

Designing a hybrid in silico/in-cell controller robust to process–model mismatch associated with dynamically regulated enzyme overexpression

Author information

Tomoki Ohkubo^{1*}, Yuichi Sakumura^{1,2}, Fuzhong Zhang³, Katsuyuki Kunida^{1,4}

¹ Graduate School of Science and Technology, Nara Institute of Science and Technology, Ikoma, Nara, 8916-5, Japan

² Data Science Center, Nara Institute of Science and Technology, Ikoma, Nara, 8916-5, Japan

³ Department of Energy, Environmental and Chemical Engineering, Washington University in St. Louis, St. Louis, MO 63130, USA

⁴ School of Medicine, Fujita Health University, Toyoake, Aichi, 470-1192, Japan

*Correspondence: okubo.tomoki.ou1@naist.ac.jp

Supporting information

Table S1.

Process outputs and measurement time in the experimental datasets.

Process output		Measurement time	
Index i	Name	Index l	Value [h]
1	Relative cell density	1	0
		2	1
		3	5
		4	9
		5	13
		6	17
		7	21
		8 (= N_1)	25
2	Fatty acid concentration	1	0
		2 (= N_2)	25

Table S2.

E. coli strains and IPTG input levels in the experimental datasets.

Strain		IPTG input level	
Index j	Name	Index k	Value [μM]
1	FA2	1	0
		2	10
		3	40
		4	100
		5	400
		6 ($= M_1$)	1000
2	FA3	1 ($= M_2$)	100