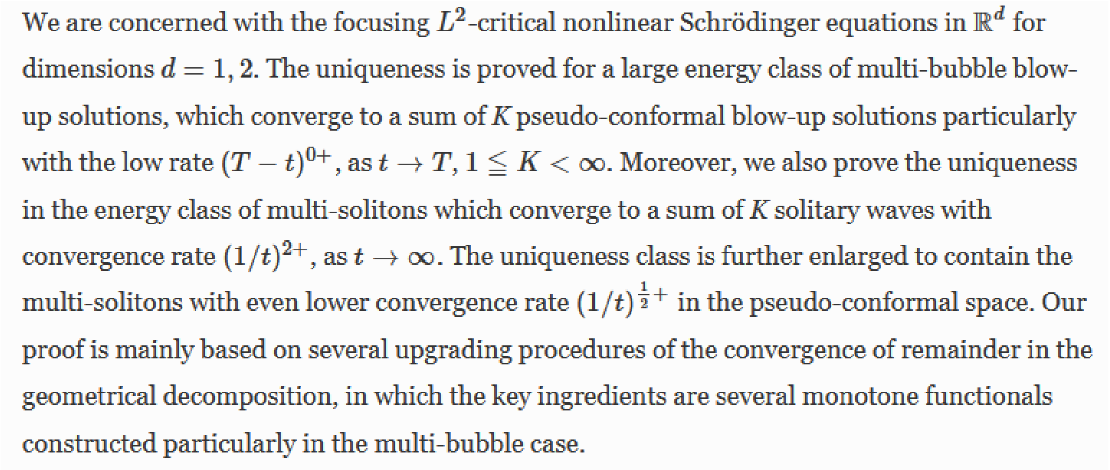
应用所科研人员近期研究成果

一、曹道民研究员等的论文 On Uniqueness of Multi-bubble Blow-Up Solutions and Multi-solitons to L^2-Critical Nonlinear Schrodinger Equations 被 ARCHIVE FOR RATIONAL MECHANICS AND ANALYSIS 发表。

摘要：



We are concerned with the focusing L^2-critical nonlinear Schrödinger equations in $\mathbb{R}^d$ for dimensions $d = 1, 2$. The uniqueness is proved for a large energy class of multi-bubble blow-up solutions, which converge to a sum of K pseudo-conformal blow-up solutions particularly with the low rate $(T - t)^{0+}$, as $t \to T$, $1 \leqq K < \infty$. Moreover, we also prove the uniqueness in the energy class of multi-solitons which converge to a sum of K solitary waves with convergence rate $(1/t)^{2+}$, as $t \to \infty$. The uniqueness class is further enlarged to contain the multi-solitons with even lower convergence rate $(1/t)^{\frac{1}{2}+}$ in the pseudo-conformal space. Our proof is mainly based on several upgrading procedures of the convergence of remainder in the geometrical decomposition, in which the key ingredients are several monotone functionals constructed particularly in the multi-bubble case.

论文链接：http://dx.doi.org/10.1007/s00205-022-01832-x

二、董昭研究员等的论文 Ergodicity for Stochastic Conservation Laws with Multiplicative Noise 被 COMMUNICATIONS IN MATHEMATICAL PHYSICS 发表。

摘要：We proved that there exists a unique invariant measure for solutions of stochastic conservation laws with Dirichlet boundary condition driven by multiplicative noise. Moreover, a polynomial mixing property is established. This is done in the setting of kinetic solutions taking values in an L^1-weighted space.

论文链接：http://dx.doi.org/10.1007/s00220-022-04629-x

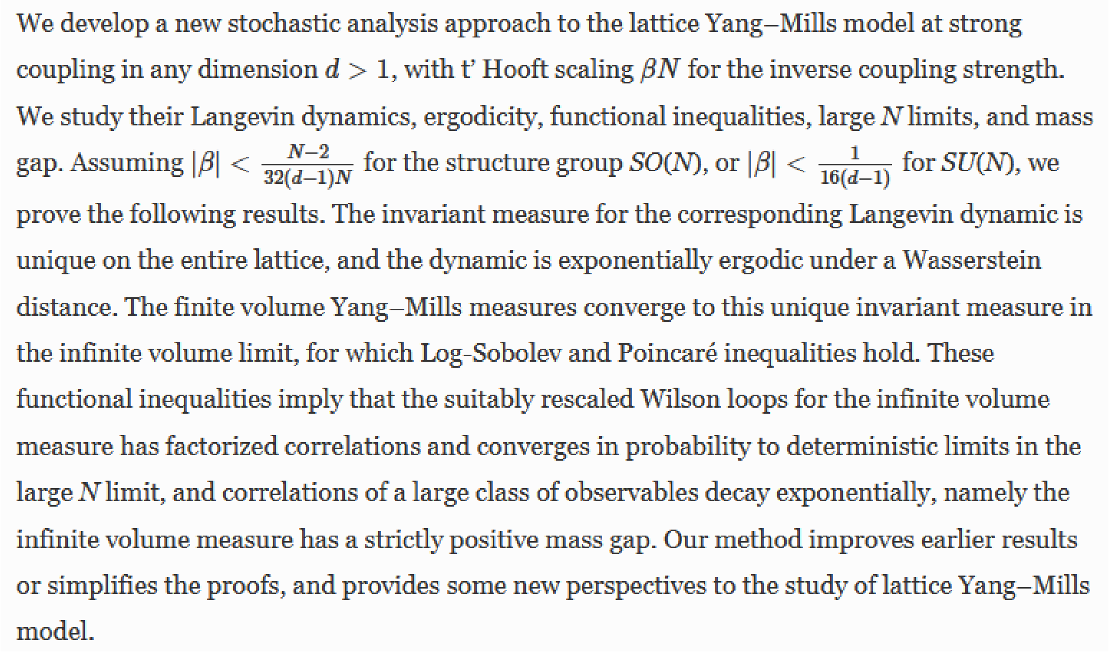
三、曹道民研究员等的论文 GLOBAL SOLUTIONS FOR THE GENERALIZED SQG EQUATION AND REARRANGEMENTS 被 TRANSACTIONS OF THE AMERICAN MATHEMATICAL SOCIETY 发表。

摘要：In this paper, we study the existence of rotating and traveling wave solutions for the generalized surface quasi-geostrophic (gSQG) equation. The solutions are obtained by maximization of the energy over the set of rearrangements of a fixed function. The rotating solutions take the form of co-rotating vortices with N-fold symmetry. The traveling-wave solutions take the form of translating vortex pairs. Moreover, these solutions constitute the desingularization of co-rotating N point vortices and counter-rotating pairs. Some other quantitative properties are also established.

论文链接：http://dx.doi.org/10.1090/tran/8835

四、朱湘婵研究员的论文 A Stochastic Analysis Approach to Lattice Yang-Mills at Strong Coupling 被 COMMUNICATIONS IN MATHEMATICAL PHYSICS 发表。

摘要：



We develop a new stochastic analysis approach to the lattice Yang–Mills model at strong coupling in any dimension $d > 1$, with t' Hooft scaling βN for the inverse coupling strength. We study their Langevin dynamics, ergodicity, functional inequalities, large N limits, and mass gap. Assuming $|\beta| < \frac{N-2}{32(d-1)N}$ for the structure group $SO(N)$, or $|\beta| < \frac{1}{16(d-1)}$ for $SU(N)$, we prove the following results. The invariant measure for the corresponding Langevin dynamic is unique on the entire lattice, and the dynamic is exponentially ergodic under a Wasserstein distance. The finite volume Yang–Mills measures converge to this unique invariant measure in the infinite volume limit, for which Log-Sobolev and Poincaré inequalities hold. These functional inequalities imply that the suitably rescaled Wilson loops for the infinite volume measure has factorized correlations and converges in probability to deterministic limits in the large N limit, and correlations of a large class of observables decay exponentially, namely the infinite volume measure has a strictly positive mass gap. Our method improves earlier results or simplifies the proofs, and provides some new perspectives to the study of lattice Yang–Mills model.

论文链接：http://dx.doi.org/10.1007/s00220-022-04609-1

五、骆顺龙研究员等的论文 Detecting quantum phase transition via magic resource in the XY spin model 被 PHYSICAL REVIEW A 发表。

摘要：Quantum phase transition in the XY spin model with three-spin interaction is investigated using magic resource (non-stabilizerness), which is crucial in universal fault-tolerant quantum computation. The magic quantifier we employ here is defined straightforwardly via characteristic functions of quantum states, which are well defined for all dimensional quantum systems (in sharp contrast to those defined by discrete Wigner functions) and can be easily calculated. We show that the magic quantifier of both the reduced single-site spins and two-site spins of the system ground state increase to their maximum around the critical points for quantum phase transition. This indicates that the magic resource can be used to detect the critical phenomena in the XY spin model and reveals a connection between quantum phase transition in many-body systems and quantum resource in stabilizer quantum computation.

论文链接：http://dx.doi.org/10.1103/PhysRevA.106.062405

六、张世华研究员等的论文 A single-nucleus transcriptomic atlas of the dog hippocampus reveals the potential relationship between specific cell types and domestication 被 NATIONAL SCIENCE REVIEW 发表。

摘要：The process of domestication has led to dramatic differences in behavioral traits between domestic dogs and gray wolves. Whole-genome research found that a class of putative positively selected genes were related to various aspects of learning and memory, such as long-term potentiation and long-term depression. In this study, we constructed a single-nucleus transcriptomic atlas of the dog hippocampus to illustrate its cell types, cell lineage and molecular features. Using the transcriptomes of 105 057 nuclei from the hippocampus of a Beagle dog, we identified 26 cell clusters and a putative trajectory of oligodendrocyte development. Comparative analysis revealed a significant convergence between dog differentially expressed genes (DEGs) and putative positively selected genes (PSGs). Forty putative PSGs were DEGs in glutamatergic neurons, especially in Cluster 14, which is related to the regulation of nervous system development. In summary, this study provides a blueprint to understand the cellular mechanism of dog domestication.

论文链接：http://dx.doi.org/10.1093/nsr/nwac147

七、张世华研究员的论文 Information-theoretic Classification Accuracy: A Criterion that Guides Data-driven Combination of Ambiguous Outcome Labels in Multi-class Classification 被 Journal of Machine Learning Research 发表。

摘要：Outcome labeling ambiguity and subjectivity are ubiquitous in real-world datasets. While practitioners commonly combine ambiguous outcome labels for all data points (instances) in an ad hoc way to improve the accuracy of multi-class classification, there lacks a principled approach to guide the label combination for all data points by any optimality criterion. To address this problem, we propose the information-theoretic classification accuracy (ITCA), a criterion that balances the trade-off between prediction accuracy (how well do predicted labels agree with actual labels) and classification resolution (how many labels are predictable), to guide practitioners on how to combine ambiguous outcome labels.

To find the optimal label combination indicated by ITCA, we propose two search strategies: greedy search and breadth-first search. Notably, ITCA and the two search strategies are adaptive to all machine-learning classification algorithms. Coupled with a classification algorithm and a search strategy, ITCA has two uses: improving prediction accuracy and identifying ambiguous labels. We first verify that ITCA achieves high accuracy with both search strategies in finding the correct label combinations on synthetic and real data. Then we demonstrate the effectiveness of ITCA in diverse applications, including medical prognosis, cancer survival prediction, user demographics prediction, and cell type classification. We also provide theoretical insights into ITCA by studying the oracle and the linear discriminant analysis classification algorithms. Python package `itca` (available at `https://github.com/JSB-UCLA/ITCA`) implements ITCA and the search strategie.

论文链接：https://www.jmlr.org/papers/volume23/21-1150/21-1150.pdf

八、张世华研究员的论文Cross-species cell-type assignment of single-cell RNA-seq by heterogeneous graph neural network被Genome Research发表。

摘要：Cross-species comparative analyses of single-cell RNA sequencing (scRNA-seq) data allow us to explore, at single-cell resolution, the origins of the cellular diversity and evolutionary mechanisms that shape cellular form and function. Cell-type assignment is a crucial step to achieve that. However, the poorly annotated genome and limited known biomarkers hinder us from assigning cell identities for nonmodel species. Here, we design a heterogeneous graph neural network model, CAME, to learn aligned and interpretable cell and gene embeddings for cross-species cell-type assignment and gene module extraction from scRNA-seq data. CAME achieves significant improvements in cell-type characterization across distant species owing to the utilization of non-one-to-one homologous gene mapping ignored by early methods. Our large-scale benchmarking study shows that CAME significantly outperforms five classical methods in terms of cell-type assignment and model robustness to insufficiency and inconsistency of sequencing depths. CAME can transfer the major cell types and interneuron subtypes of human brains to mouse and discover shared cell-type-specific functions in homologous gene modules. CAME can align the trajectories of human and macaque spermatogenesis and reveal their conservative expression dynamics. In short, CAME can make accurate cross-species cell-type assignments even for nonmodel species and uncover shared and divergent characteristics between two species from scRNA-seq data.

论文链接：https://genome.cshlp.org/content/33/1/96.short

九、我院张世华研究员的论文Define the separation landscape of topological domains for decoding consensus domain organization of 3D genome被Genome Research发表。

摘要：Topologically associating domains (TADs) have emerged as basic structural and functional units of genome organization, and have been determined by many computational methods from

Hi-C contact maps. However, the TADs obtained by different methods vary greatly, which makes the accurate determination of TADs a challenging issue and hinders subsequent biological analyses about their organization and functions. Obvious inconsistencies among the TADs identified by different methods indeed make the statistical and biological properties of TADs overly depend on the method we chose rather than on the data. To this end, we employ the consensus structural information captured by these methods to define the TAD separation landscape for decoding consensus domain organization of the 3D genome. We demonstrate that the TAD separation landscape could be used to compare domain boundaries across multiple cell types for discovering conserved and divergent topological structures, decipher three types of boundary regions with diverse biological features, and identify Consensus Topological Associating Domains (ConsTADs). We illustrate that these analyses could deepen our understanding of the relationships between the topological domains and chromatin states, gene expression, and DNA replication timing. In short, we provide an alternative solution to deal with the serious inconsistencies of TADs obtained via different methods by defining the TAD separation landscape and ConsTAD.

论文链接：https://genome.cshlp.org/content/early/2023/03/09/gr.277187.122