

Data and Decision Analysis

Project work

A bioreactor for bacterial fermentation is described by the following discrete-time system

$$\begin{aligned}x_1(k+1) &= x_1(k) - T_c u(k) x_1(k) + T_c \alpha(k) x_1(k) x_2(k) \\x_2(k+1) &= x_2(k) + T_c u(k) [S_{in} - x_2(k)] - T_c K_p \alpha(k) x_1(k) x_2(k)\end{aligned}$$

where

- T_c is the sampling time;
- $x_1(k)$ is the bacterial concentration at time k ;
- $x_2(k)$ is the concentration of the substrate necessary for the growth of the bacterial population, at time k ;
- $u(k)$ is the dilution rate at time k ;
- $\alpha(k)$ is the specific growth rate at time k ;
- S_{in} e K_p are known constant parameters.

Measurements of the bacterial concentration are collected at each time k

$$y(k) = x_1(k) + v(k)$$

where $v(k)$ represents measurement noise and is modeled as a white zero-mean stochastic process, with variance σ_v^2 .

- a) Design and implement an Extended Kalman Filter for estimating the state variables $x_1(k)$ and $x_2(k)$ at each time k , based on the measurements $y(t)$ and the input signals $u(t)$ and $\alpha(t)$, with $t = 1, 2, \dots, k$.
- b) Assume now that the input $\alpha(k)$ is not known and therefore it must be estimated along with the state variables. Define an extended model in which the state vector contains a new variable $x_3(k) = \alpha(k)$, whose dynamics can be modeled according to

$$x_3(k+1) = x_3(k) + w(k)$$

in which $w(k)$ is modeled as a white zero-mean stochastic process, with variance σ_w^2 . Design and implement an Extended Kalman Filter for estimating the state variables $x_i(k)$, $i = 1, 2, 3$, using the same data employed in item a) for $y(k)$ and $u(k)$. Compare the estimation errors of x_1 e x_2 , and the corresponding variances, to the values obtained in the case in which α is known.

[Suggestion: choose carefully the value of the process noise variance σ_w^2 in the equation of the state variable $x_3(k)$ and discuss the results for different values of σ_w^2].

- c) In both items a) and b) evaluate:

- the consistency of the filter, by comparing the estimation errors of each state variable $x_i(k) - \hat{x}_i(k|k)$ with the corresponding confidence intervals $\pm 3\sqrt{P_{ii}(k|k)}$;
- the behavior of the filter as a function of the initial conditions $\hat{x}(0|-1)$, $P(0|-1)$.

Data available in the file `dati#_bioreactor.mat`:

y: vector of measurements $y(k)$, $k = 0, \dots, N$;

u: vector of inputs $u(k)$, $k = 0, \dots, N$;

alfa: vector of inputs $\alpha(k)$, $k = 0, \dots, N$, to be used in item a) as known input, (while in item b) only for the comparisons described in item c));

X: matrix $N \times 2$ of true states $x_i(k)$, $i = 1, 2$, $k = 0, \dots, N$, to be used only for the comparisons described in item c) (the entry k,i in the matrix corresponds to $x_i(k)$);

R: variance σ_v^2 of the measurement noise $v(k)$;

Tc, Kp, Sin: values of the parameters T_c , K_p , S_{in} .