

# Advanced Parameter Estimation for Stochastic Epidemics with Individual Variability Using the Stochastic EM Algorithm

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## Introduction

In the realm of epidemiological modeling, particularly when dealing with stochastic epidemics where the disease spread is governed by random processes, parameter estimation becomes challenging, especially when data is incomplete. The Stochastic Expectation-maximization (EM) algorithm offers a robust framework for handling these difficulties, especially when incorporating individual heterogeneity into the model. This approach is crucial for understanding and predicting the dynamics of disease spread in real-world scenarios where complete data is rarely available.

## Description

Stochastic epidemics are characterized by the inherent randomness in the transmission and progression of diseases, which makes modeling and forecasting complex. Individual heterogeneity further complicates the situation, as it involves variations in susceptibility, infectiousness, and other individual-specific factors that can significantly affect disease dynamics. Traditional deterministic models may fail to capture these complexities adequately, making stochastic models and advanced estimation techniques like the Stochastic EM algorithm essential. The Stochastic EM algorithm addresses the challenge of incomplete data in stochastic epidemic models by iteratively refining parameter estimates through a two-step process. In the context of a partially observed epidemic, where only a subset of the true data is available, the algorithm uses a combination of simulation and optimization to estimate both the missing data and the model parameters. The first step in the Stochastic EM algorithm is the **Expectation (E) step**, where the goal is to estimate the expected value of the complete-data log-likelihood function. In this step, we consider both observed data and the unobserved or latent variables, such as the exact timing and number of infections for each individual. Since these latent variables are not directly observed, the E-step involves using simulations or Bayesian methods to infer their possible values. For instance, one approach is to generate multiple possible epidemic trajectories based on the current estimates of the parameters. This can be achieved through Monte Carlo simulations, where numerous realizations of the epidemic are simulated, reflecting different possible scenarios of disease spread. Each realization provides a set of imputed data points that represent plausible states of the epidemic. The E-step thus involves calculating the average likelihood of the observed data under these simulated scenarios, giving a comprehensive view of the epidemic's progression and the missing data. The second step is the **Maximization (M) step**, where the algorithm updates the parameter estimates to maximize the expected complete-data log-likelihood obtained from the E-step. This involves finding parameter values that best fit the observed data and the imputed latent variables. For stochastic epidemics with individual heterogeneity, this step can be particularly challenging due to the non-linearity and complexity of the likelihood function. Optimization techniques are employed to adjust parameters such as transmission rates, recovery rates, and individual-specific factors. Gradient-based methods, numerical optimization, or advanced heuristics might be used depending on the nature of the likelihood function and the complexity of the model. The M-step refines the estimates of these parameters, improving the fit of the model to the observed epidemic data and the simulated imputed data. The Stochastic EM algorithm iterates between these E and M steps until convergence is achieved. Convergence is assessed by monitoring changes in the parameter estimates or the log-likelihood between iterations. When these changes fall below a certain threshold, the algorithm is considered to have reached a stable set of parameter estimates. Once the algorithm converges, the final parameter estimates provide insights into the disease dynamics and individual heterogeneity. This information is critical for understanding the spread of the epidemic, evaluating potential interventions, and predicting future outbreaks. Moreover, post-processing techniques can be used to validate the model and ensure that the estimates are robust and reliable [1-4].

## Conclusion

In summary, the Stochastic EM algorithm is a powerful tool for estimating parameters in partially observed stochastic epidemic models with individual heterogeneity. By combining simulation with iterative optimization, this approach addresses the complexities of incomplete data and varying individual factors, offering a deeper understanding of



epidemic dynamics and more accurate predictions. This advanced methodology is essential for tackling real-world epidemiological challenges and improving public health responses.

## **Acknowledgement**

None.

## **Conflict of Interest**

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