On some approximate methods for nonlinear models

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Abstract

We show that recent applications of the homotopy perturbation method the Adomian decomposition method and the variational iteration method are completely useless for the treatment of nonlinear problems.

1 Introduction

In a series of papers we have shown that some particular applications of some variational and perturbation approaches (VAPA) like, for example, the homotopy perturbation method (HPM), homotopy analysis method (HAM), Adomian decomposition method (ADM) and variational iteration method (VIM) are utterly useless for the study of nonlinear systems, even for the simplest models [1–7]. Unfortunately some journals do not accept criticisms of the papers they publish.

The purpose of this paper is the analysis of some recent applications of VAPA to simple models of nonlinear phenomena published in this journal. In Sec. 2...
we discuss the application of HPM to an exactly solvable Riccati equation. In Sec. 3 we analyse the application of the same approach to an exactly-solvable model for the interaction between a prey and a predator. In Sec. 4 we discuss the application of other VAPA to the simplest epidemic model. Finally, in Sec. 5 we draw some conclusions on the achievements and future of those VAPA.

2 Homotopy perturbation method for a quadratic differential equation

Lately, there has been great interest in the application of analytical approximate methods to the solution of several problems of nonlinear dynamics [8–13], some of which lead to time–power series [8–11]. Some of the models considered by those authors are suitable for the study of prey–predator interactions [8, 9, 11–13].

It is curious that most of those authors resort to a power series description of the dynamics of the system because it is known that such approach is unable to provide a reasonable overall picture of the evolution which is what really matters in the case of, for example, prey–predator models. A time–power series is limited to a neighbourhood of the origin (for example, initial species population) by its convergence radius that is determined by the singularity closest to that point. Besides, most equations for nonlinear dynamics generate singularities spontaneously that move when the initial conditions change. We have already pointed out the limitations of several of those approaches in earlier communications [1–7].

The purpose of this section is to discuss some of those features of the nonlinear dynamics by means of the simple Riccati equation solved by Abbasbandy [10] by means of the HPM.
The model chosen by Abbasbandy [10]

\[
\frac{dY(t)}{dt} = 2Y(t) - Y(t)^2 + 1, \quad Y(0) = 0 \tag{1}
\]

for the application of the HPM is useful for present discussion because the Riccati equation can be solved exactly:

\[
Y(t) = \frac{e^{2\sqrt{2}t} - 1}{\left(\sqrt{2} - 1\right)e^{2\sqrt{2}t} + \sqrt{2} + 1} \tag{2}
\]

One clearly appreciates that there is a pole in the complex \(t\)–plane that limits the convergence of the time–power series to \(t < |t_c|\), where

\[
|t_c| = \frac{\sqrt{2}}{4}\sqrt{4 \left[ \ln \left(\sqrt{2} + 1\right) \right]^2 + \pi^2} \approx 1.274 \tag{3}
\]

In other words, the HPM proposed by Abbasbandy [10] will be useless for \(t > |t_c|\) disregarding the order of the perturbation approach. In particular, the resulting time–power series will not reveal the stationary point \(Y_s = \sqrt{2}+1\) [14] to which the solution approaches as \(t \to \infty\). Such stationary points are most important for any physical description of a dynamical system [15, 16].

The solution to the Riccati equation (1) with an arbitrary initial condition \(Y(0) = Y_0\) is

\[
Y(t) = \frac{\left(\sqrt{2} + 1\right)\left(Y_0 + \sqrt{2} - 1\right)e^{2\sqrt{2}t} + Y_0\left(\sqrt{2} - 1\right) - 1}{\left(Y_0 + \sqrt{2} - 1\right)e^{2\sqrt{2}t} - Y_0 + \sqrt{2} + 1} \tag{4}
\]

and the radius of convergence of the time–series is

\[
|t_c| = \frac{\sqrt{2}}{4} \ln \left(\frac{Y_0 - \sqrt{2} - 1}{Y_0 + \sqrt{2} - 1}\right) \tag{5}
\]

Notice that the singularity closest to the origin of the complex \(t\)–plane moves as the initial condition changes as mentioned above. The HPM performs even more poorly if \(Y_0 > Y_s\); for example, if \(Y_0 = 5\) then \(|t_c| \approx 0.261\).
From the discussion above we clearly appreciate that the HPM proposed by Abbasbandy [10] (and also the time–power series produced by any other approach [8, 9, 11]) is unable to reveal the main features of nonlinear dynamical models.

Straightforward application of the ADM [8, 14] also produces a time–power series, however, El–Tawil et al [14] proposed a multistage ADM that basically leads to the expansion of \( Y(t + \Delta t) \) in \( \Delta t \)–power series. The radius of convergence of this series is given by

\[
|\Delta t_c(t)| = \frac{\sqrt{2}}{4} \sqrt{4 \ln \left( \frac{\sqrt{2} + 1}{\sqrt{2} - 1} \right)^2 - 8 \sqrt{2} \ln \left( \sqrt{2} + 1 \right) t + 8t^2 + \pi^2} > \frac{\sqrt{2}\pi}{4} \approx 1.11
\]

when \( Y_0 = 0 \). El–Tawil et al [14] chose \( \Delta T \ll 1.11 \) and their multistage ADM yielded accurate results of \( Y(t) \) even for values of \( t \) sufficiently large that \( Y(t) \approx Y_s \). However, this approach is more closely related to numerical integration algorithms such as Runge–Kutta than to the analytical methods discussed above.

Analytical approaches like the HPM and ADM that lead to time–power series [8–11] are completely useless for a serious study of nonlinear dynamics because they fail to provide the overall features of the problem that any physical or ecological application requires [1–7]. Other approaches like the VIM [13] also yield expressions that are just valid in a meaningless neighbourhood of origin [3].

3 Homotopy perturbation method for a prey–predator model

In a recent paper Rafei et al [12] proposed the application of the HPM to the simplest model of prey–predator interaction. After a rather tedious develop-
ment of the main equations, their particular implementation of the HPM leads to a series solution of the population of the species. It is difficult to justify the application of the HPM in this way because one obtains the same solution more easily and straightforwardly by direct expansion of the nonlinear differential equation in time–power series [9]. Besides, we have recently shown that the time–power series developed by Chowdhury et al [11] by means of an alternative implementation of the HPM completely fails to yield the main features of the population dynamics [1]. The ADM also leads to a time–series solutions although in this case they are slightly different from the correct ones [8].

The purpose of this section is to analyze the results of Rafei et al [12] in terms of what one expects from an approach designed to solve problems of population dynamics. The results of this analysis applies also to the other methods already mentioned above [8, 9, 11].

Rafei et al [12] chose the prey–predator system

\[
\begin{align*}
\frac{dx(t)}{dt} &= x(t)[a - by(t)], \quad a, b > 0 \\
\frac{dy(t)}{dt} &= -y(t)[c - dx(t)], \quad c, d > 0
\end{align*}
\]  

(7)

where \(x(t)\) and \(y(t)\) are the populations of rabbits and foxes, respectively. This nonlinear system (7) exhibits a saddle point at \((x_s, y_s) = (0, 0)\) and a center at \((x_s, y_s) = (c/d, a/b)\). Besides, the populations obey the following curve in the \(x - y\) plane:

\[
\ln (x^c y^a) - dx - by = \ln (x_0^c y_0^a) - dx_0 - by_0
\]

(8)

where \(x_0\) and \(y_0\) are the initial populations at time \(t = 0\).

The HPM proposed by Rafei et al [12] leads to time–series expansions of the form
\begin{align}
x(t) &= x_0 + x_0(a - by_0)t + \ldots \\
y(t) &= y_0 + y_0(dx_0 - c)t + \ldots
\end{align}

that are exactly the same as those obtained earlier by Biazar et al [9]. Obviously, they are suitable about the point \((x_0, y_0)\) and will not predict the main features of the population dynamics which is what really matters in this field [15].

Fig. 1 shows the populations for Case I \((a = b = d = 1, c = 0.1, x_0 = 14, y_0 = 18)\) in a time scale larger than that considered in the earlier studies already mentioned above [8, 9, 12]. We clearly appreciate that all those approaches predict a wrong behaviour of the populations.

Case V \((a = b = c = d = 1, x_0 = 3, y_0 = 2)\) is much more interesting. Fig. 2 shows the results in the plane \(x - y\). The time series predict a completely wrong behaviour and the resulting curve cross itself which can never happen as everyone knows [15].

Present analysis clearly shows that the HPM [11, 12], the ADM [9] and the straightforward time–series expansion [8] are completely useless for a reasonable prediction of the evolution of even the simplest prey–predator systems.

4 Simple epidemic model for non–fatal disease

In a series of papers Biazar [17] and Rafei et al [18, 19] discussed the application of VAPA to the simplest epidemic model of a non–fatal disease, commonly called SIR and attributed to Kermack and McKendrick [20]. Those authors applied ADM [17], VIM [19], and HPM [19], and obtained the Taylor expansions of the number of susceptibles, infectives, and removed about the initial time \(t = 0\). In those papers the authors verified that the three methods yield exactly the same expansions, and, consequently, they showed the same figures
for the evolution of the epidemic.

However, Biazar [17] and Rafei et al [18,19] did not try to simulate any real epidemic situation and did not explain the reason for choosing their particular values of the model parameters and initial conditions.

The purpose of this section is to investigate to which extent the analytical expressions derived by those authors are useful for a reasonable prediction of the behaviour of an epidemic within the realm of the rather oversimplified SIR model. We first answer some relevant questions about the epidemic dynamics by means of the exact solution. Then we choose particular model parameters and study if the approximate analytical expressions proposed by Biazar [17] and Rafei et al [18,19] are suitable for answering those questions. Finally, we give our opinion about the utility of those analytical expressions.

The nonlinear ordinary differential equations that predict the evolution of the epidemic according to the SIR model are:

\[
\begin{align*}
\frac{dx}{dt} &= -\beta xy, \\
\frac{dy}{dt} &= \beta xy - \gamma y, \\
\frac{dz}{dt} &= \gamma y
\end{align*}
\]  

(10)

where \(x\) is the number of susceptibles, who do not have the disease but could get it, \(y\) is the number of infectives, who have the disease and can transmit it to others, \(z\) is the number of removed, who cannot get the disease or transmit it, and \(\beta, \gamma > 0\) are model parameters that determine the epidemic evolution.

Biazar [17] proposed to solve the SIR equations (10) by means of the ADM and merely obtained the Taylor expansion of the solutions about \(t = 0\):

\[
\begin{align*}
x(t) &= \sum_{j=0}^{\infty} x_j t^j, & y(t) &= \sum_{j=0}^{\infty} y_j t^j, & z(t) &= \sum_{j=0}^{\infty} z_j t^j
\end{align*}
\]  

(11)
where \( x_0 = x(0), y_0 = y(0), z_0 = z(0) \) are the initial conditions. Obviously, if we substitute the series (11) into the differential equations (10) we easily obtain the coefficients \( x_j, y_j \) and \( z_j \) in terms of the initial conditions and the model parameters without recourse to any elaborate method like the ADM.

Later, Rafei et al applied the VIM [18] and the HPM [19] and obtained the same Taylor series. In fact, the three papers show almost the same partial sums of the series (11) and for that reason display approximately the same figures for the discussion of the results [17–19].

The SIR model is the simplest description of the evolution of an epidemic of a non-fatal disease. It does not consider birth or death of the individuals and therefore the total population is constant

\[
x(t) + y(t) + z(t) = x_0 + y_0 + z_0
\]

(12)

Besides, the model is so simple that it can be solved exactly and one obtains

\[
y(x) = y_0 + x_0 - x + \frac{\gamma}{\beta} \ln \frac{x}{x_0}
\]

\[
z(x) = z_0 - \frac{\gamma}{\beta} \ln \frac{x}{x_0}
\]

(13)

However, if one needs the solutions in terms of \( t \) one has to solve the following integral numerically:

\[
t = \frac{1}{\beta} \int_x^{x_0} \frac{dx'}{x'(y_0 + x_0 - x' + \frac{\gamma}{\beta} \ln \frac{x'}{x_0})}
\]

(14)

There are several important questions about the epidemic that one would like to answer, for example, if we introduce a small number of infectives in a population of susceptibles, will the number of infectives increase, causing an epidemic, or will the disease fizzle out?. Assuming there is an epidemic, how will it end?, will there still be susceptibles left when it is over?. How long will the epidemic last? [21]. Biazar and Rafei et al [17–19] merely showed some
figures that are meaningless if they did not answer any important question about the epidemic.

The exact solution enables one to answer the questions above. As an example we analyze how the epidemic dies out. Notice that \( dx/dt = dy/dt = dz/dt = 0 \) when \( y = 0 \), which according to the exact solution takes place when \( x = x_L \) that is a solution of

\[
y_0 + x_0 - x_L + \frac{\gamma}{\beta} \ln \frac{x_L}{x_0} = 0
\]

(15)

We may say that the epidemic is over when the number of infectives is similar to the one we had at the beginning: \( y_{over} = y_0 \); in this case we have

\[
x_0 - x_{over} + \frac{\gamma}{\beta} \ln \frac{x_{over}}{x_0} = 0
\]

(16)

Biazar and Rafei et al [17–19] chose the following example

\[
x_0 = 20, \ y_0 = 15, \ z_0 = 10, \ \beta = 0.01, \ \gamma = 0.02
\]

(17)

What we first appreciate here is that the number of infectives is rather large: 1/3 of the total population. This situation does not define the beginning of the epidemic but and advanced stage of it. However, we analyze the results anyway.

The fifth–degree polynomials proposed by Biazar and Rafei et al [17,19] do not give acceptable solutions for \( y = 0 \) or \( y = y_0 \); therefore, they cannot answer the relevant questions raised above. In order to find the cause of the failure of the time–power series, we show \( y(x) \) and \( z(x) \) in Fig. 3. We appreciate that the time series do not follow the exact curve in the region were we expect to find \( x_L = 5.02 \times 10^{-7} \) and \( x_{over} = 0.000908 \).

If \( x_0 > \gamma/\beta \) the number of infectives increases up to a maximum at \( x_m = \gamma/\beta \) and then decreases. The figures shown by Biazar and Rafei et al [17–19] are
restricted to a rather small time interval and do not show this maximum. Besides, they suggest an ever increasing number of infectives and do no reveal anything relevant about the future of the dynamics of the epidemic process. For the particular model parameters (17) we obtain \( x_m = 2 \) and \( y_m = 28.39 \).

Although the power-series approach is unable to show the overall picture of the epidemic dynamics it does not perform too poorly in the case of the conveniently chosen model parameters (17). One expects that the range of utility of the time-power series decreases as the model parameters \( \beta \) and \( \gamma \) increases. For example, if we choose

\[
x_0 = 20, \quad y_0 = 4, \quad z_0 = 10, \quad \beta = \gamma = 1
\]  

the situation is considerably worse than in the preceding case. Fig. 4 shows the exact curves \( y(x) \) and \( z(x) \) and those predicted by the fifth-degree power-series approach. We appreciate that in this case the time series fails to give any reasonable account of the epidemic dynamics.

The results derived above clearly show that the ADM, VIM and HPM implemented by Biazar [17] and Rafei et al [18, 19] are unsuitable for the description of the epidemic dynamics. The reason is that the time-power series is a local approximation valid in a relatively small neighbourhood of the initial stages of the epidemic. Consequently, it cannot provide the long-term behaviour of the infectious process that is needed for understanding its future evolution. As we have already seen, the analytical expressions provided by Biazar [17] and Rafei et al [18, 19] do not allow us to answer the most relevant questions about the epidemic dynamics, even in the case of an oversimplified model with exact analytical solution. It is most probable that their performance may be even poorer in the case of a more elaborated model.

In conclusion, we do not recommend a health-care system to rely on the ADM, VIM or HPM time-power series to cope with an actual epidemic emergency.
5 Conclusions

In our opinion most of the recent applications of VAPA are responsible for the poorest scientific papers ever published. They are spreading like an epidemic overcoming the refereeing mechanism of the journals. I believe that the main reason for it is that the authors of such papers referee themselves and accept the manuscripts that give them a considerable number of citations. Unfortunately, it seems that some editors are accomplices of this situation favouring such papers and banning criticisms of them. For example, some editors think that a prey–predator model that predicts a negative number of rabbits is a valuable scientific contribution to the journal [5]. The reader may find some more examples elsewhere [1–7].

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Fig. 1. Exact (solid, e) and series (dashed, s) populations for Case I

Fig. 2. Exact (solid) and approximate (dashed) populations for Case V in the $x - y$ plane
Fig. 3. Number of infectives $y$ and recovered $z$ in terms of the number of susceptibles $x$ for the model parameters (17). The solid and dashed lines correspond to the exact and approximate results, respectively.

Fig. 4. Number of infectives $y$ and recovered $z$ in terms of the number of susceptibles $x$ for the model parameters (18). The solid and dashed lines correspond to the exact and approximate results, respectively.