A hybrid approach for efficient and robust parameter
estimation in biochemical pathways

#	Paper	IF	Citations
234	Insights into the behaviour of systems biology models from dynamic sensitivity and identifiability analysis: a case study of an NF-kappaB signalling pathway. **2006**, 2, 640-9		106
233	Dynamic modelling and analysis of biochemical networks: mechanism-based models and model-based experiments. **2006**, 7, 364-74		182
232	Systems interface biology. **2006**, 3, 603-16		40
231	Bringing metabolic networks to life: integration of kinetic, metabolic, and proteomic data. **2006**, 3, 42		53
230	Linking data to models: data regression. **2006**, 7, 813-9		177
229	Novel metaheuristic for parameter estimation in nonlinear dynamic biological systems. **2006**, 7, 483		191
228	Information Technology in Systems Biology (Informationstechnologien in der Systembiologie). **2006**, 48, 133-139		0
227	Complex parameter landscape for a complex neuron model. *PLoS Computational Biology*, **2006**, 2, e94	5	185
226	Robust parameter estimation in a model for glucose kinetics in type 1 diabetes subjects. **2006**, 2006, 319-22		5
225	Universally sloppy parameter sensitivities in systems biology models. *PLoS Computational Biology*, **2007**, 3, 1871-78	5	774
224	Optimal experimental design based on global sensitivity analysis. **2007**, 63-68		16
223	Bioengineering novel in vitro metabolic pathways using synthetic biology. **2007**, 10, 246-53		44
222	Systems biology--an engineering perspective. **2007**, 129, 329-51		57
221	Efficient algorithms for ordinary differential equation model identification of biological systems. *IET Systems Biology*, **2007**, 1, 120-9	1.4	38
220	Metabolomic biomarkers: search, discovery and validation. **2007**, 7, 329-33		37
219	Systems Level Modeling of the Cell Cycle Using Budding Yeast. *Cancer Informatics*, **2007**, 3, 117693510700300		4
218	Optimal design of dynamic experiments for improved estimation of kinetic parameters of thermal degradation. **2007**, 82, 178-188		40

199	A set-based framework for coherent model invalidation and parameter estimation of discrete time nonlinear systems. **2009**,	13
198	A new probabilistic generative model of parameter inference in biochemical networks. **2009**,	4
197	Modeling metabolic networks in C. glutamicum: a comparison of rate laws in combination with various parameter optimization strategies. **2009**, 3, 5	53
196	Systematic identifiability testing for unambiguous mechanistic modeling--application to JAK-STAT, MAP kinase, and NF-kappaB signaling pathway models. **2009**, 3, 50	68
195	Inferring Drosophila gap gene regulatory network: a parameter sensitivity and perturbation analysis. **2009**, 3, 94	22
194	Optimal Design of Experiments for Parameter Identification of Ceramic Porous Membranes. **2009**, 32, 641-649	4
193	Parameter estimation for linear compartmental models--a sensitivity analysis approach. **2009**, 37, 1028-42	4
192	Iron behaving badly: inappropriate iron chelation as a major contributor to the aetiology of vascular and other progressive inflammatory and degenerative diseases. **2009**, 2, 2	349
191	Systems biology: experimental design. **2009**, 276, 923-42	180
190	Systems biology: parameter estimation for biochemical models. **2009**, 276, 886-902	223
189	Bioinformatics and computational methods for lipidomics. **2009**, 877, 2855-62	78
188	Calibration of a kinetic model for wet air oxidation (WAO) of substituted phenols: Influence of experimental data on model prediction and practical identifiability. **2009**, 150, 328-336	4
187	Improving prediction capabilities of complex dynamic models via parameter selection and estimation. **2009**, 64, 4178-4185	28
186	An anticipatory approach to optimal experimental design for model discrimination. *Chemometrics and Intelligent Laboratory Systems*, **2009**, 95, 53-63	3.8	27
185	Hybrid differential evolution with geometric mean mutation in parameter estimation of bioreaction systems with large parameter search space. **2009**, 33, 1851-1860	20
184	Gene regulatory network inference: data integration in dynamic models-a review. *BioSystems*, **2009**, 96, 86-103	1.9	537
183	Mass Transport in Multilayer Porous Metallic Membranes □Diagnosis, Identification and Validation. **2009**, 32, 632-640	4
182	Input-output behavior of ErbB signaling pathways as revealed by a mass action model trained against dynamic data. **2009**, 5, 239	287

163	Transport Phenomena in Porous Membranes and Membrane Reactors. **2010**, 85-132	
162	Mathematical modeling: bridging the gap between concept and realization in synthetic biology. **2010**, 2010, 541609	26
161	Computational Challenges in Systems Biology. **2010**, 175-223	2
160	Automating Mathematical Modeling of Biochemical Reaction Networks. **2010**, 159-205	3
159	Delineating role of ubiquitination on nuclear factor-kappa B pathway by a computational modeling approach. **2010**, 391, 33-7	5
158	Parameter Scanning by Parallel Model Checking with Applications in Systems Biology. **2010**,	5
157	Sloppy models, parameter uncertainty, and the role of experimental design. **2010**, 6, 1890-900	90
156	Identification of optimal drug combinations targeting cellular networks: integrating phospho-proteomics and computational network analysis. **2010**, 70, 6704-14	161
155	A cooperative strategy for parameter estimation problems in Systems Biology: Preliminary results. **2011**,	
154	ON IDENTIFIABILITY OF NONLINEAR ODE MODELS AND APPLICATIONS IN VIRAL DYNAMICS. **2011**, 53, 3-39	286
153	Computational modeling of mitochondrial energy transduction. **2011**, 39, 363-77	7
152	Inference of Signalling Pathway Models. **2011**, 417-439	
151	Development of a simple unified volatility-based scheme (SUVS) for secondary organic aerosol formation using genetic algorithms. **2011**, 11, 6185-6205	2
150	Reaction kinetics of catalyzed competitive heteropolymer cleavage. **2011**, 115, 11017-27	6
149	An integrative and practical evolutionary optimization for a complex, dynamic model of biological networks. **2011**, 34, 433-46	11
148	Parameter estimation with a novel gradient-based optimization method for biological lattice-gas cellular automaton models. **2011**, 63, 173-200	13
147	Parameter estimation and dynamic control analysis of central carbon metabolism in Escherichia coli. **2011**, 16, 216-228	8
146	An Artificial Neural Network approximation based decomposition approach for parameter estimation of system of ordinary differential equations. **2011**, 35, 545-553	38

145	Inference in HIV dynamics models via hierarchical likelihood. **2011**, 55, 446-456	5
144	Detailed kinetic model describing new oligosaccharides synthesis using different ꞵgalactosidases. **2011**, 153, 116-24	18
143	Dynamics of rate limiting enzymes involved in the sequential substrate uptake by Pseudomonas putida CSV86: Modeling and experimental validation. **2011**, 46, 701-708	3
142	Modeling and analysis of biopathways dynamics. **2012**, 10, 1231001	8
141	A Novel Multi-Objective Optimization based Experimental Design and its Application for Physiological Model of Type 1 Diabetes. **2012**, 45, 638-643	4
140	Parameter estimation using meta-heuristics in systems biology: a comprehensive review. **2012**, 9, 185-202	85
139	A Bayesian approach to targeted experiment design. **2012**, 28, 1136-42	64
138	On parameter synthesis by parallel model checking. **2012**, 9, 693-705	34
137	A Bio-inspired Optimization Algorithm for Modeling the Dynamics of Biological Systems. **2012**,	1
136	Optimal experiment selection for parameter estimation in biological differential equation models. **2012**, 13, 181	20
135	A novel cost function to estimate parameters of oscillatory biochemical systems. **2012**, 2012, 3	1
134	Set membership experimental design for biological systems. **2012**, 6, 21	11
133	Two stage optimization of biochemical pathways using parallel runs of global stochastic optimization methods. **2012**,	2
132	A Simultaneous Approach for Parameter Estimation of a System of Ordinary Differential Equations, Using Artificial Neural Network Approximation. **2012**, 51, 1809-1814	9
131	Novel global sensitivity analysis methodology accounting for the crucial role of the distribution of input parameters: application to systems biology models. **2012**, 22, 1082-1102	33
130	Indirect method for quantification of cellular biomass in a solidscontaining medium used as pre-culture for cellulase production. **2012**, 17, 100-108	11
129	Model-based global sensitivity analysis as applied to identification of anti-cancer drug targets and biomarkers of drug resistance in the ErbB2/3 network. **2012**, 46, 244-58	25
128	ConvAn: a convergence analyzing tool for optimization of biochemical networks. *BioSystems*, **2012**, 108, 73-7	1.9	11

127	Model-based selection of the robust JAK-STAT activation mechanism. **2012**, 309, 34-46	7
126	A global parallel model based design of experiments method to minimize model output uncertainty. **2012**, 74, 688-716	20
125	Smooth functional tempering for nonlinear differential equation models. **2012**, 22, 429-443	28
124	The relation between growth phases, cell volume changes and metabolism of adherent cells during cultivation. **2013**, 164, 489-99	12
123	Advances in Food Process Engineering Research and Applications. *Food Engineering Series*, **2013**,	0.5	5
122	Identification of parameter correlations for parameter estimation in dynamic biological models. **2013**, 7, 91	46
121	Simultaneous model discrimination and parameter estimation in dynamic models of cellular systems. **2013**, 7, 76	25
120	Estimation of neoplasia-related biological parameters through modeling and sensitivity analysis of optical molecular imaging data. **2013**, 60, 1241-9	3
119	Model-based design of experiments for cellular processes. **2013**, 5, 181-203	32
118	Modeling of a Biobutanol Adsorption Process for Designing an Extractive Fermentor. **2013**, 52, 603-611	31
117	Modeling antiretroviral drug responses for HIV-1 infected patients using differential equation models. **2013**, 65, 940-53	42
116	Modeling the Semicontinuous Heterophase Polymerization for Synthesizing Poly(n-butyl methacrylate) Nanoparticles. **2013**, 7, 440-452	3
115	Multiobjective Framework for Model-based Design of Experiments to Improve Parameter Precision and Minimize Parameter Correlation. **2013**, 52, 8289-8304	14
114	KInfer: a tool for model calibration. **2013**, 280-321	
113	Reverse-engineering post-transcriptional regulation of gap genes in Drosophila melanogaster. *PLoS Computational Biology*, **2013**, 9, e1003281	5	31
112	Systematic parameter estimation in data-rich environments for cell signalling dynamics. **2013**, 29, 1044-51	9
111	SPEDRE: a web server for estimating rate parameters for cell signaling dynamics in data-rich environments. **2013**, 41, W187-91	2
110	Automated parameters retrieval for energetic model identification of servers in datacenters. **2013**,	1

109	CHAOTIC ANALOG-TO-INFORMATION CONVERSION: PRINCIPLE AND RECONSTRUCTABILITY WITH PARAMETER IDENTIFIABILITY. **2013**, 23, 1350198		1
108	Multi-Criteria Optimization Based Experimental Design for Parameter Estimation of a Double Feedback Gene Switching Model. **2013**, 46, 333-337		1
107	An improved swarm optimization for parameter estimation and biological model selection. *PLoS ONE*, **2013**, 8, e61258	3.7	13
106	Integrated signaling pathway and gene expression regulatory model to dissect dynamics of Escherichia coli challenged mammary epithelial cells. *BioSystems*, **2014**, 126, 27-40	1.9	6
105	On structural identifiability of S-system. **2014**,		1
104	On the Choice of Nugget in Kriging Modeling for Deterministic Computer Experiments. **2014**, 23, 151-168		30
103	Metabolomics and systems pharmacology: why and how to model the human metabolic network for drug discovery. **2014**, 19, 171-82		122
102	Kinetic models in industrial biotechnology - Improving cell factory performance. **2014**, 24, 38-60		183
101	Model identification of a template-directed peptide network for optimization in a continuous reactor. **2014**, 50, 3849-51		4
100	Differential simulated annealing: a robust and efficient global optimization algorithm for parameter estimation of biological networks. **2014**, 10, 1385-92		8
99	An extended dynamic model of Lactococcus lactis metabolism for mannitol and 2,3-butanediol production. **2014**, 10, 628-39		12
98	Recursive estimation of selective catalyst reduction system parameters using modified Gauss-Newton method. **2014**,		
97	A model comparison study of the flowering time regulatory network in Arabidopsis. **2014**, 8, 15		12
96	An ANOVA test for parameter estimability using data cloning with application to statistical inference for dynamic systems. **2014**, 70, 257-267		19
95	Stochastic differential equations as a tool to regularize the parameter estimation problem for continuous time dynamical systems given discrete time measurements. **2014**, 251, 54-62		24
94	Dynamic Model Building Using Optimal Identification Strategies, with Applications in Bioprocess Engineering. **2014**, 441-467		
93	Data Analytical Methods for the Application of Systems Biology in Nutrition. **2015**, 235-249		
92	Automated parameter estimation for biological models using Bayesian statistical model checking. **2015**, 16 Suppl 17, S8		10

91	Run-to-Run Optimization of Biodiesel Production using Probabilistic Tendency Models: A Simulation Study. **2015**, 93, 1613-1623		4
90	A unified framework for estimating parameters of kinetic biological models. **2015**, 16, 104		12
89	Parameter identification and validation analysis for a small USV. **2015**,		3
88	Structural and practical identifiability analysis of S-system. *IET Systems Biology*, **2015**, 9, 285-93	1.4	4
87	Parameters identification in the mathematical model of immune competition cells. **2015**, 23,		0
86	Embedded multiple shooting methodology in a genetic algorithm framework for parameter estimation and state identification of complex systems. **2015**, 134, 605-618		5
85	Reverse engineering of logic-based differential equation models using a mixed-integer dynamic optimization approach. **2015**, 31, 2999-3007		16
84	Robust and efficient parameter estimation in dynamic models of biological systems. **2015**, 9, 74		76
83	New trends and perspectives in nonlinear intracellular dynamics: one century from MichaelisMenten paper. **2015**, 27, 659-684		31
82	Model-based analysis of chemical-looping combustion experiments. Part I: Structural identifiability of kinetic models for NiO reduction. **2016**, 62, 2419-2431		27
81	Concentrations monitoring via software sensor for bioreactors under model parametric uncertainty: Application to cadmium removal in an anaerobic process. **2016**, 55, 1893-1902		6
80	Time Course Analysis of Enzyme-Catalyzed DNA Polymerization. **2016**, 55, 5622-5634		7
79	Adaptive position-dependent friction characteristics for electromagnetic actuators. **2016**,		0
78	Inverse problem studies of biochemical systems with structure identification of S-systems by embedding training functions in a genetic algorithm. **2016**, 275, 93-106		1
77	Global optimization advances in Mixed-Integer Nonlinear Programming, MINLP, and Constrained Derivative-Free Optimization, CDFO. **2016**, 252, 701-727		126
76	Search for a Minimal Set of Parameters by Assessing the Total Optimization Potential for a Dynamic Model of a Biochemical Network. **2017**, 14, 978-985		5
75	Predicting network modules of cell cycle regulators using relative protein abundance statistics. **2017**, 11, 30		5
74	An improved hybrid of particle swarm optimization and the gravitational search algorithm to produce a kinetic parameter estimation of aspartate biochemical pathways. *BioSystems*, **2017**, 162, 81-89	1.9	5

| 73 | Identification of microbiota dynamics using robust parameter estimation methods. **2017**, 294, 71-84 | 8 |

| 72 | State Estimation Based on Nonlinear Observer for Hydrogen Production in a Photocatalytic Anaerobic Bioreactor. **2017**, 15, | 6 |

| 71 | Sequential-Optimization-Based Framework for Robust Modeling and Design of Heterogeneous Catalytic Systems. **2017**, 121, 25847-25863 | 30 |

| 70 | How graphical analysis helps interpreting optimal experimental designs for nonlinear enzyme kinetic models. **2017**, 63, 4870-4880 | 13 |

| 69 | Parameter identifiability analysis and visualization in large-scale kinetic models of biosystems. **2017**, 11, 54 | 51 |

| 68 | In Silico Approaches to Metabolic Engineering. **2017**, 161-200 | 2 |

| 67 | Optimal Model Parameter Estimation from EEG Power Spectrum Features Observed during General Anesthesia. **2018**, 16, 231-251 | 9 |

| 66 | Diffusion kurtosis imaging with free water elimination: A bayesian estimation approach. **2018**, 80, 802-813 | 13 |

| 65 | Estimation of biophysical parameters in a neuron model under random fluctuations. **2018**, 329, 364-373 | 2 |

| 64 | Computational Modeling of the Early Development of Embryonic Leaves in Maize. **2018**, | |

| 63 | Comparison and Identifiability Analysis of Friction Models for the Dither Motion of a Solenoid. **2018**, | 0 |

| 62 | libRCGA: a C library for real-coded genetic algorithms for rapid parameter estimation of kinetic models. **2018**, 11, 31-40 | 4 |

| 61 | Identification of parameters in systems biology. **2018**, 305, 133-145 | 3 |

| 60 | Descriptive Modeling of the Dynamical Systems and Determination of Feedback Homeostasis at Different Levels of Life Organization. **2018**, 66, 177-199 | |

| 59 | Adaptive optimal input design and parametric estimation of nonlinear dynamical systems: application to neuronal modeling. **2018**, 15, 046028 | 2 |

| 58 | On the Identifiability of Physiological Models: Optimal Design of Clinical Tests. **2018**, 85-110 | 1 |

| 57 | Evaluation and Calibration of In Silico Models of Thrombin Generation Using Experimental Data from Healthy and Haemophilic Subjects. **2018**, 80, 1989-2025 | 6 |

| 56 | Predicting perturbation patterns from the topology of biological networks. **2018**, 115, E6375-E6383 | 88 |

55	Unwinding the model manifold: Choosing similarity measures to remove local minima in sloppy dynamical systems. **2019**, 100, 012206	0
54	A new efficient parameter estimation algorithm for high-dimensional complex nonlinear turbulent dynamical systems with partial observations. **2019**, 397, 108836	4
53	Comprehensive Review of Models and Methods for Inferences in Bio-Chemical Reaction Networks. **2019**, 10, 549	16
52	Global sensitivity analysis for the design of nonlinear identification experiments. **2019**, 98, 375-394	6
51	A scalable method for parameter identification in kinetic models of metabolism using steady-state data. **2019**, 35, 5216-5225	3
50	Model validation in dynamic systems for time-course data with complex error structures. **2019**, 33, e3108	
49	Global optimization using Gaussian processes to estimate biological parameters from image data. **2019**, 481, 233-248	1
48	Sequential state prediction and parameter estimation with constrained dual extended Kalman filter for building zone thermal responses. **2019**, 183, 538-546	11
47	The costs and benefits of estimating T of tissue alongside cerebral blood flow and arterial transit time in pseudo-continuous arterial spin labeling. **2020**, 33, e4182	5
46	Parameter estimation and sensitivity analysis for dynamic modelling and simulation of beer fermentation. **2020**, 136, 106665	3
45	. **2020**,	3
44	Virtual Sensor Design for State Estimation in a Photocatalytic Bioreactor for Hydrogen Production. **2020**, 255-276	
43	Identifiability and Regression Analysis of Biological Systems Models. *SpringerBriefs in Statistics*, **2020**,	0.2
42	Learning nonlinear turbulent dynamics from partial observations via analytically solvable conditional statistics. **2020**, 418, 109635	6
41	Effective Parameterization of PEM Fuel Cell Models─Part I: Sensitivity Analysis and Parameter Identifiability. **2020**, 167, 044504	12
40	Identification of parameters for large-scale kinetic models. **2021**, 429, 110026	1
39	Use of Non-linear Empirical Models to Predict the Substrate Degradation, Enzymatic Activity and Cell Growth in a Bioreactor with Aspergillus niger and Sugarcane Bagasse. **2021**, 12, 4433	
38	Using Shooting Approaches to Generate Initial Guesses for ODE Parameter Estimation. **2021**, 267-276	

No.	Title	IF	Cit.
37	Optimal Experimental Design for Systems and Synthetic Biology Using AMIGO2. *Methods in Molecular Biology*, **2021**, 2229, 221-239	1.4	2
36	An integrated framework for building trustworthy data-driven epidemiological models: Application to the COVID-19 outbreak in New York City.		1
35	Bilevel optimal control of urban traffic-related air pollution by means of Stackelberg strategies. 1		0
34	Introducing Parameter Clustering to the OED Procedure for Model Calibration of a Synthetic Inducible Promoter in S. cerevisiae. *Processes*, **2021**, 9, 1053	2.9	
33	Parameter Estimation of Partially Observed Turbulent Systems Using Conditional Gaussian Path-Wise Sampler. *Computation*, **2021**, 9, 91	2.2	
32	Quantifying biochemical reaction rates from static population variability within complex networks.		
31	An integrated framework for building trustworthy data-driven epidemiological models: Application to the COVID-19 outbreak in New York City. *PLoS Computational Biology*, **2021**, 17, e1009334	5	2
30	Parameter inference and model selection in signaling pathway models. *Methods in Molecular Biology*, **2010**, 673, 283-95	1.4	11
29	Improved Parameter Estimation in Kinetic Models: Selection and Tuning of Regularization Methods. *Lecture Notes in Computer Science*, **2014**, 45-60	0.9	4
28	Sloppiness and the Geometry of Parameter Space. *Studies in Mechanobiology, Tissue Engineering and Biomaterials*, **2016**, 271-299	0.5	12
27	A Heuristic Search for Optimal Parameter Values of Three Biokinetic Growth Models for Describing Batch Cultivations of Streptococcus Pneumoniae in Bioreactors. *Lecture Notes in Computer Science*, **2008**, 359-368	0.9	3
26	Global Sensitivity Analysis of a Biochemical Pathway Model. *Advances in Soft Computing*, **2009**, 233-242		3
25	Improved Parameter Estimation for Completely Observed Ordinary Differential Equations with Application to Biological Systems. *Lecture Notes in Computer Science*, **2009**, 205-217	0.9	1
24	Hierarchy cuckoo search algorithm for parameter estimation in biological systems. *Chemometrics and Intelligent Laboratory Systems*, **2016**, 159, 97-107	3.8	17
23	Parameter estimation and optimal experimental design. *Essays in Biochemistry*, **2008**, 45, 195-209	7.6	102
22	Application of conditional robust calibration to ordinary differential equations models in computational systems biology: a comparison of two sampling strategies. *IET Systems Biology*, **2020**, 14, 107-119	1.4	5
21	Predicting perturbation patterns from the topology of biological networks.		3
20	Systems biology informed deep learning for inferring parameters and hidden dynamics.		1

19	A Quasi-Monte Carlo Approach to Bayesian Parameter Estimation for Nonlinear Dynamic Process Models. *Journal of Chemical Engineering of Japan*, **2013**, 46, 467-479	0.8	0
18	Systems biology informed deep learning for inferring parameters and hidden dynamics. *PLoS Computational Biology*, **2020**, 16, e1007575	5	37
17	Modeling the intra- and extracellular cytokine signaling pathway under heat stroke in the liver. *PLoS ONE*, **2013**, 8, e73393	3.7	13
16	The impact of parameter identification methods on drug therapy control in an intensive care unit. *Open Medical Informatics Journal*, **2008**, 2, 92-104	1	10
15	Automatic Control in Systems Biology. **2009**, 1335-1360		
14	Dynamic Model Building Using Optimal Identification Strategies, with Applications in Bioprocess Engineering. 441-467		
13	Developing Next-Generation Predictive Models: Systems Biology Approach. *Food Engineering Series*, **2013**, 547-565	0.5	
12	Determinition of best set of adjustable parameters with full search and limited search methods. *Biosystems and Information Technology*, **2013**, 2, 11-14		1
11	Direct Sequential Based Firefly Algorithm for the (alpha)-Pinene Isomerization Problem. *Lecture Notes in Computer Science*, **2016**, 386-401	0.9	1
10	Structural and Practical Identifiability of Dual-input Kinetic Modeling in Dynamic PET of Liver Inflammation.		
9	Model Identifiability. *SpringerBriefs in Statistics*, **2020**, 37-48	0.2	
8	The Present and the Future Perspectives of Biological Network Inference. *Advances in Bioinformatics and Biomedical Engineering Book Series*, 118-140	0.4	0
7	Systems level modeling of the cell cycle using budding yeast. *Cancer Informatics*, **2007**, 3, 357-70	2.4	3
6	Isotope-assisted metabolic flux analysis as an equality-constrained nonlinear program for improved scalability and robustness.. *PLoS Computational Biology*, **2022**, 18, e1009831	5	0
5	Data_Sheet_1.PDF. **2019**,		
4	Simulation-Based Inference for Whole-Brain Network Modeling of Epilepsy using Deep Neural Density Estimators.		0
3	Quantifying biochemical reaction rates from static population variability within incompletely observed complex networks. *PLoS Computational Biology*, **2022**, 18, e1010183	5	
2	Mini-batching ecological data to improve ecosystem models with machine learning.		

1   A reinforcement learning-based hybrid modeling framework for bioprocess kinetics identification.   0