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Research article

A quantitative approach for mathematical model of doping in high performance sport

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Abstract: Doping or administration of substances for purpose of improving the performances in various sport has a long history, even in the modern era to most common association of doping is connected to professional cycling. The usage of doping substances has become a major public health issue. Also, some abuse of doping substance was a major cause of death in some cases. As results of effort in fighting against doping, World Anti-Doping Agency (WADA) coordinated the implementation of the athlete hematological passport, or more commonly athlete biological passport (ABP). The decision of doped or not doped based on biological markers is made using Bayesian inference. But the code of implementation and the code of software used in decisions is not available to the public, and as sequels there are also some approaches in research, as methods based on psychological questionaries. In this case, the statistical analysis using structural equation models offer a valuable tool for management of antidoping policies in order to reduce this phenomenon. **Material and method.** In this paper, a novel method is novel model for quantitative analysis of doping is proposed. The model doesn't use the biological markers but the effect of this as declared doping persons in a quantitative analysis over a lot of high performance athletes. The model is based on nonlinear equations as result of compartmental model with quantitative time dependent evolution of them. **Results and discussions.** The model was implemented in MATLAB and numerical solutions were obtained using ODE (Ordinary Differential Equations) tool. The stability of model was analyzed using analogies with an epidemic SIRS compartmental model. The implementation uses a GUI (Graphical User Interface) that make the application user friendly. The fitting tools model is in stage of implementation and the parameter are finding out using a data collected and optimization tools (an objective function and genetic algorithms in order to prevent the phenomenon in a trapping minima). **Conclusions**. The result is very encouraging, the model fit 99.7% in preliminary set of data. The future development will include the fitting module and a set of results structured on various high performance sports.

Keywords: *doping in sport, compartmental models, anti-doping policy, modeling and simulation, data fitting*

1. Introduction

The usage of performance-enhancing substances (PES) in sport by athletes, that is the doping is a prohibited practice, but this tendence is global ([1]-[4]). In order to be a PE-SE, three basic criteria are taken into account: (1) the substance has the potential to increase the athlete's performance; (2) the substance is a potential risk for the athlete's health; and (3) the substance is against the ethics rules of the sport. The presence of forbidden substance in the body is identifiable by biomarkers, in an using standardized tests ([5]-[6]).

The World Anti-Doping Agency (WADA) is the leader of a globalnetwork of international and national organisations that attempt to reduce or eliminate doping in sport. Athlete Biological Passport (ABP) was proposed in 2000 as personalized monitoring of biomarkers of doping and hematological passport was validated empirically in 2003 [7].

One of the tools used to identify blood doping is Abnormal Blood Profile Score (ABPS) [8]. The original method was developed in Swiss Laboratory for Doping Analyses (LAD) in Lausanne [9], and actually combines 7 hematological markers (reticulocytes percent, hemoglobin level, haematocrit level, red blood cell count, mean corpuscular volume, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration) into a single score using Bayesian adaptive method. Even the code or software details for ABS used by WADA are not available, some suggestions are in literature, usually in paper published by the authors of software. Actually, the ABP has three modules (Doping Control Form - DCF information entered into ADAMS): Hematological Module (the module collect details about blood doping markers), Steroidal Module (the module collect details about steroid doping markers), and Endocrine Module (the module can detect several direct or indirect types of steroidal doping). The incorporation of new markers in the hematological system is a continuous challenge.

In [10], authors show a Bayesian network used to evaluate the evidence for an indirect marker used in ABS evaluation along with a GUI (Graphic User Interface) for automatic calculation of inferences. In this paper, the longitudinal approach is made along with heterogeneous factors as gender, ethnic origin, sport, instrument, age, altitude, as causality factors in order to evaluate the influence on result for a specific marker [10].

The behavioral sciences frameworks (social cognition models, threat (or fear) appeals, and instrumental and normative approaches) offers the possibility to construct sport drug control model (SCMD) ([11]-[12]). These types of models are empirical ones and the validation of result are made by real data. The calculus of weight are made by using the with inherent possible subjectivism of respondent due to method of questionnaire used in most of the cases. There number of papers in this area that take into account the contribution of self-regulatory efficacy team efficacy and moral disengagement [12], a framework for construction of one predictor of athletes' use of performance-enhancing drugs [13] or WADA's questionnaire package [14].

Structural equation modeling (SEM) is useful method than can be extended to modelling the Sport Drug Control Model(SCDM). WADA's questionnaire package was used in [14] using the following constructs: (1) morality; (2) legitimacy; (3) benefits appraisal; (4) threat appraisal; (5) personality traits; (6) beliefs about reference groups' endorsement of doping methods/substances; (7) use of legal supplements; (8) beliefs about the availability of PES and relevant authorities' control over trafficking of doping methods/substances; (9) beliefs about the affordability of doping methods/substances; (10) attitudes toward doping, (11) susceptibility to doping; and (12) self-reported use of banned PES or methods.

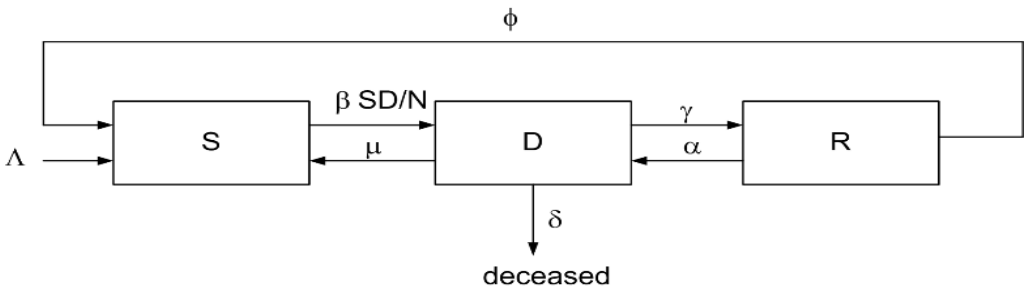

Fig. 1. The proposed SDRS model.

A simpler model that uses three constructs (athletes' attitudes, sport orientation and doping behavior) was proposed to model the relationship among these entities in [15]. A usually solution to deal with this approach is regression model that fit to experimental data.

2 Methods

In order to model the doping for a quantitative analysis, we propose to use a compartmental model inspired by SIRS epidemic model ([16]-[18]), an SDRS (S-Susceptible, S-Doped, R-Recovery) model.

These criteria, as WADA define them, are as follows[23]:

- athletes who are part of the national team in major sporting events or other priority sports at the national level (or who may be selected for these groups);
- performance history, performance patterns, and/or high performance without appropriate testing;
- reintegration into sports activity after a period of suspension;
- doping test history;
- withdrawal or absence from the planned competition;
- violations of previous anti-doping regulations, including abnormal biological parameters;
- moving or performing training in an isolated location;
- trusted information from a third party or secret information obtained or provided by other anti-doing agency;
- athletes who are serving a suspension period or those who are in the temporary suspension period due to a violation of anti-doping regulations;

As WADA International Standard for Testing and Investigation assumes, we were also taking into account the following criteria[23]:

- athletes who participate at major events but train by themselves
- public financed athletes
- high level athletes who train and live abroad
- international level athlete's toughener with the international federations
- repeated breaches of location information obligations;
- suspicious habits of transmitting location information;
- association with a third party with a history of doping involvement;
- injury;
- age/career stage (transition from junior to senior level);
- financial incentives for improved performance, such as cash prizes or sponsorship opportunities;

By grouping these criteria, three broad categories emerged. In this article, these categories have been adopted as query items: S-Susceptible, D-Doped, R-Recovery.

The compartmental model is presented in Fig. 1, where βSD/N is the "infectious" rate, that is the doping rate μ-the rate of sportive that occasionally tested a drug, γ-rate of athletes that are entered in a program of recovery from PES consume, α-the rate of athletes that fails in recovery program, ϕ-the rate of athletes that completed the recovery

and return to sport but they continue to take nutritional supplements, Λ-the influx of new athletes, and δ-the rate of deceased as result abuse of PES consume.
The system of ODEs (Ordinary Differential Equations) corresponding to compartmental model from Fig 1 are:

$$\frac{dS}{dt} = \Lambda - \beta\frac{SD}{N} + \phi R + \mu D.$$
$$\frac{dD}{dt} = \beta\frac{SD}{N} - (\mu + \gamma - \delta)D + \alpha R \quad (1)$$
$$\frac{dR}{dt} = \gamma D - (\alpha + \phi R)$$

In the equation (1), the population N=S+D+R is constant. The model can have new athletes or no flux of new athletes. In this last case, the model will have Λ=0, and the letter Λ can be omitted.
In fact, there can be various forms of doping rate, that is βSD/N can have a more general form, S·g(D) where g can be a periodic function (based on sin(t)) for modeling breaks or waves, or a particular one that can have additional factor included (as attitude) in a mathematical form:

$$g(D) = \frac{kD^m}{1+pD^h}. \quad (2)$$

where k, m, p and h are the parameters that can be determined by fitting data and optimization on global error in the sense or RMS (Root Mean Square).
The main points of interest in mathematical models of epidemics are (a) Disease Free Equilibriums (DFE); (b) Endemic equilibrium (EE) and (c) R_0 – the basic reproductive number. In some cases, bifurcations are also a point of interest but in this paper, we resumed to calculation of R_0, as measure for asymptotic stability and decrease/explode the number of doping athletes. From R_0 it can be see how the doping phenomenon is spread in athletes and we can control this.
The calculation of R0 [19] was made using the method of next generation matrix [20]. The first step is the identification of type of doping substances used: stimulants, anabolic, hormones, peptide hormones, masking agents, analgesics, anabolic agents, diuretics, etc. Each type of effort required in sports (strength, endurance, speed, flexibility, concentration, etc.) leads to the use of different types of substances (in this case it is about the second equation from (1)) and methods of improving non-chemical performance (it is about the first and the third equation from (1)). The DFE is $(S^*, D^*, R^*)=(N, 0, 0)$:

$$F(D) = \beta SD/N.$$

$$V(D) = (\mu+\gamma-\delta)D+\alpha R .$$

$$F = \partial F/\partial D = \beta S/N \Rightarrow F = \beta.$$

$$V = \partial V/\partial D = \mu+\gamma-\delta.$$

$$V^{-1} = \frac{1}{\mu+\gamma-\delta}.$$

$$V^{-1} = \frac{1}{\mu+\gamma-\delta}.$$

$$FV^{-1} = \frac{\beta}{\mu+\gamma-\delta}.$$

In this case we have only one eigenvalue so this is the dominant eigenvalue that is, R_0= $\beta/(\mu+\gamma-\delta)$. In model with more than one compartment of infections (le's say SEIR), the calculus (3)-(8) is matriceal.

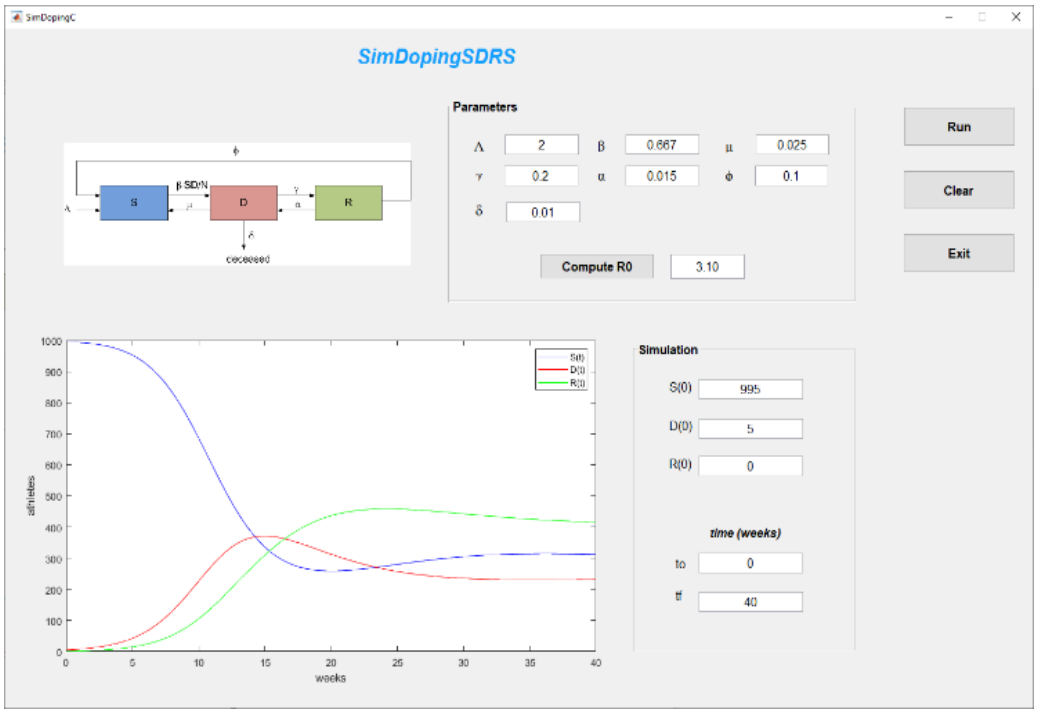

Fig. 2. The GUI proposed SDRS model

3 Results and Discussions

A GUI was constructed MATLAB in order to made simulation of proposed SDRS model. In Fig. 2 the simulation was made using initial values (S_0, D_0, R_0) = (995, 5, 0), N = S_0+ D_0+R_0=1000, and parameters Λ=2.0, β=0.667, μ=0.025, γ=0.2, α=0.015, ϕ = 0.1 , δ= 0.01.

The compartment S has no sport dropout in this model. We approximate it due to fact that The statistical data available at the moment (relevant for the period 2015-2020) did not show any cases of leaving sports careers due to doping and be neglected in modelling. However, if a s rate is considered, the calculus of R_0 will be more visible as matrix calculus.

An interesting development for future exploration is given in [21]. In this approach ([21]-[22]), the main ideea is to formulate SIRS model and to assign mixtures/finite mixtures prior to heterogeneity learning using Markov chain Monte Carlo sampling algorithm for posterior distribution. The data in this models are presumed to come from conditional independent Poisson distributions. The development of this model imply clustering so the geographic localization of competiona ang groups that participate to competitions must be made.

4 Conclusions

A new model based on quantitative analysis is proposed. The stability and reproduction number are calculated and possible extensions of the model are taken into account. A GUI is constructed in order to facilitate the experiments with parameters and data for model. The R0 can be calculated automatically directly in the interface.

The future development will include a model for finding out the parameters based on experimental data using optimization function and heuristic search of optimum (Genetic algorithms) and a model that is based on heterogenic learning and Poisson distributions.

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