Abstract—A whole-cell bioluminescent biosensor dynamics based on genetically engineered Escherichia coli bacteria carrying a promoter-reporter fusion is often determined by a series of chemical reactions such as gene expression and reactions involving protein concentrations at nanomolar volume. In this paper, we derive an analytical model of a whole-cell bioluminescent biosensor based on the Michaelis–Menten kinetics of simple enzymatic reactions. The proposed model is characterized by three measurable set of parameters: the biosensor effective rate constant, the total number of the emitted photons and the biosensor reaction order. We get a good agreement between the simulation results of the model and the measured light signal, correlating the input signal (toxin concentration) and the output signal (the bioluminescent light). The model is tested and verified for various prompters (recA, KatG, and micF). This model is useful in the design process of bio-electronic circuits.

Index Terms—Bioluminescent, integrating sphere, promoter-reporter fusion, quasi-steady-state approximation, whole-cell biosensor.

I. INTRODUCTION

WHOLE-CELL biosensor systems have been recently introduced for screening and monitoring applications. Those biosensors consist of living microbial cell as sensing elements (bioreporters); e.g., genetically engineered bacteria integrated with electronic circuit. In this paper, the discussed whole-cell bioluminescent biosensors can detect and quantify chemical or physical agents in the environment by producing measurable bioluminescent signal in response to the agent concentration [1]–[6]. The living microbial cell which is integrated on chip is engineered to emit light when a chemical with a specific function is encountered, while the electronic circuit is designed to detect the luminescent signal, process it, and analyze the obtained information. Whole-cell biosensors can be applied in other fields, including health care and medical applications, pharmaceutical screening and environmental monitoring.

Successful whole-cell biosensors should be well defined for the purpose of the analysis, and stable under normal storage conditions. The reaction should be independent of physical parameters such as stirring, pH and temperature as is manageable. The response should be accurate, precise, reproducible, and linear over the useful analytical range. It should also be free from electrical noise and the complete biosensor should be compact, reliable, and cost effective.

Under those beneficial features, it is necessary to set the bio-circuit design rules followed by a computer simulation. At this stage, it is useful to introduce the results of the system characterization, the mathematical modeling, and fitting parameters. Recently, our group has derived analytical and simulation model for the whole-cell biosensor based on genetically engineered living cells [6], [7]. In these works, we focused on the bioreporter enzymatic reaction without consideration to the genetic system and gene expression biophysical functions when we assumed that the generation rate of bioreporter enzyme is proportionally to the analyte and living cells concentrations. In this paper, we present an analytical model with consideration to the biophysical functions of analyte-receptor binding reaction, genetic system and gene expression. We built an experimental setup to characterize the bio-system. In this work, we use genetically engineered Escherichia coli bacteria carrying a recA::luxCDABE promoter-reporter fusion which exhibit SOS response to large group of toxin [6], [8]–[10]. The analytical model and the characterization experimental setup are tested and verified for various prompters (KatG and micF). Moreover, the proposed model can be beneficial in planning simulation program for bio-integrated circuit and other bacteria based biosensors.

II. ANALYTICAL MODEL

Typically, E.coli bacteria are used as harboring cells, in which plasmids containing promoter-reporter gene conjugation are introduced. Promoter gene functions as activators of the process of the bioreporter expression in the presence of a toxin. Consequently, turning on the promoter gene now causes the reporter gene to be turned on. The promoter/reporter gene is transcribed into messenger RNA (mRNA) and then translated into a reporter enzyme (protein) that function as light sources or electron sources for monitoring metabolic cell activity [10], [11]. In the case of bioluminescent biosensor, the microbial cell sensors have been constructed by genetically binding the Lux gene with an inducible gene promoter for toxicity testing. Bioluminescence phenomenon (in living organisms) accompanies the oxidation of organic compounds, such as luciferin, mediated by an enzyme catalyst, known as luciferase [12]. The bacterial bioluminescent reaction, which is catalyzed by luciferase, involves the oxidation of a long-chain aliphatic aldehyde (R-CHO) and reduced flavin mononucleotide (FMN+2) with the liberation of excess free energy in the form of light [12]. The generation
process of the bioreporter enzyme in genetically engineered microbial cells involves series of biochemical cascade genetic reactions such as DNA repair, SOS response, and gene expression. A limitation of a model which combines all the biochemical reactions is that require detailed information about chemical kinetics often unavailable in biology systems. Fig. 1 shows a schematic model of genetically engineered microbial cells. We consider a model with one input (X) – concentration of the analyte and one output (P) – concentration of the product (fatty acid). The model consists of four types of reactions: 1) analyte – receptor binding reaction; 2) biochemical genetic cascade system; 3) gene expression; and 4) bioreporter enzymatic reaction. For the simple case, we assume that all the rates are constants and time independent.

A. Analyte–Receptor Binding Reaction

If the reaction between the analyte X, and the receptor W has binding rate \( k_1 \) (1/M·min) and dissociation rate \( k_2 \) (1/min), then we can write

\[ \frac{d[Y_0]}{dt} = k_1 \left[ W \right] \cdot [X] - k_2 [Y_0] \]  

(1)

where the symbol \([\cdot]\) indicates concentrations of the species. In the case that \([X(0)][W(0)] >> [Y]\), the solution of (1) is:

\[ [Y_0] = \frac{k_1 [W(0)] \cdot [X(0)]}{k} \left( 1 - \exp(-kt) \right) \]  

(2)

where \(k \equiv k_1 [W(0)] + k_2 [X(0)] + k_2\), and \([W(0)]\) and \([X(0)]\) are the initial concentrations of the analyte and the receptor, respectively.

B. A Biochemical Genetic Cascade System

Includes a set of linear biochemical reactions from the first-order rates which every stage depends only on the previous one with differential amplification rates \( a_i \) (1/min) and decay rates \( b_i \) (1/min)

\[ \frac{d[Y_i]}{dt} = a_i [Y_{i-1}] - b_i [Y_i] \]  

(3)

\(i = 1 \sim n\), and \(n\) is the length of the cascade.

C. Gene Expression

The transcription process of the mRNA (\(R\)) and the translation process of the reporter enzyme (\(ET\)) are described by a set of linear reactions

\[ \frac{d[R]}{dt} = a_n [Y_{n-1}] - b_n [R] \]  

\[ \frac{d[ET]}{dt} = c_1 [R] - c_2 [ET] \]  

(4)

where \(a_n\) and \(c_1\) represent the transcription and translation rates, respectively, and \(b_n\) and \(c_2\) represent the decay rates of mRNA and enzyme, respectively. Equation (4) can be solved by numerical method, however, for simplicity, the solution we used the fact that the synthesized proteins and enzymes are usually considered to be stable compared to mRNA molecules and other chemical species \(b_i \gg c_2\) [14] which yields

\[ [ET] = \frac{k_3 [W(0)][X(0)]}{k} c_1 \left( \frac{n}{c_2} \right) \left( \frac{1 - \exp(-c_2t)}{c_2} + \frac{\exp(-c_2t) - \exp(-kt)}{c_2 - k} \right) \]  

(5)

With initial conditions \([ET(0)] = 0\), \([Y_2(0)] = 0\). Here, we discuss two cases, the first one when \(k \approx c_2\) and the second case when \(k \gg c_2\). In the both cases; an approximation to the reporter enzyme concentration near \(t_0(\sigma^{-1} < t_0 < c_2^{-1})\) is given by

\[ [ET] = \frac{k_3 [W(0)][X(0)]}{2} c_1 \left( \frac{n}{c_2} \right) \cdot t^2 \quad k \approx c_2 \]  

(6)

\[ [ET] = \frac{k_3 [W(0)][X(0)]}{k} c_1 \left( \frac{n}{c_2} \right) \cdot t \quad k \gg c_2 \]  

(7)

Based on the assumption that the reporter enzyme is stable with a long halftime compared to mRNA molecules and other chemical species, we obtain that the reporter enzyme concentration is proportionally to the analyte concentration and can be expressed as

\[ [ET(t)] = \mu_m W(0)X(0) \cdot t^m \]  

(8)

\(m = 1, 2\) is the time power and \(\mu_m\) is a rate constant which depends on the ratio between \(k\) and \(c_2\). Equation (8) is constituted with the assumption which was used in [6] and [7] and fits nicely to the data.

D. Bioreporter Enzymatic Reaction

The light generation kinetics of the bioluminescence process depends on the enzyme – substrate interaction which is described by the Michaelis–Menten model [15] with binding rate \(h_1\) (1/M·min), dissociation rate \(h_{-1}\) (1/min) and kinetics rate \(h_2\) (1/min). The generating reporter enzyme concentration \([ET] \) is equal to the free enzyme concentration \([E]\) and to the complex concentration \([SE]\) \([ET] = [E] + [SE]\). The Michaelis–Menten constant is defined as \(h_m = (h_2 + h_{-1})/h_1\). In order to simplify the system, we will use the quasi-steady-state approximation (QSSA), \(d[SE]/dt \approx 0\), the complex \(SE\) will arrive to steady
state in the beginning of the measurement or the concentration of the complex SE changes much more slowly than those of the product and substrate. In the QSSA, the rates of formation and breakdown of the complex SE are equal. In our model, the time constant of the bioluminescence enzymatic reaction [16] is much shorter than the time constant of the reporter enzyme production rate (the SOS response is very slow process [17], [18]). Therefore, in our case, in every particular time scale the QSSA for enzymatic reaction can be considered.

We consider two practical cases: 1) When excess substrate is used \( [S(t)] \gg h_m \), which yields \( [SE] \approx [E_T] \) and \( P/dt \approx h_2[E_T] \), such as, in whole-cell electrochemical biosensor [7]. 2) There is no excess substrate, such as in the case of the whole-cell bioluminescent biosensor [6], [10]. In this case, we claim that \( [S(t)] \ll h_m \) (see Lineweaver–Burk plot in the Appendix), which yields \( [E] \approx [E_T] \) and

\[
\frac{d[P]}{dt} = \frac{d[S]}{dt} = -\frac{h_2}{h_m}[E_T][S],
\]

(9)

The light generation rate is equal to \( I(t) = \eta \cdot V \cdot N_A \cdot d[P]/dt \) [2], when \( \eta \) is the quantum yield of the bioluminescence process [19], \( V \) is the reaction chamber volume of single bacteria and \( N_A \) is Avogadro’s number. Substituting the solution of (9) into the light generation rate term yields

\[
I = N_0 \mu_{eff} X(0) \mu^m \exp \left( -\frac{\mu_{eff} X(0)}{m+1} \cdot \mu^{m+1} \right)
\]

(10)

where \( N_0 = \eta \cdot V \cdot N_A \cdot [S_0]_0 \), \( [S_0]_0 \) is the initial substrate concentration \( ([S(t = 0)] = [S_0]) \). \( \mu_{eff} = \mu_t W(0) h_2/h_m \).

The model of the whole-cell biosensor is presented in expression (10) and characterized by three parameters: 1) \( \mu_{eff} \), the biosensor effective rate constant which simply describes the reaction \( X(0) \), \( P \) (\( r(t) = \mu_{eff} S(0) \mu^m \), \( d[P]/dt = r(t) X(0) \)) ; 2) \( N_0 \) is the total number of the emitted photons which is related to initial condition of the biosensor \( N_0 = \lim_{t \to -\infty} N(t) \); and 3) \( m = 1.2 \), the biosensor reaction order which depends on the stability of the biochemical reactions.

### III. EXPERIMENTAL SETUP AND METHODS

#### A. Biological Material

In this work, we measure and characterize an assay which is used as a biosensor detecting water toxicity [6]. We used three different promoters \( recA, micF, \) and \( katG \). For every promoter we used different toxin (Table I). The reporter strains (RFM/2TTS – \( recA/micF/KatG::luxCDABE \) fusion) were kept as colonies at \( 4^\circ \)C or in a 50% glycerol suspension at \( -80^\circ \)C. Just prior to the experiment, the bacteria were grown overnight with shaking at \( 37^\circ \)C in Luria Bertani (LB) broth containing \( 100 \) mg/liter of ampicillin. Overnight-grown cultures were diluted 200-fold in fresh LB broth (without ampicillin) and grown with shaking at \( 30^\circ \)C to the early exponential growth phase (optical density of 0.12 at 600 nm). The chambers were filled by solution containing LB medium with bacteria concentration of \( 5 \times 10^{11} \) bacteria/L and adding toxin to the solution. For each promoter, we use different toxin, as shown in Table I.

#### B. Calibration of the Absolute Sensitivity of the Photodetector

It is important to understand the type of the measurement to be made: photometric, radiometric, spectrum-radiometric. In this work, we have measured the power (\( \rho W \)) and the total photon flux (\( \#ph/s \)) of the bioluminescent solution. In radiometric measurements, it is preferred to use a detector with wide flat response. The conventional bioluminescent detection for low light level is based on a photon counting detector, due to its low dark current. The readout signal in \( counts/s \) units can be expressed as: \( C = \int g(\lambda) d\lambda \), where \( g(\lambda) \) is the bioluminescent spectrum \( [counts/s \cdot \text{nm}] \). The power of the radiant light is calculated, respectively, to the absolute sensitivity of the photon counting detector \( S_p(\lambda) [W^{-1} \cdot s^{-1}] \): \( \phi = \int g(\lambda)/S_p(\lambda) d\lambda \), and for a detector with wide flat response \( S_p(\lambda) = S_p \), the power in \( watt \) units is simply calculated by

\[
\phi = \frac{1}{S} \int g(\lambda) d\lambda = \frac{C}{S_p}.
\]

(11)

We assume that most of the emitted photons of the bioluminescent solution are narrowly centered at wavelength \( \lambda_0 = 495 \) nm [9], and therefore, the calculation of the number of photons emitted is

\[
\text{number of photons} = \int g(\lambda) d\lambda = \frac{C}{S_p}.
\]
the emitted photons is by dividing the power (11) by the energy of the photon around $\lambda_0 = 495$ nm ($N = \phi \cdot \lambda_0 / h \cdot c$, $h$ is plank constant $6.62 \times 10^{-34}$ J · s and $c$ is the speed-of-light $3 \times 10^{10}$ cm/s). We used a photon counting detector based on a photomultiplier tube (PMT), Hamamatsu model 7155 with absolute sensitivity $S_p = 2.2 \times 10^2$ pW$^{-1}$sr$^{-1}$ (one counts will be equal to 11 photons near wave length 495 nm).

C. Estimation the Total Flux of the Bioluminescent Solution and the Geometrical Light-Collection Efficiency

Since the light emission of the bioluminescent solution occurs practically isotropically, only a fraction of the light will reach the detector and determines the geometrical light-collection efficiency $\eta_g$ of the sensor. The geometrical light-collection efficiency is defined as the ratio of the number of photons reaching the detector ($N_{\phi}$) divided by the number of the photons emitted by the sample ($N$). The collection efficiency depends on the geometry and the wall coating material of the chamber and on the optical system between the chamber and the photodetector. Quantitative evaluation of the collection efficiency by computer simulation or numerical calculation is possible [20], however, to get accurate results detailed information about the chamber geometry and bioluminescent solution are required. In this work, we estimate the collection efficiency via measurement using an original method, which do not require any external standard light source (for calibrating the tested bioluminescent solution) and allow a direct determination of the total photon flux of the bioluminescent solution. The method is based on a new design of double integrating sphere system [21], which is illustrated in Fig. 2(a). In our design, we required that the two spheres are symmetric (have the same radius and reflectance) with a surface area larger than the cut cap area between the spheres. The measured flux of the light source (bioluminescent solution) is equal to

$$\phi_0 = \frac{\phi_{D1}^2}{\phi_{D2}}$$

(12)

where $\phi_{D1}$ and $\phi_{D2}$ are the measured detector flux for the first and the second sphere in the system, respectively. The relation between the flux of the bioluminescent solution and the number of the photons emitted by the sample ($N$) is described in the previous section. We also compared the results of the double integrating sphere system method to another method which is based on reference double-plate cell within isotropic light source [22], [23] and is illustrated in Fig. 2(b) and (c). The collection efficiency of the reference double-plate cell is expressed as [22]

$$\eta_b = 1 - \sqrt{1 - \left(\frac{NA}{n_i}\right)^2}$$

(13)

where $NA$ is the external numerical aperture ($NA = \sin\theta$), and $n_i$ is the refractive index of the bioluminescent solution. In this method, we can assume that the collection efficiency has a weak dependency on the wavelength.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

In this section, we present the experimental characterization results of the whole-cell bioluminescent biosensor by measuring $\mu_{eff}$, $N_0$, and $m = 1$ or 2. Fig. 3(a) shows the measured optical signal of whole-cell bioluminescent biosensor for three different concentrations of analyte toxin (Nalidixic Acid) (5 ppm, 7.5 ppm, 10 ppm) by using photon counting detector. We reorganize (10) as

$$\ln \left(\frac{I_1}{I_2}\right) = \ln \left(\frac{X(0)_1}{X(0)_2}\right) - \frac{\mu_{eff}}{m + 1} \cdot \frac{m + 1}{m + 1} (X(0)_1 - X(0)_2)$$

(14)

where $X(0)_1$ and $X(0)_2$ are different toxin concentrations, yielding the measured signals $I_1$ and $I_2$, respectively. Fig. 3(b) describes (14), when the $x$ axis is $m + 1$ and the $y$ axis is $\ln(I_1/I_2)$. Experimentally, we found that for $m = 2$, the plot of Fig. 2(b) is linear. By calculation, the slope ($\alpha$) of the linear plot of Fig. 3(b), one can estimate the biosensor effective rate constant

$$\mu_{eff} = \frac{3 \cdot \alpha}{(X(0)_1 - X(0)_2)}.$$  

(15)

For $X(0)_1 > X(0)_2$, We performed the measurements of signals $I_1$ and $I_2$ in the same time using the same conditions (two similar photon counting devices and two similar chambers). The
The collection efficiency of the reference double-plate cell within isotropic light source method is equal to 0.262% [22]. The experimental results for recA promoter using the reference double-plate cell within isotropic light source method is presented in Fig. 4(a). The relation between the signal and the toxin concentration, as described in (16). The slope of the linear plot is a function of the time and is presented in Fig. 4(b). By calculation, the slope (of the linear plot with $y$ axis will give the ratio between the toxin concentrations $X(0)_1/X(0)_2$). Note that $\mu_{\text{eff}}$ is independent on the optical geometry of the measuring chamber.

The light generation rate (10) near $t_0(\mu_{\text{eff}} \cdot X(0)^{d+1} \ll 1)$ can be approximated as

$$I = \eta_l^2 N_0 \mu_{\text{eff}} X(0)^{d+1}$$

where $\eta_l$ is the geometrical light-collection efficiency of the system. The relation between the signal and the toxin concentrations for recA promoter using the reference double-plate cell within isotropic light source method is presented in Fig. 4(a). The experimental results show that the signal has a linear dependency on the toxin concentration, as described in (16). The slope of the linear plot is a function of the time and is presented in Fig. 4(b). By calculation, the slope (of the linear plot of Fig. 4(b), one can estimate the total number of the emitted photons $N_0 = \eta \cdot V \cdot N_A \cdot S_0$

$$\beta(t) \equiv \frac{\Delta I}{\Delta X(0)} = \eta_l \mu_{\text{eff}} N_0 \cdot t^2$$

$$N_0 = \frac{1}{\eta_l \mu_{\text{eff}}} \cdot \frac{\Delta \beta}{\Delta (E_0^2)}.$$ (16)

The collection efficiency of the reference double-plate cell within isotropic light source method is equal to 0.262% [22] and of the double integrating sphere system method is equal to 0.1% [21].

The toxin concentration is given in “parts per million-ppm” units which is equivalent to mg/L. The conversion to molar units is given by 1 ppm/1000 $\cdot M_w$, where $M_w$ is the molecular weight (in g/mol). Table I summarized all the results for three different promoters (recA, micF and katG). The experimental results for katG and micF promoters are presented in Fig. 6(a) and (b) and in the Appendix, respectively. We normalized the total number of the emitted photons by dividing it on the photodetector area ($r = 2 \text{ mm}$, $A = 0.125 \text{ cm}^2$). The simulation results based on (10)
with \( n = 2 \), \( \mu_{\text{eff}} = 9.26 \times 10^{-8} \text{ ppm}^{-1} \text{min}^{-3} \) and \( N_0 = 4 \times 10^{14} \text{ ph/cm}^2 \) (Table 1) for toxin concentrations (5 ppm, 7.5 ppm, 10 ppm) are presented in Fig. 3(a). The dashed black lines present the simulation results. We can see a good agreement between the simulation and the experimental results (error 2.5%). If we compare between the different promoters with toxin concentration of 1 M, we obtain that recA will give the maximum signal and micF have the longest half time.

We can also estimate physiological parameters of the microbial cell sensors, such as, the initial substrate concentration \( S(0) \). In our case, the quantum yield \( \eta = 0.3 \) [24], thus we obtain that the initial concentration is equal to 80–4000 \( \mu \text{M} \) depends on the promoter kind and the bacteria optical density. When the substrate concentration is larger than Michaelis–Menten constant, the \( N_0/\eta \cdot V \cdot N_A \) will give the Michaelis–Menten constant. We found experimentally that \( m = 2 \), however, according to [5], for whole-cell electrochemical biosensor, it was found that \( m = 1 \), which can also be explained by our model (7).

### V. Conclusion

In this work, we present an analytical model of a whole-cell bioluminescent biosensor (bacteria based). The model takes into consideration the biophysical functions of the bacteria and the physical properties of the microbes–electronic circuits interface. We showed that typically, the signal has a linear or power law dependency on the time, which is determined by the ratio between the half time of the reporter enzyme and the dissociation rate of the analyte-receptor binding reaction. The model can be fitted to the measured signal and demonstrates the relation between the analyte (input) and the output signal. Furthermore, the model is characterized by three measurable parameters; the biosensor effective rate constant, the total number of the emitted photons and the biosensor reaction order. We presented experimental methods to estimate the parameters of the model. The model is tested and verified for various promoters (recA, KatG, and micF). The proposed model can be useful in designing bioelectronic circuits, as well as in validation and testing. For future work, we will consider more biophysical functions in the model such as, the growth of the bacteria during the bioluminescence process and dependency of the physiological coefficients and rate constants on the time. We will also model the kinetics of the bioluminescent signal after a few hours and we will study the decay of the signal [5].

### Appendix

#### Lineweaver–Burk Plot

Undoubtedly the most popular and familiar, manual technique for calculating kinetic parameters is that known as the Lineweaver–Burk plot [25]. In the case that the substrate \( [S_{\text{ext}}] \) will externally be add to the bioluminescent solution, we will express the product rate as:

\[
\frac{d[P]}{dt} = \frac{k_2^*[E_{T0}]}{k_m^* + ([S_{\text{ext}}] + [S_0])},
\]

(19)

where \( [E_{T0}] \) is the initial total enzyme concentration (without adding toxin to the solution), and \( [S_0] \) is the (initial) internal substrate concentration inside the cells. We worked when the promoter is in “off” (without adding toxin to the solution) and there is no generation of the reporter enzyme. Only a part of the external substrate will diffuse inside the cells and will be used in the reporter enzyme reaction. For simplifying the analysis, we assume that this relation can be expressed as a linear relation:

\[\frac{[S_{\text{ext}}]}{[S_0]} = \alpha \frac{[S_{\text{ext}}]}{[S_0]} \]

Substituting the previous relation into (19), then the measured signal can be expressed as

\[ I = \frac{\eta \cdot V \cdot N_A \cdot k_2^*[E_{T0}]}{\frac{k_m^*}{\alpha} + \left( \frac{[S_{\text{ext}}]}{[S_0]} + \frac{[S_0]}{\alpha} \right)} \]

(20)

Reorganization (20) in form of Lineweaver–Burk plot, we obtain that

\[ \left( \frac{1}{I(t)} \right)_0 = \frac{1}{\frac{\eta \cdot V \cdot N_A \cdot k_2^*[E_{T0}]}{\frac{k_m^*}{\alpha} + \left( \frac{[S_{\text{ext}}]}{[S_0]} + \frac{[S_0]}{\alpha} \right)}} \]

(21)

where \( k_m^* = \frac{k_m}{\alpha} \) and \( S_0^* = \frac{S_0}{\alpha} \). Fig. 5(a) shows the signal kinetics as a function of the external substrate concentration. The figure shows a strong dependency on the substrate concentration. Only by estimating the correct (internal) initial substrate concentration \( S_0^* \), one will obtain the linear form of Lineweaver–Burk plot. Fig. 5(b) shows the Lineweaver–Burk plot when \( S_0^* = 2.5 \text{ mM} \). The measurements were taken after 3 min. The plot gives an intercept of Michaelis-Menten constant \( (k_m^*) \) on the x axis \( (k_m^* = 20 \text{ mM}) \). We are interested in the relation \( S_0/k_m = S_0^*/k_m^* = 0.125 \) which is matching our assumption.
katG and micF Results: Fig. 6(a) and (b) presents the experimental and the simulation results of katG promoter with three different concentrations of Hydrogen peroxide analyte toxin (15 ppm, 11 ppm, 7.5 ppm) and micF promoter with three different concentrations of Methyl viologen analyte toxin (100 ppm, 75 ppm, 50 ppm), respectively. The model is fitted well to the experimental results for both promoters.

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