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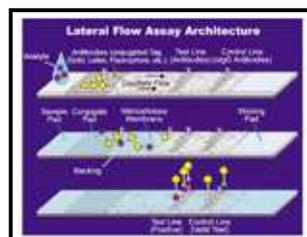
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From the March/April 2012 Issue

### **A Hybrid EKF and Switching PSO Algorithm for Joint State and Parameter Estimation of Lateral Flow Immunoassay Models**

By Nianyin Zeng, Zidong Wang, Yurong Li, Min Du, & Xiaohui Liu



In this paper, a hybrid extended Kalman filter (EKF) and switching particle swarm optimization (SPSO) algorithm is proposed for jointly estimating both the parameters and states of the lateral flow immunoassay model through available short time-series measurement. Our proposed method generalizes the well-known EKF algorithm by imposing physical constraints on the system states. Note that the state constraints are encountered very often in practice that give rise to considerable difficulties in system analysis and design. The main purpose of this paper is to handle the dynamic modeling problem with state constraints by combining the extended Kalman filtering and constrained optimization algorithms via the maximization probability method.



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#### PrePrint: Inferring Gene Regulatory Networks via Nonlinear State-Space Models and Exploiting Sparsity

This paper considers the problem of learning the structure of gene regulatory networks from gene expression time series data. A more realistic scenario when the state space model representing a gene network evolves nonlinearly is considered while a linear model is assumed for the microarray data. To capture the nonlinearity, a particle filter based state estimation algorithm is considered instead of the contemporary linear approximation based approaches. The parameters characterizing the regulatory relations among various genes are estimated online using a Kalman filter. The state estimates delivered by the particle filter and the observed microarray data are then subjected to a LASSO based least squares regression which yields a parsimonious and efficient description of the regulatory network. The performance of the aforementioned algorithm is compared with the extended Kalman filter (EKF) and Unscented



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Kalman Filter (UKF) employing the Mean Square Error (MSE) as the fidelity criterion in recovering the parameters of gene regulatory networks from synthetic data and real biological data. The proposed particle filter based network inference algorithm outperforms EKF and UKF, and therefore, it can serve as a natural framework for modeling gene regulatory networks with nonlinear and sparse structure.

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