7th Singapore Mathematics Symposium

Date: 30 September, 2016 (Friday)
Venue: National University of Singapore, Institute of Mathematical Sciences
Auditorium; see http://www2.ims.nus.edu.sg/getims.php for directions).
Time: 1pm – 5:30pm

Schedule:
1:00 – 1:10: Welcome by Ling San, SMS president
1:10 – 2:00: Ajay Jasra (NUS, DSAP): Multilevel Sequential Monte Carlo Samplers
2:05 – 2:55: Dinh Tien Cuong (NUS Math): Fekete points and Beta ensembles on a complex manifold
2:55 – 3:25: Tea break
3:25 – 4:15: Hoang Viet Ha (NTU SPMS): Stochastic Partial Differential Equations and Uncertainty Quantification
4:20 – 5:10: Zhang Louxin (NUS Math): Spaced Seed Technique for DNA Sequence Comparison
5:15 – 5:30: Poster Prize Presentation and Closing Remarks

Organizing Committee: Gan Wee Teck (NUS Math), Lim Tiong Wee (NUS DSAP) and Chua Chek Beng (NTU SPMS).

Title and Abstract:

(1) Speaker: Prof. Ajay Jasra (NUS Department of Statistic and Applied Probability)

Title: Multilevel Sequential Monte Carlo Samplers.

Abstract: In this talk I consider the approximation of expectations w.r.t. probability distributions associated to the solution of partial differential equations (PDEs); this scenario appears routinely in Bayesian inverse problems. In practice, one often has to solve the associated PDE numerically, using, for instance finite element methods which depends on the step-size level h_L. In addition, the expectation cannot be computed analytically and one often resorts to Monte Carlo methods.

In the context of this problem, it is known that the introduction of the multilevel Monte Carlo (MLMC) method can reduce the amount of computational effort to estimate expectations, for a given level of error. This is achieved via a telescoping identity associated to a Monte Carlo approximation of a sequence of probability distributions with discretisation levels $\infty > h_0 > h_1 .... > h_L$. In many practical problems of interest, one cannot achieve an i.i.d. sampling of the associated sequence of probability distributions. A sequential Monte Carlo (SMC) version of the MLMC method is introduced to deal with this problem. It is shown that under appropriate assumptions, the attractive property of a reduction of the amount of computational effort to estimate expectations, for a given level of error, can be maintained within the SMC context, that is, relative to exact sampling and Monte Carlo for the distribution at the finest level h_L.
The approach is numerically illustrated on a Bayesian inverse problem.

(2) Speaker: Prof. Dinh Tien Cuong (NUS Department of Mathematics)

Title: Fekete points and Beta ensembles on a complex manifold

Abstract: Let K be a compact subset with piecewise smooth boundary in $\mathbf{R}^n$ or $\mathbf{C}^n$. A Fekete configuration of order p for K is a finite subset of K maximalizing the Vandermonde determinant associated with polynomials of degree p or less than p. A theorem by Berman, Boucksom and Witt Nyström implies that Fekete configurations for K are asymptotically equidistributed with respect to a canonical equilibrium measure for K when p tends to infinity. We give an explicit estimate for the rate of convergence. The result holds in a general setting of Fekete points associated with a holomorphic line bundle. We also discuss the case of Beta ensembles. This talk is based on the joint works with Ma Xiaonan, Nguyen Viet-Anh, and a recent work of my PhD student Vu Duc-Viet.

(3) Speaker: Prof. Hoang Viet Ha (NTU, School of Physical and Mathematical Sciences)

Title: Stochastic Partial Differential Equations and Uncertainty Quantification

Abstract: Solving partial differential equations with stochastic coefficients is exceedingly complicated. The Monte Carlo method, which computes expectation of the solutions, requires an enormous amount of computation resources, which surpasses the current available computers' capacity. In this talk, we review the recent research on the (quasi-) best N term approximation of the generalized polynomial chaos expansion of the solution, and the adaptive approximation of these terms according to the magnitude of their norms. The method achieves a prescribed level of accuracy with optimal complexity. We consider both the case where the coefficients are uniformly bounded, and the far more complicated case where the coefficients are of the log-normal form (i.e. the logarithm of the coefficient follows the normal distribution) and can get arbitrarily close to zero, and arbitrarily large.

In the second part, we discuss our recent work on Bayesian inverse problems where the coefficient of a (forward) partial differential equation is constructed from limited available information on the solution. We find the posterior probability measure of the coefficient, which is the conditional probability given the noisy information, in a prior probability space. This measure is sampled by the Markov Chain Monte Carlo (MCMC) method. The plain MCMC method solves a large number of realizations of the forward equation, and is prohibitively expensive. We introduce two methods that accelerate this process drastically. We show that the generalized polynomial chaos MCMC method, which employs the best N term approximation above, can do the task with optimal complexity. We then review the multilevel MCMC method, (which is first introduced in V. H. Hoang, Ch. Schwab and A. M. Stuart (2013), Complexity analysis of accelerated MCMC methods for Bayesian inversion, Inverse Problems,29, 085010, 37 pp, for Bayesian inverse problems with bounded coefficients and extended recently for Gaussian priors for unbounded coefficients), also samples this posterior measure with optimal complexity.

This is the joint work with Jia Hao Quek (NTU), Christoph Schwab (ETH, Zurich), Andrew Stuart (Caltech) and Bingxing Xia (NTU).

(4) Speaker: Prof. Zhang Louxin (NUS Department of Mathematics)

Title: Spaced Seed Technique for DNA Sequence Comparison

Abstract: Decoding DNA information creates formidable computational challenges in data storage and analysis. Thirty years ago, there were little sequences, but computer was slow. Presently, computers are improving at a rate much less than the rate sequencing machines are. With thousands of so-called next-generation sequencers sitting in medical laboratories and hospitals across the world, DNA sequence data have been increasing about three- to fivefold every year since 2008.In this talk, I will discuss the space seed technique for DNA sequence comparison and explain why it is powerful using simple mathematical facts.