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Data-driven polynomial MPC and application to blood glucose regulation in a diabetic patient

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Abstract— **The majority of control design approaches assume that an accurate first-principle model of the system to control is available. However, in many real-world applications, deriving an accurate model is extremely difficult, since the system dynamics may be not well known and/or too complex. In this paper, a polynomial model predictive control (PMPC) approach for nonlinear systems is presented, relying on the identification from data of a polynomial prediction model. The main advantages of this approach over the standard methods are that it does not require a detailed knowledge of the plant to control and it is computationally efficient. A real-data application is presented, concerned with regulation of blood glucose concentration in a type 1 diabetic patient. This application shows that the PMPC approach can be effective in the biomedical field, where accurate first-principle model can seldom be found.**

I. Introduction

The majority of control design approaches assume that an accurate first-principle model describing the dynamics of the system to control is available. In the case of nonlinear systems, classical examples are feedback linearization [21], [18], Lyapunov function based control [8], [25] and NMPC (Nonlinear Model Predictive Control) [3], [4], [5]. However, in most real-world situations, deriving an accurate first-principle model is difficult: the system dynamics is often not well understood and/or too complex; there are parameters that are difficult to measure/estimate. Robust methods have been developed to deal with this issue, [17], [33], [35]. However, deriving the required uncertainty models is hard even for LTI (Linear Time Invariant) systems (see e.g. [13] and the references therein), and is still an open problem in the case of nonlinear systems. Another relevant issue is that, in the case of nonlinear systems with a non-affine structure, even when a reliable model can be derived, designing a controller is in general difficult.

Data-driven methods may represent a solution to all these problems, see, e.g., [24], [12], [32], [36], [11], [16], [10], [27], [23], [26]. However, guaranteeing general a-priori stability and accuracy properties is not easy for many data-driven methods. Typically, the controller is first synthesized using some heuristic procedure, then tested/tuned in simulation, and finally implemented (and possibly tuned) on the real plant to control. Moreover, many data-driven methods are based on neural networks or similar approximating functions, whose design involves non-convex optimization in large dimensional spaces. For this reason, the resulting controller may be not adequate for the considered application.

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A data-driven control method for nonlinear systems has been proposed in [28], [29], which allows us to overcome all these problems: the method does not require a physical model of the plant to control; it can ensure a priori important properties such as closed-loop stability and tracking error accuracy; it is numerically efficient. The method is based on the identification from data of a polynomial prediction model and its online inversion through an efficient optimization algorithm. An important point is that closed-loop stability can be enforced directly in the identification algorithm used to derive the prediction model. The method is here named polynomial model predictive control (PMPC), while in [28], [29] it is called nonlinear inversion control (NIC) (for reasons that will be clear in Section II-C).

Thanks to the features discussed above, the PMPC approach may be particularly effective in the biomedical field, for the treatment of various diseases, where deriving accurate physiological models is difficult and there is a strong variability among the patient population. The PMPC approach allows indeed the design of treatment strategies that are personalized for each patient, avoiding the population variability problem. Also, it does not require accurate physiological models: control design is carried out from a set of data acquired in a preliminary phase of the treatment.

The main contribution of this paper is a real-data study, concerning regulation of blood glucose concentration in a type 1 diabetic patient. First, a model of a diabetic patient is identified from a subset of the available experimental data. This model represents the (unknown) patient, for which a glucose regulator has to be designed. In other words, this patient model is here used instead of a real patient (future activities will be devoted to test the data-driven PMPC approach in clinical trials with real patients). Next, a disturbance estimator is derived, allowing the estimation of the unknown signals that typically affect a diabetic patient (e.g. food, physical activity, emotions, etc.). Then, a PMPC controller for glucose regulation is designed, which takes advantage of the information given by the disturbance estimator. Finally, this controller is tested using fresh data, not previously used for model identification and controller/estimator design. This study shows that the PMPC strategy is effective in regulating the blood glucose concentration of the patient model, yielding a significantly better treatment quality with respect to a "manual" strategy, where the insulin is injected by the patient on the basis of his/hers experience and of the indications coming from a semi-automated glucose regulation device.

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II. Data-driven polynomial MPC

A. Problem formulation

Consider a nonlinear discrete-time system of the form

$$\begin{aligned} y_t &= h\left(u_t^-, y_t^-\right) + \xi_t \\ u_t^- &\doteq (u_{t-1}, \ldots, u_{t-n}) \\ y_t^- &\doteq (y_{t-1}, \ldots, y_{t-n}) \end{aligned} \tag{1}$$

where $u_t \in U \subset \mathbb{R}$ is the input, $y_t \in \mathbb{R}$ is the output, $\xi_t \in \Xi \subset \mathbb{R}$ is a disturbance, n is the system order and $t \in \mathbb{Z}$ is the time index; U and $\Xi \doteq \left\{\xi \in \mathbb{R} : |\xi| \leq \bar{\xi}\right\}$ are compact sets, where U accounts for possible constraints on u_t.

Suppose that the system (1) is unknown, but a set of noise-corrupted measurements is available:

$$DS \doteq \{\tilde{u}_t, \tilde{y}_t\}_{t=1-L}^{0} \tag{2}$$

where $\tilde{u}_t \in U$, $\tilde{y}_t \in Y$, $Y \subset \mathbb{R}$ is a compact set, and the tilde is used to indicate the collected data.

Let $\mathcal{Y}^0 \subseteq R^n$ be a set of initial conditions of interest, $R \subset \mathbb{R}$ a compact set, $\mathcal{R} \doteq \{\boldsymbol{r} = (r_1, r_2, \ldots) : r_t \in R, \forall t\}$ a set of output sequences of interest and $\varXi \doteq \{\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots) : \xi_t \in \Xi, \forall t\}$ the set of all possible disturbance sequences.

The problem is to control the system (1) such that, for any $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots) \in \varXi$, and for any initial condition $y_0^- \in \mathcal{Y}^0$, the output sequence $\boldsymbol{y} = (y_1, y_2, \ldots)$ of the controlled system tracks any reference sequence $\boldsymbol{r} = (r_1, r_2, \ldots) \in \mathcal{R}$.

In the following, a data-driven polynomial model predictive control (PMPC) method is presented, based on the identification from data of a polynomial prediction model and the online inversion of this model through an efficient optimization.

B. Polynomial prediction model identification

Consider that the system (1) can be represented in the τ-step ahead prediction form

$$\begin{aligned} y_{t+\tau} &= g\left(u_t^+, q_t^-, \xi_t^v\right) \\ u_t^+ &\doteq (u_{t+\tau-1}, \ldots, u_t) \\ q_t^- &\doteq \left(u_t^-, y_t^-\right) \\ \xi_t^v &\doteq (\xi_{t+\tau-1}, \ldots, \xi_{t-n}) \end{aligned} \tag{3}$$

where $g(\cdot) \doteq h^{\tau+1}(\cdot)$, h^i indicates the ith self-composition of the function h and τ is the prediction horizon. This representation can be easily obtained by iteration of (1).

The prediction model that we introduce is an approximation of the system (3), of the form

$$\hat{y}_{t+\tau} = f\left(u_t, q_t^-\right). \tag{4}$$

For simplicity of notation, this model is supposed of the same order as the system (3). The generalization to the case where the order is different is straightforward.

A parametric structure is taken for the function f:

$$f(\cdot) = \sum_{i=1}^{N} \alpha_i \phi_i(\cdot) \tag{5}$$

where ϕ_i are polynomial basis functions, α_i are parameters to identify The basis function choice is in general a crucial step, [34], [20], [31]. Here, the motivations for choosing polynomial functions are mainly two: 1) polynomials have proven to be effective approximators in a huge number of problems; 2) as we will see later, they allow a very efficient controller evaluation. A systematic procedure for the choice of the order n, the prediction horizon τ and the polynomial degree is currently under development.

The model parameters α_i are identified from the data (2) by means of convex optimization: Define

$$z \doteq \begin{bmatrix} \tilde{y}_{n-L+\tau} \\ \vdots \\ \tilde{y}_0 \end{bmatrix}$$

$$\Phi \doteq \begin{bmatrix} \phi_1\left(\tilde{u}_{n-L}, \tilde{q}_{n-L}^-\right) & \cdots & \phi_N\left(\tilde{u}_{n-L}, \tilde{q}_{n-L}^-\right) \\ \vdots & \ddots & \vdots \\ \phi_1\left(\tilde{u}_{-\tau}, \tilde{q}_{-\tau}^-\right) & \cdots & \phi_N\left(\tilde{u}_{-\tau}, \tilde{q}_{-\tau}^-\right) \end{bmatrix}$$

where the tilde denotes the samples obtained from the data set (2). Define also the set

$$\begin{aligned} &SC(\gamma, \sigma) \doteq \{\beta \in \mathbb{R}^N : \\ &|\tilde{y}_{i+\tau} - \tilde{y}_{j+\tau} + (\boldsymbol{\Phi}_j - \boldsymbol{\Phi}_i)\beta| \\ &\leq \gamma \left\|\tilde{y}_i^- - \tilde{y}_j^-\right\| + 2\sigma,\ j \in \mathcal{T}, i \in \Upsilon_j\} \end{aligned}$$

where $\boldsymbol{\Phi}_k$ is the kth row of Φ, $\mathcal{T} \doteq \{n-L, \ldots, -\tau\}$, Υ_k is the index set

$$\Upsilon_k \doteq \left\{i : \left\|\left(\tilde{u}_k, \tilde{u}_k^-\right) - \left(\tilde{u}_i, \tilde{u}_i^-\right)\right\| \leq \zeta\right\}$$

and ζ is the minimum value for which every set Υ_k contains at least two elements. Note that SC is defined by a set of linear inequalities in β and σ, and is thus convex in β and σ. In this paper, the following notation for norms is used: $\|\cdot\| \equiv \|\cdot\|_\infty$ is the vector ℓ_∞ norm; $\|\cdot\|_p$ is in general the vector ℓ_p norm.

The vector $\alpha \in \mathbb{R}^N$, whose entries α_i are the parameters of the model (4)-(5), is identified by means of the following convex algorithm. Note that the algorithm is "self-tuning", in the sense that the required parameters are automatically chosen, without involving extensive heuristic procedures.

Identification algorithm 1: $\alpha = \text{id\_poly\_1}\left(DS, \hat{\gamma}_\Delta\right)$

Compute α as follows:

1) Solve the preliminary optimization problems

$$\begin{aligned} \sigma_0 &= \min_{\beta \in \mathbb{R}^N} \|z - \boldsymbol{\Phi}\beta\| \\ \beta_0 &= \arg\min_{\beta \in \mathbb{R}^N} \|\beta\|_1 \\ \text{s.t.} &\quad \|z - \boldsymbol{\Phi}\beta\| \leq \sigma_0 + \rho\|z\| \end{aligned}$$

where ρ is used to penalize models with high complexity (a simple choice can be $\rho = 0.01$).

2) Solve the optimization problem

$$\begin{array}{rcl}(\alpha, \hat{\sigma}_\Delta) & = & \arg\min_{(\beta,\sigma)} \sigma \\ \text{s.t.} \quad \text{(i)} & & \beta \in SC(\hat{\gamma}_\Delta, \sigma) \\ \text{(ii)} & & \|z - \Phi\beta\|_p \leq \sigma\Lambda \\ \text{(iii)} & & \|\beta\|_1 \leq \eta_0\end{array}$$

where $\eta_0 \doteq \|\beta_0\|_1$ and $\Lambda \doteq \|z - \mathbf{\Phi}\beta_0\|_p / \|z - \mathbf{\Phi}\beta_0\|$.

C. PMPC control algorithm

In this section, a control approach for nonlinear systems is proposed, called data-driven polynomial model predictive control (PMPC), relying on an efficient online inversion of the model (4). The basic idea of this approach is to invert the prediction model: at each time $t > 0$, given a reference $r_{t+\tau}$ and the current regressor q_t^-, a command u_t^* is looked for, such that the model output $\hat{y}_{t+\tau}$ is close to $r_{t+\tau}$. Such a command input is found solving the optimization problem

$$u_t^* = \arg\min_{\mathfrak{u} \in U^\tau} J\left(\mathfrak{u}, r_{t+\tau}, q_t^-\right) \tag{6}$$

$$J\left(\mathfrak{u}, r_{t+\tau}, q_t^-\right) \doteq \left(r_{t+\tau} - f\left(\mathfrak{u}, q_t^-\right)\right)^2 + \mu\mathfrak{u}^2 \tag{7}$$

where $\mu \geq 0$ is a design parameter, determining the trade-off between tracking precision and command activity. The PMPC control law is fully defined by (6).

It is important to observe that the objective function (7) is in general non-convex. Moreover, the optimization problem (6) has to be solved on-line, and this may take a long time compared to the sampling time used in the application of interest. To overcome these problems, an efficient algorithm is now proposed.

Control algorithm 1: $u_t^* = K^*\left(J, r_{t+\tau}, q_t^-\right)$

Compute the optimal input as

$$u_t^* = \arg\min_{\mathfrak{u} \in U^s} J\left(\mathfrak{u}, r_{t+\tau}, q_t^-\right)$$

where

$$U^s \doteq \left(\mathrm{Rroots}\left(J'\left(\mathfrak{u}, r_{t+\tau}, q_t^-\right)\right) \cap U\right) \cup \{\underline{u}, \overline{u}\},$$

J' is the derivative of J wrt $\mathfrak{u}$, $\mathrm{Rroots}\left(J'\right)$ denotes the set of all real roots of J', and $\underline{u}$ and $\overline{u}$ are the boundaries of U.

Remark 1: The derivative J' can be computed analytically. Moreover, U^s is composed by a small number of elements:

$$\mathrm{card}\left(U^s\right) < \deg\left(J\left(\mathfrak{u}, r_{t+\tau}, q_t^-\right)\right) + 2$$

where card is the set cardinality and deg indicates the polynomial degree. The evaluation of u^* through Algorithm 1 is thus extremely fast, since it just requires to find the real roots of a univariate polynomial whose analytical expression is known and to compute the objective function for a small number of values. □

III. Blood glucose regulation for a type 1 diabetic patient

Diabetes mellitus type 1 (DMT1) is a chronic disease which causes the pancreas to produce an incorrect amount of insulin, a protein whose function is to move the glucose from the bloodstream to the liver and muscle cells where it produces energy [1], [2]. A lack of insulin leads to a high glucose concentration in the blood (hyperglycemia), which in turn causes serious damages to various organs and tissues in the human body (e.g., heart, kidneys, eyes, nerves). On the other hand, if the insulin level is too high, the glucose concentration may decrease too much (hypoglycemia), causing again serious health problems. Without access to insulin, people affected by DMT1 have to deal with serious health conditions which typically lead to a premature death.

Control of blood glucose concentration has a fundamental role in terms of patient wellness and integrity of organs that may be damaged due to DMT1 [19], [14], [9], [22], [2]. Control in general implies the availability of reliable models able to predict and/or simulate the behavior of metabolic control in diabetes. Different models and modeling techniques have been proposed in the literature, where physiology equations are used to describe the glucose and insulin kinetics in the body [7], [15]. However, these models are generally not very accurate as their equations do not take into account all the dynamics, parameters and disturbances involved in the patient system. Moreover, physiological models do not allow us to properly cope with the high variability among patients.

Data-driven control represents a possible solution to all these issues. In the following, after a brief description of the available experimental data, a model of a DMT1 patient is identified from a subset of these data. This model, not to be confused with the prediction model of the PMPC algorithm, represents the (unknown) patient, for which a glucose regulator has to be designed. In other words, this patient model is used instead of a real patient (future activities will be devoted to test the data-driven PMPC approach in clinical trials with real patients). After patient model identification, a disturbance estimator is derived, allowing the estimation of the unknown signals that typically affect a diabetic patient (e.g. food, physical activity, emotions, etc.). Next, a PMPC controller for glucose regulation is designed, which takes advantage of the information given by the disturbance estimator. Finally, the controller is tested using fresh data, not previously used for model identification and controller/estimator design.

In a real scenario, the data needed for controller/estimator design can be collected in a preliminary phase of the diabetes treatment, where a "manual" regulation strategy is employed. For example, in this phase, the insulin can be injected by the patient on the basis of his/hers experience and of the physician indications. After this preliminary phase, the

designed controller can be applied to the patient, allowing a fully-automated treatment of diabetes.

A. Experimental dataset

Experimental measurements, collected from a DMT1 kid patient, have been considered. The measured input $\tilde{u}_t$ is the quantity of insulin injected in the patient body. A real-time insulin pump was used to perform subcutaneous injection of insulin. The measured output $\tilde{\tilde{y}}_t$ is the blood glucose concentration, measured by a Continuous Glucose Monitoring (CGM) sensor. This sensor worked continuously for about 13 days, procuring a set of 3744 measurements of blood glucose concentration, collected with a sampling time $T_s = 5$ min. The resulting dataset was partitioned in two subsets:

- Identification dataset (first 4 days): $IS \doteq \left\{\tilde{u}_t, \tilde{\tilde{y}}_t\right\}_{t=-1151}^{0}$, used for model identification and controller design.
- Validation dataset (last 9 days): $VS \doteq \left\{\tilde{u}_t, \tilde{\tilde{y}}_t\right\}_{t=1}^{2592}$, used for model validation and controller test.

B. Patient model identification

In the diabetes context, a relevant problem common to all modeling approaches is that a patient is a system affected by unmeasured (or not easily measurable) inputs (e.g. food, physical activity, emotions, etc.), and the techniques frequently used for model identification are in general not able to recover or to account for such unmeasured signals. Indeed, modeling of a diabetic patient can be seen as a blind identification problem: not only the patient system has to be identified but also some of its input signals [6].

In this paper, a model of a DMT1 patient was derived from the identification set IS, using the blind approach proposed in [30]. This approach provides models of the form (1), with estimates of both the function h and the disturbance ξ_t. The model was identified from the identification set IS, and is given by

$$y_t = h_p\left(u_t^-, y_t^-\right) + \xi_t \tag{8}$$

where u_t is the rate of insulin injected in the patient body, y_t is the patient blood glucose concentration, ξ_t is a disturbance describing the effects of all unknown inputs (e.g. food, physical activity, emotions, etc.), h_p is a function describing the metabolic system kinematics and dynamics. The identified function and disturbance are

$$\begin{aligned} h_p\left(u_t^-, y_t^-\right) &= \textstyle\sum_{i=1}^{P} a_i \chi_i\left(u_t^-, y_t^-\right) \\ \xi_t &= \textstyle\sum_{i=1}^{M} b_i \psi_i(t) \end{aligned} \tag{9}$$

where χ_i and ψ_i are basis functions, and a_i and b_i are parameters estimated solving the convex optimization problem presented in [30]. A model order $n = 9$ has been assumed, since giving the best trade-off between accuracy and complexity (no accuracy improvements were observed for larger orders). Polynomial basis functions χ_i with degree ranging in the interval $[0, 2]$ were considered for the function h. Indeed, no accuracy improvements were observed for larger degrees. On the other hand, a model accuracy degradation was observed using only polynomial functions with degree ≤ 1. Gaussian basis functions $\psi_i(t) = e^{-\beta(t-i)^2}$ were used for the disturbance ξ_t, with $i = 1, \ldots, 1152$ and $\beta = 0.03$ (this value of β was chosen through a trial-and-error procedure).

This patient model was tested on the validation set VS: A simulation of the model was performed, using as inputs the measured insulin signal $\tilde{u}_t$ and the disturbance ξ_t estimated from the validation set. This estimation was carried out solving the optimization problem in [30], only with respect to b, with a fixed and equal to the one previously estimated on the identification set. Figure 1 shows the estimated disturbance (upper plot), the measured insulin input (middle plot), and the output simulated by the model compared with the measured one (bottom plot). The root mean square error resulting from the simulation is $RMSE = 14.4$ mg/dl.

Other simulations were carried out to validate the model: In one simulation, the model was fed by the disturbance signal ξ_t estimated from the validation set and by a null insulin input u_t. Being this signal characterized by several positive peaks (presumably corresponding to meals), the output resulting from this simulation became very large, according to a typical hyperglycemia behavior. In another simulation, the model was fed by a null disturbance ξ_t and by the measured insulin input $\tilde{u}_t$, taken from the validation set. The output moved towards low values, according to a typical hypoglycemia behavior. All these simulations demonstrate that the identified patient model has a quite reasonable behavior form a physiological point of view.

In the present paper, the model (8) represents the patient for which a glucose regulator has to be designed. This model is assumed unknown (as it happens in a real situation). Only the following data are used for regulator design:

- Design dataset (first 4 days): $DS \doteq \{\tilde{u}_t, \tilde{y}_t\}_{t=-1151}^{0}$, used for controller design. $\tilde{u}_t$ is the measured insulin signal of IS and $\tilde{y}_t$ is the blood glucose concentration simulated by the patient model, fed by $\tilde{u}_t$ and the recovered disturbance signal ξ_t. Note that, in the case where not a patient model but a real patient is under therapy, the sets IS and DS coincide.

C. Disturbance estimator design

A disturbance estimator was designed, whose output was used as an input of the PMPC controller of Section (III-D), in order to enhance its performance.

As discussed in Section III-B, the blind identification method of [30] allows the estimation of the disturbance affecting a dynamic system. However, such an estimate cannot be performed on-line, since it is non-causal: the estimate at a given time instant is computed using past and future measurements.

Here, a causal estimator was built, using again the method of [30] but obtaining the estimate in a different way. The estimator is defined by

$$\hat{\xi}_t = y_t - \hat{h}_p\left(u_t^-, y_t^-\right) \tag{10}$$

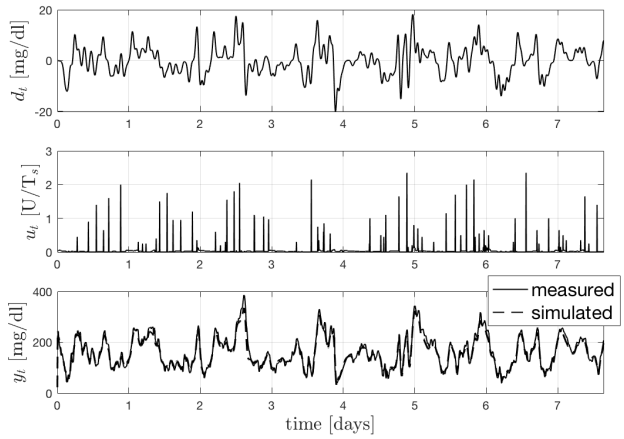

Fig. 1. Upper: estimated disturbance. Middle: insulin signal. Lower: comparison between patient model and measured output.

where $\hat{\xi}_t$ is the estimate of the unknown disturbance ξ_t affecting the patient model (8), y_t is the output of the patient model, and u_t^- and y_t^- are the corresponding input and output regressors. The identified function is

$$\hat{h}_p\left(u_t^-, y_t^-\right) = \sum_{i=1}^{P} \hat{a}_i \chi_i\left(u_t^-, y_t^-\right).$$

where χ_i are polynomial basis functions with maximum degree 2. The parameters $\hat{a}_i$ were estimated from the design set DS by means of the optimization problem in [30]. For this estimator, an order $n = 6$ has been chosen to mimic a real situation, where the order of the true system (i.e., $n = 9$) is not known.

D. Data-driven PMPC design

Using the PMPC approach described in Section II, a blood glucose regulation algorithm was designed, according to the following procedure:

1) *Prediction model identification*. A prediction model is identified from the design set DS, using the identification algorithm 1. The prediction model is of the form (4), with $q_t^- \doteq \left(u_t^-, y_t^-, \hat{\xi}_t^-\right)$, where $\hat{\xi}_t^-$ is the regressor of the on-line disturbance estimate $\hat{\xi}_t$ provided by (10).
2) *PMPC controller design*. From the prediction model identified in step 1, a PMPC controller is designed and implemented, according to the control algorithm 1.
3) *PMPC controller preliminary test*. The PMPC controller designed in step 2 is tested in closed-loop on the patient model (8). The glucose concentration reference value $r_t = 130$ mg/dl, $\forall t$, and the recovered disturbance ξ_t of the design dataset DS are used.

This procedure was repeated many times considering several prediction model orders, prediction horizons, polynomial degrees and values of μ in (7). The following parameters were chosen, since providing the best closed-loop performance: model order 5, prediction horizon 8, polynomial basis functions up to degree 2, $\mu = 0.1$. A linear model was also considered but the resulting closed-loop performance was not completely satisfactory. Note that the whole design (disturbance estimator, prediction model, control algorithm design and preliminary test) was carried out using only the design set DS.

	AUC	AAC
PMPC	0.07	0.50
"manual"	0.10	13.76

TABLE I
DIABETES TREATMENT QUALITY.

E. Blood glucose regulation

The PMPC controller designed in Section III-D was tested in closed-loop on the patient model (8). In this figure, "plant" is the patient model (8), K^* is the controller (including the disturbance estimator (10)), y_t is the patient blood glucose concentration, r_t is a desired reference value, and ξ_t is a disturbance describing the effects of all unknown inputs (e.g. food, physical activity, emotions, etc.). The glucose concentration reference value $r_t = 130$ mg/dl, $\forall t$, and the recovered disturbance ξ_t of the validation set VS were used.

For comparison, also a "manual" regulation strategy was tested, where the insulin was injected by the patient on the basis of his/hers experience and of the indications coming from a semi-automated glucose regulation device (to be close to the real situation, the measured insulin signal $\tilde{u}_t$ of the validation set VS was taken).

In general, the goal of regulation is too keep the value of the blood glucose concentration y_t inside the interval $[70, 180]$ mg/dl which, in diabetes treatment medicine, is commonly considered a safe interval. Thus, the following indexes were used to measure the quality of the treatment:

$$AUC \doteq \frac{1}{2592} \sum_{t=1}^{2592} (y_t < 70)(70 - y_t)$$
$$AAC \doteq \frac{1}{2592} \sum_{t=1}^{2592} (y_t > 180)(y_t - 180)$$

where $(y_t < 70)$ and $(y_t > 180)$ are logical operators. These indexes, called *area under the curve* (AUC) and *area above the curve* (AAC), respectively, measure the amount of glucose exceeding the bounds. The values obtained by the PMPC and "manual" strategies with the disturbance ξ_t of the validation set VS are reported in Table I. The corresponding glucose concentration signals for the two strategies are shown in Figure 2. These results demonstrate that the PMPC strategy is effective in regulating the blood glucose concentration, yielding significantly lower values of AAC with respect to the "manual" strategy. It must be remarked that this "manual" strategy is a real one, actually applied to a real diabetic patients, and the dot-dashed curve in Figure 2 represents quite accurately what happened to the blood glucose concentration in the real patient.

IV. CONCLUSIONS

A data-driven polynomial model predictive control (PMPC) approach for nonlinear systems has been presented,

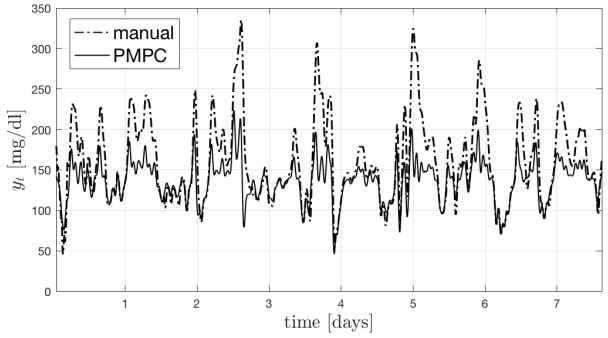

Fig. 2. Diabetes treatment test.

showing features which can make it effective in challenging real-world applications: it does not require a physical model of the system to control; it is systematic and relatively simple; it can be applied to a wide class of nonlinear systems; it is numerically efficient. The approach has been employed with success in a real data case study, regarding insulin regulation in a type 1 diabetic patient.

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