第二届 青年交叉学科论坛

从科学原理到学术研究再到业界实践

主办方： 苏州大学“基于神经生物学的金融决策行为量化研究”团队

苏州大学商学院： 沈建成 陈冬宇 王佐政 贺超

苏州大学医学院： 孟红蕊 崔家斌

苏州大学数学科学院： 马学俊

时　间： 2022年8月11日（周四）09：00-17：00 （GMT+08:00）

腾讯会议： 206-475-914；入会时请修改名称为：姓名 单位

|会议日程安排|

8：45-9：00	入会
9：00-10：00	赵瑶瑶 北京工业大学环境与生命学部 副研究员 **题目：基于液滴微流控-质谱联用技术分析脑脊液中的神经递质** **摘要：**监测大脑细胞外空间中神经递质的动态变化可以研究各种正常和病理的大脑状态。神经递质如乙酰胆碱从细胞中释放出来，在形成不同行为、药物效应、或疾病状态中起着关键作用。使用液滴微流控进行局部和连续采样，能够在检测前储存脑脊液样品，同时避免了泰勒分散和分析物扩散，从而提高检测的时间分辨率。纳升电喷雾质谱（nESI-MS）是一种能够得到丰富信息的微量分析方法，可快速，无标记，高灵敏度的分析液滴中的神经递质，同时具有一定的基质耐受性，非常适合分析纳升和皮升体积的生物样品。液滴微流控-质谱联用技术可以在单个液滴水平上分析脑脊液中的神经递质，将来有希望将其应用于活体脑神经递质的监测。
10：00-11：00	丛启飞 苏州大学神经科学研究所 教授 **Title: The complement system in thalamocortical synapse elimination** **Abstract:** Synapse elimination occurs continuously throughout brain development, but at different rates during different development periods. Many brain regions go through a maturation process comprising of two developmental periods, an initial period of net synapse formation when the rate of synapse formation exceeds that of synapse elimination, followed by a period of net synapse elimination when the rate of synapse elimination exceeds that of synapse formation. During brain development, complement-mediated microglial engulfment has been demonstrated to actively participate in postnatal establishment and refinement of brain wiring in mammals. Here, we uncovered that neurons express complement inhibitors to protect synapses against complement-mediated synapse elimination during postnatal brain development. We show that the sushi domain protein SRPX2 is a neuronally expressed complement inhibitor that regulates complement-dependent synapse elimination. SRPX2 directly binds to C1q and blocks its activity, and SRPX2-/Y mice show increased C3 deposition and microglial synapse engulfment. They also show a transient decrease in synapse numbers and increase in retinogeniculate axon segregation in the lateral geniculate nucleus. In the P60 to P90 somatosensory cortex, layer 4 thalamocortical synapses are eliminated via the complement-microglial pathway. Therefore, complement-microglial synapse elimination is a major mechanism for synapse removal in multiple brain regions during the

	developmental period of net synapse elimination.
11：00-12：00	崔家斌 苏州大学放射医学与防护学院 教授 **题目：耦合型分子影像探针的构建及其活体成像** **摘要：**癌症严重危害着人类的生命健康，已经成为目前亟待解决的前沿问题。因此实现癌症的早期灵敏诊断与精准治疗具有重要的研究意义。而基于光学探针的活体成像，能够为临床诊断提供精准的导航技术。同时发展高穿透深度以及低背景干扰的近红外荧光探针已经成为近几年研究的热点。本课题组通过纳米晶耦合探针的制备，实现了半导体纳米晶自由载流子浓度的有效调控，以及轨道能级的杂化耦合增强，成功制备了波长显著红移型近红外纳米探针。同时通过进一步表面的修饰与改性，实现了高灵敏度、高组织穿透深度的活体成像以及癌症的诊断与治疗。为肿瘤的早期诊断与精准可视化成像提供了潜在的研究策略。
13：45-14：00	入会
14：00-15：00	张群姿 山东大学经济学院 教授 **Title: A Dynamic Model of Health on Housing Price and Rent** **Abstract:** This study contributes to the health and regional economics literature by exploring the impact of health factors on local housing market and households’ choices though both demand and supply channels. Specifically, we investigate regional and individual health shocks in the housing market through migration flow. Health influences housing demand through the local labor income and amenities and affects housing supply through local labor productivity. To study the housing market heterogeneity across different Metropolitan Statistical Areas (MSAs), we develop an overlapping generations spatial equilibrium model, in which home price and rent are determined by regional and individual health factors and the migration between regions via health status. The empirical evidence suggests home value is positively related to the MSA health index and a "good" health region is more sensitive to health shocks. Additionally, likelihood of moving is negatively related to an individuals’ health status. Our simulation analysis of our theoretical model further supports the features and patterns of the main empirical findings.
15：00-16：00	李向杰 昌平实验室 副研究员 **Title: Propensity Score Matching enables batch effect corrected imputation in single-cell RNA-seq analysis** **Abstract:** Developments of single-cell RNA-sequencing (scRNA-seq) technologies have enabled biological discoveries at the single-cell resolution with high throughput. However, large scRNA-seq datasets always suffer from massive technical noises, including batch

	effects and dropouts, and the dropout is often shown to be batch-dependent. Most existing methods only address one of the problems, and we show that the popular used methods failed in trading off batch effect correction and dropout imputation. Here inspired by the idea of causal inference, we propose a novel propensity score matching method (scPSM) for scRNA-seq data by borrowing information and taking weighted average from similar cells in the deep sequenced batch, which simultaneously removes batch effect, imputes dropout and denoises data in the entire gene expression space. The proposed method is testified on two simulation datasets and a variety of real scRNA-seq datasets, and the results show that scPSM is superior to other state-of-the-art methods. First, scPSM improves clustering accuracy and mixes cells of the same type, suggesting its ability of keeping cell type separation while correcting for batch. Besides, using the scPSM-integrated data as input yields results free of batch effects or dropouts in the differential expression (DE) analysis. Moreover, scPSM not only achieves ideal denoising, but also preserves real biological structure for downstream gene-based analyses. Furthermore, scPSM is robust to hyperparameters and small datasets with a few cells but enormous genes. Comprehensive evaluations demonstrate that scPSM jointly provides desirable batch effect correction, imputation, and denoising for recovering the biologically meaningful expression in scRNA-seq data.
16：00-17：00	李喜彤 法国巴黎高等商学院(**HEC Paris**) 副教授 **Title: Reporting Technologies and Textual Readability: Evidence from the XBRL Mandate** **Abstract:** Financial reporting technologies can significantly affect how firms construct and disseminate quantitative and qualitative disclosures. Leveraging the opportunity created by the eXtensible Business Reporting Language (XBRL) mandate in the United States, we use a difference-in-differences approach to examine whether and how a firm’s XBRL adoption affects the readability of its textual disclosures. We find that the initial adopters’ HTML-formatted annual reports become harder to read after the XBRL mandate. Further analysis reveals that this effect is concentrated among adopters with more quantitative disclosures, those with smaller firm size, and those with a higher level of financial complexity. Importantly, we show that managers’ reduced attention to preparing HTML-formatted annual reports, rather than increased disclosures, is likely the explanation for this decrease in textual readability. We also find that the negative effect on textual readability persists at least in the subsequent year. Taken together, our results suggest that although XBRL can standardize numerical disclosures, its initial adoption can divert managerial attention and result in reduced readability of textual disclosures.

|学者简介|

	**赵瑶瑶** 北京工业大学环境与生命学部副研究员。本科就读于北京化工大学实验班和应用化学专业，2017 年在清华大学化学系获得博士学位。2017 年-2019 年，在日本北海道大学保健科学研究院担任助理教授。2019 年-2021 年，在美国伊利诺伊大学厄巴纳-香槟分校 Jonathan V Sweedler 教授课题组从事博士后研究，2021 年入选北京市青年人才项目。研究工作主要围绕敞开式离子源质谱用于生物分子的快速分析展开。以第一作者或通讯作者的身份在 Chemical Science 和 Analytical Chemistry 等期刊上发表了多篇研究论文。利用敞开式质谱进样的多样性，开发或者改进现有的进样系统和离子化方法，实现了对一系列复杂生物样品，尤其是小体积样品的快速质谱分析。
	**从启飞** 苏州大学特聘教授，博士生导师，入选苏州大学精英人才计划。2010 年毕业于南京大学，获得生物技术专业学士学位，2015 年毕业于中国科学院上海药物所，获得药物化学博士学位。随后在美国德州大学圣安东尼奥健康科学中心从事博士后研究工作。2021 年全职加入苏州大学神经科学研究所。实验室研究方向为调控情感和记忆的神经免疫分子机制研究，以第一或通讯作者在 Nature Neuroscience, Glia 等期刊发表研究论文。获得 2021 年长三角神经科学青年论坛脑科学青锋奖等荣誉。
	**崔家斌** 苏州大学特聘教授，博士生导师。2017 年博士毕业于北京化工大学。同年在以色列 Hebrew University of Jerusalem 化学系从事博士后研究。主持国家自然科学基金青年基金，江苏省青年基金各 1 项。目前主要的研究领域为分子与核医学影像探针的制备、基于放疗的癌症诊疗一体化、量子点耦合纳米材料的设计及其分析、传感以及活体成像研究等方面的应用。曾先后获得国家奖学金、PBC、Valazzy Pikovsky 博士后奖学金。迄今在 Nat. Commun.、J. Am. Chem. Soc.、Angew. Chem. Int. Edit.、Acc. Chem. Res.、Nano Lett.、Anal. Chem.、Small 等期刊发表论文 30 余篇。

	**张群姿** 山东大学经济学院教授，博士生导师，副院长，获评山东省金融高端人才，山东省一流本科课程负责人，教育部“双带头人”党支部书记工作室负责人,山东大学齐鲁青年学者。瑞士洛桑大学和瑞士金融学院金融学博士。从事资产定价、金融风险、金融科技和衍生品等方面的研究。在国际权威期刊《Journal of Financial Economics》、《Journal of Financial and Quantitative Analysis》、《Management Science》等发表多篇论文。主持国家自然科学基金、省部级重要项目 7 项。分别担任国际期刊 IJFE 副主编（ABS 三星）和 Energy Nexus 编委（国际交叉学科期刊）。
	**李向杰** 昌平实验室，副研究员。2019 年博士毕业于中国人民大学，2017 年 11 月-2018 年 11 月在美国宾夕法尼亚大学交流学习, 2019 年 7 月-2021 年 7 月在中国医学科学院阜外医院从事博士后工作。研究领域包括事单细胞多组学、空间组学以及在肿瘤免疫的应用。主持博士后面上基金一项，参与国自然重大项目一项。迄今在 Nature Methods, Nature Communications, Nature Machine Intelligence, cardiovascular research, Genome Research, Briefings in Bioinformatics, Journal of statistical planning of inference, Basis Research in Cardiology 等高水平期刊发表多篇论文。
	**李喜彤** 法国巴黎高等商学院（HEC Paris）信息系统副教授，Information Systems Research（UTD24 期刊）副主编。麻省理工大学和清华大学博士毕业。他的主要研究兴趣是信息技术经济学，包括社交媒体、众筹、数字营销、算法和人工智能。他的主要研究方法包括应用计量经济学分析、现场和实验室实验。在国际权威期刊 Information Systems Research、Management Information Systems Quarterly、Journal of Management Information Systems 发表多篇论文。其研究获得 ANR AAPG France (solo PI) 和 Paris Research Fellowship 资助。审阅了 Management Science、ISR、MISQ 和 JMIS 总共一百多篇投稿。曾获 2019 年 Management Science 杰出服务奖、2018 年 Management Science 功勋奖。