应用所科研人员近期研究成果

成果一：

我院杨钊副研究员等的论文 Unstable Stokes Waves 被 ARCHIVE FOR RATIONAL MECHANICS AND ANALYSIS 接收发表。

摘要： We investigate the spectral instability of a 2p/? periodic Stokes wave of sufficiently small amplitude, traveling in water of unit depth, under gravity. Numerical evidence suggests instability whenever the unperturbed wave is resonant with its infinitesimal perturbations. This has not been analytically studied except for the Benjamin-Feir instability in the vicinity of the origin of the complex plane. Here we develop a periodic Evans function approach to give an alternative proof of the Benjamin-Feir instability and, also, a first proof of spectral instability away from the origin. Specifically, we prove instability near the origin for ? > ?1 := 1.3627827.. . , and instability due to resonance of order two so long as an index function is positive. Validated numerics establishes that the index function is indeed positive for some ? < ?1, whereby there exists a Stokes wave that is spectrally unstable even though it is insusceptible to the Benjamin-Feir instability. The proofs involve center manifold reduction, Floquet theory, and methods of ordinary and partial differential equations. Numerical evaluation reveals that the index function remains positive unless ? = 1.8494040.. .. Therefore we conjecture that all Stokes waves of sufficiently small amplitude are spectrally unstable. For the proof of the conjecture, one has to verify that the index function is positive for ? sufficiently small.

论文链接：http://dx.doi.org/10.1007/s00205-023-01889-2

成果二：

我院罗德军研究员等的论文 WELL POSEDNESS AND LIMIT THEOREMS FOR A CLASS OF STOCHASTIC DYADIC MODELS 被 SIAM JOURNAL ON MATHEMATICAL ANALYSIS 接收发表。

摘要： We consider stochastic inviscid dyadic models with energy-preserving noise. It is shown that the models admit weak solutions which are unique in law. Under a certain scaling limit of the noise, the stochastic models converge weakly to a deterministic viscous dyadic model, for which we provide explicit convergence rates in terms of the parameters of noise. A central limit theorem underlying such scaling limit is also established. In case that the stochastic dyadic model is viscous, we show the phenomenon of dissipation enhancement for suitably chosen noise.

论文链接：\underline{\text{http://dx.doi.org/10.1137/22M1511497}}

成果三：

我院朱湘婵研究员等的论文 Global Existence and Non-Uniqueness for 3D Navier-Stokes Equations with Space-Time White Noise 被 ARCHIVE FOR RATIONAL MECHANICS AND ANALYSIS 接收发表。

摘要：We establish that global-in-time existence and non-uniqueness of probabilistically strong solutions to the three dimensional Navier-Stokes system driven by space-time white noise. In this setting, solutions are expected to have space regularity of at most −1/2 − ? for any ? > 0. Consequently, the convective term is ill-defined analytically and probabilistic renormalization is required. Up until now, only local well-posedness has been known. With the help of paracontrolled calculus we decompose the system in a way which makes it amenable to convex integration. By a careful analysis of the regularity of each term, we develop an iterative procedure which yields global non-unique probabilistically strong paracontrolled solutions. Our result applies to any divergence free initial condition in L-2 ? B-8,8(-1+?) (,) ? > 0, and also implies non-uniqueness in law.

论文链接：\underline{\text{http://dx.doi.org/10.1007/s00205-023-01872-x}}

成果四：

我院朱天琪副研究员等的论文 Estimation of species divergence times in presence of cross-species gene flow 被 SYSTEMATIC BIOLOGY 接收发表。

摘要：Cross-species introgression can have significant impacts on phylogenomic reconstruction of species divergence events. Here, we used simulations to show how the presence of even a small amount of introgression can bias divergence time estimates when gene flow is ignored in the analysis. Using advances in analytical methods under the multispecies coalescent (MSC) model, we demonstrate that by accounting for incomplete lineage sorting and introgression using large phylogenomic data sets this problem can be avoided. The multispecies-coalescent-with-introgression (MSci) model is capable of accurately estimating both divergence times and ancestral effective population sizes, even when only a single diploid individual per species is sampled. We characterize some general expectations for biases in divergence time estimation under three different scenarios: 1) introgression between sister species, 2) introgression between non-sister species, and 3) introgression from an unsampled (i.e., ghost) outgroup lineage. We also conducted simulations under the isolation-with-migration (IM) model and found that the MSci model assuming episodic gene flow was able to accurately estimate species divergence times despite high levels of continuous gene flow. We estimated

divergence times under the MSC and MSci models from two published empirical datasets with previous evidence of introgression, one of 372 target-enrichment loci from baobabs (Adansonia), and another of 1000 transcriptome loci from 14 species of the tomato relative, Jaltomata. The empirical analyses not only confirm our findings from simulations, demonstrating that the MSci model can reliably estimate divergence times but also show that divergence time estimation under the MSC can be robust to the presence of small amounts of introgression in empirical datasets with extensive taxon sampling. [divergence time; gene flow; hybridization; introgression; MSci model; multispecies coalescent]

论文链接：http://dx.doi.org/10.1093/sysbio/syad015

成果五：

我院常晋源研究员等的论文 Statistical Inferences for Complex Dependence of Multimodal Imaging Data 被 JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION 接收发表。

摘要：

Statistical analysis of multimodal imaging data is a challenging task, since the data involves high-dimensionality, strong spatial correlations and complex data structures. In this article, we propose rigorous statistical testing procedures for making inferences on the complex dependence of multimodal imaging data. Motivated by the analysis of multi-task fMRI data in the Human Connectome Project (HCP) study, we particularly address three hypothesis testing problems: (a) testing independence among imaging modalities over brain regions, (b) testing independence between brain regions within imaging modalities, and (c) testing independence between brain regions across different modalities. Considering a general form for all the three tests, we develop a global testing procedure and a multiple testing procedure controlling the false discovery rate. We study theoretical properties of the proposed tests and develop a computationally efficient distributed algorithm. The proposed methods and theory are general and relevant for many statistical problems of testing independence structure among the components of high-dimensional random vectors with arbitrary dependence structures. We also illustrate our proposed methods via extensive simulations and analysis of five task fMRI contrast maps in the HCP study.

论文链接：http://dx.doi.org/10.1080/01621459.2023.2200610

成果六：

我院姚大成副研究员等的论文 Dynamic pricing and production control in a two-item make-to-stock system with flexible dual sourcing and lost sales 被 PRODUCTION AND OPERATIONS MANAGEMENT 接收发表。

摘要：We consider a joint control of pricing and production in a two-item inventory system, where each item can be produced by its dedicated source or a shared flexible source, under the lost-sales setting. The demands of the two items are correlated. Due to the complexity caused by the lost-sales assumption and the interplay between pricing and production decisions, we show the optimal value function satisfies five structural properties under certain conditions. The optimal ordering and pricing policies are then fully characterized by five production curves and two pricing functions. Different from existing literature, we show that the optimal price path may not be monotone in the inventory level of either item. Next, we estimate the value of flexibility by comparing two systems, one with the flexible source only and the other with the dedicated source only, and show that the value of flexibility is positive (or negative) if the flexible source has a faster (or slower) production rate and a lower (or higher) production cost. Through numerical experiments, we find that in most cases flexibility and dynamic pricing are substitutes except for a few exceptions; and product substitution can either increase or decrease the value of flexibility.

论文链接：http://dx.doi.org/10.1111/poms.14026

成果七：

我院吴凌云研究员等的论文 Supervised learning of high-confidence phenotypic subpopulations from single-cell data 被 NATURE MACHINE INTELLIGENCE 接收发表。

摘要：Accurately identifying phenotype-relevant cell subsets from heterogeneous cell populations is crucial for delineating the underlying mechanisms driving biological or clinical phenotypes. Here by deploying a Learning with Rejection strategy, we developed a novel supervised learning framework called PENCIL to identify subpopulations associated with categorical or continuous phenotypes from single-cell data. By embedding a feature selection function into this flexible framework, for the first time, we were able to simultaneously select informative features and identify cell subpopulations, enabling accurate identification of phenotypic subpopulations otherwise missed by methods incapable of concurrent gene selection. Furthermore, the regression mode of PENCIL presents a novel ability for supervised phenotypic trajectory learning of subpopulations from single-cell data. We conducted comprehensive simulations to evaluate PENCIL's

versatility in simultaneous gene selection, subpopulation identification and phenotypic trajectory prediction. PENCIL is fast and scalable to analyse one million cells within 1 h. Using the classification mode, PENCIL detected T-cell subpopulations associated with melanoma immunotherapy outcomes. Moreover, when applied to single-cell RNA sequencing of a patient with mantle cell lymphoma with drug treatment across multiple timepoints, the regression mode of PENCIL revealed a transcriptional treatment response trajectory. Collectively, our work introduces a scalable and flexible infrastructure to accurately identify phenotype-associated subpopulations from single-cell data. To detect phenotype-related cell subpopulations from single-cell data, appropriate feature sets need to be chosen or learned simultaneously. Ren et al. present here a tool based on Learning with Rejection, a method that during training learns features from cells that can be predicted with high confidence, while cells that the model is not yet certain about are rejected.

论文链接：http://dx.doi.org/10.1038/s42256-023-00656-y

成果八：

我院朱天琪副研究员等的论文 Was Wuhan the early epicenter of the COVID-19 pandemic?-A critique 被 NATIONAL SCIENCE REVIEW 接收发表。

论文链接：http://dx.doi.org/10.1093/nsr/nwac287