

# Fiber Bragg grating sensor array interrogation using differential evolution

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We apply the differential evolution algorithm (DE) to interrogate a fiber Bragg grating sensor network, where a multi-level crossing detector comprising of reference gratings is used to track the sensor gratings which have the same Bragg wavelength but different reflectivities. The DE algorithm uses a numerical model of the system and the data collected from the network, for wavelength demodulation and direct extraction of the perturbation on each of the sensor. We show that the estimated signals are in good agreement with the actual signals. The use of DE algorithm facilitates faster data collection and offline interrogation.

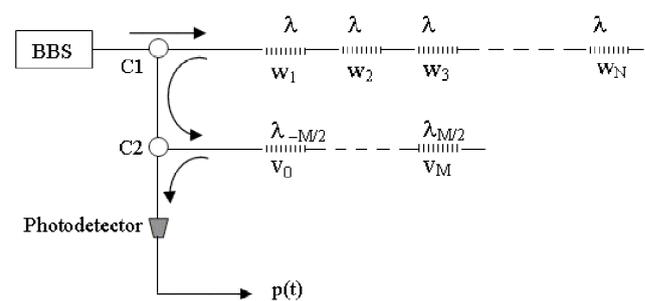
(Received August 8, 2008; in revised form September 16, 2008; accepted September 26, 2008)

*Keywords:* Fiber Bragg grating, Sensor array, Differential evolution algorithm

## 1. Introduction

The interrogation of a fiber Bragg grating (FBG) sensor array has been a challenging problem. In a typical scenario, each grating is assigned a unique Bragg wavelength and window of operation so that spectrally adjacent gratings do not overlap. The optical source for the sensor array and/or the detector, such as a tunable Fabry-Perot filter or an optical spectrum analyzer, is scanned over the range of operation of each sensor. The amount of perturbation on any given sensor is then deduced by calculating the difference between the original Bragg wavelength and the current Bragg wavelength of the sensor. This technique, called wavelength division multiplexing (WDM), limits the number of sensors that can be interrogated due to the finite spectral width of the broadband source. However, various interrogation techniques have been proposed to increase the number of sensors, such as, Wavelength Division Multiple Access (WDMA) [1], Frequency Modulated Continuous Wave (FMCW) technique [2], Code Division Multiple Access (CDMA) [3], wavelength-scanned fiber laser [4], Spatial Division Multiplexing (SDM) [5], titled Fiber Bragg Grating [6], and matched filter interrogation [7]. Majority of these interrogation techniques track the Bragg wavelength of the sensor. However, the actual perturbation on the sensor has to be still deduced indirectly. Also, the speed of interrogation is limited by the interrogation system used. In applications where data collection and post-processing is preferred over real-time observation such as civil structural health monitoring [8] for fatigue and environmental deterioration, where data is collected over few days and is processed later, a different approach is required. A wavelength-shift time stamping (WSTS) system that is capable of monitoring the perturbation on a

single sensor in real-time and at high-speeds has been demonstrated [9].



*Fig. 1. MWSTS network layout to interrogate  $N$  FBG sensors with the same Bragg wavelengths ( $\lambda$ ) and  $w_N$  reflectivities, using  $M$  reference gratings ( $\lambda_M$ ) with  $v_M$  reflectivities. (BBS: Broadband Source).*

Evolutionary optimization methods such as genetic algorithms [10] and particle swarms [11], [12] have been employed to detect the wavelengths in an FBG sensor network. The advantage of using computer algorithms lies in the fact that the data can be collected and processed offline which delinks the speed of the interrogation system used, from the dynamic nature of the perturbation. The concept of such an approach is to collect the data as fast as possible, but process it later.

In this paper, we demonstrate a multi-wavelength shift time-stamping (MWSTS) grating network that collects the data from the sensor gratings in real-time and employs differential evolution algorithm to process the data offline. The principle of operation of the network and the methodology of applying DE to interrogate the network is explained in Section II, followed by simulation results and conclusions in Sections III and IV, respectively.

## 2. Theory

The layout of the MWSTS interrogation technique is shown in Fig. 1. Using a circulator (C1), light from the broadband source (BBS) is launched into the sensor grating array (SGA), consisting of  $N$  sensors with the same Bragg wavelength  $\lambda$  and different reflectivities, represented as weights  $\{w_1, w_2, \dots, w_N\}$ . The light reflected from the sensors is redirected using another circulator (C2) into the reference grating array (RGA). The RGA consists of  $M$  gratings with different reflectivities, represented as weights  $\{v_0, \dots, v_{M-1}\}$  and Bragg wavelengths  $\lambda_k$  that are offset from  $\lambda$  by the relation,

$$\lambda_k = \lambda + kq \tag{1}$$

where,  $-M/2 \leq k \leq M/2$ ,  $k \neq 0$  and  $q$  is the spectral distance between adjacent reference gratings. We define  $q > \Delta\lambda$ , the full width at half maximum (FWHM) of the sensor gratings so that there is no simultaneous spectral overlap of the sensor spectrum and the two adjacent reference spectra.

In the absence of perturbation on SGA, the sensor gratings will have the same resonant wavelength  $\lambda$ . If a sensor grating is perturbed by an amount  $k\delta$ , then from eq. (1) we see that the light reflected from the sensor will be reflected back by the corresponding reference grating  $\lambda_k$  and directed into the photodetector by the circulator C2. The output of the photodetector,  $p(t)$ , consists of a series of pulses with amplitudes that are elements of the matrix,

$$F = \begin{pmatrix} w_1 v_0 & \dots & w_1 v_M \\ \vdots & \ddots & \vdots \\ w_N v_0 & \dots & w_N v_M \end{pmatrix} \tag{2}$$

For example, if  $N=2$  and  $M=2$ , strains  $s_1(t)$  and  $s_2(t)$  on sensors 1 and 2, respectively, will produce a series of pulses with amplitudes that are elements of the set  $\{w_1 v_0, w_1 v_1, w_1 v_2, w_2 v_0, w_2 v_1, w_2 v_2\}$ . The order of occurrence of the pulses will depend on the strain signal of the sensors. Using eq. (2), the output of the photodetector  $p(t)$  for  $N$  sensors and  $M$  reference gratings can be represented as,

$$p(t) = \sum_{i=1}^N \sum_{j=1}^M F_{ij} s_i(t) \tag{3}$$

### 2.1 Objective function

The concept of using DE for extracting the  $N$  strain signals  $s_i(t)$  from  $p(t)$  is to model the network shown in Fig. 1 numerically and generate an estimate  $r(t)$  of  $p(t)$  by assuming initial random inputs  $\hat{s}_i(t)$ . That is,

$$r(t) = \sum_{i=1}^N \sum_{j=1}^M F_{ij} \hat{s}_i(t) \tag{4}$$

The DE algorithm iteratively tunes the estimates  $\hat{s}_i(t)$  so as to minimize,

$$g(t) = \sum_{t=1}^T [p(t) - r(t)]^2 \tag{5}$$

where,  $T$  is the sample length at the output of the photodetector. A schematic of the technique is shown in Fig. 2.

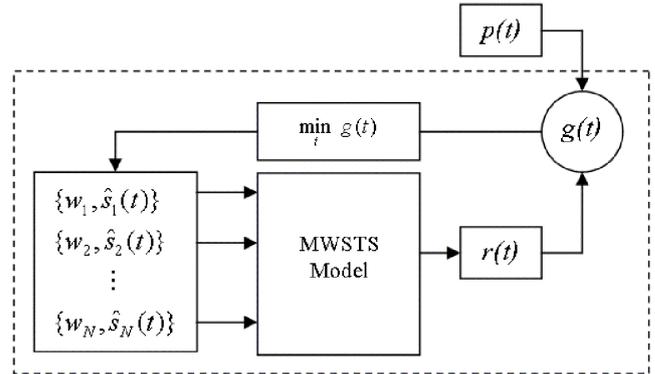


Fig. 2 Schematic of applying DE algorithm to estimate  $\hat{s}_i(t)$ .

### 2.2 Differential evolution

Differential evolution algorithm [14] is a powerful population-based stochastic search technique, which is an efficient and effective global optimizer in the continuous search domain. DE algorithm aims at evolving a population of  $NP$   $D$ -dimensional parameter vectors or individuals, which are the candidate solutions, i.e.  $X_{i,G} = \{x_{i,G}^1, \dots, x_{i,G}^D\}$ ,  $i = 1, \dots, NP$  towards the global optimum. The initial population covers the entire search space as much as possible by uniformly randomizing individuals within the search space constrained by the prescribed bounds  $s_{min}$  and  $s_{max}$ , which are the expected minimum and maximum strain values, respectively. The initial value of the  $j^{th}$  parameter in the  $i^{th}$  individual in generation  $G = 0$  is generated as,

$$x_{i,0}^j = s_{min} + rand(0,1)(s_{max} - s_{min}) \tag{6}$$

where,  $j = 1, \dots, D$ , and  $rand(0,1)$  represents a uniformly distributed random variable within the range  $[0,1]$ . After initialization, DE employs a certain mutation strategy to produce a mutant vector  $V_{i,G}$  with respect to each individual target vector  $X_{i,G}$ , in the current population. Following the mutation phase, a crossover operation is applied to a pair of target vector  $X_{i,G}$  and its corresponding mutant vector  $V_{i,G}$  to generate a trial vector  $U_{i,G} = \{U_{i,G}^1, \dots, U_{i,G}^D\}$ . If the values of some parameters of the newly generated trial vector exceed the

corresponding upper and lower bounds, they are randomly and uniformly reinitialized to values within the bounds. The objective function value of each trial vector  $g(U_{i,G})$  is compared to that of its corresponding target vector  $g(X_{i,G})$  in the current population where  $g(\cdot)$  is defined in eq. (5). If  $g(U_{i,G}) \leq g(X_{i,G})$ , the target vector is replaced by the trial vector and is included in the population of the next generation and for  $g(U_{i,G}) > g(X_{i,G})$ , the target vector is retained in the population for the next generation. The process is repeated until a termination criterion is satisfied. The DE optimization process is summarized below.

1. Set the generation counter  $G=0$ , and randomly initialize a population of  $NP$  individuals  $P_G = \{X_{1,G}, \dots, X_{NP,G}\}$  with  $X_{i,G} = \{x_{i,G}^1, \dots, x_{i,G}^D\}$ ,  $i = 1, \dots, NP$ , uniformly distributed in the range  $[s_{min}, s_{max}]$ . Find the best solution ( $\hat{S}_G$ ) based on the objective function value based on eq. (5).
2. After initialization, the following steps are executed until the stopping criterion is met. The stopping criterion may be satisfying a predefined threshold value of the mean square error as defined in eq. (5) or completion of maximum fitness evaluations (Max\_FEs).

2.1 *Mutation*: Generate a mutated vector  $V_{i,G} = \{v_{i,G}^1, \dots, v_{i,G}^D\}$  corresponding to each target vector  $X_{i,G}$ ,  $i = 1, \dots, NP$ , using,

$$V_{i,G} = X_{i,G} + F \cdot (\hat{S}_G - X_{i,G}) + F \cdot (X_{r_1,G} - X_{r_2,G}) \quad (7)$$

where, the indices  $r_1^i$  and  $r_2^i$  are mutually exclusive integers randomly generated within the range  $[1, NP]$ .

2.2 *Crossover*: Generate a trial vector  $U_{i,G} = \{u_{i,G}^1, \dots, u_{i,G}^D\}$ ,  $i = 1, \dots, NP$ , for each target vector  $X_{i,G}$ . For  $j = 1, \dots, D$ ,

$$u_{i,G}^j = \begin{cases} v_{i,G}^j & \text{if rand}[0,1] \leq CR \\ x_{i,G}^j & \text{otherwise} \end{cases} \quad (8)$$

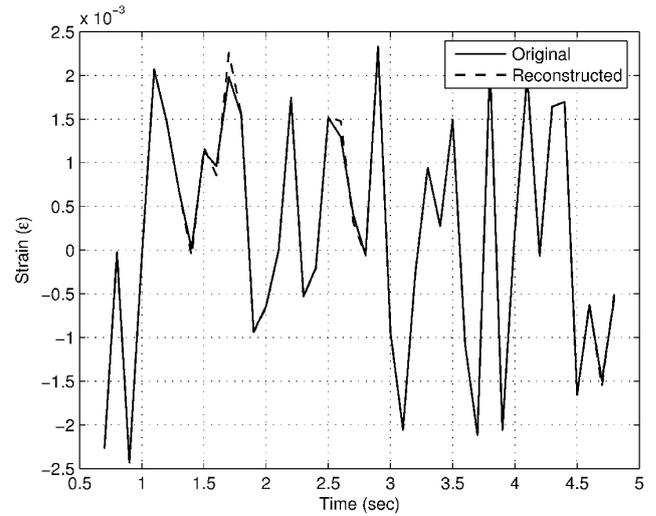
where,  $CR$  is the crossover rate, a constant within the range  $[0,1)$  that controls the fraction of parameter values copied from the mutant vector.

2.3 *Selection*: Evaluate the trial vectors. For  $i=1, \dots, NP$ , if  $g(U_{i,G}) \leq g(X_{i,G})$ ,  $X_{i,G+1} = U_{i,G}$  and  $g(X_{i,G+1}) = g(U_{i,G})$ . If  $g(U_{i,G}) > g(\hat{S}_G)$ ,  $\hat{S}_G = U_{i,G}$  and  $g(\hat{S}_G) = g(U_{i,G})$

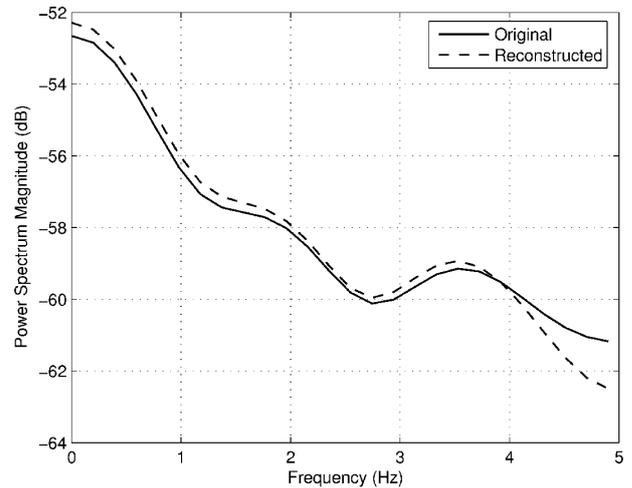
2.4 Increment the generation count,  $G = G + 1$  and set  $\hat{S}_G = \hat{S}_{G-1}$

### 3. Simulation results

The DE-MWSTS system is numerically evaluated for  $N = 10$ ,  $M = 8$ ,  $\lambda = 1560\text{nm}$ ,  $\text{Max\_FEs} = 600,000$ ,  $CR = 0.5$ ,  $T = 12$ ,  $NP = 3000$  and  $\{s_{min}, s_{max}\} = \{-2500\mu\epsilon, 2500\mu\epsilon\}$ . For  $M = 8$ , the quantization levels and their corresponding reflectivities are,  $(\pm 1639.344\mu\epsilon, 15\%, 95\%)$ ,  $(\pm 1170.960\mu\epsilon, 26\%, 84\%)$ ,  $(\pm 702.576\mu\epsilon, 38\%, 72\%)$  and  $(\pm 234.192\mu\epsilon, 49\%, 61\%)$ .



(a)



(b)

Fig. 3. (a) DE estimated and original signal (b) Power spectral density of the reconstructed and original signal.

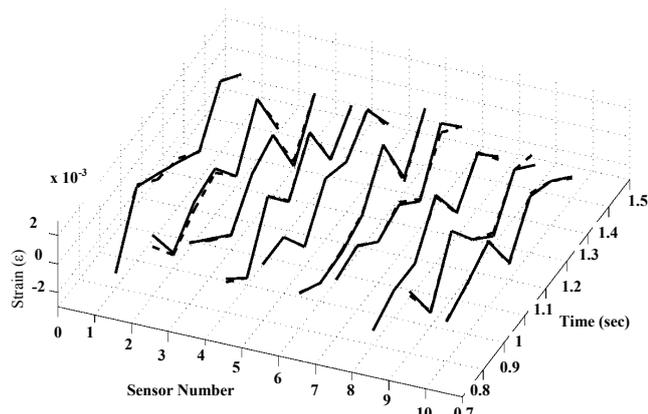


Fig. 4. A section of the DE generated estimate  $\hat{s}_i(t)$  (dashed line) of the actual signal  $s_i(t)$  (solid line), where  $i = 1, 2, \dots, 10$ .

For faster convergence and lesser processing time, the output of the photodetector  $p(t)$  is split into  $l = T/D$  smaller time length segments  $\{p_1(t), p_2(t), \dots, p_l(t)\}$  and DE is applied on each segment individually for  $D = 3$ . One of the main advantages of the proposed quantization based MWSTS interrogation is the ability to preserve the spectral content of the signal. To test the spectral reproducibility, the strain signal on a single sensor is reconstructed by using DE and the power spectral densities (PSDs) of the original and reconstructed signals are compared as shown in Fig. 3(a) and (b). It is seen that the reconstructed and original PSDs are in good agreement. Fig.4 shows the original  $s_i(t)$  and estimated  $\hat{s}_i(t)$  signals for  $N = 10$ , generated on a P4, 3GHz, 1GB RAM computer after a computation time of 40 minutes. The processing time can be reduced further by using high performance computers.

#### 4. Conclusions

The differential evolution (DE) algorithm was applied to demodulate and extract strain signals from a fiber Bragg grating sensor array network tracked by a multilevel crossing reference grating network. Numerical simulation of the proposed system shows that the estimated signals by the DE are in good agreement with the actual signals. Faster data collection is achieved by delinking the interrogation speed from the speed of sensor response and post-processing the collected data. Since MWSTS is a completely passive interrogation system, data is collected in real-time and processed later to extract the strain signals. By using dedicated processors high-speed data extraction is possible.

#### Acknowledgements

This work is supported by the A\*Star (agency for science, technology and re- search) under the grant #052 101 002010.

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