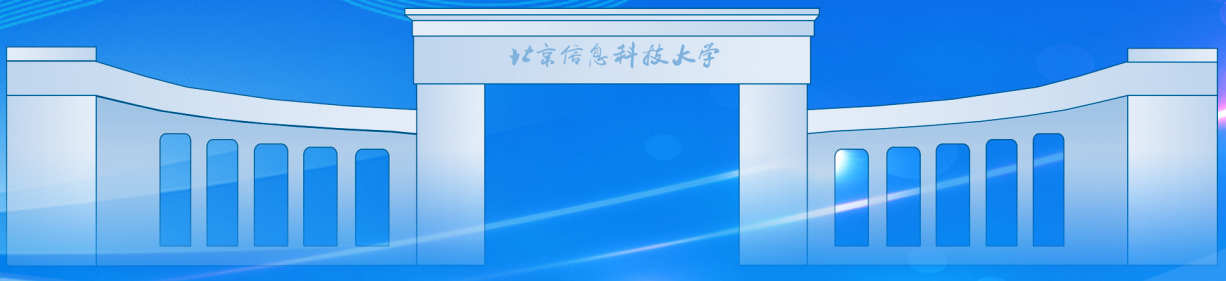
中国现场统计研究会贝叶斯统计分会
成立大会暨首届学术年会

会议手册

主办单位：中国现场统计研究会

承办单位：北京信息科技大学研究生院　科技处　理学院

云南省统计建模与数据分析重点实验室



2025年5月9–11日 北京

欢迎辞

尊敬的各位参会代表：

大家好！

在数据科学和人工智能飞速发展的时代浪潮中，贝叶斯统计分析方法正凭借其独特的优势，在处理不确定性问题和复杂数据分析方面大放异彩。值此之际，我们满怀欣喜与期待，相聚在北京信息科技大学，共同迎来“中国现场统计研究会贝叶斯统计分会成立大会暨首届学术年会”的开幕。

本次大会由中国现场统计研究会主办，北京信息科技大学研究生院、科技处、理学院和云南省统计建模与数据分析重点实验室联合承办。在此，我们谨代表大会的主办方、承办方和协办方，向每一位拨冗出席的参会代表，表示最热烈的欢迎和最衷心的感谢！

贝叶斯统计作为现代统计学的重要分支，其理论与方法的不断创新，为数据科学和人工智能的发展注入了强大动力。我们举办此次大会，旨在为贝叶斯统计领域的专家学者、科研人员以及广大从业者搭建一个深入交流的平台，共同探讨前沿学术成果，分享实践经验，携手促进我国贝叶斯统计领域的学术进步和人才培养。相信在接下来的会议中，大家将围绕贝叶斯统计分析方法在数据科学和人工智能领域的理论创新与应用拓展，展开精彩纷呈的交流与研讨。无论是理论研究的新突破，还是实际应用中的宝贵经验，都将在这里碰撞出智慧的火花。

我们衷心希望各位参会代表能够在本次大会中畅所欲言、深入交流，在收获知识的同时增进友谊。同时，也期待大家通过此次会议，建立更加紧密的合作关系，共同为贝叶斯统计领域的发展添砖加瓦，助力我国在数据科学和人工智能领域取得更加辉煌的成就！

最后，祝愿本次“中国现场统计研究会贝叶斯统计分会成立大会暨首届学术年会”取得圆满成功！祝愿各位参会代表在会议期间身体健康、欣忭盈怀、硕果盈筐！

北京信息科技大学研究生院 科技处 理学院

云南省统计建模与数据分析重点实验室

2025 年 5 月 9 日

会议组委会成员

姓名	单位
朱文圣	云南大学
李会琼	云南大学
周建军	云南大学
王爱文	北京信息科技大学
孙　妍	北京信息科技大学
程希明	北京信息科技大学

目　录

1. 温馨提醒

- 会议住宿
  - 名称：北京石油科技交流中心

    地址：北京市昌平区沙河镇黄河街与太行路交会处东北角

    电话：010-61794992
  - 名称：沙河唯实国际文化交流中心

    地址：北京市昌平区高教园中街

    电话：010-89766295

- 会议时间与地点
  - 2025 年 5 月 9 日 09:00-22:00：会议报到

    地点：北京石油科技交流中心
  - 2025 年 5 月 10 日 08:30-17:40：会议报告

    地点：北京信息科技大学沙河校区文理楼 A 座（北京市昌平区太行路 55 号）

    上午：开幕式 分会成立大会 大会报告，具体地点：212

    下午：分组报告，具体地点：301-305
  - 2025 年 5 月 11 日 8:30-17:00：会议报告

    地点：北京信息科技大学沙河校区文理楼 A 座（北京市昌平区太行路 55 号）

    上午：分组报告，具体地点：301-305

    下午：自由讨论，具体地点：不限

- 会议就餐

餐食	时间	地点
5 月 9 日晚餐	18:00-20:00	自助：北京石油科技交流中心 自助：沙河唯实国际文化交流中心
5 月 10 日午餐	12:00-13:30	自助：北京信息科技大学沙河校区一食堂一楼
5 月 10 日晚餐	18:30-20:30	晚宴：沙河唯实国际文化交流中心 D 座一楼 2 号会议厅
5 月 11 日午餐	12:10-13:30	自助：北京信息科技大学沙河校区一食堂一楼

- 大巴接送服务（具体时间可能会根据实际情况进行调整）

日期	发车时间	始发地	终到地
5 月 9 日	14:30、16:30	首都机场、大兴机场、北京站、北京西站、北京南站	北京石油科技交流中心
5 月 10 日	8:00	北京石油科技交流中心 沙河唯实国际文化交流中心	北京信息科技大学沙河校区
	18:10	北京信息科技大学沙河校区	沙河唯实国际文化交流中心
	20:45	沙河唯实国际文化交流中心	北京石油科技交流中心
5 月 11 日	8:00	北京石油科技交流中心 沙河唯实国际文化交流中心	北京信息科技大学沙河校区
	13:00、13:30	北京信息科技大学沙河校区	北京石油科技交流中心 沙河唯实国际文化交流中心
	14:00、16:00	北京石油科技交流中心 沙河唯实国际文化交流中心	首都机场、大兴机场、北京站、北京西站、北京南站

- 会议讨论与休息

  308、310 教室供参会代表自由讨论

  312、313 教室供参会代表安静休息

- 会议联系人
  - 学术事务

    李会琼 云南大学 13529152592 lihuiqiong@ynu.edu.cn

    赵建喜 北京信息科技大学 15010109846 zhaojianxi@bistu.edu.cn

    邹庆荣 北京信息科技大学 15600601956 qingrongzou@bistu.edu.cn
  - 会务安排

    周建军 云南大学 18287193405 jjzhou@ynu.edu.cn

    周　平 北京信息科技大学 15201266180 18417764@qq.com

    白永昕 北京信息科技大学 18810169585 yongxinbai2017@163.com

2. 会议日程

会议地点：北京信息科技大学沙河校区文理楼 A 座

2025 年 5 月 9 日			
09:00-22:00	会议报到		石油科技交流中心
2025 年 5 月 10 日			
时间	议程内容	主持人	地点
08:00-08:30	会议签到		一楼大厅
08:30-09:00	开幕式	王爱文 教授 北京信息科技大学	212
09:00-09:30	分会成立大会		
09:30-10:00	茶歇		二楼
10:00-11:00 大会报告 1	Bayesian Linear and Group Regression 刘军 教授 哈佛大学 清华大学	周晓华 教授 北京大学	212
11:00-12:00 大会报告 2	Recent Development of Power Priors for Leveraging Historica Data 陈明辉 教授 美国康涅狄格大学	张忠占 教授 北京工业大学	
12:00-13:20	自助午餐		一食堂一楼
13:00-14:00	图书馆参观		图书馆
13:20-13:50	分会常务理事会	朱文圣 教授 云南大学	311
14:00-15:40 分组报告 1	A 组报告 (A1-A4)	林明 厦门大学	301
	B 组报告 (B1-B4)	李周平 兰州大学	302
	C 组报告 (C1-C4)	蔡敬衡 中山大学	303
	D 组报告 (D1-D4)	郭绍俊 中国人民大学	304
	E 组报告 (E1-E4)	陈钊 复旦大学	305
15:40-16:00	茶歇		三楼
	A 组报告 (A5-A8)	冯龙 南开大学	301

16:00-17:40 分组报告 2	B 组报告 (B5-B8)	严晓东 西安交通大学	302
	C 组报告 (C5-C8)	李云仙 云南财经大学	303
	D 组报告 (D5-D8)	杜江 北京工业大学	304
	E 组报告 (E5-E8)	李新民 青岛大学	305
18:30-20:30	晚宴		唯实国际文化交流中心
2025 年 5 月 11 日			
8:30-10:10 分组报告 1	A 组报告 (A1-A4)	赵建喜 北京信息科技大学	301
	B 组报告 (B1-B4)	张思亮 华东师范大学	302
	C 组报告 (C1-C4)	兰伟 西南财经大学	303
	D 组报告 (D1-D4)	王纯杰 长春工业大学	304
	E 组报告 (E1-E4)	杨洋 南开大学	305
10:10-10:30	茶歇		三楼
10:30-12:10 分组报告 2	A 组报告 (A5-A8)	邹庆荣 北京信息科技大学	301
	B 组报告 (B5-B8)	李会琼 云南大学	302
	C 组报告 (C5-C8)	杜明月 吉林大学	303
	D 组报告 (D5-D8)	周平 北京信息科技大学	304
	E 组报告 (E5-E7)	周建军 云南大学	305
12:10-13:30	自助午餐		一食堂一楼
14:00-17:00	自由讨论		不限

3. 分组报告安排

5 月 10 日下午分组报告安排

A 组日程（地点：301）

主持人：林明，厦门大学

14:00--14:25 (A1) 题　目: Recover Concentrated Semi-Bayesian Estimation

报告人: 许杏柏，厦门大学

14:25--14:50 (A2) 题　目:　DAG Trend Filtering for Genomic Denoising via Higher-Order Bayesian Networks and DAG Shrinkage Processes

报告人: 朱蔚萱，厦门大学

14:50--15:15 (A3) 题　目: Acceleration of Approximate Bayesian Computation Methods for Complex Models

报告人: 汪时嘉，上海科技大学

15:15--15:40 (A4) 题　目: Bayes-Optimal Fair Classification with Linear Disparity Constraints via Pre-, In-, and Post-processing

报告人: 曾宪立，厦门大学

15：40--16：00　茶歇

主持人：冯龙，南开大学

16:00--16:25 (A5) 题　目: Spatial-Sign based High Dimensional Change Point Inference

报告人: 刘霁萱，南开大学

16:25--16:50 (A6) 题　目: Inverse Norm Weighted Max-sum Test for High Dimensional Location Parameters

报告人: 闫国玮，南开大学

16:50--17:15 (A7) 题　目: Robust Multi-Source Domain Adaptation under Label Shift

报告人: 钱成德，上海交通大学

17:15--17:40 (A8) 题　目: High-Dimensional Hettmansperger-Randles Estimator and Its Applications

报告人: 张晓旭，中国科学院数学院与系统科学院

B 组日程（地点：302）

主持人：李周平，兰州大学

14:00--14:25 (B1) 题　目: Bayesian Utility-driven Bandit Learning for Matching Markets with Hypothesis Testing

报告人: 严晓东，西安交通大学

14:25--14:50 (B2) 题　目: Model Average Estimation of Parameters in Linear Model with Multiple Change points

报告人: 夏志明，西北大学

14:50--15:15 (B3) 题　目: Bayesian Outlier Detection for High-dimensional Regression Models with Nonignorable Missing Data

报告人: 张韵祺，云南大学

15:15--15:40 (B4) 题　目: A New Functional Data Classifier Based on Shrinkage Functional Mahalanobis Distance

报告人: 李周平，兰州大学

15：40--16：00　茶歇

主持人：严晓东，西安交通大学

16:00--16:25 (B5) 题　目: Decomposition of WAIC for Assessing the Information Gain with Application to Educational Testing

报告人: 刘芳，苏州大学

16:25--16:50 (B6) 题　目: A Bayesian Tweedie Exponential Dispersion Process with a Change-Point for Two-Phase Degradation Data

报告人: 王平平，南京财经大学

16:50--17:15 (B7) 题　目: Learning Semi-parametric Tree Models from Mixed Data

报告人: 周灿，南京审计大学

17:15--17:40 (B8) 题　目: Composite Likelihood Variational Approximation to Generalized Linear Mixed Models

报告人: 徐礼柏，苏州大学

C 组日程（地点：303）

主持人：蔡敬衡，中山大学

14:00--14:25 (C1) 题　目: 基于 Pólya-Gamma 随机表示的两部分模型贝叶斯正则变分估计

报告人: 夏业茂，南京林业大学

14:25--14:50 (C2) 题　目: Mitigating Ambiguity in Earthquake Catastrophe Insurance Pricing: Model Averaging and Ambiguity Aversion

报告人: 李云仙，云南财经大学

14:50--15:15 (C3) 题　目: 应用贝叶斯结构方程模型元分析技术处理部分原始研究违反排他性假设的问题

报告人: 柯紫筠，中山大学

15:15--15:40 (C4) 题　目: 贝叶斯 Lasso 验证性因子分析模型

报告人: 潘俊豪，中山大学

15：40--16：00　茶歇

主持人：李云仙，云南财经大学

16:00--16:25 (C5) 题　目: Kernel Variable Importance Measure with Applications

报告人: 黄丙耀，广东工业大学

16:25--16:50 (C6) 题　目: Super-Efficient Markov Chain Monte Carlo Algorithms for Bayesian Inference in Population Genomics

报告人: 焦熙云，南方科技大学

16:50--17:15 (C7) 题　目: 代际流动感知的省域差异比较研究--基于贝叶斯 MrsP 模型

报告人: 汪燕敏，安徽财经大学

17:15--17:40 (C8) 题　目: 弗雷歇回归模型的贝叶斯分析

报告人: 刘鹤飞，云南财经大学

D 组日程（地点：304）

主持人：郭绍俊，中国人民大学

14:00--14:25 (D1) 题　目: Bayesian Integrative Region Segmentation in Spatially Resolved Transcriptomic Studies

报告人: 闫引桥，北京工业大学

14:25--14:50 (D2) 题　目: BACT: Nonparametric Bayesian Cell Typing for Single-Cell Spatial Transcriptomics Data

报告人: 罗翔宇，中国人民大学

14:50--15:15 (D3) 题　目: Functional Bayesian Additive Regression Trees with Shape Constraints

报告人: 张博海，北师香港浸会大学

15:15--15:40 (D4) 题　目: Modeling Microbial Community Coalescence via Compositional Directed Acyclic Graphical Models

报告人: 何珂俊，中国人民大学

15：40--16：00　茶歇

主持人：杜江，北京工业大学

16:00--16:25 (D5) 题　目: 基于去噪扩散隐式模型的地震缺失数据插值方法

报告人: 张春霞，西安交通大学

16:25--16:50 (D6) 题　目: Hierarchical Hidden Markov Models for Modeling Heterogeneous Time Series in Data-Scarce Scenarios

报告人: 兰慧，北京工业大学

16:50--17:15 (D7) 题　目: Two-fold Varying-coefficient Mediation Models and　Their Applications

报告人: 王文武，曲阜师范大学

17:15--17:40 (D8) 题　目: Time Series Clustering and Prediction using LSTM Combined with RBF Kernel-based Multi-head Attention

报告人: 赵娉君，西安电子科技大学

E 组日程（地点：305）

主持人：陈钊，复旦大学

14:00--14:25 (E1) 题　目: Test of Multivariate Independence via Comparing Two Bivariate Means

报告人: 许凯，安徽师范大学

14:25--14:50 (E2) 题　目: Order-Restricted Hypothesis Tests for Nonlinear Mixed-Effects Models with Measurement Errors in Covariates

报告人: 张艺馨，中国科学技术大学

14:50--15:15 (E3) 题　目: Testing the Homogeneity of a Three-Sample Problem with a Mixture Structure

报告人: 任鹏程，江苏师范大学

15:15--15:40 (E4) 题　目: Ordinal Graphical Models via a Bayesian Nonparametric　Clustering Approach

报告人: 谌自奇，华东师范大学

15：40--16：00　茶歇

主持人：李新民，青岛大学

16:00--16:25 (E5) 题　目: Log-Gaussian Process Regression with Applications in Loss Reserving

报告人: 卢志义，天津商业大学

16:25--16:50 (E6) 题　目: Improving Design and Normalization of Multiplex Proteomics Study

报告人: 方华英，首都师范大学

16:50--17:15 (E7) 题　目: Mixed-input Gaussian Process Regression

报告人: 江声，香港中文大学（深圳）

17:15--17:40 (E8) 题　目: Gaussian Process-based Calibration of Complex Computer Models with Functional Inputs

报告人: 李赵辉，中国科学院数学与系统科学研究院

5 月 11 日上午分组报告安排

A 组日程（地点：301）

主持人：赵建喜，北京信息科技大学

08:30--08:55 (A1) 题　目: Estimating IRT Models under Gaussian Mixture Modelling of Latent Traits: An Application of MSAEM Algorithm

报告人: 孟祥斌，东北师范大学

08:55--09:20 (A2) 题　目:　A Sequential Bayesian Changepoint Detection Procedure for Aberrant Behaviours in Computerized Testing

报告人: 陆婧，东北师范大学

09:20--09:45 (A3) 题　目: Bayesian Variable Selection for Optimizing Dynamic Treatment Regimes

报告人: 崔婷婷，浙江财经大学

09:45--10:10 (A4) 题　目: Similarity-Assisted Learning for Estimating Optimal Individualized Treatment Regimes

报告人: 李灿辉，河南大学

10:10--10:30 茶歇

主持人：邹庆荣，北京信息科技大学

10:30--10:55 (A5) 题　目: Time-Varying Probabilistic Forecast Combinations based on Particle Filtering: Diversity Matters

报告人: 罗雪，北京航空航天大学

10:55--11:20 (A6) 题　目: Research on the Extension of Convex Clustering

报告人: 赵建喜，北京信息科技大学

11:20--11:45 (A7) 题　目: Bayesian Spatiotemporal Modeling for the Inpatient Hospital Costs of Alcohol-related Disorders

报告人: 虞祯，对外经济贸易大学

11:45--12:10 (A8) 题　目: Development and Evaluation of the Updated Risk Prediction Model Involving in New Candidate Predictors

报告人: 曹雅琦，中央民族大学

B 组日程（地点：302）

主持人：张思亮，华东师范大学

08:30--08:55 (B1) 题　目: Imputation and Post-selection Inference in Models with Missing Data: Applications in Clinical Data

报告人: 裘予琦，华东师范大学

08:55--09:20 (B2) 题　目: Functional Differential Graphical Analysis Procedure with Application to Hard Landing Incidents in Civil Aviation

报告人: 李格非，华东师范大学

09:20--09:45 (B3) 题　目: Efficient Bayesian Reliability Assessment for Step-Stress Accelerated Wiener Degradation Model

报告人: 周世荣，温州大学

09:45--10:10 (B4) 题　目: Joint Latent Variable Modeling with a Cumulative Shrinkage Process Prior

报告人: 吕斌，华东师范大学

10:10--10:30 茶歇

主持人：李会琼，云南大学

10:30--10:55 (B5) 题　目: Bayesian Learning of Optimal Real-time Dynamic Treatment Regimes

报告人: 周迎春，华东师范大学

10:55--11:20 (B6) 题　目: Semiparametric Structural Equation Models with Interval-Censored Data

报告人: 李树威，广州大学

11:20--11:45 (B7) 题　目: Low-rank Variational Correction Estimation for Multi-Source Heterogeneous Quantile Linear Regression Models

报告人: 李会琼，云南大学

11:45--12:10 (B8) 题　目: Network Alternating Direction Method of Multipliers for Ultrahigh-Dimensional Decentralised Federated Learning

报告人: 董伟，郑州大学

C 组日程（地点：303）

主持人：兰伟，西南财经大学

08:30--08:55 (C1) 题　目: Network Assisted Approximate Factor Model Estimation

报告人: 范新妍，中国人民大学

08:55--09:20 (C2) 题　目: Graph-based Multisample Comparison with Application to Feature Selection for Multi-Category Responses

报告人: 蒲丹，西南财经大学

09:20--09:45 (C3) 题　目: High-Frequency Volatility Estimation and Forecasting with a Novel Bayesian LGI Model

报告人: 吴奔，中国人民大学

09:45--10:10 (C4) 题　目: Mixture Conditional Regression with Ultrahigh Dimensional Text Data for Estimating Extralegal Factor Effects

报告人: 师佳鑫，北京大学

10:10--10:30 茶歇

主持人：杜明月，吉林大学

10:30--10:55 (C5) 题　目: Bonus-Malus System Based on INAR(1) Model with Finite Mixtures of Erlang Distributions for the Heterogeneity

报告人: 程建华，吉林大学

10:55--11:20 (C6) 题　目: 几类门限时间序列模型在空气质量监测中的应用研究

报告人: 李聪，吉林大学

11:20--11:45 (C7) 题　目: Genomic Patterns are Associated with Different Sequelae of Patients with Long-Term COVID-19

报告人: 张楠，吉林大学

11:45--12:10 (C8) 题　目: AMPGP: A Deep Learning Framework for High-Efficacy Antimicrobial Peptide Discovery

报告人: 武润泽，吉林大学

D 组日程（地点：304）

主持人：王纯杰，长春工业大学

08:30--08:55 (D1) 题　目: On MCMC Sampling in Self-Exciting Integer-Valued Threshold Time Series Models

报告人: 杨凯，长春工业大学

08:55--09:20 (D2) 题　目: Three-Stage Communication-Efficient Surrogate Quantile Regression for Non-randomly Distributed System with Missing Data

报告人: 袁晓惠，长春工业大学

09:20--09:45 (D3) 题　目: Semiparametric Analysis of Additive-Multiplicative Hazards Model with Interval-Censored Data and Panel Count Data

报告人: 王淑影，长春工业大学

09:45--10:10 (D4) 题　目: Bayesian Empirical Likelihood for Accelerated Failure Time Model with Covariates Missing at Random

报告人: 刘新蕊，长春工业大学

10:10--10:30 茶歇

主持人：周平，北京信息科技大学

10:30--10:55 (D5) 题　目: 基于能力猜测的两参数项目反应理论模型及其随机期望最大化估计方法

报告人: 齐春香，东北师范大学

10:55--11:20 (D6) 题　目: 扩散条件后验采样引导的稀疏注意力 Transformer 地震数据插值方法

报告人: 韦晓莉，西安交通大学

11:20--11:45 (D7) 题　目: 一种基于图神经网络和神经过程的两阶段空间预测建模方法

报告人: 包丽莉，西安交通大学

11:45--12:10 (D8) 题　目: 基于 BERT+BiLSTM 的非平衡数据的情感分析

报告人: 徐子祥，南京林业大学

E 组日程（地点：305）

主持人：杨洋，南开大学

08:30--08:55 (E1) 题　目: Bayesian Optimization with Pareto-Principled Training for Economical Hyperparameter Optimization

报告人: 杨洋，南开大学

08:55--09:20 (E2) 题　目: Heritability Estimation with Genetic Similarity Representation

报告人: 王健桥，清华大学

09:20--09:45 (E3) 题　目: Multi-dimensional Domain Generalization with Low-Rank Structures

报告人: 李赛，人民大学

09:45--10:10 (E4) 题　目: Imputation-based Randomization Tests for Randomized Experiments with Interference

报告人: 韩庭萱，清华大学

10:10--10:30 茶歇

主持人：周建军，云南大学

10:30--10:55 (E5) 题　目: Block Sparse Bayesian Learning: A Diversified Scheme

报告人: 张岩昊，北京航空航天大学

10:55--11:20 (E6) 题　目: The Minimax Optimal Convergence Rate of Posterior Density in the Weighted Orthogonal Polynomials

报告人: 罗祎祺，北京航空航天大学

11:20--11:45 (E7) 题　目: Inference with Combined Data from Subgroup Selection and Validation Phases in Clinical Trials

报告人: 周建军，云南大学

4. 报告摘要

✷ *大会报告摘要*

（V1）Bayesian Linear and Group Regression

Jun S Liu
Department of Statistics, Harvard University
Department of Statistics and Data Science, Tsinghua University

Abstract: After introducing the basic framework for Bayesian linear regressions, we explain the idea of using a "neuronized" form to unify a class of popular priors and demonstrate its use in a genetic risk prediction task. We then dive into the group-variable selection problem in Bayesian regression. We show how to use an efficient variational approximation method to carry out necessary Bayesian computation so as to obtain good approximations to the marginal posterior distributions of the targeted parameters. We demonstrate its advantages by both simulations and applications to real-data examples. This is based on the joint work with Buyu Lin and Changhao Ge.

刘军教授 1981 年毕业于清华附中；1985 年于北京大学获得数学学士学位；1991 年在美国芝加哥大学获统计学博士学位。自 2000 年至今，刘军担任美国哈佛大学统计系终身教授，并于 2003-2015 年兼任哈佛生物统计系教授。他曾任哈佛统计系助理教授（1991-1994）；斯坦福大学统计系助理教授、副教授、终身教授（1994-2004）；北京大学数学学院长江讲座教授、清华大学数学系访问教授，并获国家杰出青年基金 B 类（2005）。他于 2015 年领导创建清华大学统计学研究中心，并任名誉主任至 2024 年。2024 年 7 月他以筹建发展委员会主任身份领导在清华大学创建统计与数据科学系。

刘军教授一直从事于贝叶斯统计理论、蒙特卡洛方法、统计机器学习、状态空间模型和时间序列、生物信息学、计算生物学等方向的研究，并做出杰出贡献，对大数据处理和机器学习领域有深远影响。他于 2002 年获得考普斯会长奖 （COPSS Presidents' Award，公认为国际统计学界的最高荣誉）； 2010 年获得世界华人应用数学最高荣誉晨兴应用数学金奖（三年一度，不超过 45 岁）；2014 年被 ISI 评为论文高频引用的数学家；2016 年获得泛华统计协会许宝騄奖（三年一度，不超过 51 岁）；2004、2005 年分别成为美国数理统计学会和美国统计学会会士（Fellow）； 2022 年当选国际计算生物学会会士；2025 年当选美国科学院院士。刘军教授还曾任美国统计协会会刊（JASA）联席主编及多个国际一流统计杂志副编等职。截至 2025 年 5 月，他在各类国际顶尖学术杂志（如 Science，Nature，Cell，JASA，JMLR 等）及书刊上发表论文 300 余篇和一本专著， 被引用 9 万余次（Google scholar）。他已经指导了 40 多位博士生、30 多位博士后。

（V2）Recent Development of Power Priors for Leveraging Historical Data

Ming-Hui Chen
Department of Statistics, University of Connecticut

Abstract: Historical data or real-world data are often available in clinical trials, genetics, health care, psychology, environmental health, engineering, economics, and business. The power priors have emerged as a useful class of informative priors for a variety of situations in which historical data are available. In this talk, an overview of the development of the power priors is provided. Various variations of the power priors under a binomial regression model and a normal linear regression model will be presented. Several interesting applications will be used to demonstrate the usefulness of the power priors and their variations. Finally, the directions of future research on the power priors are discussed.

Dr. Ming-Hui Chen is a Board of Trustees Distinguished Professor and Head of Department of Statistics at University of Connecticut (UConn). He was elected to Member of the Connecticut Academy of Science and Engineering (CASE) in 2025, Fellow of American Association for the Advancement of Science (AAAS) in 2024, Fellow of International Society for Bayesian Analysis in 2016, Fellow of Institute of Mathematical Statistics in 2007, and Fellow of American Statistical Association in 2005. He received the University of Connecticut AAUP Research Excellence Award in 2013, the UConn College of Liberal Arts and Sciences (CLAS) Excellence in Research Award in the Physical Sciences Division in 2013, the University of Connecticut Alumni Association's University Award for Faculty Excellence in Research and Creativity (Sciences) in 2014, the ICSA Distinguished Achievement Award in 2020, and the Distinguished Science Alumni Award from Purdue University in 2023. He has published 485+ peer-reviewed journal articles and five books including two advanced graduate-level books on Bayesian survival analysis and Monte Carlo methods in Bayesian computation. He has supervised 42 PhD students. He served as, President of ICSA (2013), Chair of the Eastern Asia Chapter of International Society for Bayesian Analysis (2018), President of New England Statistical Society (2018-2020), and the 2022 JSM Program Chair. Currently, he is Co Editor-in-Chief of Statistics and Its Interface, inaugurated Co Editor-in-Chief of New England Journal of Statistics in Data Science, and an Associate Editor for several other statistical journals.

✶ *分组报告摘要*

5 月 10 日下午分组报告摘要

主持人: 林明 厦门大学

（A1）Recover Concentrated Semi-Bayesian Estimation

许杏柏 厦门大学

Abstract: A concentrated semi-Bayesian estimation method is proposed in this paper, which is computationally attractive while maintaining the advantages of traditional Bayesian estimation methods. This approach allows for computation with Markov Chain Monte Carlo methods, and it requires considerably less computational time and memory usage compared to traditional and some recent Bayesian methods, since it reduces the dimension of the parameters to be sampled. It can be applied to either correctly specified or misspecified likelihood functions, as well as moment-based estimators. Monte Carlo studies show that the biases and root mean squared errors of our concentrated Bayesian estimators are usually less than or similar to those of the standard Bayesian estimators. We establish large sample properties of the concentrated semin-Bayesian estimator. An empirical application examining the network spillover effect of stock returns in the Chinese A-share market is used to further illustrate the advantage of our method.

（A2）DAG Trend Filtering for Genomic Denoising via Higher-Order Bayesian Networks and DAG Shrinkage Processes

朱蔚萱 厦门大学

Abstract: Graph-based denoising is a critical preprocessing step for analyzing noisy data, particularly in genomic applications where gene regulatory networks exhibit inherent directional dependencies. This paper introduces a novel directed acyclic graph trend filtering framework that leverages novel higher-order Bayesian networks and graphical shrinkage processes to enhance local adaptivity in signal smoothing along the directed edges of a graph. Unlike traditional graph trend filtering, which assumes undirected graphs, the proposed method explicitly respects the directional structure of graphs, improving interpretability and accuracy in capturing dependencies. We employ a Hamiltonian Monte Carlo algorithm for efficient posterior inference. Through simulations and genomic applications, the proposed method outperforms a state-of-the-art graph trend filtering algorithm in terms of mean squared error reduction and signal-to-noise ratio improvement, demonstrating its utility in recovering true signals while accounting for meaningful structural information.

（A3）Acceleration of Approximate Bayesian Computation Methods for Complex Models

汪时嘉 上海科技大学

Abstract: Approximate Bayesian computation (ABC) is a class of Bayesian inference algorithms that targets for problems with intractable or unavailable likelihood function. It uses synthetic data drawn from the simulation model to approximate the posterior distribution. However, ABC is computationally intensive for complex models. Firstly, we propose an early rejection Markov chain Monte Carlo (ejMCMC) sampler based on Gaussian processes to accelerate inference speed. Secondly, we introduce an adaptive ABC Markov chain Monte Carlo (MCMC) approach for complex distribution in high dimensional parameter space by combining the advantages of global and local MCMC proposals.

（A4）Bayes-Optimal Fair Classification with Linear Disparity Constraints via Pre-, In-, and Post-processing

曾宪立 厦门大学

Abstract: Machine learning algorithms may have disparate impacts on protected groups. To address this, we develop methods for Bayes-optimal fair classification, aiming to minimize classification error subject to given group fairness constraints. We find the form of Bayes-optimal fair classifiers under a single linear disparity measure, by uncovering a connection with the Neyman-Pearson lemma. Leveraging our theoretical results, we design methods that learn fair Bayes-optimal classifiers under bilinear disparity constraints. Our methods cover three popular approaches to fairness-aware classification, via pre-processing (Fair Up- and Down-Sampling), in-processing (Fair Cost-Sensitive Classification) and post-processing (a Fair Plug-In Rule). Our methods control disparity directly while achieving near-optimal fairness-accuracy tradeoffs. We show empirically that our methods compare favorably to existing algorithms.

主持人：冯龙，南开大学

（A5）Spatial-Sign based High Dimensional Change Point Inference

刘霁萱 南开大学

Abstract: High-dimensional changepoint inference, adaptable to diverse alternative scenarios, has attracted significant attention in recent years. In this study, we propose an adaptive and robust approach to changepoint testing. Specifically, by generalizing the classical cumulative sum (CUSUM) statistic, we construct CUSUM statistics based on spatial medians and spatial signs. We introduce test statistics that consider the maximum and summation of the CUSUM statistics across different dimensions, respectively, and take the maximum across all potential changepoint locations. We derive the asymptotic distributions of test statistics under the null hypothesis. Furthermore, the test statistics demonstrate strong performance under sparse and dense alternative hypotheses and exhibit asymptotic independence under mild conditions. Building on these results, we propose an adaptive testing procedure that integrates the max-L_∞-type and max-L_2-type statistics. Through numerical experiments and theoretical analysis, the proposed method demonstrates strong performance and exhibits robustness across a wide range of signal sparsity levels and heavy-tailed distributions.

（A6）Inverse Norm Weighted Max-sum Test for High Dimensional Location Parameters

闫国玮 南开大学

Abstract: In the context of high-dimensional data, we investigate the one-sample location testing problem. We introduce a max-type test based on the weighted spatial sign, which exhibits exceptional performance, particularly in the presence of sparse alternatives. Notably, we find that the inverse norm test significantly enhances the power of the test compared to several existing max-type tests. Next, we prove the asymptotic independence between the newly proposed max-type test statistic and the sum-type test statistic based on the weighted spatial sign. Then, we propose an innovative max-sum type testing procedure that integrates both test statistics. This novel procedure demonstrates remarkable robustness and effectiveness across a wide range of signal sparsity levels and heavy-tailed distributions. Through extensive simulation studies, we highlight the superior performance of the proposed method, showcasing its robustness and efficiency compared to traditional alternatives in various high-dimensional settings.

（A7）Robust Multi-Source Domain Adaptation under Label Shift

钱成德 上海交通大学

Abstract: As the volume of data continues to expand, it becomes increasingly common for data to be aggregated from multiple sources. Leveraging multiple sources for model training typically achieves better predictive performance on test datasets. Unsupervised multi-source domain adaptation aims to predict labels of unlabeled samples in the target domain by using labeled samples from source domains. This work focuses on robust multi-source domain adaptation for multi-category classification problems against the heterogeneity of label shift and data contamination. We investigate a domain-weighted empirical risk minimization framework for robust estimation of the target domain's class proportion. Inspired by outlier detection techniques, we propose a refinement procedure within this framework. With the estimated class proportion, robust classifiers for the target domain can be constructed. Theoretically, we study the finite-sample error bounds of the domain-weighted empirical risk minimization and highlight the improvement of the refinement step. Numerical simulations and real-data applications demonstrate the superiority of the proposed method.

（A8）High-Dimensional Hettmansperger-Randles Estimator and Its Applications

张晓旭 中国科学院数学院与系统科学院

Abstract: The classic Hettmansperger-Randles Estimator has found extensive use in robust statistical inference. However, it cannot be directly applied to high-dimensional data. In this paper, we propose a high-dimensional Hettmansperger-Randles Estimator for the location parameter and scatter matrix of elliptical distributions in high-dimensional scenarios. Subsequently, we apply these estimators to two prominent problems: the one-sample location test problem and quadratic discriminant analysis. We discover that the corresponding new methods exhibit high effectiveness across a broad range of distributions. Both simulation studies and real-data applications further illustrate the superiority of the newly proposed methods.

主持人： 李周平 兰州大学

（B1）Bayesian Utility-driven Bandit Learning for Matching Markets with Hypothesis Testing

严晓东 西安交通大学

Abstract: Bandit learning algorithms gradually optimize decision-making strategies by balancing exploration and exploitation and have been widely applied in scenarios such as online ride-hailing, advertising recommendation, and personalized medicine. However, the optimization goal of most bandit algorithms is to maximize cumulative rewards, which means that the strategies fail to capture the uncertainty in the decision-making process, making them unreliable. This paper constructs a bayesian utility-driven strategy by incorporating the uncertainty of rewards as a new objective, as it aims to maximize the probability of achieving the anticipated goal c while considering the expected utility. This paper theoretically proves that the proposed bayesian utility-driven bandit learning achieves the fastest convergence rate among current bandit algorithms and generates stronger statistical power than classical tests based on normality. The conducted simulation studies further support the theoretical findings. Ultimately, the proposed strategy was applied to market matching scenarios, and it was found that our strategy can maximize the fairness of market matching.

（B2）Model Average Estimation of Parameters in Linear Model with Multiple Change Points

夏志明 西北大学

Abstract: In this talk, we develops a model averaging framework for segmented linear regression with possible structural breaks. We build the asymptotic distribution theory for parameter estimators under the setting of gradual parameter change, which indicates the limitation of the traditional estimation methods under misspecification of sudden breaks. Based on this, the Mallows criterion and Mallows Model Average (MMA) estimator for multi-change-point regressions are established. We show that the Mallows criterion is an asymptotic unbiased estimator of the expected in-sample squared error plus a constant. When all candidate models are misspecified, the resulting MMA estimator is asymptotically optimal in terms of achieving the lowest squared error. Specifically, When the real model is a change-point model, the MMA estimator is proved to be root-n-consistent. Simulation results verify the theoretical properties well.

（B3）Bayesian Outlier Detection for High-dimensional Regression Models with Nonignorable Missing Data

张韵祺 云南大学

Abstract: In biomedical research, complex data often exist, including high-dimensional data, missing data, and outliers. These challenges may lead to the "curse of dimensionality," estimation bias, or overfitting—all of which are critically important and difficult to address. Our research focuses on solving these problems by proposing a Bayesian method for simultaneous variable selection and outlier detection in linear models with nonignorable missing data and outliers. Specifically, the Spike-Slab prior is introduced into the mean-shift model, and Spike-Slab-L1/2 priors are constructed for both the regression coefficients of covariates and the indicator parameters of outliers. A Skinny Gibbs algorithm is developed for posterior sampling, enabling simultaneous outlier detection and variable selection while achieving robust estimation of regression coefficients. When the response variable exhibits nonignorable missingness, a Polya-Gamma latent variable is introduced to facilitate posterior estimation of the propensity score model. Numerical analyses demonstrate that the proposed method performs well in outlier detection and regression parameter estimation, particularly in ultra-high-dimensional scenarios. Finally, an Alzheimer’s disease study is used to illustrate the method’s effectiveness and practical utility.

（B4）A New Functional Data Classifier Based on Shrinkage Functional Mahalanobis Distance

李周平 兰州大学

Abstract: Functional data classification is an important task and ubiquitous in many real applications, which has been extensively studied in the last few decades. In this talk, we propose a novel classification approach for functional data based on a shrinkage estimate of functional Mahalanobis distance. We first introduce a new shrinkage functional Mahalanobis distance (SFMD), by using this new distance, we transform the functional observations into a set of vector-valued pseudo-samples. Furthermore, we adopt some good classification algorithms designed for multivariate data to this pseudo-samples instead of the original functional data. The new approach has advantage of highly flexible and scalable, that is, it can easily combine with any classification algorithm, such as support vector machine, tree-based methods, and neural networks. We demonstrate the performance of the proposed functional classifier through both extensive simulation studies and two real data applications.

主持人：严晓东，西安交通大学

（B5）Decomposition of WAIC for Assessing the Information Gain with Application to Educational Testing

刘芳 苏州大学

Abstract: Nowadays, multidimensional data are often available from educational testing. One natural issue is to identify whether more dimensional data are useful in fitting the item response data. To address this important issue, we develop a new decomposition of Widely Applicable Information Criterion (WAIC) via the posterior predictive ordinate (PPO) under the joint model for the response, response time, and two additional educational testing scores. Based on this decomposition, a new model assessment criterion is then proposed, which allows us to determine which of the response time and two additional scores are most useful in fitting the response data and whether other dimensional data are further needed given that one of these dimensional data is already included in the joint model with the response data. In addition, an efficient Monte Carlo method is developed to compute PPO. An extensive simulation study is conducted to examine the empirical performance of the proposed joint model and the model assessment criterion in the psychological setting. The proposed methodology is further applied to an analysis of a real dataset from a computerized educational assessment program.

（B6）A Bayesian Tweedie Exponential Dispersion Process with a Change-Point for Two-Phase Degradation Data

王平平 南京财经大学

Abstract: Degradation analysis is an efficient way to evaluate a product's reliability in various applications by capturing its degradation characteristics quickly and accurately. In the degradation analysis, the accuracy of the reliability inference depends highly on the selected model for fitting observed degradation measurements. Covering popular stochastic process models as special cases, the Tweedie exponential dispersion process (TEDP) model has potential in describing more extensive degradation phenomena in engineering applications. In this work, we propose a TEDP with a change-point (CPTEDP) to model two-phase degradation pattern of products, where unit-specific two-piece drifts are considered to explain heterogeneous degradation patterns of testing units. We introduce a three-stage hierarchical Bayesian inference on the parameters of the CPTEDP model without the need for approximating its likelihood function that has no closed-form expression using Markov chain Monte Carlo (MCMC). To overcome difficulties posed by the continuity constraint of degradation processes on modeling and computation under the hierarchical Bayesian framework, we adopt the pseudo likelihood function instead of the real likelihood for computational efficiency. After fitting the three-stage hierarchical Bayesian CPTEDP model by adopting the Gibbs

algorithm, we derive the approximations of reliability measures (e.g., mean time to failure (MTTF), remaining useful life (RUL), mean residual life (MRL)) of explicit analytical forms by substituting posterior estimates obtained from the Gibbs algorithm. Analytical results from a case study and a variety of simulations demonstrate that the hierarchical Bayesian CPTEDP model can provide more suitable fits to degradation data with two-phase patterns, improving the accuracy of reliability estimation for products.

（B7）Learning Semi-parametric Tree Models from Mixed Data

周灿 南京审计大学

Abstract: Causal discovery and representation involving latent variables and structures have attracted growing interest in the era of artificial intelligence, particularly for their critical role in understanding real-world data. While many existing methods focus exclusively on either purely continuous or purely discrete data, this paper addresses the challenge of learning latent structures from mixed data. We propose a novel semi-parametric tree model capable of handling mixed data， and develop an algorithm for learning the structure of this model using additive information distances. We demonstrate that this algorithm efficiently and accurately recovers the true structure, given the information distances. Additionally, the sample-based version of the structural learning algorithm achieves probabilistic approximate correctness, with a finite sample bound established for exact structural recovery. Both simulated and real data are used to assess the performance of our proposed algorithm, with experimental results showing that our algorithm can effectively discover latent hierarchical structures behind mixed data.

（B8）Composite Likelihood Variational Approximation to Generalized Linear Mixed Models

徐礼柏 苏州大学

Abstract: Composite likelihood usually ignores dependencies among response components, while variational approximation to likelihood ignores dependencies among parameter components. What both methods have in common is that they essentially break the dependence of random effects. In this talk, we derive (1) a variational approximation to row-column composite likelihood for GLMMs, and (2) a variational approximation to marginal likelihood for multivariate GLMMs. We establish the exact asymptotic behaviors of the variational estimates' asymptotic behaviors for both composite likelihood variational approximations. Simulation studies demonstrate that our methods are computationally faster than both Laplace approximation and MCMC.

主持人：蔡敬衡 中山大学

（C1）基于 Pólya-Gamma 随机表示的两部分模型贝叶斯正则变分估计

夏业茂 南京林业大学

摘要：两部分模型在刻画“零过多”半连续数据方面具有独特的优势。然而在分析这类模型时却面临着非线性问题的困扰，这特别在处理参数惩罚时极为不便。为此，本文基于 Pólya-gamma 随机表示，将两部分模型置于类高斯分布混合框架内，其中的回归系数表现为高斯回归模型下线性形式，这大大改善了统计计算。我们在贝叶斯框架内展开统计分析。为了模型简约性，我们对回归参数赋以 spike-and-slab 收缩先验，使得在“n 小 p 大”情形下能够有效地控制参数的惩罚度。我们建立变分贝叶斯推断程序，平均场方法被用来构建变分密度。与 MCMC 抽样近似方法相比，变分贝叶斯近似能够提供确定解，且估计具备较高的精度。我们建立了基于 Pólya-gamma 随机表示的变分推断与 Jaakkola and Jordan（*Statistics and Computing,* 2000）的 logistic 似然变分近似的等价性。随机模型和实证分析展示了方法的有效性和实用性。

（C2）Mitigating Ambiguity in Earthquake Catastrophe Insurance Pricing: Model Averaging and Ambiguity Aversion

李云仙 云南财经大学

Abstract: Ambiguity, defined as uncertainty with unknown probabilities, poses a significant challenge in the pricing of earthquake catastrophe insurance, as it systematically increases premium levels relative to risks with known probabilities. Despite its practical relevance, the economic mechanisms and industry responses to ambiguity remain underexplored. This paper addresses this gap by advancing two key contributions. First, we introduce model averaging (MA) techniques into earthquake catastrophe insurance pricing, demonstrating their dual efficacy in reducing parameter uncertainty and optimizing premium calculations. Second, we extend the α-maxmin pricing framework to explicitly incorporate insurer ambiguity aversion, formalizing the relationship between model uncertainty and firm economic objectives. Using China’s earthquake loss dataset (1992–2023), we estimate jackknife model averaging (JMA), Akaike information criterion (AIC) MA, and Bayesian information criterion (BIC) MA models within a quantile regression framework. Empirical results show that MA approaches outperform traditional model selection methods in predictive accuracy, with JMA demonstrating superior performance in extreme quantile estimation when additional explanatory variables are included. Notably, JMA achieves premium reductions of up to 13.64%, suggesting that insurers may exhibit low ambiguity aversion or even ambiguity-seeking behavior under specific conditions. Sensitivity analyses highlight how ambiguity aversion (α), capital cost (δ), and quantile level (τ) systematically influence pricing outcomes, with higher values of these parameters requiring larger capital reserves to mitigate the risk of ruin, thereby increasing premium levels. This research provides a novel methodological toolkit for integrating model uncertainty into catastrophe insurance pricing, offering direct implications for risk management practices and regulatory frameworks.

（C3）应用贝叶斯结构方程模型元分析技术处理部分原始研究违反排他性假设的问题

柯紫筠 中山大学

摘要：工具变量法是一种在管理学领域广泛应用的非实验性因果推断。日前有研究将其与结构方程模型元分析技术相结合从而强化元分析层面的因果关系。排他性假设是工具变量法的其中一个关键前提假设，违反该假设将对工具变量法的有效性产生重大影响。在元分析情境中，可能存在部分原始研究违反该前提假设的情形。本研究将探索如何在贝叶斯结构方程模型元分析框架下处理部分原始研究违反排他性设计的问题，并通过模拟研究验证其有效性。

（C4）贝叶斯 Lasso 验证性因子分析模型

潘俊豪 中山大学

摘要：验证性因子分析（Confirmatory Factor Analysis，CFA）模型被广泛应用于心理学、社会学等领域的科学研究当中，以研究指标变量（Indicator）和潜变量（Latent Variable）之间的关系。在建模过程中，CFA 模型（以及其他潜变量模型）的一个重要前提假设是局部独立性（Local Independence），违反局部独立性假设的情况被称为局部项目依赖。在实际数据分析当中，研究者往往默认局部独立性假设成立从而建立测量模型。然而，随着 CFA 模型的广泛应用，研究者逐渐意识到错误地假设局部独立性会对研究结果（特别是潜变量之间关系的估算）产生严重的误导。作为最基础的潜变量模型之一，在 CFA 模型的统计分析中如何有

效地考虑指标变量间的局部依赖程度一直是学界关注的热点问题。此问题的解决也将有助于解决其他潜变量模型中不满足局部独立性时应如何建模的问题。本报告将跟大家分享我们关于这方面的一些研究。

主持人： 李云仙 云南财经大学

（C5）Kernel Variable Importance Measure with Applications

黄丙耀 广东工业大学

Abstract: This paper introduces a novel kernel variable importance measure (KvIM) based on the maximum mean discrepancy (MMD). KvIM can effectively measure the importance of each individual dimension in contributing to the distributional difference by constructing weighted MMD and applying perturbations to evaluate changes in MMD through assigned weights. KvIM has several notable advantages: it is nonparametric and model-free, accounts for dependencies among dimensions, and is suitable for high-dimensional data. We establish the consistency of the empirical KvIM under general conditions, along with its theoretical properties in high-dimensional settings. Furthermore, we apply KvIM to classification problems and streaming datasets, proposing a KvIM-enhanced classification approach and an online KvIM. These applications demonstrate the practical utility of the proposed KvIM in diverse scenarios, as justified through extensive numerical experiments.

（C6）Super-Efficient Markov Chain Monte Carlo Algorithms for Bayesian Inference in Population Genomics

焦熙云 南方科技大学

Abstract: Bayesian inference in population genomics and phylogenomics under the multispecies coalescent (MSC) model involves intense computation. The mixing efficiency of Markov chain Monte Carlo (MCMC) algorithms is inversely proportional to the computational effort required to achieve a certain precision. We describe a few super-efficient MCMC algorithms, which achieve mixing efficiency higher than the independent sampler. The first, called the mirror-type move, proposes new values of the parameters around the mirror image of the current values. The second, called Bactrian-uniform-reflection (BUR), combines a Bactrian sliding-window for the uniform target with variable transform to achieve super efficiency in the parameter. We apply the new algorithms to a problem in population genomics and the new algorithms performed favourably compared with other state-of-art MCMC algorithms.

（C7）代际流动感知的省域差异比较研究--基于贝叶斯 MrsP 模型

汪燕敏 安徽财经大学

摘要：制定科学公共政策的前提是政府能够准确了解民众的意愿。传统抽样调查受限于小样本和非代表性抽样，不足以准确获取民意。多层回归和合成分层（MrsP）可以将基于调查数据的模型估计结果扩展到普查数据，是小样本下获取民意的有效手段。基于 2020 年的中国综合社会调查数据和第七次人口普查汇总数据，本研究采用贝叶斯 MrsP 模型估计了中国各省民众对代际向上流动的支持率，并与频率方法的估计结果进行了比较。我们的研究表明：在全国层面上，有过半数成年人认为自己相对于父辈实现了向上流动。在省域层面，民族自治地区和安徽福建的民众向上流动感知的排名最高，东北和华北地区民众感知排名最低。

（C8）弗雷歇回归模型的贝叶斯分析

刘鹤飞 云南财经大学

摘要：随着数据科学的发展，数据分析的对象越来越宽泛，数据分析中的“数据”越来越广义。在回归分析中，当感兴趣的响应变量不是实数，而是非欧几里得空间中的一个随机对象时，Petersen 基于条件弗雷歇均值提出了弗雷歇回归的概念。我们在此研究的基础上，详细分析了弗雷歇回归的原理，采用贝叶斯分析的方法对弗雷歇回归模型进行了模型估计和变量选择。

主持人： 郭绍俊 中国人民大学

（D1）Bayesian Integrative Region Segmentation in Spatially Resolved Transcriptomic Studies

闫引桥 北京工业大学

Abstract: The spatially resolved transcriptomic study is a recently developed biological experiment that can measure gene expressions and retain spatial information simultaneously, opening a new avenue to characterize fine-grained tissue structures. In this article, we propose a nonparametric Bayesian method named BINRES to carry out the region segmentation for a tissue section by integrating all the three types of data generated during the study---gene expressions, spatial coordinates, and the histology image. BINRES is able to capture more subtle regions than existing statistical partitioning models that only partially make use of the three data modes and is more interpretable than neural-network-based region segmentation approaches. Specifically, due to a nonparametric spatial prior, BINRES does not require a prespecified region number and can learn it automatically. BINRES also combines the image and the gene expressions in the Bayesian consensus clustering framework and thus flexibly adjusts their label alignment contribution weights in a data-adaptive manner. A computationally scalable extension is developed for large-scale studies. Both simulation studies and the real application to three mouse spatial transcriptomic datasets demonstrate that BINRES outperforms the competing methods and easily achieves the uncertainty quantification of the integrative partition. The R package of the proposed method is publicly available at https://github.com/yinqiaoyan/BINRES.

（D2）BACT: Nonparametric Bayesian Cell Typing for Single-Cell Spatial Transcriptomics Data

罗翔宇 中国人民大学

Abstract: The spatial transcriptomics is a rapidly evolving biological technology that simultaneously measures the gene expression profiles and the spatial locations of spots. With progressive advances, current spatial transcriptomic techniques can achieve the cellular or even the subcellular resolution, making it possible to explore the fine-grained spatial pattern of cell types within one tissue section. However, most existing cell spatial clustering methods require a correct specification of the cell type number, which is hard to determine in the practical exploratory data analysis. To address this issue, we present a nonparametric Bayesian model BACT to perform BAyesian Cell Typing by utilizing gene expression information and spatial coordinates of cells. BACT incorporates a nonparametric Potts prior to induce neighboring cells' spatial dependency, and more importantly it can automatically learn the cell type number directly from the data without prespecification. Evaluations on three single-cell spatial transcriptomic datasets demonstrate the better performance of BACT than competing spatial cell typing methods.

（D3）Functional Bayesian Additive Regression Trees with Shape Constraints

张博海 北师香港浸会大学

Abstract: Motivated by the great success of Bayesian additive regression trees (BART) on regression, we propose a nonparametric Bayesian approach for the function-on-scalar regression problem, termed as Functional BART (FBART). Utilizing spline-based function representation and tree-based domain partition model, FBART offers great flexibility in characterizing the complex and heterogeneous relationship between the response curve and scalar covariates. We devise a tailored Bayesian backfitting algorithm for estimating the parameters in the FBART model. Furthermore, we introduce an FBART model with shape constraints on the response curve, enhancing estimation and prediction performance when prior shape information of response curves is available. By incorporating a shape-constrained prior, we ensure that the posterior samples of the response curve satisfy the required shape constraints (e.g., monotonicity and/or convexity). Under certain regularity conditions, we derive the posterior convergence results for both FBART and its shape-constrained version. Finally, the superiority of the proposed methods over other competitive counterparts is validated through simulation experiments under various settings and analyses of two real

datasets.

（D4）Modeling Microbial Community Coalescence via Compositional Directed Acyclic Graphical Models

何珂俊 中国人民大学

Abstract: The process of microbial community coalescence, i.e., the admixture of two or more separate communities, is widespread in microbial ecology. Although microbial community coalescence is significantly related to several human diseases, the mechanism of the coalescence process has not been rigorously studied due to the lack of causal discovery models for compositional data. To investigate the causal relationships across microbial communities, we propose a novel compositional directed acyclic graphical model (compDAG), which is identifiable at both the community and microbe levels. The structure of the graph is learned by a score-based method, which utilizes Hamiltonian Monte Carlo. We demonstrate our approach through simulation studies and two applications of studying coalescence in the female genital tract and oral-stool microbial communities. In both applications, we found evidence of microbial community coalescence and generated genus-level causal hypotheses regarding the participating microbes in the coalescence processes.

主持人：杜江 北京工业大学

（D5）基于去噪扩散隐式模型的地震缺失数据插值方法

张春霞 西安交通大学

摘要：在地震勘探采集过程中，由于复杂的地表环境、地下障碍物或经济因素影响，采集到的地震数据往往存在随机缺失或连续缺失情况，这对后续地震数据的处理解释都造成了很大影响。因此，构建高效、准确的缺失数据插值模型对该问题有重要意义。我们提出了一种基于去噪扩散隐式模型的插值方法，其主要思想是基于已有地震道的信息采用扩散模型建模，通过逆过程对缺失地震道进行重建，并采用变分 Bayes 方法进行模型的高效训练。在人工合成数据和实际工区数据上都验证了我们新提出插值方法的有效性和稳健性。

（D6）Hierarchical Hidden Markov Models for Modeling Heterogeneous Time Series in Data-Scarce Scenarios

兰慧 北京工业大学

Abstract: Modeling time series data from heterogeneous, independent sources is challenging, particularly in data-scarce settings prevalent in fields such as cognitive science, finance, and engineering. Each time series exhibits unique local dynamics while adhering to shared global patterns across sources. Traditional methods, such as fitting separate models for each series, risk overfitting, while a single global model often fails to capture critical individual variations. Time Series Clustering and Prediction using LSTM Combined with RBF Kernel-based Multi-head Attention To address these challenges, we propose a hierarchical framework for Hidden Markov Models (HMMs) that jointly learns group-level and individual-level models. The group model serves as a Bayesian regularizer, improving the robustness of individual models and mitigating overfitting. We further introduce co-clustering across sources, enabling the group model to share information across related sources while retaining individual-specific dynamics. This is implemented within a tree-structured probabilistic framework, where group models (parents) guide and regularize the learning of individual models (children), with iterative optimization ensuring joint refinement. Our method is particularly effective in data-scarce scenarios. Empirical results on synthetic and real-world datasets demonstrate its superiority over existing approaches, with significant performance improvements under limited training data conditions.

（D7）Two-fold Varying-coefficient Mediation Models and Their Applications

王文武 曲阜师范大学

Abstract: Mediation analysis provides a technical approach to reveal the complex relationships between variables, and researchers can use causal mediation analysis to distinguish more targeted interventions for different individuals and different scenarios. In real life, the strength of the effects between the variables in a causal relationship is often influenced by many other variables. Meanwhile, there are still relatively few studies on the theories and applications of the multiple varying-coefficient mediation models. In this paper, we study two influence mechanisms of two mediators in the two-fold varying-coefficient mediation model. In the first case, the mediators are in a parallel relationship, and in the second case, the mediators are sequential, where one mediator has a fixed coefficient and the other has a varying coefficient. Following these two cases, we propose the parallel two-fold varying-coefficient mediation model and the chain two-fold varying-coefficient mediation model, and regard the coefficient functions as smooth functions of the effect modifier. We further derive the spline estimators of the direct and indirect effects, as well as establish the asymptotic normality of all or part of the estimators. Simulation studies show that our new models and methods for the direct and indirect effects perform well. In two real data examples, they are also able to capture the dynamic changes of the coefficient functions, compared to the classic mediation model with constant coefficients.

（D8）Time Series Clustering and Prediction using LSTM Combined with RBF Kernel-based Multi-head Attention

赵娉君 西安电子科技大学

Abstract: This paper proposes a deep learning architecture for time series clustering by integrating long short-term memory (LSTM) network with a multi-head attention mechanism employing radial basis function kernel (RBF kernel), which is applicable to perform prediction and clustering analysis on the time series of air pollutant concentrations. To fully exploit local features and long-term dependency in time series, an enhanced LSTM architecture with RBF kernel-based multi-head attention is proposed adopting a hierarchical design. The bottom layer employs bidirectional LSTM network to capture long-term dependence features through gating mechanisms. The middle layer innovatively incorporates an RBF kernel-based multi-head attention module to adaptively capture local correlation patterns of pollutant concentration fluctuations across different time scales by replacing conventional dot-product method for similarity calculation. The top layer utilizes residual connections to fuse outputs from multiple attention heads, combined with Dropout layers to prevent overfitting. Bayesian optimization is implemented to determine the optimal gamma parameter for RBF kernels. Using dynamic time warping (DTW) distance on the Multi-Attention-LSTM outputs in hierarchical clustering analysis, three distinct temporal patterns are identified in pollutant concentration variations. Further a novel clustering assignment module is designed to dynamically allocate new time series samples to predefined clusters based on DTW similarity. This mechanism provides data-driven support for describing the evolutionary patterns of pollutant concentrations and enables the formulation of targeted mitigation strategies. Comparative prediction evaluation of mean squared error demonstrates that the RBF kernel-based multi-head attention mechanism significantly improves forecasting accuracy by optimizing feature weight. This integrated framework offers new insights into temporal pattern mining and predictive modeling of environmental time series data.

主持人: 陈钊 复旦大学

（E1）Test of Multivariate Independence via Comparing Two Bivariate Means

许凯 安徽师范大学

Abstract: Testing for independence between two random vectors is a fundamental problem in statistics. It is observed from empirical studies that many existing omnibus consistent tests may not perform well for some strongly nonmonotonic and nonlinear dependence. To get insights into this issue, this paper discovers that the multivariate independence testing problem can be cast into an equivalent test of the equality of two bivariate means, and further reveals the power loss phenomenon is mainly due to cancellation of positive and negative terms in dependence metrics. The cancellation leads to the sum of these terms very close to zero. Motivated by this finding, we propose a class of consistent metrics indexed by a positive integer ξ\gammaξ to characterize independence. We further prove that the metrics with even or infinity ξ\gammaξ can effectively avoid the cancellation, and have better powers under the alternatives in which two mean differences offset each other. In practice, it is desirable to target at a wide range of dependence scenarios. Thus, we further advocate to combine the p-values of test statistics with different ξ\gammaξ's through the Fisher's method. The advantages of the newly proposed tests are illustrated by numerical studies.

（E2）Order-Restricted Hypothesis Tests for Nonlinear Mixed-Effects Models with Measurement Errors in Covariates

张艺馨 中国科学技术大学

Abstract: Order-restricted hypothesis testing problems frequently arise in practice, including studies involving regression models for longitudinal data. These tests are known to be more powerful than tests that ignore such restrictions. In this article, we consider order-restricted tests for nonlinear mixed-effects models with measurement errors in time-dependent covariates. We propose to use a multiple imputation method to address measurement errors, since this approach allows us to use existing complete-data methods for order-restricted tests. Some theoretical results are presented. We evaluate our proposed methods via simulation studies that demonstrate they are more powerful than either a competing naive method or a two-step approach to testing hypotheses. We illustrate the use of our proposed approach by analyzing data from an HIV/AIDS study.

（E3）Testing the Homogeneity of a Three-Sample Problem with a Mixture Structure

任鹏程 江苏师范大学

Abstract: The three-sample model plays an important role in analyzing data from two different distributions as well as from a mixture of them. Most previous work involving this model has been focused on estimating the mixing proportion, and the methods used were based on the fact that the model is heterogeneous. However, before estimating the mixing proportion, the homogeneity of this model should be tested. Proposed here are the likelihood ratio and generalized fiducial methods to test the three-sample model for homogeneity. Compared with these methods by simulation studies, the likelihood ratio method is more powerful and computes much faster than the generalized fiducial methods under relatively large sized samples, while the generalized fiducial methods perform more powerful under small or moderately sized samples. An example involving halibut data is used to illustrate the proposed methods.

（E4）Ordinal Graphical Models via a Bayesian Nonparametric Clustering Approach

谌自奇 华东师范大学

Abstract: Graphical models are powerful tools for capturing conditional dependence structures in complex systems but remain underexplored in analyzing ordinal data, especially in sports analytics. Ordinal variables, such as team

rankings, player performance ratings, and survey responses, are pervasive in sports data but present unique challenges, particularly when accounting for heterogeneous subgroups, such as teams with varying styles or players with distinct roles. Existing methods, including probit graphical models, struggle with modeling heterogeneity and selecting the number of subgroups effectively. We propose a novel nonparametric Bayesian framework using the Mixture of Finite Mixtures (MFM) approach to address these challenges. Our method allows for flexible subgroup discovery and models each subgroup with a probit graphical model, simultaneously estimating the number of clusters and their configurations. We develop an efficient Gibbs sampling algorithm for inference, enabling robust estimation of cluster-specific structures and parameters. This framework is particularly suited to sports analytics, uncovering latent patterns in player performance metrics. Our work bridges critical gaps in modeling ordinal data and provides a foundation for advanced decision-making in sports performance and strategy.

主持人: 李新民 青岛大学

（E5）Log-Gaussian Process Regression with Applications in Loss Reserving

卢志义 天津商业大学

Abstract: Gaussian processes (GP) are known for their excellent smoothing properties and flexibility in modeling complex nonlinear relationships. Recently, they have been utilized in actuarial science to estimate potential insurance losses. However, in insurance practice, loss data often exhibits non-negative support and heavy tails, leading to significant model errors when using the GP model for loss prediction. This paper aims to replace the Gaussian distribution in GP with a log-Gaussian distribution to construct a log-Gaussian process (LGP) model. The properties and training methods of LGP are discussed. Furthermore, the LGP regression model is employed for estimating loss reserves. It is shown that the LGP regression model offers higher prediction accuracy and reliability compared to other models, particularly the GP regression model, making it more suitable for claims reserving.

（E6）Improving Design and Normalization of Multiplex Proteomics Study

方华英 首都师范大学

Abstract: Advances in multiplex mass spectrometry-based technologies have enabled high-throughput, quantitative proteome profiling of large cohort. However, certain experimental design configurations can amplify sample variability and introduce systematic biases. To address these challenges, we incorporated two novel features in a recent proteogenomic investigation: (1) the inclusion of two reference samples within each mass spectrometry run to serve as internal standards, and (2) the analysis of each specimen as technical replicates across two distinct mass spectrometry runs. Building on these enhancements, we present ProMix, a flexible analytical framework designed to fully leverage these supplementary experimental components. Using both simulated and real-world datasets, we demonstrate the improved performance of ProMix and highlight the advantages conferred by these refined experimental design strategies.

（E7）Mixed-input Gaussian Process Regression

江声 香港中文大学（深圳）

Abstract: Specifying an appropriate covariance kernel is crucial for Gaussian Process (GP) regression. However, selecting an optimal kernel remains challenging when dealing with both quantitative and qualitative (Q\&Q) inputs. We propose a novel latent variable approach which models the qualitative inputs as functions of latent numerical inputs. By imputing the qualitative inputs into numerical ones, the mixed-input GP regression problem reduces to a standard GP regression with only numerical inputs, allowing for flexible and well-understood kernel choices. The

latent variable model unifies many influential methods in the literature; it immediately improves computer emulators with Q\&Q inputs in prediction accuracy and uncertainty quantification, as well as downstream applications, such as mixed-variable Bayesian optimization and inverse problems. This paper also develops an efficient Markov Chain Monte Carlo algorithm for sampling from the posterior distribution and making predictions.

（E8）Gaussian Process-based Calibration of Complex Computer Models with Functional Inputs

李赵辉 中国科学院数学与系统科学研究院

Abstract: Bayesian calibration of a functional input/parameter to a time-consuming simulator based on a Gaussian process (GP) emulator involves two challenges that distinguish it from other parameter calibration problems. First, one needs to specify a flexible stochastic process prior for the input, and reduce it to a tractable number of random variables. Second, a sequential experiment design criterion that decreases the effect of emulator prediction uncertainty on calibration results is needed and the criterion should be scalable for high-dimensional input and output. In this article, we address these two issues. For the first issue, we employ a GP with a prior density for its correlation parameter as prior for the functional input, and the KarhunenLoève (KL) expansion of this non-Gaussian stochastic process to reduce its dimension. We show that this prior gives far more robust inference results than a GP with a fixed correlation parameter. For the second issue, we propose the weighted prediction variance (WPV) criterion (with posterior density of the calibration parameter as weight) and prove the consistency of the sequence of emulator-based likelihoods given by the criterion. The proposed method is illustrated with examples on hydraulic transmissivity estimation for groundwater models.

5 月 11 日上午分组报告摘要

主持人: 赵建喜 北京信息科技大学

（A1）Estimating IRT Models under Gaussian Mixture Modelling of Latent Traits: An Application of MSAEM Algorithm

孟祥斌 东北师范大学

Abstract: The assumption of a normal distribution for latent traits is a common practice in item response theory (IRT) models. Numerous studies have demonstrated that this assumption is often inadequate, impacting the accuracy of statistical inferences in IRT models. To mitigate this issue, Gaussian mixture modeling (GMM) for latent traits, known as GMM-IRT, has been proposed. Moreover, the GMM-IRT models can also serve as powerful tools for exploring the heterogeneity of latent traits. However, the computation of GMM-IRT model estimation encounters several challenges, impeding its widespread application. The purpose of this paper is to propose a reliable and robust computing method for GMM-IRT model estimation. Specifically, we develop a mixed stochastic approximation EM (MSAEM) algorithm for estimating the three--parameter normal ogive model with GMM for latent traits (GMM-3PNO). Crucially, the GMM-3PNO is augmented to be a complete data model within the exponential family, thereby substantially streamlining the computation of the MSAEM algorithm. Furthermore, the MSAEM algorithm adeptly avoid the label-switching issue, ensuring its convergence. Finally, simulation and empirical studies are conducted to validate the performance of the MSAEM algorithm and demonstrate the superiority of the GMM-IRT models.

（A2）A Sequential Bayesian Changepoint Detection Procedure for Aberrant Behaviours in Computerized Testing

陆婧 东北师范大学

Abstract: Changepoints are abrupt variations in a sequence of data in statistical inference. In educational and psychological assessments, it is essential to properly differentiate examinees' aberrant behaviors from solution behaviour to ensure test reliability and validity. In this paper, we propose a sequential Bayesian changepoint detection algorithm to monitor the locations of changepoints for response times in real time and, subsequently, further identify types of aberrant behaviors in conjunction with response patterns. Two simulation studies were conducted to investigate the efficiency and accuracy of the proposed detection procedure in terms of identifying one or multiple changepoints at different locations. In addition to manipulating the number and locations of changepoints, two types of aberrant behaviors were also considered: rapid guessing behaviour and cheating behaviour. Simulation results indicate that ability estimates could be improved after removing responses from aberrant behaviors identified by our approach. Two empirical examples were analyzed to illustrate the application of the proposed sequential Bayesian changepoint detection procedure.

（A3）Bayesian Variable Selection for Optimizing Dynamic Treatment Regimes

崔婷婷 浙江财经大学

Abstract: The heterogeneity of treatment responses poses a significant challenge in selecting optimal treatments for many diseases. Recognizing this heterogeneity among patients, contemporary clinical trials collect an extraordinarily large number of prognostic factors, such as disease history, demographic characteristics, clinical measurements and genetic information, to improve treatment efficacy. Given such a high volume of pretreatment variables, identifying essential variables for clinical decision-making becomes critical. However, current personalized medicine literature focusing on high-dimensional data is predominantly based on penalized frequentist methods. Motivated by this problem, we propose High-dimensional Bayesian Q-learning (HBQL), a novel approach for

optimizing dynamic treatment regimes through a series of Bayesian hierarchical models, one for each stage, in reverse sequential order. The proposed method simultaneously estimates optimal dynamic treatment regimes and identifies variables truly predictive of individual treatment responses. Numerical experiments demonstrate that our proposed method can achieve superior performance compared to existing state-of-the-art methods in both variable selection and treatment rule optimization.

（A4）Similarity-Assisted Learning for Estimating Optimal Individualized Treatment Regimes

李灿辉 河南大学

Abstract: In precision medicine, estimating optimal individualized treatment regimes presents a critical challenge, where patient heterogeneity often leads to highly individualized treatment responses. We propose a novel framework called Similarity-Assisted Learning for estimating optimal individualized treatment regimes. This method incorporates patient similarity information to construct assisted learning tasks, effectively capturing underlying patient heterogeneity and generating more accurate treatment recommendations. Our method aligns treatment decisions with patient similarity by constructing a similarity-weighted large-margin classification model. We further integrate SCAD penalty for variable selection, enhancing the interpretability of the model. In addition, the method reduces reliance on specific model assumptions, thereby improving the robustness of the estimates. Theoretical analysis establishes the consistency and efficiency of the proposed estimators under appropriate regularity conditions. Extensive simulation studies and real data analyses show that our proposed method outperforms existing methods.

主持人： 邹庆荣 北京信息科技大学

（A5）Time-Varying Probabilistic Forecast Combinations based on Particle Filtering: Diversity Matters

罗雪 北京航空航天大学

Abstract: Mitigating uncertainty in probabilistic forecasts requires adaptive strategies to address model redundancy and the dynamic nature of economic conditions. This study introduces a novel framework that integrates diversity regularization into a Bayesian ensemble forecasting system. In this system, time-varying model weights are optimized dynamically using particle filtering. By incorporating real-time diversity metrics, our approach enhances prior knowledge and enables continuous updates of predictive densities while penalizing correlated predictors. This method expands on traditional combination techniques by jointly estimating time-varying biases, inter-model dependencies, and calibration uncertainties within a unified nonlinear filtering framework. Empirical results in macroeconomic and commodity price forecasting demonstrate significant improvements in both point and density accuracy, outperforming individual models and other time-varying combination methods. Additionally, the framework includes diagnostic tools for identifying model incompleteness, further advancing ensemble forecasting in the face of uncertainty.

（A6）Research on the Extension of Convex Clustering

赵建喜 北京信息科技大学

Abstract: In recent years, convex clustering has attracted intensive attentions because it has basically overcome the three shortcomings of traditional clustering methods: non-global convergence, poor robustness and the need for prior information. Due to the data type and the limitation of existing methods nowadays, we extend the classic convex clustering model and conduct appropriate theoretical analysis. In addition, we present a solving algorithm and analyze its theoretical property. Experiments performed on several benchmark datasets show that the proposed method achieves the better clustering performance in comparison with some state-of-the-art clustering methods.

（A7）Bayesian Spatiotemporal Modeling for the Inpatient Hospital Costs of Alcohol-related Disorders

虞祯 对外经济贸易大学

Abstract: Understanding how healthcare costs vary across different demographics and health conditions is essential to developing policies for healthcare cost reduction. It may not be optimal to apply the conventional mean regression due to its sensitivity to the high level of skewness and spatiotemporal heterogeneity presented in the cost data. To find an alternative method for spatiotemporal analysis with robustness and high estimation efficiency, we combine information across multiple quantiles and propose a Bayesian spatiotemporal weighted composite quantile regression (ST-WCQR) model. An easy-to-implement Gibbs sampling algorithm is provided based on the asymmetric Laplace mixture representation of the error term. Extensive simulation studies show that ST-WCQR outperforms existing methods for skewed error distributions. We apply ST-WCQR to investigate how patients' characteristics affected the inpatient hospital costs for alcohol-related disorders and identify areas that could be targeted for cost reduction in New York State from 2015 to 2017.

（A8）Development and Evaluation of the Updated Risk Prediction Model Involving in New Candidate Predictors

曹雅琦 中央民族大学

Abstract: Assessing the incremental predictive value of new biomarkers is critical for improving clinical risk models. However, conventional metrics such as the area under the ROC curve (AUC) often lack sensitivity to quantify meaningful model enhancements. We propose a statistically rigorous evaluation framework that introduces two novel metrics, Net Reclassification Improvement (NRI), and Integrated Discrimination Improvement (IDI), derived from U-statistics theory, offering robust asymptotic properties and improved interpretability for quantifying model improvement. Our framework integrates discrimination, calibration, and reclassification-based assessments to evaluate the impact of new predictors. It addresses key limitations of AUC, particularly in high-performing baseline models. This work contributes generalizable statistical tools for enhancing model evaluation, bridging the gap between statistical significance and clinical utility in risk prediction research. We conduct extensive simulation studies under multiple scenarios, varying effect sizes, event rates, and baseline model strengths.We apply the methods to real-world data from STEMI patients, evaluating whether incorporating tryptase and hsCRP improves prediction of major adverse cardiovascular events (MACE). Although AUC changes are limited, our new metrics reveal meaningful reclassification and discrimination gains.

主持人：张思亮 华东师范大学

（B1）Imputation and Post-selection Inference in Models with Missing Data: Applications in Clinical Data

裘予琦 华东师范大学

Abstract: Missing data are a common and challenging feature in clinical predictive modeling, particularly in the context of variable selection. In a study aiming to improve U.S. guidelines for colorectal cancer risk stratification following screening colonoscopy (Cancer Causes Control 27 (2016) 1175–1185), we sought to incorporate additional informative predictors into neoplasia risk models, extending beyond three established risk factors. We compared three post-imputation inference strategies. The first used multiple imputation followed by Rubin's Rules for variance estimation. The second applied single imputation and variable selection followed by bootstrap percentile intervals. The third used bootstrap model averaging with variance estimation inspired by Efron's approach. Simulations showed that Rubin's Rules frequently led to undercoverage when variable selection was data-driven. Bootstrap methods performed better, with model averaging yielding the best results when effect sizes were moderate and model uncertainty was present. We further considered Bayesian model averaging (BMA) to address uncertainty from both imputation and model selection. BMA allows coherent integration over missing data and model space, producing posterior inference that reflects all sources of uncertainty. This approach is particularly useful in high-dimensional settings with correlated predictors and incomplete data. We applied these methods to a colorectal neoplasia risk-prediction problem. The results support Bayesian techniques as a robust alternative to traditional methods, improving inference and clinical decision-making in complex data settings.

（B2）Functional Differential Graphical Analysis Procedure with Application to Hard Landing Incidents in Civil Aviation

李格非 华东师范大学

Abstract: The hard landing incident, a critical safety event during the landing phase, has drawn significant attention from civil aviation due to its potential threats to aircraft structures and passenger safety. While existing studies have focused on predicting hard landings based on individual flight parameters, they often overlook the complex interdependencies among these parameters' functional characteristics. In this paper, we introduce a functional differential graphical analysis procedure for flight parameters. The key components of our procedure include proposing the functional differential node-wise regression (FDNR) method to estimate the differential coefficient matrix across two groups of flights and a basis rotation technique to construct conditional canonical functions, which interpret the information within the differential coefficient matrix. By applying our procedure to the landing curves of 10 flight parameters from 1,282 normal flights and 629 flights at risk of hard landings, we uncover significant differences in the conditional dependency structures between normal and hard landings, providing precautionary suggestions for enhancing flight safety.

（B3）Efficient Bayesian Reliability Assessment for Step-Stress Accelerated Wiener Degradation Model

周世荣 温州大学

Abstract: Step-stress accelerated degradation testing (SSADT) plays a critical role in evaluating the reliability of high-performance industrial products under harsh conditions, where performance deterioration is not significant under normal operating conditions. However, existing Bayesian inference methods for SSADT models face significant challenges due to computational inefficiency, particularly in achieving convergence and handling complex stochastic processes. These limitations hinder practical applications where rapid and precise reliability assessment is essential. To address this, we propose a novel iterative integrated nested Laplace approximation framework combined with a fixed-point iteration technique. By reformulating the Wiener-process-based SSADT model into a latent

Gaussian model via Taylor linearization, our approach leverages quadratic polynomial approximation and expansion-and-contraction strategies to optimize computational efficiency. Simulation studies demonstrate that the proposed method achieves comparable accuracy to traditional Bayesian methods like Gibbs sampling while significantly reducing computational costs, even for small sample sizes. Additionally, empirical validation using two real-world datasets confirms its applicability and effectiveness in practical reliability analysis.

（B4）Joint Latent Variable Modeling with a Cumulative Shrinkage Process Prior

吕斌 华东师范大学

Abstract: Network latent space models assume that each node is associated with a set of unobserved latent variables, which determine the probability of links between nodes. Although numerous latent variable models based on network data have been proposed, most overlook the estimation of latent variable dimensions. Furthermore, the network link information is often collected along with high dimensional node variables, which provide additional information for the links and may play a critical role in estimating the latent structure of the network. This paper proposes a joint latent variable model based on cumulative shrinkage priors, which simultaneously models network structures and node variables. The model assumes that both network links and node variables are generated by a set of latent variables, which are linked to the network structure and node variables through a dot product model and a generalized linear model, respectively. To achieve adaptive estimation of the latent variable dimensions, a cumulative shrinkage prior is introduced, allowing for an infinite dimensionality of the latent variables, which shrink to zero as the dimension increases. For different types of node variables, corresponding Gibbs algorithms are developed for Bayesian inference. The paper also establishes the convergence properties of parameter estimation and latent variable dimension estimation under maximum a posteriori estimation. Both simulation experiments and real data analysis validate the effectiveness and robustness of the proposed method in recovering latent structures and predicting performance.

主持人：李会琼 云南大学

（B5）Bayesian Learning of Optimal Real-time Dynamic Treatment Regimes

周迎春 华东师范大学

Abstract: Real-time dynamic treatment regimes (real-time DTRs) refers to decision rules that personalize patient treatment in real-time based on treatment and covariate histories. These rules are crucial for real-time clinical decision support systems and automated drug delivery systems for chronic diseases. Although considerable statistical and machine learning DTR methods have been developed, they are designed for a small number of fixed decision points, and thus cannot adapt to real-time cases. This paper proposes a new semiparametric Bayesian method for estimating an optimal treatment regime in real-time, which allows for the existence of latent individual level variables. Specifically, random real-time DTRs are defined through interventional parameters, the optimal values of which are estimated by maximizing the posterior predictive utility. The proposed approach is compared with alternative methods using simulated datasets, and applied to estimate the optimal real time oxytocin administration regime for preventing postpartum hemorrhage.

（B6）Semiparametric Structural Equation Models with Interval-Censored Data

李树威 广州大学

Abstract: Structural equation models offer a valuable tool for delineating the complicated interrelationships among multiple variables, including observed and latent variables. Over the last few decades, structural equation models

have successfully analyzed complete and right-censored survival data, exemplified by wide applications in psychological, social, or genomic studies. However, the existing methodology for structural equation modeling is not concerned with interval-censored data, a type of coarse survival data arising typically from periodic examinations for the occurrence of asymptomatic disease. The present study aims to fill this gap and provide a flexible semiparametric structural equation modeling framework. A general class of factor-augmented transformation models is proposed to model the interval-censored outcome of interest in the presence of latent risk factors. An expectation-maximization algorithm is subtly designed to conduct the nonparametric maximum likelihood estimation. Furthermore, the asymptotic properties of the proposed estimators are established by leveraging the empirical process theory. The numerical results obtained from extensive simulations and an application to the Alzheimer's disease data set demonstrate the proposed method's empirical performance and practical utility.

（B7）Low-rank Variational Correction Estimation for Multi-Source Heterogeneous Quantile Linear Regression Models

李会琼 云南大学

Abstract: High-dimensional data, prevalent in genomics, econometrics, and clinical medicine, often exhibit inherent heterogeneity. While existing methods address either multi-source data or heterogeneity separately, they fail to jointly model high-dimensional, multi-source heterogeneous data. To bridge this gap, we propose a scalable Bayesian framework for multi-source heterogeneous quantile regression, employing spike-and-slab priors for feature selection. Our approach integrates mean-field variational and Laplace approximations to tackle computational challenges, with a particular emphasis on a novel low-rank correction mechanism that significantly enhances adaptability to high-dimensional heterogeneous structures. This mechanism is crucial for capturing the intrinsic structure of the data, ensuring robust and efficient modeling. For comprehensive diagnostics, we develop a Bayesian score test combined with local influence analysis. Through extensive empirical evaluations using both simulations and TCGA myeloid leukemia data, our method demonstrates remarkable computational efficiency and exceptional scalability in processing complex, high-dimensional heterogeneous datasets.

（B8）Network Alternating Direction Method of Multipliers for Ultrahigh-Dimensional Decentralised Federated Learning

董伟 郑州大学

Abstract: Ultrahigh-dimensional data analysis has received great achievement in recent years. When the data are stored in multiple clients and the clients can be connected only with each other through a network structure, the implementation of ultrahigh-dimensional analysis can be numerically challenging or even infeasible. In this work, we study decentralised federated learning for ultrahigh-dimensional data analysis, where the parameters of interest are estimated via a large amount of devices without data sharing by a network structure. In the local machines, each parallel runs gradient ascent to obtain estimators via the sparsity-restricted constrained methods. Also, we obtain a global model by aggregating each machine's information via an alternating direction method of multipliers (ADMM) using a concave pairwise fusion penalty between different machines through a network structure. The proposed method can mitigate privacy risks from traditional machine learning, recover the sparsity and provide estimates of all regression coefficients simultaneously. Under mild conditions, we show the convergence and estimation consistency of our method. The promising performance of the method is supported by both simulated and real data examples.

主持人：兰伟 西南财经大学

（C1）Network Assisted Approximate Factor Model Estimation

范新妍 中国人民大学

Abstract: The factor models are powerful tools for uncovering patterns of similarity or co-movement among individuals, and they have been successfully applied in the fields of finance and biology. However, the classical approximate factor model encounters limitations when dealing with small sample sizes. To overcome this challenge, we leverage auxiliary network information and propose a novel joint quasi-maximum likelihood estimation, which can use the network information flexibly and allow network heterogeneity. The theoretical properties of these estimators are rigorously established. We obtain a new convergence rate, which is faster than the rate of classical maximum likelihood estimators when the sample size is small. Numerous numerical studies have been conducted to evaluate the performance of the proposed methods.

（C2）Graph-based Multisample Comparison with Application to Feature Selection for Multi-Category Responses

蒲丹 西南财经大学

Abstract: This article proposes a graph-based maximum pairwise difference (MPD) test to compare K-sample distributions. This test can be utilized to identify the most informative variables contributing to the heterogeneity of multiple multivariate dis- tributions. To construct the test, we first pool observations from multiple samples to create a similarity graph based on the distances between any two observations. For each observation, we next evaluate its connection probability to each sample. Then, we doubly maximize the squared differences of these connection probabilities via the within and between samples. Accordingly, the MPD test is a max-of-squares test and can effectively detect sparse alternatives. In addition, we show the asymptotic null distribution of the test statistic and establish its consistency under alternatives. To illustrate the finite sample performance of the proposed test, we conduct exten- sive simulation studies. The results indicate that the MPD test outperforms some commonly used multisample tests. Finally, we employ it to select relevant features related to corporate credit ratings.

（C3）High-Frequency Volatility Estimation and Forecasting with a Novel Bayesian LGI Model

吴奔 中国人民大学

Abstract: Volatility modeling is a challenging topic in high-frequency financial data analysis. In this paper, we propose a novel Bayesian framework for modeling and forecasting spot volatility by assuming a latent GARCH structure is embedded into the volatility process at a series of unobserved “anchor” time points, which can well describe the evolving volatility of financial assets in high frequency. We introduce an ideal approximation of latent anchors, which shares similar posterior distribution with true latent anchors. Furthermore, we develop an efficient two-stage inference framework with its corresponding two-stage MCMC sampling algorithm. The simulation study and real data analysis both show our method outperforms the existing alternatives in explanation of latent anchors and the estimation and forecasting of volatility.

（C4）Mixture Conditional Regression with Ultrahigh Dimensional Text Data for Estimating Extralegal Factor Effects

师佳鑫 北京大学

Abstract: Testing judicial impartiality is a problem of fundamental importance in empirical legal studies, for which standard regression methods have been popularly used to estimate the extralegal factor effects. However, those methods cannot handle control variables with ultrahigh dimensionality, such as those found in judgment documents

recorded in text format. To solve this problem, we develop a novel mixture conditional regression (MCR) approach, assuming that the whole sample can be classified into a number of latent classes. Within each latent class, a standard linear regression model can be used to model the relationship between the response and a key feature vector, which is assumed to be of a fixed dimension. Meanwhile, ultrahigh dimensional control variables are then used to determine the latent class membership, where a na\"ive Bayes type model is used to describe the relationship. Hence, the dimension of control variables is allowed to be arbitrarily high. A novel expectation-maximization algorithm is developed for model estimation. Therefore, we are able to estimate the key parameters of interest as efficiently as if the true class membership were known in advance. Simulation studies are presented to demonstrate the proposed MCR method. A real dataset of Chinese burglary offenses is analyzed for illustration purposes.

主持人：杜明月 吉林大学

（C5）Bonus-Malus System Based on INAR(1) Model with Finite Mixtures of Erlang Distributions for the Heterogeneity

程建华 吉林大学

Abstract: We consider a bonus-malus system based on first-order coefficient inter-valued autoregressive (INAR(1)) model, in which the unobservable heterogeneity is assumed to follow a finite mixture of Erlang distributions. We study some distributional properties of the proposed model, and apply it to Bayesian credibility premium updating in the automobile insurance to investigate how the claim history affects the future premium. We also present some numerical examples. By comparing with other existing models, we find that our model can exploit the past information more efficiently.

（C6）几类门限时间序列模型在空气质量监测中的应用研究

李聪 吉林大学

摘要：随着城市化的加速，空气质量监测对于公共健康和环境管理变得越来越重要。本文探讨了用整数值时间序列模型捕捉空气质量指标之间的复杂相依关系的方法，并根据模型性质提出新的控制图，以监控过程均值和方差的变化。本研究还利用我国部分地区一段时期的 AQI 指标等时间序列数据，展示了这些方法在空气质量评估方面的应用，该研究可为决策制定和政策规划提供支持。

（C7）Genomic Patterns are Associated with Different Sequelae of Patients with Long-Term COVID-19

张楠 吉林大学

Abstract: In the post-large era, various COVID-19 sequelae are getting more and more attention to health problems. Although the mortality rate of the COVID-19 infection is now declining, it is often accompanied by new clinical sequelae with different symptoms such as fatigue after infection, loss of smell. The degree of age, gender, virus infection seems to be weakly correlated with clinical symptoms. Human genetic variation plays a significant role in the sequelae of the COVID-19 infection. This study aims to analyze the genomic differences between individuals with different COVID-19 sequelae. In this study, the exomes of 97 patients with Omicron with 8 unique clinical manifestations are sequenced, and conducted a systematic analysis. Based on non-negative matrix factorization algorithms, the trinucleotide mutation spectrum of four long-term COVID-19 genomes is summarized and found that individuals with different clinical symptoms have unique DNA mutation patterns and indel patterns. By constructing a Genomic Fingerprinting Framework, the driver genes of variation in each symptomatic population are deciphered and analyzed. This study showed that population-specific mutational fingerprint differences are the main cause of heterogeneity in long-term COVID-19 sequelae. This study provides new ideas and insights into the causes of the long-term COVID-19 sequelae.

（C8）AMPGP: A Deep Learning Framework for High-Efficacy Antimicrobial Peptide Discovery

武润泽 吉林大学

Abstract: Antimicrobial peptides (AMPs) have emerged as vital candidates in the fight against antibiotic resistance. The traditional processes for AMPs design and discovery are often time-consuming and inefficient. Here, we propose AMPGP model, which employs deep learning algorithms for both generation and prediction. The generation model incorporates an attention mechanism into the seqGAN framework to generate high-quality AMPs. The prediction model is structured into four distinct feature channels to address the limitations of relying on a single source of information. The evaluation on the independent test set achieved an accuracy of 98.06%, surpassing several advanced models. Ultimately, we identified ten candidated AMPs and the experiment indicated that peptide No. 1 (LITHLFRFKNSGRILM) and No. 2 (FKLSVLYLGRGNIMKAYYGIKIARAG) exhibited broad-spectrum antibacterial and cellular viability, with no significant hemolytic activity observed. The AMPGP model thus presents a promising approach for discovering effective peptides and enhances the potential for clinical applications.

主持人：王纯杰 长春工业大学

（D1）On MCMC Sampling in Self-Exciting Integer-Valued Threshold Time Series Models

杨凯 长春工业大学

Abstract: Markov Chain Monte Carlo (MCMC) methods have been shown to be a useful tool in many branches in statistics. However, due to the complex structure of the models, this method remains an open problem for threshold integer-valued time series models. This study develops Bayesian inference for a class of self-exciting integer-valued threshold autoregressive models, which is implemented by means of a new MCMC algorithm. By introducing the latent variables series, a complete data likelihood is obtained. Based on which, the full conditional distributions are easily obtained with familiar forms.Furthermore, by maximizing the complete data likelihood, the threshold parameter is also accurately estimated. Finally, the performance of the MCMC algorithm is evaluated via some simulations and a real data example.

（D2）Three-Stage Communication-Efficient Surrogate Quantile Regression for Non-randomly Distributed System with Missing Data

袁晓惠 长春工业大学

Abstract: Traditional distributed quantile regression (QR) methods rely on restrictive assumptions of randomly distributed or fully observed data. However, real-world datasets often exhibit non-random storage patterns and contain missing values, posing significant challenges for existing approaches. To tackle this issue, we develop a three-stage communication-efficient framework that first obtains a small size random pilot sample, then estimates a parametric propensity model based on pilot sample and applies inverse probability weighting (IPW) to correct bias, and finally constructs a weighted surrogate loss for distributed QR estimation. Theoretically, without any restrictive randomness assumption, the established asymptotical results show that the proposed method performs as well as all data were stored on one single machine. By extending this approach to high-dimensional settings, we introduce a three-stage communication-efficient distributed penalized quantile regression approach, where include SCAD and adaptive Lasso (ALasso) penalty functions. The oracle properties are also validated without any restrictive assumption about randomness. Simulation studies evaluate the finite-sample performance of the proposed method. The practical utility of the proposed method is illustrated using a greenhouse gas (GHG) observing network dataset.

（D3）Semiparametric Analysis of Additive–Multiplicative Hazards Model with Interval-Censored Data and Panel Count Data

王淑影 长春工业大学

Abstract: In survival analysis, interval-censored data and panel count data represent two prevalent types of incomplete data. Given that, within certain research contexts, the events of interest may simultaneously involve both data types, it is imperative to perform a joint analysis of these data to fully comprehend the occurrence process of the events being studied. In this paper, a novel semiparametric joint regression analysis framework is proposed for the analysis of interval-censored data and panel count data. It is hypothesized that the failure time follows an additive–multiplicative hazards model, while the recurrent events follow a nonhomogeneous Poisson process. Additionally, a gamma-distributed frailty is introduced to describe the correlation between the failure time and the count process of recurrent events. To estimate the model parameters, a sieve maximum likelihood estimation method based on Bernstein polynomials is proposed. The performance of this estimation method under finite sample conditions is evaluated through a series of simulation studies, and an empirical study is illustrated.

（D4）Bayesian Empirical Likelihood for Accelerated Failure Time Model with Covariates Missing at Random

刘新蕊 长春工业大学

Abstract: This study proposes a Bayesian empirical likelihood (BEL) procedure based on the inverse probability weighted (IPW) Buckley-James estimation equation to analyze semiparametric accelerated failure time (AFT) models in the presence of right-censored failure time and missing covariates. Unlike the traditional Bayesian method that relies on an assessable likelihood function constructed by assigning specific distributions to the model's random errors and missing covariates, the proposed BEL-based approach does not make any distributional assumption, yielding highly reliable and robust estimation results. In addition, by exploring the entire posterior distribution of unknowns, the BEL methods can construct credible intervals based on empirical percentiles and reveal the uncertainty of the Bayesian estimator in a straightforward manner, avoiding the challenge of deriving the asymptotic distribution of empirical likelihood ratio statistics. We develop an efficient Markov Chain Monte Carlo method coupled with the Metropolis-Hastings algorithm to conduct posterior inference and investigate the asymptotic behavior of the posterior distribution. Simulation studies show that the BEL procedure performs satisfactorily in various settings and consistently outperforms several existing methods. The application of the proposed method to a real-life dataset from the mouse leukemia study further confirms the practical utility of our method.

主持人：周平 北京信息科技大学

（D5）基于能力猜测的两参数项目反应理论模型及其随机期望最大化估计方法

齐春香 东北师范大学

摘要：本研究提出了一种基于能力猜测（Ability-Based Guessing, AG）的两参数正态肩型模型（Two-Parameter Normal Ogive, 2PNO-AG），为项目反应理论提供更加灵活且适应性更强的建模方式。针对 2PNO-AG 模型的参数估计问题，本研究构建了一种随机期望最大化算法（Stochastic Expectation-Maximization, StEM），通过引入随机抽样步骤，有效缓解了传统 EM 算法在复杂模型估计中的计算不稳定性以及对初始值的敏感性。在此基础上，本文通过模拟研究验证了 StEM 对 2PNO-AG 模型的反真性、比较了 StEM 与马尔可夫链蒙特卡洛方法（MCMC）的估计效果，并从整体拟合表现方面对 2PNO-AG 模型、1PNO-AG 模型以及 3PNO 进行了对比分析。最后，基于实证数据验证了 2PNO-AG 模型拟合性能。

（D6）扩散条件后验采样引导的稀疏注意力 Transformer 地震数据插值方法

韦晓莉 西安交通大学

摘要：由于地质、预算等方面的限制，地震采集系统收集的叠前数据很容易出现道集缺失现象，通常是不规则或稀疏的空间坐标采样的形式。为了方便地震资料的处理和解释，获得高质量的完整叠前资料至关重要。针对现有扩散插值方法中重采样计算效率低的问题，我们提出了扩散增强稀疏注意力 Transformer 模型。多尺度全层特征提取器高效建模长序列相关性，扩散生成器从已知信号出发实现条件后验采样，增强插值信号与已知信号的分布一致性。同时，稀疏注意力计算策略显著降低高维表示的计算负担，并结合自适应门控抑制无效注意力值。我们的模型在单阶段训练框架下，仅需少量扩散步即可完成高保真插值。实验表明，我们的方法在随机及连续缺失场景中均显著优于现有扩散模型，展现出在复杂地质条件下的优越性能与更广的应用前景。

（D7）一种基于图神经网络和神经过程的两阶段空间预测建模方法

包丽莉 西安交通大学

摘要：空间预测模型在环境科学、经济发展和地质勘探等领域具有广泛的应用前景。近年来，深度学习技术的快速发展为空间数据建模提供了新的机遇，其中图神经网络（GNNs）因其强大的表达能力和可扩展性而备受关注。在基于 GNN 的空间预测模型中，每个空间位置被抽象为一个顶点，其对应的解释变量被转化为顶点特征，而目标变量则作为顶点标签。GNN 通过学习顶点间的关系来预测顶点标签，从而实现空间预测。然而，现有研究表明，GNN 预测的残差通常表现出显著的空间自相关性，这暗示着传统 GNN 在捕捉复杂的空间关系方面存在局限性，导致预测结果次优。为解决上述问题，我们提出了一种两阶段空间预测方法，即位置嵌入图神经网络-残差神经过程（Location Embedded Graph Neural Networks-Residual Neural Processes, LEGNN-RNP）。该方法首先利用 LEGNNs 学习空间数据的复杂模式，它通过注意力机制将位置信息显式地融入到 GNN 的学习过程中，从而能够同时考虑空间上下文和属性特征，增强模型对复杂空间关系的建模能力。随后，在第二阶段，我们对 LEGNN 预测的残差进行建模，以进一步提取数据中蕴含的空间模式。具体而言，我们引入残差神经过程(RNP），一种基于神经过程的方法，来建模残差的高斯过程（Gaussian Process, GP）分布。RNP 利用神经网络参数化 GP 分布的均值和协方差，其中均值用于估计残差，而协方差则用于量化预测的不确定性。最终的预测结果是两个阶段预测结果之和。在四个真实数据集上的实验结果表明，与现有方法相比，LEGNN-RNP 能够更有效地捕捉空间关系，显著提高空间预测的精度。

（D8）基于 BERT+BiLSTM 的非平衡数据的情感分析

徐子祥 南京林业大学

摘要：影片评论数据集中类不平衡现象广泛存在。对少类数据处理方式往往直接影响到模型的预测效果。本文基于 BERT 和 BiLSTM 以及注意力机制对不平衡中文文本展开情感分析模型。主要的策略是对少类数据进行 SMOTE 过采样来进行扩充。平衡后的数据通过 BERT 预训练模型将评论转变为矩阵向量, 并建立融合注意力机制的 BiLSTM 神经网络对文本信息进行特征提取, 最后将信息特征按照不同的权重输入到 Softmax 分类器进行预测。我们针对电影评论数据展开实证分析。模型比较结果显示，该模型的预测效果在常见的不平衡数据中优于相关网络模型；在准确率、召回率和精确率上均有优秀表现，准确率和精确率分别达到 93.78%和 98.02%。

主持人：杨洋 南开大学

（E1）Bayesian Optimization with Pareto-Principled Training for Economical Hyperparameter Optimization

杨洋 南开大学

Abstract: The specification of hyperparameters plays a critical role in determining the practical performance of a machine learning method. Hyperparameter Optimization (HPO), i.e., the searching for optimal specification of hyperparameters, however, often faces critical computational challenges due to the vast searching space and the high computational cost on model training under a given hyperparameter specification. In this study, we propose BOPT-HPO, a systematic approach for efficient HPO by leveraging Bayesian optimization with Pareto-principled training, based on the observation that the training procedure of a machine learning method under a given hyperparameter specification often follows the Pareto principle (the 80/20 rule) that about 80% of the total improvement in the objective function is achieved in 20% of the training time. By introducing two levels of training corresponding to the Pareto principle, i.e., the eighty-percent training (ET) and the complete training (CT), and establishing a joint surrogate model for CT runs and ET runs, BOPT-HPO reduces the computational cost of HPO significantly under the framework of Bayesian optimization with multi-fidelity measurements. A wide range of experimental studies confirm that the proposed approach achieves economical HPO for various machine learning models, including support vector machines, fully connected networks, and convolutional neural networks.

（E2）Heritability Estimation with Genetic Similarity Representation

王健桥 清华大学

Abstract: We introduce a similarity representation framework for robust heritability estimation in Genome-Wide Association Studies (GWAS). This problem parallels the signal-to-noise ratio estimation problem in the presence of a large number of predictors in linear models. Traditional fixed and random-effects methods for heritability estimation often impose restrictive assumptions on regression coefficients or the design (genotype) matrix. These assumptions are usually violated by the heterogeneous effects of genetic variants (regression coefficients) that depend on the genotype distribution and the correlation among genotypes due to linkage disequilibrium. This leads to the non-robust estimation of heritability using these existing methods in practice. To overcome these limitations, we propose a SiMILarity rEpresentation method (SMILE) by modeling the dependence of the gram matrix of the outcome vector (outcome similarity) on the gram matrix of the genetic signal vector (genetic similarity). We represent the genetic similarity using a weighted gram matrix of genotypes, where a specified weight matrix is used to disentangle the heterogeneous variant effects from the genotype distribution. SMILE includes the classical random-effects model as a special case and improves the fixed-effects model by not requiring accurate estimation of the precision matrix or the regression coefficients. We develop a scalable implementation for efficient analysis of large biobank GWAS data. Extensive simulations and the analysis of the UK biobank data demonstrate the robustness of the proposed method over the existing methods across a range of genetic architectures, and show that SMILE provides a versatile approach for heritability estimation.

（E3）Multi-dimensional Domain Generalization with Low-Rank Structures

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Abstract: In conventional statistical and machine learning methods, it is typically assumed that the test data are identically distributed with the training data. However, this assumption does not always hold, especially in applications where the target population are not well-represented in the training data. This is a notable issue in health-related studies, where specific ethnic populations may be underrepresented, posing a significant challenge for

researchers aiming to make statistical inferences about these minority groups. In this work, we present a novel approach to addressing this challenge in linear regression models. We organize the model parameters for all the sub-populations into a tensor. We establish rigorous theoretical guarantees for the proposed method and demonstrate its minimax optimality.

（E4）Imputation-based Randomization Tests for Randomized Experiments with Interference

韩庭萱　清华大学

Abstract: The presence of interference renders classic Fisher randomization tests infeasible due to nuisance unknowns. To address this issue, we propose imputing the nuisance unknowns and computing Fisher randomization p-values multiple times, then averaging them. We term this approach the imputation-based randomization test and provide theoretical results on its asymptotic validity. Our method leverages the merits of randomization and the flexibility of the Bayesian framework: for multiple imputations, we can either employ the empirical distribution of observed outcomes to achieve robustness against model mis-specification or utilize a parametric model to incorporate prior information. Simulation results demonstrate that our method effectively controls the type I error rate and significantly enhances the testing power compared to existing randomization tests for randomized experiments with interference. We apply our method to a two-round randomized experiment with multiple treatments and one-way interference, where existing randomization tests exhibit limited power.

主持人：周建军 云南大学

（E5）Block Sparse Bayesian Learning: A Diversified Scheme

张岩昊 北京航空航天大学

Abstract: This paper introduces a novel prior called Diversified Block Sparse Prior to characterize the widespread block sparsity phenomenon in real-world data. By allowing diversification on intra-block variance and inter-block correlation matrices, we effectively address the sensitivity issue of existing block sparse learning methods to pre-defined block information, which enables adaptive block estimation while mitigating the risk of overfitting. Based on this, a diversified block sparse Bayesian learning method (DivSBL) is proposed, utilizing EM algorithm and dual ascent method for hyperparameter estimation. Moreover, we establish the global and local optimality theory of our model. Experiments validate the advantages of DivSBL over existing algorithms.

（E6）The Minimax Optimal Convergence Rate of Posterior Density in the Weighted Orthogonal Polynomials

罗祎祺 北京航空航天大学

Abstract: In this paper, we tackle the challenge of constructing priors that can attain minimax optimal convergence rates for mixture models, which represents a crucial problem within non-parametric Bayesian density estimation. Although existing theorems have provided conditions for reaching the minimax optimal convergence rate ξ\varepsilon_n = nˆ{-p/(2p+1)} ξ , where ξp\geq 1ξ is an arbitrary integer, the task of constructing priors that meet these conditions still remains arduous. The underlying density is represented as a weighted sum of orthogonal polynomials. We then construct a sieve prior from the exponential family for the weight coefficients, imposing specific constraints such as continuity and boundedness. We prove that, under the prior we have constructed, the Bayesian posterior attains the minimax optimal convergence rate. The primary innovation of our work lies in the construction of a highly flexible prior. It is not restricted to a single, fixed type of density function; instead, it is applicable to a broad spectrum of density functions, including those on finite intervals, and many others. Our study,

for the first time, presents a novel approach to constructing effective priors for mixture models on ξ\Rξ, that achieve the minimax convergence rate. Furthermore, we derive a more refined upper bound for the posterior probability.

（E7）Inference with Combined Data from Subgroup Selection and Validation Phases in Clinical Trials

周建军 云南大学

Abstract: When a promising subgroup is identified from an unsuccessful trial with a broad target population, we often need to evaluate and possibly confirm the selected subgroup with a follow-up study, typically a validation trial, on the subgroup. In this paper, we focus on the panitumumab study and ask the question of how to utilize data from both trials to improve the efficiency of subgroup evaluation without selection bias there. We propose a new resampling-based approach to quantify and remove selection bias and then to perform data combination from both trials for valid and efficient inference on the subgroup effect. The proposed method is model-free and asymptotically sharp. We apply the proposed method to analyze the panitumumab trial and show how much data combination could help improve the analysis of clinical trials when a promising subgroup is identified from part of the data and accelerate the delivery of new treatment to the patients in need.

5. 学校和学院简介

北京信息科技大学简介

北京信息科技大学是北京市重点支持建设的高校，是一所信息类学科齐全、信息特色鲜明，以本科、研究生教育为主体的多科性大学。学校现有沙河、小营、金台路、酒仙桥四个校区，占地面积 81 万余平米，设有二级教学单位 15 个。现有全日制本硕博学生 14210 人，留学生 137 人。现有 44 个本科专业，国家级一流专业 14 个、国家级特色专业 4 个，北京市一流专业 17 个，北京市特色专业 9 个，北京高校 “重点建设一流专业” 3 个。3 个专业入选教育部 “卓越工程师教育培养计划”，9 个专业通过工程教育专业认证，2 个专业获批教育部“地方高校本科专业综合改革试点专业”。实现 “信息+ 智能+”专业全覆盖，专业大类 “双万计划” 一流专业全覆盖。获评国家级一流课程 10 门，国家级规划教材 24 种。深化产教融合，突出实践创新能力培养，拥有国家级实验教学示范中心 2 个，以及国家级大学生校外实践教育基地、国家级工程实践教育中心建设单位，入选首批国家级创新创业教育实践基地，人才培养改革成果获北京市教学成果一等奖。在全国“互联网+”大学生创新创业大赛中，第 6 次获国赛铜奖，居市属应用型高校第一。在全国普通高校大学生机器人竞赛指数中，评级 A+，持续位居 TOP 2%。毕业生薪酬长期稳居薪酬网排名全国前 40 名。

目前师资队伍水平不断优化。现有专任教师 1053 人，拥有博士生导师 53 人，硕士生导师 518 人。拥有万人计划领军人才 1 人，国家级百千万人才 3 人，国家级青年人才项目 2 人，全国优秀教师 1 人，享受国务院政府特殊津贴专家 7 人，北京学者 3 人，北京市有突出贡献的科学、技术、管理人才 2 人，教育部高等学校教学指导委员会委员 4 人。8 名学者入选 “全球前 2% 顶尖科学家榜单”。现有博士后科研流动站 1 个、博士学位授权点 2 个、一级学科硕士学位授权点 14 个、专业硕士学位类别 7 个，具有推荐优秀应届本科毕业生免试攻读硕士研究生资格。6 个学科在 2023 年软科中国最好学科排名进入前 50%。现有北京市高校高精尖学科 2 个，参与共建北京市高精尖学科 1 个，北京市属高校新兴交叉学科平台 1 个。学科布局不断优化，实现学科对本科专业、优势学科对一流本科专业的支撑全覆盖。踏上新征程，建功新时代。学校坚持以政治建设为统领，以“双一流”建设为导向，科学把握新发展阶段，认真贯彻新发展理念，积极融入新发展格局，持续推进内涵发展、特色发展、差异化发展，加快建设信息特色鲜明的高水平应用型大学。

北京信息科技大学理学院简介

北京信息科技大学理学院是以数学、物理为基础，以工学为依托，理工相融的学院。设有信息与计算科学系、应用统计系、电子信息科学与技术系、数学教学部和物理教学部 5 个教学单位。学院拥有传感技术研究中心、绿色发展与大数据决策北京市重点实验室、智能决策与大数据应用北京市国际科技合作基地和应用数学研究所、数学物理研究所 2 个校级科研机构。现有数学和电子科学与技术 2 个一级学科硕士学位授权点，集成电路工程 1 个专业硕士学位授权点。数学学科近 3 年在软科中国大学学科排名中居前 40% 左右。

学院拥有在职教职工 123 人，其中专任教学科研人员 113 人，包括教授、副教授 85 人，硕士生导师 54 人， 具有博士学位教师占专任教师比例为 81.7%。教师中有青年北京学者、北京市教学名师、北京市青年拔尖、北京市中青年骨干等各类人才近 30 人次。学院有高等数学国家级教学团队 1 个。 理学院现有本科专业 3 个，“信息与计算科学” 专业入选国家一流本科专业建设点，“电子信息科学与技术” 和 “应用统计学”2 个专业入选北京市一流本科专业建设点。学院目前在校本科生 622 人，在校硕士研究生 167 名，研究生考博深造率平均 25%，核心就业率近 100%。

近年来，学院科研成果丰硕。曾荣获国家科技进步二等奖和国家技术发明二等奖各 1 项；获北京市科技进步奖二等奖 1 项、省部级奖 2 项、行业奖 3 项；近 5 年获国家自然科学基金 37 项（含重点项目 3 项）、北京市自然科学基金、北京市社科基金等各级各类项目 100 余项，科研经费达 4610 万元；发表科研论文 620 余篇，其中 SCI 检索 400 余篇，出版专著 7 部，获得专利 37 项，为学校学科建设高水平发展奠定了坚实基础。

学院坚持 “加强基础，精化专业，优化学科，融合信息”的办学定位，着力于为学校高素质应用型人才培养提供坚实的数理支撑，致力于培养具有较强实践能力、创新意识与国际化意识的高素质应用型人才；秉持 “明理慎思，笃学善行” 的院训精神，紧密围绕国家、首都和行业发展需求及学校的人才培养目标，开展教学改革和专业建设，提升学院教育教学水平。

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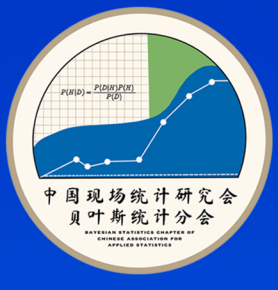
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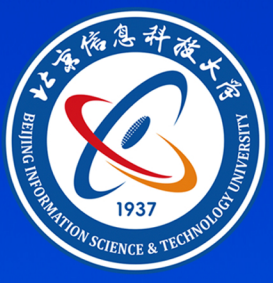
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