成果一.

我院 Panu Lahti 副研究员与其合作者的论文 NONLOCAL FUNCTIONALS, TOTAL VARIATION, AND Γ -CONVERGENCE WITH RESPECT TO AREA-STRICT CONVERGENCE 被 SIAM JOURNAL ON MATHEMATICAL ANALYSIS 接收发表。

摘要：We study a class of nonlo cal functionals that was introduced by Brezis et al. [Atti Accad. Naz. Lincei Rend. Lincei Mat. Appl., 33 (2022), pp. 413--437] and can be used to characterize the total variation of functions. We establish the Gamma-limit of these functionals with respect to area-strict convergence.

论文链接：http://dx.doi.org/10.1137/25M1739522

成果二.

我院李向东研究员与其合作者的论文 ON THE NAVIER-STOKES EQUATIONS AND THE HAMILTON-JACOBI-BELLMAN EQUATION ON THE GROUP OF VOLUME PRESERVING DIFFEOMORPHISMS 被 SIAM JOURNAL ON CONTROL AND OPTIMIZATION 接收发表。

摘要：

In this paper, we give a new characterization of the incompressible Navier–Stokes equations on a compact Riemannian manifold M via the Bellman dynamic programming principle on $SG = \mathrm{SDiff}(M)$, the group of volume preserving diffeomorphisms on M. The main result of this paper indicates the interesting relationships among the incompressible Navier–Stokes equations on M, the Hamilton–Jacobi–Bellman equation, and the viscous Burgers equation on $SG = \mathrm{SDiff}(M)$. In particular, we derive the incompressible Navier–Stokes equations and the revised incompressible Navier–Stokes equations on the two-dimensional torus. This extends Arnold's famous theorem on the geometric interpretation of the incompressible Euler equation to the incompressible Navier–Stokes equations on compact Riemannian manifolds.

论文链接：http://dx.doi.org/10.1137/24M1658103

成果三.

我院施展研究员与其合作者的论文 THE STOCHASTIC JACOBI FLOW 被 ANNALS OF PROBABILITY 接收发表。

摘要：

The problem of conditioning on the occupation field was investigated for the Brownian motion in 1998 independently by Aldous (*Electron. Commun. Probab.* **3** (1998) 79–90) and Warren and Yor (In *Séminaire de Probabilités, XXXII* (1998) 328–342, Springer) and recently for the loop soup at intensity $1/2$ by Werner (In *Séminaire de Probabilités XLVIII* (2016) 481–503 Springer), Sabot and Tarrès (*Probab. Theory Related Fields* **165** (2016) 559–580), and Lupu, Sabot and Tarrès (*Electron. J. Probab.* **24** (2019) 1–28). We consider this problem in the case of the Brownian loop soup on the real line, and show that it is connected with a flow version of Jacobi processes, called Jacobi flow. We show that such flows naturally appear in the setting of the perturbed reflecting Brownian motion. The Jacobi flow is also related to Fleming–Viot processes, as established by Bertoin and Le Gall (*Probab. Theory Related Fields* **126** (2003) 261–288, *Ann. Inst. Henri Poincaré Probab. Stat.* **41** (2005) 307–333) and Dawson and Li (*Ann. Probab.* **40** (2012) 813–857). This relation allows us to interpret Perkins' disintegration theorem between Feller continuous state branching-processes and Fleming–Viot processes as a decomposition of Gaussian measures. Our approach gives a unified framework for the problems of disintegrating on the real line. The connection with Bass–Burdzy flows which was drawn in Warren (*Probab. Theory Related Fields* **133** (2005) 559–572) and Lupu, Sabot and Tarrès (*Electron. J. Probab.* **26** (2021) 1–25) is shown to be valid in the general case.

论文链接：http://dx.doi.org/10.1214/24-AOP1737

成果四.

我院肖惠副研究员与其合作者的论文 Conditioned random walks on linear groups I: construction of the target harmonic measure 被 PROBABILITY THEORY AND RELATED FIELDS 接收发表。

摘要：Our objective is to explore random walks on the general linear group, constrained to a specific domain, with a primary focus on establishing the conditioned local limit theorem. This paper represents the first step toward achieving this goal, specifically entailing the construction of a novel entity - the target harmonic measure. This measure, together with the harmonic function, serves as a pivotal component in establishing the conditioned local limit theorem. Using a reversal identity, we introduce a reversed sequence characterized as a dual random walk with a perturbation depending on future observations. The investigation of such walks, which rely on future information, lies at the heart of this paper. To carry out this study, we develop an approach grounded in the finite-size approximation of perturbations, enabling us to simplify the investigation to an array of Markov chains with increasing dimensions.

论文链接：http://dx.doi.org/10.1007/s00440-026-01508-7

成果五.

我院张驰浩助理研究员与其合作者的论文 Dynamical Causality Under Latent Confounders for Biological Network Reconstruction 被 IEEE TRANSACTIONS ON PATTERN ANALYSIS AND MACHINE INTELLIGENCE 接收发表。

摘要：Causal interaction inference is prone to spurious causal interactions, due to the

substantial confounders in a biological system. While many existing methods attempt to address misidentification challenges, there remains a notable lack of effective methods to infer causal interaction under latent/unobserved confounders. In this work, we propose a method to overcome such challenges to infer dynamical causality under invisible confounders (CIC) and further reconstruct the latent confounders from time-series data by developing an orthogonal decomposition theorem in a delay embedding space. This theoretical foundation ensures the causal detection for any high-dimensional system even with only two observed variables under many latent confounders, which is a long-standing problem in the field. In addition to the latent confounder problem, such a decomposition makes the coupled variables separable in the embedding space, thus also solving the non-separability problem of causal inference. Extensive validation of the CIC method is carried out using various real datasets, which all demonstrates its effectiveness to reconstruct real biological networks and unobserved confounders.

论文链接：http://dx.doi.org/10.1109/TPAMI.2026.3658839

成果六.

我院王勇研究员与其合作者的论文 CellNiche represents cellular microenvironments in atlas-scale spatial omics data with contrastive learning 被 NATURE COMMUNICATIONS 接收发表。

摘要：Deciphering cellular microenvironments at atlas scale remains challenging because molecular identity, spatial context, and platform heterogeneity are tightly coupled. Here we present CellNiche, a scalable contrastive-learning framework that identifies and characterizes cellular microenvironments from spatial omics data using cell-centric spatial-proximity subgraphs. CellNiche combines spatial co-localization and molecular co-expression cues to learn microenvironment-aware embeddings. Across spatial omics datasets from multiple platforms (>10 million cells in total), scaling experiments show improved representations with more training data and competitive clustering and embedding-quality performance with efficient computation. In a multi-sample human non-small-cell lung cancer (NSCLC) cohort, CellNiche identifies conserved and sample-specific tumor and immune microenvironments and captures localized spatial transitions. In four independent mouse brain atlases, CellNiche integrates 293 slices into a unified virtual brain map for cross-atlas annotation transfer and spatial refinement.

论文链接：http://dx.doi.org/10.1038/s41467-026-71759-4

成果七.

我院张世华研究员与其合作者的论文 CellLoop: Identifying single-cell 3D genome chromatin loops 被 NATURE COMMUNICATIONS 接收发表。

摘要：Single-cell 3D genome technologies provide unprecedented views of chromatin architecture, but the extreme sparsity and noise of contact maps limit robust detection

of chromatin loops at the individual cell level. Here we present CellLoop, a computational framework for identifying chromatin loops from single-cell contact data by integrating intra-cellular and neighboring inter-cellular contacts through a density-based voting strategy. Applied to Dip-C data from the mouse brain, CellLoop achieves improved loop detection consistent with spatial distances and compartmentalization signals, revealing single cell-specific chromatin loops associated with transcriptional regulation and cell identity. In HiRES embryogenesis data, CellLoop enables finer cell subtype delineation by reducing confounding cell cycle effects. Integration with GAGE-seq and MERFISH data redefines spatial domain functions through chromatin loop dynamics. Together, CellLoop provides a scalable and accurate approach for characterizing chromatin loop variability at single-cell resolution and highlights the utility of 3D genome features in interpreting transcriptional and spatial heterogeneity.

论文链接：http://dx.doi.org/10.1038/s41467-026-71406-y