

A GENETIC ALGORITHM TO CALIBRATE SYSTEMS: A CASE IN PSYCHOLOGY

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Abstract

The present study attempts to deal with personality dynamics measured by the *General Factor of Personality (GFP)*. The *response model*, an integro-differential equation, is capable to reproduce the personality dynamics as a consequence of a determined stimulus. An application case is presented. The model is calibrated with a Genetic Algorithm (GA) ad-hoc designed and herein described that reveals to be very efficient to find the optimal set of values for the 8 model parameters.

Keywords: *general factor of personality; response model; integro-differential equation; genetic algorithm; calibration; system.*

1. Introduction

In the application case presented, methylphenidate is the drug being used. It is a powerful psycho-stimulant. This psycho-stimulation can be measured by the *General Factor of Personality (GFP)*, as a universal observable of personality. The five adjectives scale to measure the *GFP* described by Amigó, Micó & Caselles, (2009a) has been used. This scale is based on the *General Factor of Personality Questionnaire* (Amigó, Caselles & Micó, 2010), which has been constructed specifically to assess *GFP* in the context of the *Unique Trait Personality Theory (UTPT)* (Amigó, 2005; Amigó et al., 2010). The *UTPT* claims for a unique trait, as synonymous of single trait, substituted later by the equivalent concept of *GFP*, to represent the overall human personality. The *GFP* is the psychological expression of the activation level of the organism stress system. In fact, in the context of the *UTPT*, *GFP* is called also *extraversion* in a wider sense than the one used in behavioral science, i.e., in the sense of activation level of the organism stress system.

The *response model* is an integro-differential equation that has been widely assessed in the context of different experimental designs. It can reproduce the acute effect of a stimulant drug (Amigó, Caselles & Micó 2008; Caselles, Micó & Amigó, 2011; Micó, Amigó & Caselles, 2012; Micó, Caselles, Amigó, Cotolí & Sanz, 2013; Micó, Amigó & Caselles, 2014). The model reproduces the dynamical pattern forecasted by Solomon & Corbit (1974) and Grossberg (2000), by using the hedonic scale, and by Amigó (2005) for the *GFP*, i.e., a typical inverted-U.

The performed calibration of the model is based on a genetic algorithm. Genetic algorithms (GAs) are Evolutionary Algorithms (EAs) (they adapt their parameters according to previous results) that try to imitate Natural Selection inside a population through parent selection, recombination, mutation and migration. About details on GAs and its use in systems calibration, see for instance: Guzmán-Cruz et al., (2009) and Muraro & Dilao (2013). Nevertheless there are a lot of possible options for their definition.

2. The response model

The kinetic part of the response model provides the evolution of the stimulus amount $s(t)$, present in plasma after intake by the individual. It is given by the time function:

$$s(t) = \begin{cases} \frac{\alpha \cdot M}{\beta - \alpha} (\exp(-\alpha \cdot t) - \exp(-\beta \cdot t)) : \alpha \neq \beta \\ \alpha \cdot M \cdot t \cdot \exp(-\alpha \cdot t) : \alpha = \beta \end{cases} \quad (1)$$

Equation (1) is the solution of two coupled differential equations (Micó et al., 2014), which assumes that no drug/stimulus is present in the organism before consumption. In (1) M is the initial amount of a drug single dose, α is the stimulus assimilation rate and β is the stimulus elimination rate. The dynamics of the *GFP* is given by the following integro-differential equation (Micó et al., 2014):

$$\left. \begin{aligned} \frac{dy(t)}{dt} &= a(b - y(t)) + \frac{p}{b} s(t) - b \cdot q \cdot \int_0^t e^{-\frac{x-t}{\tau}} \cdot s(x) \cdot y(x) dx \\ y(0) &= y_0 \end{aligned} \right\} \quad (2)$$

In (2), $s(t)$ represents the stimulus; $y(t)$ represents the *GFP* dynamics; and b and y_0 are respectively its tonic level and its initial value. Its dynamics is a balance of three terms, which provide the time derivative of the *GFP*: the *homeostatic control* ($a(b - y(t))$), i.e., the cause of the fast recovering of the tonic level b , the *excitation effect* ($p \cdot s(t)/b$), which tends to increase the *GFP*, and the *inhibitor effect* ($\int_0^t e^{-\frac{x-t}{\tau}} \cdot s(x) \cdot y(x) dx$), which tends to decrease the *GFP* and is the cause of a continuously delayed recovering, with the weight $e^{-\frac{x-t}{\tau}}$. Parameters a , p , q and τ are named respectively the *homeostatic control power*, the *excitation effect power*, the *inhibitor effect power* and the *inhibitor effect delay*. All the parameters of the model depend on the individual personality or individual biology and on the type of stimulus.

3. The genetic algorithm used for the response model calibration

The program we use for calibration has been ad hoc designed for the previously described model but it can be adapted easily for systems with the following characteristics:

- (1) Real data are deterministic. In the case of the *response model*, real *GFP* is measured by the responses of an individual to a questionnaire every some minutes. And model parameters are specific of the individual.
- (2) The system to be calibrated is deterministic.
- (3) All parameters have a continuous range of possible or plausible values from a maximum to a minimum value.
- (4) A single objective variable (function) must be considered, but it may be designed as a weighted combination of several other ones.
- (5) Parameter space (search space) is a multidimensional compact space.
- (6) In order to assure the global character of the found optimum three strategies are considered:
 - a. A random sample may be analyzed, from the entire search space or from specific zones, in order to identify starting points.
 - b. Random migrants with reproduction capacity are introduced inside the current population in every generation.
 - c. Several iterations are performed using the previous optimum as a new starting point, up to no improvement is found or the top number of iterations is reached.

3.1. The needed data

The *response mode* has seven parameters: α , β , a , b , p , q , τ and M (M may also be adjusted like the other parameters), which meaning has been previously explained. A vector of nine components containing a value for each parameter plus the corresponding *GFP* (y) may be considered as an individual of a population of possible characterizations of the system. The starting values of the parameters (given by previous knowledge), their maximum values, their minimum values, their search window width (% of their initial value), and their search step width (% of their initial value) have to be introduced at the beginning of the search process. Other needed data are the number of experimental values, their time step, and their values. The integration method (Euler or Runge-Kutta-4) and the integration step size have to be also specified. The function to be optimized may be the mean squared deviation (s^2), the determination coefficient (R^2) or the relative mean deviation.

The *GA* may be optionally used, and in the case it is used the following options must be specified: number of individuals of the population, percentage of the population corresponding to reproducers (the best individuals), number of immigrants per generation, mutant genes per thousand in a new individual, number of generations inside a given iteration, and maximum number of iterations. In the case of not using the *GA* but only analyzing a sample, it may be exhaustive or uniformly random. This sampling process also admits iterations.

3.2 The GA pseudo-code

The proposed *GA* intends to be the simplest possible one in order to be as fast as possible without restricting the possibility to find a global optimum. The following pseudo-code might be enough descriptive of the *GA*.

Introduce data and options

Define the initial population (vectors with random values for parameters and the objective function value)

For $i=1$ to "number of iterations"

For $j=1$ to "number of generations"

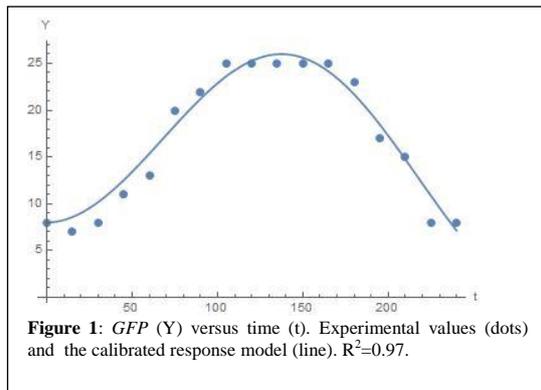
Arrange population from lower to higher the objective function

Retain the best individuals and eliminate the remaining ones

Incorporate some immigrants (randomly defined inside parameters' ranges)
 "Complete the population by reproduction (with mutation) of the present individuals, i.e.:"
 For $k = \text{"number of reproducers"} + 1$ to "population size", "create a new individual, i.e.:"
 Choose randomly the "father" and the "mother" of the new individual
 For each gen (parameter) choose randomly whether it comes from father or mother
 For each gen (parameter) choose randomly whether it is newly randomly defined or not
 Next new individual
 Next generation
 If "previous optimum is not improved" Then Exit-Iterations-Loop Else Continue
 Use the optimum individual as new starting point
 Next iteration
 Calculate residuals by comparing the found optimum with the experimental values
 Test residuals for Normality and zero-mean
 If "yes" Then "calculate confidence intervals to define the optimal fitting evolution band"
 Write results

4. The response model calibration

The studied application case consists in one subject that consumed 20 mg of methylphenidate. The Five Adjectives scale questionnaire (adventurous, daring, enthusiastic, merry and bored) was filled out before consumption and after consumption every 15 minutes during 4 hours. The interval of the *GFP* measures is $y \in [0,25]$. The calibration result of the response model for the *GFP* dynamics is provided in Figure 1.



5. Conclusions

Figure 1 shows the calibration result of the response model for the *GFP* response as a consequence of 20 mg of methylphenidate obtained with the proposed *GA*. The obtained determination coefficient value R^2 supports model validation as in other studies from literature (see Section 1). The herein proposed *GA* presented a great efficiency.

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