ cm}^2$ with variable sample thickness. The samples were frozen at −22 °C for 24 h before freeze drying, well below the glass transition temperature. During drying, the sample temperature was measured using an infrared thermometer and the recorded temperature was used to identify the end point of the primary drying cycle. The basis behind this was the reduction in residual ice content as drying proceeded which will induce an increase in temperature of the food product beyond the triple point of water (0.01 °C). Moisture reduction in the samples was monitored with drying time to indicate end of freeze drying when two consecutive constant weights were obtained at the end of the secondary drying cycle.

Rehydration ratio

Rehydration capacity is defined as the ability of a product to retain its original structure after soaking in the liquid medium which it was deprived of during drying. For determination of rehydration ratio, known amount of dried mushroom sample was placed in 100 mL distilled water at 50 °C. The mushrooms were taken out every 30 min for weighing. Weight of the dried samples was measured after draining the excess water first over a muslin cloth followed by removal of residual surface water over a blotting paper. The process was stopped when two constant consecutive weights were obtained. The Rehydration ratio (RR) was estimated by the following equation:

$$RR = \frac{\text{Mass of rehydrated sample (g)}}{\text{Dry sample weight (g)}} \quad (2)$$

Shrinkage ratio

The shrinkage in the dried sample was determined as the ratio of the reduced volume to that of the initial volume (V_i) as described by Mayor and Sereno (2004). Shrinkage ratio (SR) can be expressed mathematically as:

$$SR = \frac{V_i - V_d}{V_i} \quad (3)$$

where V_d is the volume of the dried sample.

Volume of the dried sample was estimated using toluene displacement method. Toluene was recommended by Dursun and Dursun (2005) due to its inertness to being absorbed by any material to which it is a surrounding medium.

Protein content

Modified Lowry's method for stability of absorbance readings as suggested by Pomory (2008) was referred for protein estimation. The sample was prepared by adding 10 mL of 0.1 M sodium phosphate buffer (pH 8.0) to a known amount of grounded freeze dried mushroom sample. The mixture was centrifuged at 9000 rpm for 20 min. Five millilitres of reagent A (copper-tartrate-carbonate complex) was then added to 1 mL of the supernatant collected from the centrifuged sample. This solution was then allowed to stand for 10 min after which 0.5 mL of 2 N Folin–Ciocalteu reagent was added to it. The mixture was shaken vigorously and kept in dark for 2–3 h for stable spectrophotometric reading. The blank was prepared using the same procedure without addition of the sample. The absorbance was measured at 660 nm. The standard curve for protein was generated at 660 nm using different concentrations (0.2, 0.4, 0.6, 0.8, 1.0 mg/mL) of Bovine Serum Albumin (BSA) in sodium

Table 1 BBD design matrix with experimental responses for 4 variables at 3 levels

Run no.	X ₁ : PDT (°C)	X ₂ : SDT (°C)	X ₃ : P (mbar)	X ₄ : ST (cm)	Rehydration ratio	Shrinkage ratio	Ascorbic acid (mg/100 g)	Antioxidant (mg/g)	Protein (mg/mL)
1	− 8	25	0.07	0.5	3.091	0.851	20.090	3.870	3.808
2	− 2	25	0.07	0.5	3.280	0.982	26.250	3.445	5.824
3	− 8	31	0.07	0.5	3.036	0.887	17.984	5.470	6.352
4	− 2	31	0.07	0.5	3.018	0.904	20.000	2.989	5.392
5	− 5	28	0.04	0.2	2.414	0.822	25.646	2.480	3.136
6	− 5	28	0.1	0.2	3.712	0.755	22.704	3.132	1.288
7	− 5	28	0.04	0.8	2.987	0.833	25.859	2.970	1.672
8	− 5	28	0.1	0.8	2.785	0.867	26.097	3.274	1.887
9	− 8	28	0.07	0.2	3.991	0.784	23.673	3.920	5.920
10	− 2	28	0.07	0.2	4.190	0.810	24.691	3.226	4.528
11	− 8	28	0.07	0.8	3.770	0.844	21.830	5.440	1.582
12	− 2	28	0.07	0.8	4.000	0.930	24.370	4.373	2.432
13	− 5	25	0.04	0.5	2.980	0.898	22.667	3.368	6.640
14	− 5	31	0.04	0.5	2.330	0.820	19.382	3.809	7.280
15	− 5	25	0.1	0.5	2.010	0.811	22.429	3.251	5.510
16	− 5	31	0.1	0.5	2.397	0.868	18.750	3.726	5.856
17	− 8	28	0.04	0.5	2.667	0.867	23.529	3.376	5.568
18	− 2	28	0.04	0.5	2.560	0.964	17.891	3.440	5.408
19	− 8	28	0.1	0.5	2.667	0.929	18.549	3.102	5.184
20	− 2	28	0.1	0.5	2.558	0.876	21.600	2.153	5.792
21	− 5	25	0.07	0.2	2.882	0.733	26.916	2.472	1.864
22	− 5	31	0.07	0.2	2.940	0.800	21.528	4.878	3.664
23	− 5	25	0.07	0.8	2.625	0.813	25.600	8.604	4.448
24	− 5	31	0.07	0.8	3.114	0.822	22.885	5.332	3.952
25	− 5	28	0.07	0.5	2.600	0.964	23.762	2.300	3.200
26	− 5	28	0.07	0.5	2.400	0.946	21.818	2.780	2.920
27	− 5	28	0.07	0.5	2.290	0.946	23.301	2.300	1.894
28	− 5	28	0.07	0.5	2.220	0.964	23.529	2.900	2.540
29	− 5	28	0.07	0.5	2.320	0.946	23.762	3.340	1.700
Fresh sample	na	na	na	na	na	na	28.000	9.105	8.432
^a S.D. (1–24)					0.146	0.010	0.815	0.440	0.645

X₁: Primary drying temperature (PDT)X₂: Secondary drying temperature (SDT)X₃: Pressure (P)X₄: Sample thickness (ST)

na not applicable

^aStandard deviation for experiments 1–24 is defined by central point experiments (25–29)

phosphate buffer. The protein content in the sample (*Pn*) was estimated by tracing the absorbance against the concentration from the standard curve.

Ascorbic acid

Indophenol method was followed for ascorbic acid determination as described by Ranganna (2001).

Estimation of antioxidants

DPPH (2,2-diphenyl-1-picrylhydrazyl) assay was followed for determination of antioxidant content. DPPH is a stable free radical due to its spare electron delocalization over the entire molecule. Due to this delocalization, DPPH gives a deep violet colour at a wavelength ($\lambda_{\max}$) of 520 nm (Cheung et al. 2003). When DPPH is added to a

substance which acts as a hydrogen donor like phenols, a stable non-radical form of DPPH is generated with subsequent change of violet colour to pale yellow colour.

The phenolic components of the sample were extracted with 50 mL methanol in an incubator shaker at 30 °C and 120 rpm. The mixture was filtered using Whatman I filter paper and the extract was collected. Four millilitres of different concentrations (0.5, 1.5, 2.5, 3.5 and 4.5 mg/mL) of the sample in methanol was made in separate test tubes and 1 mL of 0.1 mM DPPH were added to each. The test tubes were then shaken vigorously and kept under dark conditions for 1 h for the reaction to proceed. Control was prepared by the same procedure without the sample. Methanol was taken as blank. The absorbance for the samples (A_s) and control (A_c) was measured at 520 nm. Antioxidant content (AO) was expressed as the concentration in mg/mL corresponding to 50% DPPH inhibition or IC_{50} . The percent Free Radical Scavenging Activity (FRSA) was determined by the equation described by Barros et al. 2006:

$$FRSA(\%) = \frac{A_c - A_s}{A_c} \times 100 \quad (4)$$

Data modelling and statistics

The general regression equation for a 4 variable (X_1, X_2, X_3, X_4) quadratic model for the k th response, Y_k , can be mathematically expressed as:

$$Y_k = \beta_0 + \sum_{i=1}^n \beta_i X_i + \sum_{i=1}^{n-1} \sum_{j=i+1}^n \beta_{ij} X_i X_j + \sum_{i=1}^n \beta_{ii} X_i^2 \quad (5)$$

where $\beta_0, \beta_i, \beta_{ij}, \beta_{ii}$ are the model coefficients, X_i, X_j, X_i^2 are the process variables and i, j correspond to the i th and j th variable respectively. The regression models for the current study were developed in Microsoft Excel v.2012 using the 'regression' function under Data Analysis Toolpak. Models with a correlation coefficient (R) > 0.85 were considered for development of the multi-objective function for optimization.

Genetic algorithm

GA is an Evolutionary Algorithm (EA) which works on Darwin's theory of natural selection. It mixes and matches the independent variables to produce superior 'offsprings' thereby increasing flexibility, efficiency and efficacy of the model to be optimized. GA performs three operations: selection, crossover and mutation in a generated population based on an objective function. Initially strings are selected randomly as per higher relative fitness. They are then allowed to enter the mating zone where random crossover

points are chosen with a certain probability of crossover (P_c). Crossover implies the interchange of bit values (genes) i.e., 1–0 and vice versa. This continues until a particular population size is reached. Finally, mutation occurs with a probability of mutation (P_m), when random genes within the new population are changed. The result is a population (new generation) with improved average fitness. The procedure for implementation of genetic algorithm with regression model as fitness function is shown in Fig. 1. A detailed version of the steps involved in genetic algorithm from initiation to termination can be found in various literatures (Murata et al. 1996; Reed et al. 2000; Konak et al. 2006; Blaifi et al. 2016). The search for optimal points of process variables was conducted using the ga-multiobjective function available under the optimization toolbox of MATLAB software v.2009b.

Mathematical optimization

Multi-objective goal attainment function ($f_{goalattain}$) in optimization toolbox of MATLAB v.2009b was used for derivative based/mathematical optimization. The function finds the minimum of a problem as specified by the goal, constraints and weight. The minimization process completes when the objective function, γ , attains a value close to the goal as defined by:

Fig. 1 Genetic algorithm optimization process

$$\text{minimize } \gamma, \text{ such that } \begin{cases} F(x) - w.\gamma \leq \text{goal} \\ lb \leq x \leq ub \end{cases} \quad (6)$$

where x and w are the variable and weight vectors respectively, $F(x)$ is the function that returns vectors and lb and ub are the lower and upper bounds respectively. The function may also prematurely terminate if the number of set iterations or function evaluation limit exceeds. In this case, a further study is required with increased values of termination criteria, to see if the solution set remains unchanged or if global minima can be obtained successfully.

Results and discussion

Regression models

Second order polynomials of the form described in Eq. (5) were obtained for rehydration ratio, shrinkage ratio, ascorbic acid, antioxidant and protein content for freeze dried mushrooms. The model coefficients with statistical information (p value, coefficient of correlation, coefficient of determination and standard error) for the responses are shown in Table 2. The regression models developed, were found significant ($p < 0.01$) except for the model corresponding to antioxidant content ($p > 0.05$). The model for antioxidant content was therefore, not considered in the objective/fitness function as it did not meet the selection criteria ($R > 0.85$).

Analysis of the model coefficients (Table 2) revealed that the secondary drying temperature (SDT) affected the protein, antioxidant and shrinkage ratio significantly ($p < 0.01$) with no prominent effect due to variation in primary drying temperature and pressure ($p > 0.05$). Increase in temperature to near ambient conditions during secondary drying may have triggered formation of reactants which led to slight decrease in the antioxidant content. Moreover, due to desorption during the secondary drying phase, increase in shrinkage may have indirectly altered the protein structure, thereby declining it. The effect of sample thickness on the physical properties (rehydration and shrinkage) was significant ($p < 0.01$) and expected as thickness affects the drying rate and time which in turn is associated with the microstructure of the product. Ascorbic acid content was also influenced by the variation in sample thickness.

The quadratic model terms (X_i^2) are responsible for non-linearity in data which is crucial for optimization. Higher non-linearity gives us a better incentive to proceed towards an optimization problem. From Table 2, it is clear that each response has significant non-linearity in data contributed by at least two process variables to a maximum of all four

variables as in the case of protein. Comparatively lower variations in shrinkage ratio were observed followed by rest of the responses. The interaction effect of the process variables ($X_i.X_j$) was significant ($p < 0.05$) in physical properties with common effect of pressure (X_3).

GA optimization

Using the regression models which satisfied the correlation criteria, a multi-objective fitness function was created (“Appendix”) with a function handle as: @multiobjective. The function was defined to search for solutions with maximum rehydration ratio, ascorbic acid and protein and minimum shrinkage ratio. Since multi-objective GA function in MATLAB is a minimization function, a negative sign was added to the objectives with maximization goals. This facilitated the minimization of those objectives towards the negative direction with a higher absolute value. The absolute values for these objectives were considered as final optimized solution. An initial population size of 60 was generated at random using a constraint dependent creation function. The constraints were set using the upper and lower bounds of the levels of process variables in the order: [PDT, SDT, P, ST] with the lower bound corresponding to [− 8 25 0.04 0.2] and upper bound as [− 2 31 0.10 0.8]. Selection of the population individuals for crossover was done using the tournament scheme with a default size of 2. The crossover probability was set at a default value of 0.8 with a scattered crossover function. An adaptive feasible function generated better optimized solutions as compared to a constrained dependent function for population mutation. The stopping criterion for the search algorithm was defined as 1000 generations or a functional tolerance limit of 10^{-5} , whichever is earlier.

The search for optimal solution started with 1.87, 0.77, 22.02 and 3.80 for rehydration ratio, shrinkage ratio, ascorbic acid and protein content respectively. The values for best fitness increased across generations until it converged to a relatively constant value at around 800 generations. The search algorithm was allowed to run up to 1000 generations which resulted in a total of 21 solution sets (Table 3). The spread of the solutions or average pareto spread was plotted with increasing generations (Fig. 2) to visualize the solution convergence. Convergence was identified as the solutions being closer to each other and eventually attaining the same values. The final converged solution set was considered as overall best fit for the multi-objective optimization problem.

Table 2 Model coefficients with *p* statistic

Model term	Rehydration ratio		Shrinkage ratio		Ascorbic acid		Antioxidant		Protein	
	Coefficient	<i>p</i> value	Coefficient	<i>p</i> value	Coefficient	<i>p</i> value	Coefficient	<i>p</i> value	Coefficient	<i>p</i> value
Intercept	13.059	0.298	− 3.196	0.007 ^a	− 39.496	0.545	114.313	0.010 ^a	190.526	0.002 ^a
X_1 : PDT	0.912	0.105	0.088	0.072	1.490	0.602	1.942	0.277	3.723	0.109
X_2 : SDT	− 0.416	0.612	0.306	0.000 ^a	5.666	0.200	− 7.740	0.009 ^a	− 12.488	0.002 ^a
X_3 : P	− 32.102	0.567	− 5.833	0.233	131.322	0.656	68.300	0.707	− 231.180	0.323
X_4 : ST	− 5.532	0.019 ^a	1.143	0.000 ^a	− 29.428	0.018 ^a	− 8.908	0.213	11.520	0.206
X_1^2	0.074	0.000 ^a	− 0.000	0.927	− 0.178	0.029 ^a	0.045 ^a	0.346	0.180	0.007 ^a
X_2^2	0.003	0.818	− 0.006	0.000 ^a	− 0.122	0.121	0.134	0.010 ^a	0.219	0.002 ^a
X_3^2	− 194.213	0.187	− 45.296	0.002 ^a	− 1130.731	0.148	− 488.194	0.303	1447.519	0.025 ^a
X_4^2	8.256	0.000 ^a	− 1.143	0.000 ^a	25.770	0.003 ^a	11.813	0.020 ^a	− 14.480	0.025 ^a
$X_1 \cdot X_2$	− 0.006	0.753	− 0.003	0.056	− 0.115	0.241	− 0.057	0.342	− 0.083	0.282
$X_2 \cdot X_3$	2.881	0.128	0.375	0.027 ^a	− 1.094	0.909	0.094	0.987	− 0.817	0.914
$X_3 \cdot X_4$	− 41.667	0.034 ^a	2.806	0.087	88.333	0.364	− 9.667	0.871	85.083	0.269
$X_4 \cdot X_1$	0.009	0.962	0.017	0.295	0.423	0.661	− 0.104	0.861	0.901	0.243
Multiple R	0.906		0.951		0.868		0.797		0.859	
R^2	0.820		0.905		0.753		0.634		0.737	
SE	0.323		0.027		1.703		1.051		1.337	
Model <i>p</i> value	0.001 ^a		0.000 ^a		0.005 ^a		0.059		0.008 ^a	

^a*p* < 0.05 indicates significance

Mathematical optimization

The derivative required in ‘*fgoalattain*’ function was approximated by the solver. Forward difference type of derivative was used for the approximation. The initial start point was set as the minimum values attained in the experimental runs (Table 1). The vector form of the start point was defined as: [2.01 0.98 17.89 1.58] with a goal vector corresponding to the best values attained during experiments: [4.19 0.73 26.91 7.28]. Absolute weights: [0 0 0 0] were set for all variables. Lower and upper bounds were provided as described during optimization with genetic algorithm. The stopping criteria were defined as maximum function evaluation of 800 or a maximum iteration of 400, whichever is earlier. Also the function tolerance was set at 10^{-6} . The remaining solver options were kept as default software values. The solver stopped after 133 iterations as maximum number of function evaluation exceeded 800. Due to premature termination of the search function, the function evaluation value was incremented in steps of 1000 till 10,000. It was found that the change in solutions obtained did not vary with the increased limit at a function tolerance of 10^{-6} . The constant solution set obtained was therefore, considered the final solution.

Comparison of optimization techniques

It is evident from Table 4 that GA performed superior to the derivative based optimization technique while

searching for an optimum solution for physical characteristics (rehydration and shrinkage ratio). Shankar and Bandyopadhyay observed also reported similar results while comparing response surface (RSM) optimization to GA in extrusion processing of fish and rice flour blend (Shankar and Bandyopadhyay 2004). Mathematical optimizers were found to efficiently recognize the trend but GA precisely pinpointed the processing conditions. However, the performance of *fgoalattain* function was better for nutritional responses (ascorbic acid and protein). On comparison of the variation in results for the two solvers from the fresh sample, it was observed that *fgoalattain* was fairly close to the initial sample quality conditions (Table 1). Moreover, the difference in the results for shrinkage ratio (Table 4) is quite insignificant among other differences which tip the balance in favour of *fgoalattain*.

Verification of optimized results

Five experimental runs for each processing condition described in Table 4 were performed. The variation in mean actual data to the predicted optimized results was compared using a *t* test. The results of the test (Table 4) revealed that the predicted values obtained from the solvers were in good agreement with the experimentally determined values. However, the predicted value of protein given by *fgoalattain* could not be verified ($t_{\text{calculated}} > t_{\text{critical}}$). Even though the verification was not successful,

Table 3 Converging optimal solution set generated by genetic algorithm

Solution set	PDT	SDT	P	ST	Rehydration ratio	Shrinkage ratio	Ascorbic acid (mg/g)	Protein (mg/mL)
1	– 5.942	26.077	0.100	0.549	1.871	0.770	22.029	3.801
2	– 6.168	25.269	0.100	0.478	1.940	0.711	21.588	4.524
3	– 6.029	25.135	0.077	0.506	2.210	0.780	22.947	3.567
4	– 7.237	25.004	0.084	0.760	2.722	0.684	23.177	2.670
5	– 7.918	25.007	0.100	0.339	2.825	0.609	19.635	5.453
6	– 6.861	25.455	0.071	0.769	2.937	0.730	24.011	1.569
7	– 6.242	25.800	0.070	0.795	2.942	0.746	25.136	0.957
8	– 5.830	26.140	0.063	0.800	3.016	0.765	25.439	0.666
9	– 2.000	25.002	0.040	0.452	3.017	0.864	23.487	7.842
10	– 2.001	25.140	0.057	0.553	3.082	0.888	24.085	6.432
11	– 2.934	25.000	0.077	0.800	3.124	0.785	27.128	4.206
12	– 7.849	30.903	0.100	0.358	3.234	0.806	17.518	7.355
13	– 7.860	30.387	0.100	0.316	3.366	0.784	18.305	6.463
14	– 2.113	25.072	0.059	0.723	3.452	0.851	25.534	5.623
15	– 7.942	25.007	0.100	0.201	3.571	0.514	20.988	4.775
16	– 7.943	25.007	0.100	0.200	3.576	0.514	20.995	4.771
17	– 2.289	25.048	0.060	0.778	3.599	0.822	26.365	4.986
18	– 7.929	29.184	0.100	0.203	3.895	0.692	20.382	4.594
19	– 2.001	25.002	0.040	0.800	4.101	0.791	25.412	6.099
20	– 2.000	25.002	0.040	0.800	4.102	0.791	25.409	6.102
21 ^a	– 2.000	25.002	0.040	0.800	4.102	0.791	25.409	6.102

^aFinal solution**Table 4** Comparison of solutions obtained from genetic and mathematical (*fgoalattain*) solvers

Parameter	GA		*t value	<i>fgoalattain</i>		t value
	**Actual	Predicted		Actual	Predicted	
<i>Dependent</i>						
Rehydration ratio	3.92	4.10	− 1.78	2.77	2.86	− 0.43
Shrinkage ratio	0.74	0.79	− 1.17	0.77	0.75	0.49
Ascorbic acid	23.14	25.40	− 2.22	25.94	26.38	− 0.96
Protein	5.96	6.10	− 0.88	6.88	7.25	− 2.59
<i>Independent</i>						
PDT	− 2			− 2		
SDT	25			25		
P	0.04			0.10		
ST	0.8			0.8		

 $t_{\text{critical}} = 2.306$ ($\alpha = 0.05$)*|t| > t_{critical} indicates significant difference

**Mean value of 5 experimental runs

Fig. 2 Declining pareto spread with generations for optimum solution depicting solution convergence

the experimental value obtained for protein from a derivative based optimizer was 13% higher than that obtained from GA. The obtained deviation of experimental and predicted data was found similar to the findings of Khawas et al. (2016) during vacuum drying of culinary banana.

Conclusion

The current investigation reports the use of genetic (GA) and mathematical based optimization (*fgoalattain*) techniques for freeze drying of button mushroom. The process variables were optimized by both techniques on the basis of superior physico-chemical characteristics of the freeze-dried product. Physical properties of the dried mushroom were better optimized by GA whereas mathematical optimizer gave a better solution for nutritional properties. From a broad perspective, the mathematical optimization technique may have performed better overall but from the consumer point of view, physical characteristics would be more appealing. Since the rehydration and shrinkage ratio would directly affect the selling ability of the dried product, it may be concluded that GA would be the better optimizer in the present study with little compromise to nutritional composition.

Acknowledgements The authors would like to thank MRC, G.B. Pant University of Agriculture and Technology for providing the experimental material to conduct this study. Further, the authors extend their gratitude towards Ms. Kusum Pandey for sharing her valuable views on genetic algorithm, which aided in successful completion of this work.

Appendix: Fitness function for optimization using genetic algorithm in MATLAB

```
function y = mutiobjective (x)

% minus (-) sign multiplied to [objective function] represents a
% maximization problem

%objective function for rehydration ratio
y(1) = -[13.059+0.912*x(1)-0.416*x(2)-32.102*x(3)-
5.532*x(4)+0.074*(x(1)^2)+0.003*(x(2)^2)-
194.213*(x(3)^2)+8.256*(x(4)^2)-0.006*x(1)*x(2)+2.881*x(2)*x(3)-
41.667*x(3)*x(4)+0.009*x(4)*x(1)];

%objective function for shrinkage ratio
y(2) = -3.196+0.088*x(1)+0.306*x(2)-5.833*x(3)+1.143*x(4)-0.000*(x(1)^2)-
0.006*(x(2)^2)-45.296*(x(3)^2)-1.143*(x(4)^2)-
0.003*x(1)*x(2)+0.375*x(2)*x(3)+2.806*x(3)*x(4)+0.017*x(4)*x(1);

%objective function for ascorbic acid
y(3) = -[-39.496+1.490*x(1)+5.666*x(2)+131.322*x(3)-29.428*x(4)-
0.178*(x(1)^2)-0.122*(x(2)^2)-1130.731*(x(3)^2)+25.770*(x(4)^2)-
0.115*x(1)*x(2)-1.094*x(2)*x(3)+88.333*x(3)*x(4)+0.423*x(4)*x(1)];

%objective function for protein content
y(4) = -[190.526+3.723*x(1)-12.488*x(2)-
231.180*x(3)+11.520*x(4)+0.180*(x(1)^2)+0.219*(x(2)^2)+1447.519*(x(3)^2)-
14.480*(x(4)^2)-0.083*x(1)*x(2)-
0.817*x(2)*x(3)+85.083*x(3)*x(4)+0.901*x(4)*x(1)];

end
```

References

- Amine KM, Champagne CP, Salmieri S, Britten M, St-Gelais D, Fustier P, Lacroix M (2014) Effect of palmitoylated alginate microencapsulation on viability of *Bifidobacterium longum* during freeze drying. *LWT Food Sci Technol* 56:111–117. <https://doi.org/10.1016/j.lwt.2013.11.003>
- Aykin E, Erbas M (2016) Quality properties and adsorption behaviour of freeze dried beef meat from the *Biceps femoris* and *Semimembranosus* muscles. *Meat Sci* 121:272–277. <https://doi.org/10.1016/j.meatsci.2016.06.030>
- Barros L, Ferreira MJ, Queiros B, Ferreira ICFR, Baptista P (2006) Total phenols, ascorbic acid, β -carotene and lycopene in Portuguese wild edible mushrooms and their antioxidant activities. *Food Chem* 103:413–419. <https://doi.org/10.1016/j.foodchem.2006.07.038>
- Blaifi S, Moulahoum S, Colak I, Merrouche W (2016) An enhanced dynamic model of battery using genetic algorithm suitable for photovoltaic applications. *Appl Energy* 169:888–898. <https://doi.org/10.1016/j.apenergy.2016.02.062>
- Cheung LM, Cheung PCK, Ooi VEC (2003) Antioxidant activity and total phenolics of edible mushroom extracts. *Food Chem* 81:249–255. [https://doi.org/10.1016/S0308-8146\(02\)00419-3](https://doi.org/10.1016/S0308-8146(02)00419-3)
- Ciurzyn'ska A, Lenart A (2011) Freeze drying-application in food processing and biotechnology-a review. *Pol J Food Nutr Sci* 61:165–171
- Dursun E, Dursun I (2005) Some physical properties of caper seed. *Biosyst Eng* 92:237–245. <https://doi.org/10.1016/j.biosystemeng.2005.06.003>
- Erenturk S, Erenturk K (2007) Comparison of genetic algorithm and neural approaches for the drying process of carrot. *J Food Eng* 78:905–912
- Fellows P (2017) Freeze drying and freeze concentration. In: Food processing technology, 4th edn. Woodhead publications Ltd., England, pp 441–451
- Ferreira SLC, Bruns RE, Ferreira HS, Matos GD, David JM, Brandao GC, Silva EGP, Portugal LA, Reis PS, Souza AS, Santos WNL (2007) Box-Behnken design: an alternative for the optimization of analytical methods. *Anal Chim Acta* 597:179–186. <https://doi.org/10.1016/j.aca.2007.07.011>
- Goshima H, Do G, Nakagawa K (2016) Impact of ice morphology on design space of pharmaceutical freeze drying. *J Pharm Sci* 105:1920–1933. <https://doi.org/10.1016/j.xphs.2016.04.001>
- Khawas P, Dash KK, Das AJ, Deka SC (2016) Modeling and optimization of the process parameters in vacuum drying of culinary banana (*Musa ABB*) slices by application of artificial neural network and genetic algorithm. *Dry Technol* 34:491–503. <https://doi.org/10.1080/07373937.2015.1060605>
- Konak A, Coit DW, Smith AE (2006) Multi-objective optimization using genetic algorithm: a tutorial. *Reliab Eng Syst Saf* 91:992–1007. <https://doi.org/10.1016/j.res.2005.11.018>
- Mayor L, Sereno AM (2004) Modelling shrinkage during convective drying of food materials: a review. *J Food Eng* 61:373–386. [https://doi.org/10.1016/S0260-8774\(03\)00144-4](https://doi.org/10.1016/S0260-8774(03)00144-4)
- Murata T, Ishibuchi H, Tanaka H (1996) Multi-objective genetic algorithm and its application to fellowship scheduling. *Comput Ind Eng* 30:957–968
- Pikal MJ, Cardon S, Bhugra C, Jameel F, Rambhatla S, Mascarenhas WJ, Akay HU (2005) The non-steady state modeling of freeze drying: in-process product temperature and moisture content mapping and pharmaceutical product quality applications. *Pharm Dev Technol* 1:17–32. <https://doi.org/10.1081/PDT-35869>
- Pomory CM (2008) Color development time of the Lowry protein assay. *Anal Biochem* 378:216–217. <https://doi.org/10.1016/j.ab.2008.04.015>

- Ranganna S (2001) Vitamins. Handbook of analysis and quality control for fruit and vegetable products, 7th edn. Tata McGraw Hill Book Co., New Delhi, pp 105–118
- Reed P, Minsker B, Goldberg DE (2000) Designing a competent simple genetic algorithm for search and optimization. Water Resour Res 32:3757–3761
- Shankar TJ, Bandyopadhyay S (2004) Optimization of extrusion process variables using a genetic algorithm. Food Bioprod Process 82:143–150. <https://doi.org/10.1205/0960308041614855>
- Tarafdar A, Shahi NC, Singh A, Sirohi R (2017) Optimization of freeze-drying process parameters for qualitative evaluation of button mushroom (*Agaricus bisporus*) using response surface methodology. J Food Qual. <https://doi.org/10.1155/2017/5043612>