# 2016 随机过程的理论与应用研讨会

**2016** 年 **8** 月 **27-28** 日 北京大学

**1.** 日程安排

**2.** 会议报告摘要

会议学术委员会：

陈大岳 任艳霞 杨静平 席福宝 方海涛

会议组织委员会：

邓明华 刘勇 蒋达权

本次会议受到以下基金的支持：

国家自然科学基金

国家重大科学研究计划

会议地点： 北京大学英杰交流中心星光厅

会务组联系方式：刘勇 **(liuyong@math.pku.edu.cn)**

# 日程安排

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|---|---|---|---|
| 8 月 27 日上午 | | | |
| 8:00- | 注册 | | |
| 8:30-8:50 | 开幕式、照相 | | |
| 8:50-9:20 | 主持人<br>邓迎春 | 熊　捷 | Unique strong solutions of Levy processes driven Stochastic equations |
| 9:20-9:50 | | 谢践生 | 连分数中的"值域更新"结构 |
| 9:50-10:20 | 休息 | | |
| 10:20-10:50 | 主持人<br>杨文强 | 王家赠 | 异质媒体中传播规模对于参数的敏感性 |
| 10:50-11:20 | | 万　林 | Modeling the Crosstalk in High-throughput DNA Sequencing Data |
| 11:20-11:50 | | 侯　琳 | Incorporating Network Information to Prioritize Results in Genome Wide Association Studies |
| 12:00-13:30 | 午餐 | | |
| 8 月 27 日下午 | | | |
| 13:00-14:00 | 主持人<br>李秋月 | 陈新兴 | Gaussian Bounds and Collisions of Random Walks on Weighted Lattice |
| 14:00-14:30 | | 姚　强 | Exponential Extinction Time for the Contact Process on the Hypercube |
| 14:30-15:00 | | 薛晓峰 | Phase Transition for Large Dimensional Contact Processes with Random Recovery Rates on Open Clusters |
| 15:00-15:30 | 休息 | | |
| 15:30-16:00 | 主持人<br>褚为娟 | 宋　凯 | A new method to detect differentially methylated regions from bisulfite sequencing data |
| 16:00-16:30 | | 王艺舒 | Network Clustering Analysis Using Mixture Exponential-family Random Graph Models and Its Application in Genetic Interaction Data |
| 8 月 28 日上午 | | | |
| 8:30-9:00 | 主持人<br>向绪言 | 徐礼虎 | Asymptotics of Sample Entropy Production Rate for Stochastic Differential Equations |
| 9:00-9:30 | | 赵国焕 | Well-posedness of SDE Driven by $\alpha$ -stable Processes with Holder Drifts |
| 9:30-10:00 | | 李　英 | 广义扩散算子 |
| 10:00-10:30 | 休息 | | |
| 10:30-11:00 | 主持人<br>刘荣丽 | 程　雪 | Optimal execution with dynamical risk measure characterized by g-expectations |
| 11:00-11:30 | | 张志祥 | Conditional exact law of large numbers and a coordination game |
| | 闭幕式、午餐 | | |

# 2016 随机过程的理论与应用研讨会

# 报告题目与摘要

## Gaussian Bounds and Collisions of Random Walks on Weighted Lattice

陈新兴

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**Abstract:** We consider a weighted lattice $\mathbb{Z}^d$ with conductance $\mu_e = |e|^{-\alpha}$. We show that the heat kernel of a variable speed random walk on it satisfies a two-sided Gaussian bound by using an intrinsic metric. We also show that when $d = 2$ and $\alpha \in (-1, 0)$, two independent random walks on such weighted lattice will collide infinite many times while they are transient.

## Optimal execution with dynamical risk measure characterized by g-expectations

程雪

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**Abstract:** The problem of optimal execution is formulated as a stochastic control problem aiming at maximizing a generalized risk-adjusted profit and loss. The risk consists of a g-expectation and a cumulative risk. This formulation is on the one hand regarded as a natural generalization of utility maximization subject to a dynamical constraint on trading risks such as value at risk or expected shortfall. On the other hand, from economics viewpoint it is a generalization of maximizing the risk premia subject to constraints. As an illustration, we work out examples with closed form and quasi closed form expressions in the Almgren-Chriss framework. This is a joint work with Marina Di Giacinto and Tai-Ho Wang.

## Incorporating Network Information to Prioritize Results in Genome Wide Association Studies

侯琳

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**Abstract:** Although Genome Wide Association Studies (GWAS) have identified many susceptibility loci for common diseases, they only explain a small portion of heritability. It is challenging to identify the remaining disease loci because their association signals are likely weak and difficult to identify among millions of candidates. One potentially useful direction to increase statistical power is to integrate other information, such as functional genomics and gene pleiotropy, to prioritize GWAS signals. In this talk, we will discuss the methods we developed recently for post-GWAS prioritization. We use Markov random field framework to incorporate biological networks. Applications to real data demonstrated that our method can identify more replicable genes, and the prioritized genes are enriched in disease related pathways.

## 广义扩散算子

李英

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**Abstract:** 作为(一维)扩散算子和生灭矩阵的推广，我们定义了广义扩散算子。首先从分析角度研究了广义扩散算子的特征值问题，如特征值估计，变分公式和Hardy不等式中的最佳常数问题。然后试图建立相应的广义扩散过程，从而使用前面的分析结果得到该过程的稳定性质。

## A new method to detect differentially methylated regions from bisulfite sequencing data

宋凯

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**Abstract:** DNA methylation is an important epigenetic modification that has essential roles in cellular processes including gene regulation, development and disease and is widely dysregulated in most types of cancer. Recent advances in sequencing technology have enabled the measurement of DNA methylation at single nucleotide resolution through methods such as whole-genome bisulfite sequencing and reduced representation bisulfite sequencing. In DNA methylation studies, a key task is to detect differentially methylated regions (DMRs) under distinct biological contexts, for example, between tumor and normal tissue.

## Modeling the Crosstalk in High-throughput DNA Sequencing Data

万林

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**Abstract:** Base-calling accuracy is crucial for high-throughput DNA sequencing and downstream analysis. Accordingly, we made an endeavor to reduce DNA sequencing errors of Illumina systems by correcting three kinds of crosstalk in the cluster intensity data. We discovered that signal crosstalk between adjacent clusters accounts for a large portion of sequencing errors in Illumina systems, even after correcting color crosstalk caused by the overlap of dye emission spectra and phasing/pre-phasing caused by out-of-step nucleotide synthesis. Interestingly and importantly, spatial crosstalk between adjacent clusters is cluster-specific and often asymmetric, which cannot be corrected by existing deconvolution methods. Therefore, we introduce a novel mathematical method able to estimate and remove spatial crosstalk, thereby reducing base-calling errors by 44-69% at a given mapping rate from Illumina systems. This is a joint work with Bo Wang, Anqi Wang and Lei M Li.

## 异质媒体中传播规模对于参数的敏感性

王家赠

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**Abstract:** 对于不均匀媒介中的两种基本的传播问题，SIS和SIR。我们研究了爆发后，播发规模对于传播参数的敏感性。对于SIS型传播，我们利用了一种构造解，得到均衡点传播规模的表达式。对于SIR型传播，我们利用生成函数的重整化方法，得到传播规模的表达式。研究结果可看作为结构对动力学影响的一个例子。

## Network Clustering Analysis Using Mixture Exponential-family Random Graph Models and Its Application in Genetic Interaction Data

王艺舒

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**Abstract:** Epistatic miniarrary prole (EMAP) studies have enabled the mapping of large-scale genetic interaction networks and generated large amounts of data in model organisms. It provide an incredible set of molecular tools and advanced technologies that should be efficiently understanding

the relationship between the genotypes and phenotypes of individuals. However, the network information gained from EMAP cannot be fully exploited using the traditional statistical network models. Because the genetic network are always heterogeneous, for example, the network structure features for one subset of nodes are different from those of the left nodes. Exponential-family random graph models (ERGMs) are a family of statistical models, which provides a principled and flexible way to describe the structural features (e.g. the density, centrality and assortativity) of an observed network. However, the single ERGM is not enough to capture this heterogeneity of networks. In this paper, we consider a mixture EGRM (mixEGRM) networks, which model a network consisted of several communities, where the subnetwork of each community is describe by a single EGRM.

EM algorithm is a classical method to solve the mixture problem, hower, it will be very slow when the data size is huge in the numerous application. We adopt an efficient novel online graph clustering algorithm to classify the class of the graph nodes and estimate the ERGM parameters for the mixERGM. In simulation studies, the mixERGM outperforms the role analysis for the network cluster in which the mixture of exponential-family random graph model is developed for many ego-network according to their roles. One genetic interaction network of yeast and Two real social networks show the wide potential application of the mixERGM.

## 连分数中的“值域更新”结构

谢践生

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**Abstract:** 我们考察了无理数的连分数展式中前 $n$ “位”里出现的不同自然数个数 (记作 Rn) 等数学量，利用概率论与遍历论相结合的办法证明了对于“几乎处处”的小数而言，这些数学量关于 $n$ 的增长阶具有特定的规律和结构；利用分形分析中发展的非自治共形函数迭代系统的方法，得到了 Rn 的水平集的 Hausdorff 维数。

## Unique strong solutions of Levy processes driven Stochastic equations

熊捷

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**Abstract:** We establish the existence and uniqueness for one-dimensional stochastic differential equations driven by a Brownian motion and a pure jump Levy processes. It was shown that under fairly general conditions on the coefficients, pathwise uniqueness still holds based on the methods of weak uniqueness and local time technique. This talk is based on a joint work with Zheng and Zhou.

## Asymptotics of Sample Entropy Production Rate for Stochastic Differential Equations

徐礼虎

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**Abstract:** Using the dimension-free Harnack inequality and the integration by parts formula for the associated diffusion semigroup, we prove the central limit theorem, the moderate deviation principle, and the logarithmic iteration law for the sample entropy production rate of a family of stochastic differential equations.

(Joint work with Feng-Yu Wang and Jie Xiong)

## Phase Transition for Large Dimensional Contact Processes with Random Recovery Rates on Open Clusters

薛晓峰

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**Abstract:** In this talk we are concerned with contact process with random recovery rates on open clusters of bond percolation on $\mathbb{Z}^d$. Let $\zeta$ be a positive random variable, then we assign i.i.d. copies of $\zeta$ on the vertices as the random recovery rates. Assuming that each edge is open with probability $p$ and $\log d$ vertices are occupied at $t = 0$, we prove that the following phase transition occurs. When the infection rate $\lambda < 1/(pE\frac{1}{\zeta})$, then the process dies out at time $O(\log d)$ with high probability, while when $\lambda > 1/(pE\frac{1}{\zeta})$, the process survives with high probability.

## Exponential Extinction Time for the Contact Process on the Hypercube

姚强

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**Abstract:** We consider the contact process on the hypercube. We show that, for any positive infection rate, the extinction time for the contact process on this graph grows exponentially with the number of vertices.

## Conditional exact law of large numbers and a coordination game

张志祥

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**Abstract:** Some results on conditional exact law of large numbers are presented. They are used to establish the existence and uniqueness of equilibrium for a coordination game.

## Well-posedness of SDE Driven by $\alpha$-stable Processes with Hölder Drifts

赵国焕

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**Abstract:** In this talk, we will show the strong uniqueness of following SDE:

$$X_t^x = x + \int_0^t b(X_s^x)ds + Z_t.$$

Here $Z_t$ is a non-degenerate $\alpha$-stable noise $(\alpha \in (0,2))$ and $b \in C^\beta$ with $\beta \in (1-\alpha/2, 1)$. We will also show a Davie's type uniqueness theorem for the related random ODE and some analytic results about nonlocal operators.