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# **Optimization of Compartment Models by Using Metaheuristic Approaches**

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#### **Motivation**

# Problem Parameter estimation of compartment models

#### Goal

# Parameter estimation without linearization of the response function

# Method

#### **Metaheuristic methods - Genetic Algorithm (GA)**

## **Compartment Model**

Modeling of dynamical systems plays a very important role in applied science.

Compartment models are among the most important tools used for analyzing dynamical systems.

Compartment models are often used to describe transport of material in biological systems. These are widely used in many fields of science and engineering, e.g. biochemistry, physiology, radioactive isotopes, and pharmacokinetics.

# **Compartment Model**

 A pharmacokinetic model explains how the concentration of a drug in blood plasma declines over time.
 This model can be shown as a compartmental diagram which helps clarify what is going on.



Figure 1. A compartmental diagram

#### **Polyexponential Form**

Under certain assumptions, integration of differential equation leads to be polyexponential form as



The Eq.(1) express the response as a polyexponential function of time t.

#### **Stripping (Back-projection) Method**

In order to obtain the estimates of coefficients and exponents, an operation called "stripping or back projection" is used for pharmacokinetic studies.

For stripping method, straight lines are drawn through sets of data points "by sight", and these lines are extrapolated back to the ordinate scale on semilogarithmic graph.

## **Stripping (Back-projection) Method**



Figure 2.a The original graph for C-t



Figure 2.b The semilogarithmic graph for C-t

The major problem with performing the method this way is that each person who applies the method to the same data set will usually obtain a different answer than the next person.

#### **Polyexponential Regression Model**

The statistical problems in the present context are basically those of parameter estimation for polyexponential regression model.



# **Objective Function**

$$\phi(\boldsymbol{\theta}) = \sum_{i=1}^{n} \left(Y_{i} - \hat{Y}_{i}\right)^{2} = \sum_{i=1}^{n} \varepsilon_{i}^{2}$$

$$\left[\alpha_{1} \ \alpha_{2} \dots \alpha_{k}; \lambda_{1} \ \lambda_{2} \dots \lambda_{k}\right]$$

$$\left[\alpha_{1} \ \alpha_{2} \dots \alpha_{k}; \lambda_{1} \ \lambda_{2} \dots \lambda_{k}\right]$$

$$(3)$$

It is clear that the objective function has nonlinearity in parameters.

In this case derivative free methods should be more proper rather than derivative based methods for Eq.(3).

#### **Metaheuristic Methods**

Metaheuristics are the general class of stochastic optimization methods which employ some degree of randomness to find optimal solutions for hard problems.

Genetic Algorithm (GA) is a metaheuristic method based on natural selection and genetic mechanism.

The basic principle of it is the Darwinion "survival of the fittest" approach.

# **Genetic Algorithm**



- GAs are intelligent exploitation of random search used in many NP hard, complex, and nonlinear problems.
- GAs search from a population points, not a single point.
- GAs use objective function information, not derivatives.
- GAs use probabilistic transition rules, not deterministic rules.
- GAs can produce the solution without requiring initial solutions by searching from many search points simultaneously.

# How does the GA work for parameter estimation?



# **Application: (One-compartment model)**



Figure 3. Plasma concentrations for one-compartment model

$$C_p = \alpha_1 e^{-\lambda_1 t} + \alpha_2 e^{-\lambda_2 t}$$

## Data Set:

Observed plasma concentrations for 500 mg erythromycin

*t*(*hr*): 0.75, 1.5, 3, 4.5, 6, 8, 10, 12, 14

 $C_p(mg/ml)$ : 0.33, 1.3, 1.44, 1.14, 0.61, 0.27, 0.13, 0.062, 0.026

Estimate the pharmacokinetic parameters?



Figure 4. The original graph for  $C_{p}$ -t

#### Model:

$$Y_i = \alpha_1 e^{-\lambda_1 t_i} + \alpha_2 e^{-\lambda_2 t_i} + \varepsilon_i, \quad i = 1, 2, ..., 9$$

**Objective Function:** 

$$\phi(\mathbf{\theta}) = \sum_{i=1}^{9} \left[ Y_i - \left(\alpha_1 e^{-\lambda_1 t_i} + \alpha_2 e^{-\lambda_2 t_i}\right) \right]^2$$

## Parameters for GA:

$$n_{pop} = 100; n_{gen} = 200$$
  
 $Pr_{cr} = 0.90; Pr_{mut} = 0.01; m_{cr} = 20; m_{mut} = 20$   
Roulette Wheel Selection  
Single Point Crossover  
Bit flip mutation

### Interval of Parameters:

	$\alpha_1$	$\lambda_1$	$\alpha_{2}$	$\lambda_2$
<u>Lower bound:</u>	5	0	-10	0
<u>Upper bound:</u>	8	1	-8	1

#### Parameter Estimates:

	$\alpha_1$	$\lambda_1$	$\alpha_{2}$	$\lambda_2$	MSE
<u>Stripping</u>	6.51	0.392	-9.14	0.926	0.0315
GA	6.8456	0.3708	-8.9305	0.8206	0.0195
	(0.6994)	(0.0165)	(0.6239)	(0.0892)	

#### **Application: (Two-compartment model)**



Figure 5. Plasma concentrations for two-compartment model

$$C_{p} = \alpha_{1}e^{-\lambda_{1}t} + \alpha_{2}e^{-\lambda_{2}t}$$

$$k_{21} = \frac{\alpha_{1}\lambda_{2} + \alpha_{2}\lambda_{1}}{\alpha_{1} + \alpha_{2}}$$

$$k_{el} = \frac{\lambda_{1}\lambda_{2}}{k_{21}}$$

$$k_{12} = \lambda_{1} + \lambda_{2} - k_{21} - k_{el}$$

#### Data Set:

#### Observed plasma concentrations for 75 mg I.V.

t(hr):	0, 0.25, 0.50, 0.75, 1, 2, 3, 4, 6, 8, 12, 16, 24				
$C_{n}(mg / ml)$ :	16.4, 14.2, 12.53, 11.17, 10.09, 7.56, 6.44, 5.85,				
p < 0	5.16, 4.65, 3.18, 3.12, 2.09				

Estimate the pharmacokinetic parameters?



Figure 6. The original graph for  $C_p$ -t

#### Model:

$$Y_i = \alpha_1 e^{-\lambda_1 t_i} + \alpha_2 e^{-\lambda_2 t_i} + \varepsilon_i, \quad i = 1, 2, ..., 13$$

**Objective Function:** 

$$\phi(\mathbf{\theta}) = \sum_{i=1}^{13} \left[ Y_i - \left(\alpha_1 e^{-\lambda_1 t_i} + \alpha_2 e^{-\lambda_2 t_i}\right) \right]^2$$

## **Interval of Parameters:**

	$\alpha_{_1}$	$\lambda_1$	$\alpha_{_2}$	$\lambda_2$
Lower bound:	9	0	6.5	0
<u>Upper bound:</u>	10	1.5	7.5	1

#### Parameter Estimates:

	$\alpha_1$	$\lambda_1$	$\alpha_{2}$	$\lambda_2$	<i>k</i> <sub>12</sub>	k <sub>21</sub>	k <sub>el</sub>	MSE
Stripping	9.59	1.06	7.05	0.0509	0.5197	0.4784	0.1128	0.5066
<u>GA</u>	9.4381	0.9876	6.946	0.053	0.4749	0.4492	0.1165	0.3102
	(0.2216)	(0.0442)	(0.2449)	(0.0035)				

# **Conclusions**

- ✓ Compartment models are considered as nonlinear response problems.
- ✓ Basic definitions about them, related to the pharmacokinetic studies, are given.
- ✓ The compartment models are represented as polyexponential regression models in the statistical context.
- ✓ Stripping (back-projection) method, a well used method in the literature for parameter estimation, is explained.
- ✓ Basic definitions and working principle about GA are given.
- ✓ The GA is applied one and two compartment models for parameter estimation.
- ✓ It is seen from the results that GA gives smaller MSE value than stripping method.

#### **References**

[1] Blomhoj, M., Kjeldsen, T.H., Ottesen, J., (2014), Compartment Models, 1-47.

[2] Deb, K., (2004), Multi-Objective Optimization Using Evolutionary Algorithms, John Wiley and Sons, New York.

**[3]** Dreo, J., Petrowski, A., Siarry, P., Taillard, E., (2006), Metaheuristics for Hard Optimization, Springer-Verlag Berlin, Heidelberg.

**[4]** Lai, T.L., (1985), Regression Analysis of Compartmental Models, Journal of Research of the National Bureau of Standards, 90 (6), 525-530.

**[5]** Motulsky, H., Christopoulas, A., (2003), Fitting Models to Biological Data Using Linear and Nonlinear Regression, GrandPad Software.

[6] Türkşen, Ö., (2011), Fuzzy and Heuristic Approach to the Solution of Multi-Response Surface Problems, Ph.D. thesis, Ankara University.

[7] Wagner, J.G., (1975), Fundamentals of Clinical Pharmacokinetics, Drug Intelligence Publications, Hamilton.