SCMS Seminar



校庆一百一十四周年暨五十三届科学报告讨论会

时间: 5月27日1:30-5:30 地点: 上海数学中心谷超豪报告厅

Chair: Quanshui Wu (吴泉水)

Lecture 1 13:30-14:05 Speaker: Jun Li (李骏)

Title: All genus GW invariants of quintic Calabi-Yau, after BCOV and YY **Abstract:** We will outline the theories that lead to a mathematical proof of the Bershadsky-Cecotti-Ooguri-Vafa and Yamaguchi-Yau conjectures on all genus GW invariants of quintic Calabi-Yau threefold. This is a joint work with Huailiang Chang and Shuai Guo.

Lecture 2 14:05-14:40 Speaker: Zhiyuan Li (李志远)

Title: 超开勒代数簇上的算术周期映射及应用

Abstract: 由霍奇结构所定义出的周期映射是研究复代数簇模空间的一个核心工具。过去几年中,随着志村簇 integral 模型的建立以及 Langlands-Rapoport 猜想的解决,探索周期映射的算术性已经成为研究不同特征模空间理论的重要手段。在本次报告中,我们将介绍有关超开勒代数簇特别是 K3 曲面上算术周期映射方面的工作,它包括算术周期映射的建立和应用,例如 Tate 猜想和 Shafarevich 猜想等。

Lecture 3 14:40-15:15 Speaker: Shanwen Wang (王善文)

Title: 模型式的 Iwasawa 主猜想

Abstract: 我们将回顾 Iwasawa 主猜想的历史并介绍 Kato 欧拉系的形变理论在该猜想中的应用。

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Tea Break 15:15-15:45

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Chair: Weixiao Shen (沈维孝)

Lecture 4 15:45-16:20 Speaker: Peng Wu (吴鹏)

Title: Einstein four-manifolds of positive determinant self-dual Weyl curvature **Abstract:** The question that when a four-manifold with a complex structure admits a compatible Einstein metric of positive scalar curvature has been answered by Tian, LeBrun, respectively. Tian classified Kahler-Einstein four-manifolds with positive scalar curvature, LeBrun classified Hermitian Einstein four-manifolds with positive scalar curvature. In this talk we consider the inverse problem, that is, when a four-manifold with an Einstein metric of positive scalar curvature admits a compatible complex structure. We will show that if the determinant of the self-dual Weyl curvature is positive then the manifold admits a compatible complex structure.

Lecture 5 16:20-16:55 Speaker: Kei Yuen Chan (陈佳源)

Title: 表示论上的分歧问题

Abstract: 分歧问题是研究当一个群或代数的表示限制在子群或子代数时的结构。这个报告会讨论表示论上各个分歧法则的问题。 会从一些经典的例子说起,这包括对称群和酋群,然从讨论近年的发展趋势,包括著名的 Gan-Gross-Prasad 猜想及其同调相关的问题。

Lecture 6 16:55-17:30 Speaker: Chunhe Li (李春贺)

Title: Landscape of gene networks

Abstract: Cellular functions in biological systems are regulated by the underlying gene regulatory networks. How to investigate the global properties of gene networks is a challenging problem. In this talk, I will present some approaches we recently developed, i.e. the potential landscape and path framework, to study the stochastic dynamics of gene networks. The basins on the landscape characterize different cell states. The landscape topography in terms of barrier heights between stable states quantifies the global stability of the gene regulatory system. The kinetic paths based on the minimum action principles quantify the transition processes between different cell states. I will also discuss some applications of this approach in the biological systems, including cancer, cell cycle, and epithelial-mesenchymal transitions (EMT).

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 $(y_n + 0.5\tau k_1)$