



# Approximation of trajectories of non-linear systems by iterates of systems with linear state dynamics

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## Abstract

A modification of an iterative Picard process is proposed to approximate the output of a non-linear system by a concatenation of systems with linear state dynamics and non-linear outputs. A local uniform convergence result is given. The motivating example is a non-linear system that arises in surface plasmon resonance experiments to determine protein–protein interaction constants. We show with simulations that for this example the approximants converge not only locally but over the full time interval of interest in the application.

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## 1. Introduction

Over the years a large array of powerful tools have been developed for the study of linear systems. In contrast, due to the significant technical problems involved the tools available for the study of non-linear systems are more limited. This immediately leads to the question of whether or not non-linear systems can be effectively approximated by linear ones in some appropriate sense.

Our particular approach is motivated by a data analysis problem that arises in the biophysical study of protein–protein interactions using the surface plasmon resonance methodology (see Section 3 for more details). To describe the underlying phenomena a non-linear system is often advocated as an appropriate model to explain the dynamics of the kinetic process. Since many analysis techniques are only available for linear systems, we were therefore led to investigate how to best approximate trajectories or outputs of non-linear systems. Here we present a modified Picard process that under certain conditions leads to local uniform approximation of the trajectories of a non-linear system by a concatenation of systems with linear state dynamics.

The ‘classical’ Picard iteration is a well-known method which is typically introduced in university

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classes on ordinary differential equations. This process is not well suited for our application since the approximations are not easily interpreted in a system-theoretic setting.

Recently, a Picard process (in which each step is linear) was introduced to find the solution of a non-linear system that is bounded for all time in response to an input that is bounded for all time and to provide sufficient conditions under which such a solution exists [1,3]. In [1] the input and solution are assumed to be integrable as well as bounded. The bounded solution cannot be computed by solving an initial value problem since the initial condition is not known until the solution is found. In contrast the current paper introduces a Picard process to address initial value problems for non-linear systems.

We begin with a non-linear system of the form

$$\dot{x}(t) = f(t, x) + u(t), \quad x(t_0) = x_0,$$

where  $x(t) \in \mathfrak{R}^n$ ,  $f(t, 0) = 0$ ,  $f$  is continuously differentiable and  $u(t)$  denotes an  $n$ -tuple of time functions that are considered to be the input to the system. More general systems of the form  $\dot{x} = f(t, x, u)$  could be considered, and the requirement that  $f(t, 0) = 0$  can be ignored by simply moving any constant or strictly time dependent terms to the input  $u$ . We re-write the above equation as

$$\dot{x}(t) = Ax(t) + F(t, x) + u(t), \quad x(t_0) = x_0,$$

where  $A$  is a constant square matrix and  $F(t, x)$  contains non-linear terms. A standard example would be to take  $A = \partial f(0, 0)/\partial x$  and define  $F$  accordingly. We could also define  $A$  by “expanding” about any point  $x$  and adjusting  $u$  accordingly.

For an appropriate class of inputs  $u$  the initial value problem

$$\dot{x}(t) = f(t, x) + u(t), \quad x(0) = x_0$$

has a (local in time) solution if and only if the solution takes the form

$$x(t) = e^{At}x_0 + \int_0^t e^{A(t-\tau)}(F(\tau, x(\tau)) + u(\tau)) d\tau.$$

We introduce the following Picard process, where the superscripts denote the iterates:

$$x^1(t) = e^{A(t-t_0)}x_0 + \int_{t_0}^t e^{A(t-\tau)}u(\tau) d\tau,$$

$$x^2(t) = e^{A(t-t_0)}x_0 + \int_{t_0}^t e^{A(t-\tau)}(F(\tau, x^1(\tau)) + u(\tau)) d\tau,$$

⋮

$$x^{j+1}(t) = e^{A(t-t_0)}x_0 + \int_{t_0}^t e^{A(t-\tau)}(F(\tau, x^j(\tau)) + u(\tau)) d\tau,$$

⋮

Of course there are standard perturbation methods in systems theory that deal with approximation of the trajectories of a non-linear system by trajectories of a linear system. For example, there is classic standard stable, unstable manifold theory [7] about an equilibrium point. This assumes zero driving input for the non-linear system, whereas we study systems with non-zero input. There are also perturbation techniques with particular emphasis on periodic inputs and periodic solutions [7]. However, as our theory and simulations indicate, we cannot restrict ourselves to periodic inputs or trajectories. In our application the non-linear system is first excited by an input that results in a rising and leveling off of the states of the system. Then the input is withdrawn and the states decline and level off again. After a number of iterates the Picard method we introduce represents the states of the non-linear systems over the entire time interval in which the rising, leveling off, declining, and leveling off take place.

In Section 2 we state a result indicating that this process converges under relatively weak conditions. Our Picard process is applicable to general non-linear systems, not just mildly non-linear ones. The vector valued functions  $f(t, x)$  and  $F(t, x)$  are simply assumed to be continuously differentiable. The final section demonstrates the convergence process for the above mentioned biophysical example.

## 2. Convergence

In this section we establish local convergence of the modified Picard iteration that we consider here. The proof, which is omitted for brevity, follows that of the proof of convergence for the standard Picard process as in [7, Theorem 4.6, p. 56]. However, several modifications are necessary to deal with our situation.

**Theorem 2.1.** Let  $D$  be a domain in  $\mathfrak{R} \times \mathfrak{R}^n$ , i.e. an open, connected and non-empty subset. Let  $(t_0, x_0) \in D$  and let  $U_0$  be a positive constant. Assume that

1.  $A$  is a constant  $n \times n$  matrix.
2.  $u$  is an arbitrary vector valued function of time such that  $|u(t)| \leq U_0$  for  $t \geq t_0$  and which for the sake of simplicity can be assumed to be piecewise continuous.
3. the non-linearity

$$F : D \mapsto \mathfrak{R}^n$$

is continuously differentiable.

With  $(t_0, x_0) \in D$  given, let  $a > 0$ ,  $b > 0$  be such that

$$S = \{(t, x) \in \mathfrak{R} \times \mathfrak{R}^n \mid t_0 \leq t \leq t_0 + a, \|x - x_0\| \leq b\} \subseteq D.$$

For our Picard process with iterates  $x^j(t)$

1. there exists  $t_1$  with  $t_0 < t_1 \leq t_0 + a$  such that  $(t, x^j(t)) \in S$  for  $j \geq 1$  and  $t_0 \leq t \leq t_1$ ,
2.  $(x^j)_{j \geq 1}$  converges uniformly on  $[t_0, t_1]$  to a continuous function

$$x := \lim_{j \rightarrow \infty} x^j,$$

3. there exist positive constants  $C$  and  $E$  such that for  $t_0 \leq t \leq t_1$

$$\|x(t) - x^j(t)\| \leq C \sum_{k=j}^{\infty} \frac{E^k}{k!},$$

4. the limit function  $x$ , is the unique solution on  $[t_0, t_1]$  to the initial value problem,

$$\dot{x}(t) = Ax(t) + F(t, x(t)) + u(t), \quad x(t_0) = x_0.$$

Note that the bound in part 3 of the theorem is independent of the particular input  $u$ . This shows that the convergence properties are not dependent on the particular input, provided that the input is bounded by the constant  $U_0$ . This means that the approximation can be interpreted as a system theoretic convergence in the sense that the original non-linear system is approximated by a concatenation of  $j$  linear systems with non-linear outputs. Given an arbitrary bound  $U_0$ , the state  $x^j$  of the approximant system provides a good approximation to the state of the original system in a

uniform sense for arbitrary input if the input is less than the prespecified bound  $U_0$ .

Established techniques for the approximation of outputs of non-linear systems are Volterra expansions and Fliess expansions [4]. For those expansions convergence results that are local in time exist that are analogous to the convergence result that we have established for the expansion introduced here. In [2,6] functional expansions are discussed that are uniform on a specified interval. However, those results only apply for sufficiently small inputs, a condition that is not satisfied for many applications including the ones that we are interested in.

### 3. A mass transport model

In the following we are going to discuss an example whose analysis has motivated the previous result. Estimating the kinetic parameters of protein–protein interactions is an important problem in molecular biology and chemistry. A method that has attracted much attention recently is based on the use of surface plasmon resonance methodology. Here one of the proteins, protein A, is immobilized on a surface and the other protein, protein B, is flowed across the surface using a microfluidic device. The measured signal is time-dependent and is proportional to the mass that is accumulated on the surface.

As part of the model the mass transport of protein A to and from the surface has to be modeled. The following compartmental model has been advocated as an adequate model to describe the protein–protein interaction in the presence of mass transport (see e.g. [5,8]):

$$\frac{dC}{dt} = -k_a C(R_T - B) + k_d B + k_M(C_T - C),$$

$$\frac{dB}{dt} = k_a C(R_T - B) - k_d B.$$

Here  $C_T$  is the concentration of analyte (protein B) in the flow cell (compartment 1) and  $C$  is the concentration of the analyte (protein A) on the cell surface (compartment 2).  $k_M$  is a transport coefficient.  $C_T$  is treated as an input.  $B$  is the amount bound to the cell surface, i.e. is proportional to the protein A/protein B complexes.  $R_T$  is the total receptor

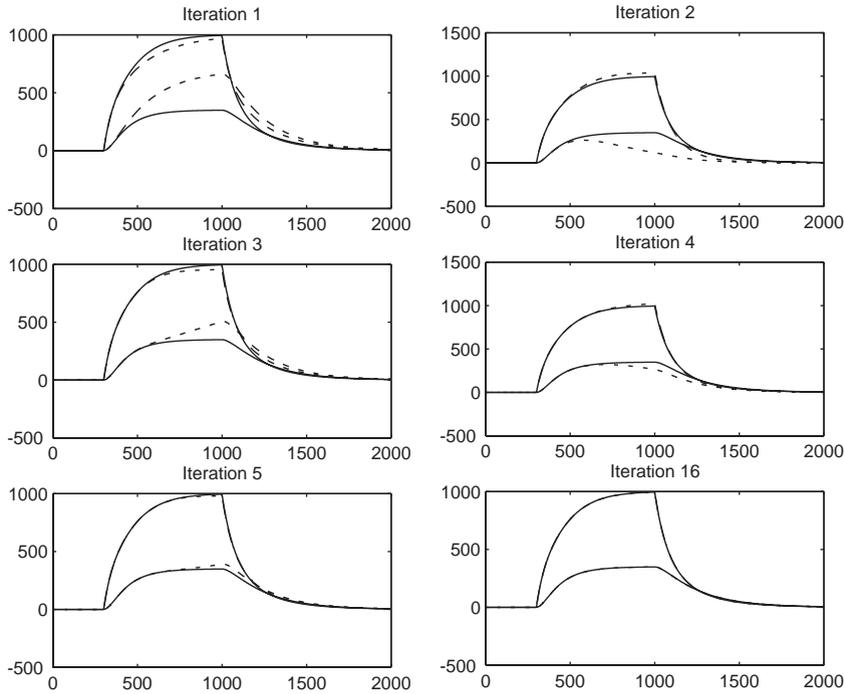


Fig. 1. Iteratives; solid lines indicate system trajectories; dashed lines indicate trajectories of iteratives.

concentration, i.e. the concentration of protein A on the surface.

We relabel some variables by setting

$$x := \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} := \begin{pmatrix} C \\ B \end{pmatrix}, \quad v := C_T.$$

Then

$$\dot{x} = \begin{pmatrix} -k_a R_T - k_M & k_d \\ k_a R_T & -k_d \end{pmatrix} x + \begin{pmatrix} k_a \\ -k_a \end{pmatrix} x_1 x_2 + \begin{pmatrix} k_M \\ 0 \end{pmatrix} v.$$

The measured signal is given by

$$y = \begin{pmatrix} 0 & 1 \end{pmatrix} x.$$

The system of equations clearly falls into the class of non-linear systems that we are considering by setting

$$A := \begin{pmatrix} -k_a R_T - k_M & k_d \\ k_a R_T & -k_d \end{pmatrix},$$

$$F(t, x(t)) := \begin{pmatrix} k_a \\ -k_a \end{pmatrix} x_1(t)x_2(t),$$

$$u(t) := \begin{pmatrix} k_M \\ 0 \end{pmatrix} v(t).$$

The Picard iterations that we discussed earlier can now be applied to this system. In Fig. 1, a simulation of a solution to the system of equations is shown which is typical of the data that is being acquired in an actual experiment with parameters  $k_a = 10^{-5}$ ,  $k_d = 0.01$ ,  $R_T = 700$ ,  $k_M = 0.01$ ,  $x_0 = [0; 0]$  and  $v(t) = 1000$  on the interval  $[300, 1000]$  and  $v(t) = 0$  elsewhere. State 1 is given by the solid “higher curve” and state 2 (the amount bound) is indicated by the solid “lower curve”. Fig. 1 shows the behaviour of the Picard iteratives for this particular system. It shows clearly that state 1 converges extremely fast. The graphs also show how the quality of the approximation by the iteratives improves step by step for state 2 (indicated by dashed lines). At iteration 16 no difference is recognizable

between state 2 of the iterative and state 2 of the system.

It is important to note that an explicit solution can be given for the state equation of the approximating system. In contrast, there is no analytical representation of the state of the non-linear system. Having an analytical representation for the state of the approximating system available makes it possible to analyze such questions as the dependence of the solution on a particular parameter. Such studies are, however, beyond the scope of the current paper.

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### References

- [1] S. Devasia, B. Paden, D. Chen, Nonlinear inversion-based output tracking, *IEEE Trans. Automat. Control* 41 (1996) 930–942.
- [2] E.G. Gilbert, Functional expansions for the response of nonlinear differential equations, *IEEE Trans. Automat. Control* 22 (1977) 909–921.
- [3] L.R. Hunt, G. Meyer, Stable inversion for nonlinear systems, *Automatica* 33 (1997) 1549–1554.
- [4] A. Isidori, *Nonlinear Control Systems*, Springer, London, 1995.
- [5] R. Karlsson, Real-time competitive kinetic analysis of interactions between low-molecular-weight ligands in solution and surface-immobilized receptors, *Anal. Biochem.* 221 (1994) 142–151.
- [6] C. Lesiak, A.J. Krener, The existence and uniqueness of Volterra series for nonlinear systems, *IEEE Trans. Automat. Control* 23 (1978) 1090–1095.
- [7] R.K. Miller, A.N. Michel, *Ordinary Differential Equations*, Academic Press, New York, 1982.
- [8] P. Schuck, Kinetics of ligand binding to receptor immobilized in a polymer matrix, as detected with an evanescent wave biosensor. I. A computer simulation of the influence of mass transport, *Biophys. J.* 70 (1996) 1230–1249.