논문 요약 보고서

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How Effectively Can BERT Models Interpret Context and Detect Bengali Communal Violent Text?

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초록:

The spread of cyber hatred has led to communal violence, fueling aggression and conflicts between various religious, ethnic, and social groups, posing a significant threat to social harmony. Despite its critical importance, the classification of communal violent text remains an underexplored area in existing research. This study aims to enhance the accuracy of detecting text that incites communal violence, focusing specifically on Bengali textual data sourced from social media platforms. We introduce a fine-tuned BanglaBERT model tailored for this task, achieving a macro F1 score of 0.60. To address the issue of data imbalance, our dataset was expanded by adding 1,794 instances, which facilitated the development and evaluation of a fine-tuned ensemble model. This ensemble model demonstrated an improved performance, achieving a macro F1 score of 0.63, thus highlighting its effectiveness in this domain. In addition to quantitative performance metrics, qualitative analysis revealed instances where the models struggled with context understanding, leading to occasional misclassifications, even when predictions were made with high confidence. Through analyzing the cosine similarity between words, we identified certain limitations in the pre-trained BanglaBERT models, particularly in their ability to distinguish between closely related communal and non-communal terms. To further interpret the model's decisions, we applied LIME, which helped to uncover specific areas where the model struggled in understanding context, contributing to errors in classification. These findings highlight the promise of NLP and interpretability tools in reducing online communal violence. Our work contributes to the growing body of research in communal violence detection and offers a foundation for future studies aiming to refine these techniques for better accuracy and societal impact.

Evaluating Compliance with Visualization Guidelines in Diagrams for Scientific Publications Using Large Vision Language Models

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플랫폼: arxiv

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초록:

Diagrams are widely used to visualize data in publications. The research field of data visualization deals with defining principles and guidelines for the creation and use of these diagrams, which are often not known or adhered to by researchers, leading to misinformation caused by providing inaccurate or incomplete information. In this work, large Vision Language Models (VLMs) are used to analyze diagrams in order to identify potential problems in regards to selected data visualization principles and guidelines. To determine the suitability of VLMs for these tasks, five open source VLMs and five prompting strategies are compared using a set of questions derived from selected data visualization guidelines. The results show that the employed VLMs work well to accurately analyze diagram types (F1-score 82.49 %), 3D effects (F1-score 98.55 %), axes labels (F1-score 76.74 %), lines (RMSE 1.16), colors (RMSE 1.60) and legends (F1-score 96.64 %, RMSE 0.70), while they cannot reliably provide feedback about the image quality (F1-score 0.74 %) and tick marks/labels (F1-score 46.13 %). Among the employed VLMs, Qwen2.5VL performs best, and the summarizing prompting strategy performs best for most of the experimental questions. It is shown that VLMs can be used to automatically identify a number of potential issues in diagrams, such as missing axes labels, missing legends, and unnecessary 3D effects. The approach laid out in this work can be extended for further aspects of data visualization.

Curating art exhibitions using machine learning

초록:

Art curatorship has always been mostly the subjective work of human experts, who, with extensive knowledge of many and diverse artworks, select a few of those to present in communal spaces, spaces that evolved into what we now call art galleries. There are no hard and fast set of rules on how to select these artworks, given a theme which either is presented to the art curator or constructed by her/him. Here we present a series of artificial models -- a total of four related models -- based on machine learning techniques (a subset of artificial intelligence) that attempt to learn from existing exhibitions which have been curated by human experts, in order to be able to do similar curatorship work. We focus exclusively on the last 25 years of past exhibitions at the Metropolitan Museum of Art in New York, due to the quality of the data available and the physical and time limitations of our research. Our four artificial intelligence models achieve a reasonable ability at imitating these various curators responsible for all those exhibitions, with various degrees of precision and curatorial coherence. In particular, we can conclude two key insights: first, that there is sufficient information in these exhibitions to construct an artificial intelligence model that replicates past exhibitions with an accuracy well above random choices; second, that using feature engineering and carefully designing the architecture of modest size models can make them as good as those using the so-called large language models such as GPT in a brute force approach. We also believe, based on small attempts to use the models in out-of-sample experiments, that given more much more data, it should be possible for these kinds of artificial intelligence agents to be closer and closer to the aesthetic and curatorial judgment of human art curators.

LLM-Based Social Simulations Require a Boundary

저자: Zengqing Wu, Run Peng, Takayuki Ito, Chuan Xiao

초록:

This position paper argues that large language model (LLM)-based social simulations should establish clear boundaries to meaningfully contribute to social science research. While LLMs offer promising capabilities for modeling human-like agents compared to traditional agent-based modeling, they face fundamental limitations that constrain their reliability for social pattern discovery. The core issue lies in LLMs' tendency towards an ``average persona'' that lacks sufficient behavioral heterogeneity, a critical requirement for simulating complex social dynamics. We examine three key boundary problems: alignment (simulated behaviors matching real-world patterns), consistency (maintaining coherent agent behavior over time), and robustness (reproducibility under varying conditions). We propose heuristic boundaries for determining when LLM-based simulations can reliably advance social science understanding. We believe that these simulations are more valuable when focusing on (1) collective patterns rather than individual trajectories, (2) agent behaviors aligning with real population averages despite limited variance, and (3) proper validation methods available for testing simulation robustness. We provide a practical checklist to guide researchers in determining the appropriate scope and claims for LLM-based social simulations.

KnowML: Improving Generalization of ML-NIDS with Attack Knowledge Graphs

저자: Xin Fan Guo, Albert Merono Penuela, Sergio Maffeis, Fabio Pierazzi

초록:

Despite extensive research on Machine Learning-based Network Intrusion Detection Systems (ML-NIDS), their capability to detect diverse attack variants remains uncertain. Prior studies have largely relied on homogeneous datasets, which artificially inflate performance scores and offer a false sense of security. Designing systems that can effectively detect a wide range of attack variants remains a significant challenge. The progress of ML-NIDS continues to depend heavily on human expertise, which can embed subjective judgments of system designers into the model, potentially hindering its ability to generalize across diverse attack types. To address this gap, we propose KnowML, a framework for knowledge-guided machine learning that integrates attack knowledge into ML-NIDS. KnowML systematically explores the threat landscape by leveraging Large Language Models (LLMs) to perform automated analysis of attack implementations. It constructs a unified Knowledge Graph (KG) of attack strategies, on which it applies symbolic reasoning to generate KG-Augmented Input, embedding domain knowledge directly into the design process of ML-NIDS. We evaluate KnowML on 28 realistic attack variants, of which 10 are newly collected for this study. Our findings reveal that baseline ML-NIDS models fail to detect several variants entirely, achieving F1 scores as low as 0 %. In contrast, our knowledge-guided approach achieves up to 99 % F1 score while maintaining a False Positive Rate below 0.1 %.

The Starlink Robot: A Platform and Dataset for Mobile Satellite Communication

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카테고리: cs.RO, cs.NI

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초록:

The integration of satellite communication into mobile devices represents a paradigm shift in connectivity, yet the performance characteristics under motion and environmental occlusion remain poorly understood. We present the Starlink Robot, the first mobile robotic platform equipped with Starlink satellite internet, comprehensive sensor suite including upward-facing camera, LiDAR, and IMU, designed to systematically study satellite communication performance during movement. Our multi-modal dataset captures synchronized communication metrics, motion dynamics, sky visibility, and 3D environmental context across diverse scenarios including steady-state motion, variable speeds, and different occlusion conditions. This platform and dataset enable researchers to develop motion-aware communication protocols, predict connectivity disruptions, and optimize satellite communication for emerging mobile applications from smartphones to autonomous vehicles. The project is available at https://github.com/StarlinkRobot.

Canary in the Mine: An LLM Augmented Survey of Disciplinary Complaints to the Ordre des ingénieurs du Québec (OIQ)

저자: Tammy Mackenzie, Varsha Kesavan, Thomas Mekhael, Animesh Paul, Branislav Radeljic, Sara Kodeiri, Sreyoshi Bhaduri

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카테고리: cs.CY

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초록:

This study uses pre-trained LLMs to conduct thematic analysis to investigate disciplinary incidents involving engineers in Quebec, shedding light on critical gaps in engineering education. Through a comprehensive review of the disciplinary register of the Ordre des ing₩'enieurs du Qu₩'ebec (OIQ)'s disciplinary register for 2010 to 2024, researchers from engineering education and human resources management in technological development laboratories conducted a thematic analysis of reported incidents to identify patterns, trends, and areas for improvement. The analysis aims to uncover the most common types of disciplinary incidents, underlying causes, and implications for the field in how engineering education addresses (or fails to address) these issues. Our findings identify recurring themes, analyze root causes, and offer recommendations for engineering educators and students to mitigate similar incidents. This research has implications for informing curriculum development, professional development, and performance evaluation, ultimately fostering a culture of professionalism and ethical responsibility in engineering. By providing empirical evidence of disciplinary incidents and their causes, this study contributes to evidence-based practices for engineering education and professional development, enhancing the engineering education community's understanding of professionalism and ethics.

A Survey of Multi-sensor Fusion Perception for Embodied AI: Background, Methods, Challenges and Prospects

저자: Shulan Ruan, Rongwei Wang, Xuchen Shen, Huijie Liu, Baihui Xiao, Jun Shi, Kun Zhang, Zhenya Huang, Yu Liu, Enhong Chen, You He

초록:

Multi-sensor fusion perception (MSFP) is a key technology for embodied AI, which can serve a variety of downstream tasks (e.g., 3D object detection and semantic segmentation) and application scenarios (e.g., autonomous driving and swarm robotics). Recently, impressive achievements on AI-based MSFP methods have been reviewed in relevant surveys. However, we observe that the existing surveys have some limitations after a rigorous and detailed investigation. For one thing, most surveys are oriented to a single task or research field, such as 3D object detection or autonomous driving. Therefore, researchers in other related tasks often find it difficult to benefit directly. For another, most surveys only introduce MSFP from a single perspective of multi-modal fusion, while lacking consideration of the diversity of MSFP methods, such as multi-view fusion and time-series fusion. To this end, in this paper, we hope to organize MSFP research from a task-agnostic perspective, where methods are reported from various technical views. Specifically, we first introduce the background of MSFP. Next, we review multi-modal and multi-agent fusion methods. A step further, time-series fusion methods are analyzed. In the era of LLM, we also investigate multimodal LLM fusion methods. Finally, we discuss open challenges and future directions for MSFP. We hope this survey can help researchers understand the important progress in MSFP and provide possible insights for future research.

Accurate, fast, cheap: Choose three. Replacing Multi-Head-Attention with Bidirectional Recurrent Attention for Long-Form ASR

저자: Martin Ratajczak, Jean-Philippe Robichaud, Jennifer Drexler Fox

초록:

Long-form speech recognition is an application area of increasing research focus. ASR models based on multi-head attention (MHA) are ill-suited to long-form ASR because of their quadratic complexity in sequence length. We build on recent work that has investigated linear complexity recurrent attention (RA) layers for ASR. We find that bidirectional RA layers can match the accuracy of MHA for both short- and long-form applications. We present a strong limited-context attention (LCA) baseline, and show that RA layers are just as accurate while being more efficient. We develop a long-form training paradigm which further improves RA performance, leading to better accuracy than LCA with 44% higher throughput. We also present Direction Dropout, a novel regularization method that improves accuracy, provides fine-grained control of the accuracy/throughput trade-off of bidirectional RA, and enables a new alternating directions decoding mode with even higher throughput.

Exploring Developer Experience Factors in Software Ecosystems

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카테고리: cs.SE, cs.HC

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초록:

Context: Developer experience (DX) plays a key role in developers' performance and their continued involvement in a software ecosystem (SECO) platform. While researchers and practitioners have recognized several factors affecting DX in SECO platforms, a clear roadmap of the most influential factors is still missing. This is particularly important given the direct impact on developers' interest in SECO and their ongoing engagement with the common technological platform. Goal: This work aims to identify key DX factors and understand how they influence third-party developers' decisions to adopt and keep contributing to a SECO. Methods: We conducted a systematic mapping study (SMS), analyzing 29 studies to assess the state-of-the-art of DX in SECO. Additionally, we conducted a Delphi study to evaluate the influence of 27 DX factors (identified in our SMS) from the perspective of 21 third-party developers to adopt and keep contributing to a SECO. Results: The factors that most strongly influence developers' adoption and ongoing contributions to a SECO are: financial costs for using the platform, desired technical resources for development, low barriers to entry into the applications market, and more financial gains. Conclusion: DX is essential for the success and sustainability of SECO. Our set of DX factors provides valuable insights and recommendations for researchers and practitioners to address key DX concerns from the perspective of third-party developers.

Exploring Low-Dimensional Magnetism in Cobalt Vanadates, ${A}$CoV$_{2}$O$_{7}$~(${A}$~=~Ca, Sr) : Crystal Growth and Magnetic Properties of Effective Spin-1/2 Zigzag Chains

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초록:

We report the successful growth of high-quality single crystals of ₩ACVO, a quasi-one-dimensional zigzag chain compound containing Co^{2+} ions, using the optical floating zone method. The crystal growth was stabilized under high-pressure argon-oxygen gas with slow growth rates, overcoming challenges associated with the incongruent melting behavior of this material. X-ray diffraction confirms the zigzag arrangement of Co^{2+} ions, forming a quasi-one-dimensional chain structure. Magnetic susceptibility and heat capacity measurements reveal an antiferromagnetic phase transition at the N₩'eel temperature ($T_{₩text{N}} ₩sim 3.5$ K) and negative Curie-Weiss temperatures, indicative of dominant antiferromagnetic interactions. The distorted CoO$_6$ octahedral geometry and strong spin-orbit coupling suggest that Co^{2+} ions likely exhibit an effective $J = 1/2$ Kramers doublet state. The results presented here demonstrate the potential of ₩ACVO₩ as a platform for investigating low-dimensional magnetism and quantum magnetic phenomena. These insights shed light on the role of the ${A}$-site ion in tuning the magnetic interactions, which will foster future research into the field-induced behavior in these cobalt vanadates.

From Reproduction to Replication: Evaluating Research Agents with Progressive Code Masking

저자: Gyeongwon James Kim, Alex Wilf, Louis-Philippe Morency, Daniel Fried

초록:

Recent progress in autonomous code generation has fueled excitement around AI agents capable of accelerating scientific discovery by running experiments. However, there is currently no benchmark that evaluates whether such agents can implement scientific ideas when given varied amounts of code as a starting point, interpolating between reproduction (running code) and from-scratch replication (fully re-implementing and running code). We introduce AutoExperiment, a benchmark that evaluates AI agents' ability to implement and run machine learning experiments based on natural language descriptions in research papers. In each task, agents are given a research paper, a codebase with key functions masked out, and a command to run the experiment. The goal is to generate the missing code, execute the experiment in a sandboxed environment, and reproduce the results. AutoExperiment scales in difficulty by varying the number of missing functions n, ranging from partial reproduction to full replication. We evaluate state-of-the-art agents and find that performance degrades rapidly as n increases. Agents that can dynamically interact with the environment (e.g. to debug their code) can outperform agents in fixed "agentless" harnesses, and there exists a significant gap between single-shot and multi-trial success rates (Pass@1 vs. Pass@5), motivating verifier approaches to our benchmark. Our findings highlight critical challenges in long-horizon code generation, context retrieval, and autonomous experiment execution, establishing AutoExperiment as a new benchmark for evaluating progress in AI-driven scientific experimentation. Our data and code are open-sourced at https://github.com/j1mk1m/AutoExperiment .

Orbital FFLO and layer-selective FFLO phases in trilayer NbSe$_2$

저자: Michiya Chazono, Youichi Yanase

초록:

Finite-momentum superconductivity has become an important research topic in condensed matter physics. In particular, the orbital Fulde-Ferrell-Larkin-Ovchinnikov (FFLO) state, which is stabi lized in atomically thin films by the orbital effect of an external magnetic field, has been getting attention as a fascinating finite-momentum superconducting state recently. We study the phase diagram of the trilayer Ising superconductor NbSe$_2$ in the in-plane magnetic field, taking into ac count the orbital effect, the paramagnetic effect, and the spin-orbit coupling. The finite-momentum gap structure in the high-field region is shown by a large-scale numerical calculation based on the Bogoliubov-de Gennes equation. We find an exotic superconducting phase, a layer-selective FFLO phase, in which finite-momentum Cooper pairs coexist with zero-momentum Cooper pairs, separated from the orbital FFLO phase.

Toward Decision-Oriented Prognostics: An Integrated Estimate-Optimize Framework for Predictive Maintenance

저자: Zhuojun Xie, Adam Abdin, Yiping Fang

플랫폼: arxiv

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카테고리: cs.AI, math.OC

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초록:

Recent research increasingly integrates machine learning (ML) into predictive maintenance (PdM) to reduce operational and maintenance costs in data-rich operational settings. However, uncertainty due to model misspecification continues to limit widespread industrial adoption. This paper proposes a PdM framework in which sensor-driven prognostics inform decision-making under economic trade-offs within a finite decision space. We investigate two key questions: (1) Does higher predictive accuracy necessarily lead to better maintenance decisions? (2) If not, how can the impact of prediction errors on downstream maintenance decisions be mitigated? We first demonstrate that in the traditional estimate-then-optimize (ETO) framework, errors in probabilistic prediction can result in inconsistent and suboptimal maintenance decisions. To address this, we propose an integrated estimate-optimize (IEO) framework that jointly tunes predictive models while directly optimizing for maintenance outcomes. We establish theoretical finite-sample guarantees on decision consistency under standard assumptions. Specifically, we develop a stochastic perturbation gradient descent algorithm suitable for small run-to-failure datasets. Empirical evaluations on a turbofan maintenance case study show that the IEO framework reduces average maintenance regret up to 22% compared to ETO. This study provides a principled approach to managing prediction errors in data-driven PdM. By aligning prognostic model training with maintenance objectives, the IEO framework improves robustness under model misspecification and improves decision quality. The improvement is particularly pronounced when the decision-making policy is misaligned with the decision-maker's target. These findings support more reliable maintenance planning in uncertain operational environments.

ReBoot: Encrypted Training of Deep Neural Networks with CKKS Bootstrapping

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플랫폼: arxiv

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카테고리: cs.LG, I.2.6	
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초록:	

Growing concerns over data privacy underscore the need for deep learning methods capable of processing sensitive information without compromising confidentiality. Among privacy-enhancing technologies, Homomorphic Encryption (HE) stands out by providing post-quantum cryptographic security and end-to-end data protection, safeguarding data even during computation. While Deep Neural Networks (DNNs) have gained attention in HE settings, their use has largely been restricted to encrypted inference. Prior research on encrypted training has primarily focused on logistic regression or has relied on multi-party computation to enable model fine-tuning. This stems from the substantial computational overhead and algorithmic complexity involved in DNNs training under HE. In this paper, we present ReBoot, the first framework to enable fully encrypted and non-interactive training of DNNs. Built upon the CKKS scheme, ReBoot introduces a novel HE-compliant neural network architecture based on local error signals, specifically designed to minimize multiplicative depth and reduce noise accumulation. ReBoot employs a tailored packing strategy that leverages real-number arithmetic via SIMD operations, significantly lowering both computational and memory overhead. Furthermore, by integrating approximate bootstrapping, ReBoot learning algorithm supports effective training of arbitrarily deep multi-layer perceptrons, making it well-suited for machine learning as-a-service. ReBoot is evaluated on both image recognition and tabular benchmarks, achieving accuracy comparable to 32-bit floating-point plaintext training while enabling fully encrypted training. It improves test accuracy by up to +3.27% over encrypted logistic regression, and up to +6.83% over existing encrypted DNN frameworks, while reducing training latency by up to 8.83x. ReBoot is made available to the scientific community as a public repository.

Performance Analysis of OAMP Detection for ODDM Modulation in Satellite Communications

저자: Yu Liu, Cunhua Pan, Tantao Gong, Yinlu Wang, Ming Chen

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카테고리: cs.IT, eess.SP, math.IT	
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초록:	

Towards future 6G wireless networks, low earth orbit (LEO) satellites have been widely considered as a promising component to enhance the terrestrial communications. To ensure the link reliability of high-mobility satellite communication scenarios, the emerging orthogonal delay-Doppler division multiplexing (ODDM) modulation has attracted significant research attention. In this paper, we study the diversity gain achieved by ODDM modulation along with the mathematical analysis and numerical simulations. Additionally, we propose an orthogonal approximate message passing (OAMP) algorithm based detector to harvest the diversity gain promised by ODDM modulation. By operating the linear and non-linear estimator iteratively, the orthogonal approximate message passing (OAMP) detector can utilize the sparsity of the effective delay-Doppler (DD) domain channel and extract the full diversity. Simulation results reveal the relationship between diversity gain and system parameters, and demonstrate that our proposed detector can achieve better performance than the conventional message passing methods with significantly reduced complexity.

A Survey of LLM-Driven AI Agent Communication: Protocols, Security Risks, and Defense Countermeasures

저자: Dezhang Kong, Shi Lin, Zhenhua Xu, Zhebo Wang, Minghao Li, Yufeng Li, Yilun Zhang, Zeyang Sha, Yuyuan Li, Changting Lin, Xun Wang, Xuan Liu, Muhammad Khurram Khan, Ningyu Zhang, Chaochao Chen, Meng Han

초록:

In recent years, Large-Language-Model-driven AI agents have exhibited unprecedented intelligence, flexibility, and adaptability, and are rapidly changing human production and lifestyle. Nowadays, agents are undergoing a new round of evolution. They no longer act as an isolated island like LLMs. Instead, they start to communicate with diverse external entities, such as other agents and tools, to collectively perform more complex tasks. Under this trend, agent communication is regarded as a foundational pillar of the future AI ecosystem, and many organizations intensively begin to design related communication protocols (e.g., Anthropic's MCP and Google's A2A) within the recent few months. However, this new field exposes significant security hazard, which can cause severe damage to real-world scenarios. To help researchers to quickly figure out this promising topic and benefit the future agent communication development, this paper presents a comprehensive survey of agent communication security. More precisely, we first present a clear definition of agent communication and categorize the entire lifecyle of agent communication into three stages: user-agent interaction, agent-agent communication, and agent-environment communication. Next, for each communication phase, we dissect related protocols and analyze its security risks according to the communication characteristics. Then, we summarize and outlook on the possible defense countermeasures for each risk. Finally, we discuss open issues and future directions in this promising research field.

Multimodal large language models and physics visual tasks: comparative analysis of performance and costs

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플랫폼: arxiv

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카테고리: physics.ed-ph

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초록:

Multimodal large language models (MLLMs) capable of processing both text and visual inputs are increasingly being explored for uses in physics education, such as tutoring, formative assessment, and grading. This study evaluates a range of publicly available MLLMs on a set of standardized, image-based physics research-based conceptual assessments (concept inventories). We benchmark 15 models from three major providers (Anthropic, Google, and OpenAI) across 102 physics items, focusing on two main questions: (1) How well do these models perform on conceptual physics tasks involving visual representations? and (2) What are the financial costs associated with their use? The results show high variability in both performance and cost. The performance of the tested models ranges from around 76₩% to as low as 21₩%. We also found that expensive models do not always outperform cheaper ones and that, depending on the demands of the context, cheaper models may be sufficiently capable for some tasks. This is especially relevant in contexts where financial resources are limited or for large-scale educational implementation of MLLMs. By providing these analyses, our aim is to inform teachers, institutions, and other educational stakeholders so that they can make evidence-based decisions about the selection of models for use in AI-supported physics education.

ReLink: Computational Circular Design of Planar Linkage Mechanisms Using Available Standard Parts

저자: Maxime Escande, Kristina Shea

플랫폼: arxiv

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카테고리: cs.CE, cs.RO

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초록:

The Circular Economy framework emphasizes sustainability by reducing resource consumption and waste through the reuse of components and materials. This paper presents ReLink, a computational framework for the circular design of planar linkage mechanisms using available standard parts. Unlike most mechanism design methods, which assume the ability to create custom parts and infinite part availability, ReLink prioritizes the reuse of discrete, standardized components, thus minimizing the need for new parts. The framework consists of two main components: design generation, where a generative design algorithm generates mechanisms from an inventory of available parts, and inverse design, which uses optimization methods to identify designs that match a user-defined trajectory curve. The paper also examines the trade-offs between kinematic performance and CO_2 footprint when incorporating new parts. Challenges such as the combinatorial nature of the design problem and the enforcement of valid solutions are addressed. By combining sustainability principles with kinematic synthesis, ReLink lays the groundwork for further research into computational circular design to support the development of systems that integrate reused components into mechanical products.

Simulating the Waterfall Model: A Systematic Review

저자: Antonios Saravanos

초록:

This systematic mapping study examines how the Waterfall Model has been represented in computational simulations within peer-reviewed literature. While Agile methodologies dominate contemporary software design practices, the Waterfall Model persists, particularly, within hybrid approaches that fuse structured, sequential workflows with the adaptability of agile practices. Despite its continued presence, little attention has been given to how the Waterfall Model is simulated in research contexts. A structured search of major academic databases identified 68 peer-reviewed studies published between 2000 and 2024. After applying inclusion criteria, selected studies were analyzed across four dimensions: (1) simulation methodologies (e.g., discrete-event simulation, system dynamics), (2) platforms and tools (e.g., Simphony.NET, SimPy), (3) geographic and temporal trends, and (4) fidelity to Royce's original seven-phase model. Discrete-event simulation was most commonly used, reflecting the model's sequential nature. Early work relied on proprietary platforms, while recent studies increasingly use open-source, Python-based tools. No studies fully implemented Royce's original formulation, most employed adaptations. These findings suggest that although niche, simulation of the Waterfall Model is present in academic discourse. This work highlights the need for accessible modeling tools and calls for future research that integrates the waterfall software process model with modern hybrid practices.

Unsupervised Data Generation for Offline Reinforcement Learning: A Perspective from Model

저자: Shuncheng He, Hongchang Zhang, Jianzhun Shao, Yuhang Jiang, Xiangyang Ji

초록:

Offline reinforcement learning (RL) recently gains growing interests from RL researchers. However, the performance of offline RL suffers from the out-of-distribution problem, which can be corrected by feedback in online RL. Previous offline RL research focuses on restricting the offline algorithm in in-distribution even in-sample action sampling. In contrast, fewer work pays attention to the influence of the batch data. In this paper, we first build a bridge over the batch data and the performance of offline RL algorithms theoretically, from the perspective of model-based offline RL optimization. We draw a conclusion that, with mild assumptions, the distance between the state-action pair distribution generated by the behavioural policy and the distribution generated by the optimal policy, accounts for the performance gap between the policy learned by model-based offline RL and the optimal policy. Secondly, we reveal that in task-agnostic settings, a series of policies trained by unsupervised RL can minimize the worst-case regret in the performance gap. Inspired by the theoretical conclusions, UDG (Unsupervised Data Generation) is devised to generate data and select proper data for offline training under tasks-agnostic settings. Empirical results demonstrate that UDG can outperform supervised data generation on solving unknown tasks.

HOIverse: A Synthetic Scene Graph Dataset With Human Object Interactions

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카테고리: cs.CV

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초록:

When humans and robotic agents coexist in an environment, scene understanding becomes crucial for the agents to carry out various downstream tasks like navigation and planning. Hence, an agent must be capable of localizing and identifying actions performed by the human. Current research lacks reliable datasets for performing scene understanding within indoor environments where humans are also a part of the scene. Scene Graphs enable us to generate a structured representation of a scene or an image to perform visual scene understanding. To tackle this, we present HOIverse a synthetic dataset at the intersection of scene graph and human-object interaction, consisting of accurate and dense relationship ground truths between humans and surrounding objects along with corresponding RGB images, segmentation masks, depth images and human keypoints. We compute parametric relations between various pairs of objects and human-object pairs, resulting in an accurate and unambiguous relation definitions. In addition, we benchmark our dataset on state-of-the-art scene graph generation models to predict parametric relations and human-object interactions. Through this dataset, we aim to accelerate research in the field of scene understanding involving people.

Hierarchical Time Series Forecasting Via Latent Mean Encoding

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초록:

Coherently forecasting the behaviour of a target variable across both coarse and fine temporal scales is crucial for profit-optimized decision-making in several business applications, and remains an open research problem in temporal hierarchical forecasting. Here, we propose a new hierarchical architecture that tackles this problem by leveraging modules that specialize in forecasting the different temporal aggregation levels of interest. The architecture, which learns to encode the average behaviour of the target variable within its hidden layers, makes accurate and coherent forecasts across the target temporal hierarchies. We validate our architecture on the challenging, real-world M5 dataset and show that it outperforms established methods, such as the TSMixer model.

Decompiling Smart Contracts with a Large Language Model

저자: Isaac David, Liyi Zhou, Dawn Song, Arthur Gervais, Kaihua Qin

초록:

The widespread lack of broad source code verification on blockchain explorers such as Etherscan, where despite 78,047,845 smart contracts deployed on Ethereum (as of May 26, 2025), a mere 767,520 (< 1%) are open source, presents a severe impediment to blockchain security. This opacity necessitates the automated semantic analysis of on-chain smart contract bytecode, a fundamental research challenge with direct implications for identifying vulnerabilities and understanding malicious behavior. Prevailing decompilers struggle to reverse bytecode in a readable manner, often yielding convoluted code that critically hampers vulnerability analysis and thwarts efforts to dissect contract functionalities for security auditing. This paper addresses this challenge by introducing a pioneering decompilation pipeline that, for the first time, successfully leverages Large Language Models (LLMs) to transform Ethereum Virtual Machine (EVM) bytecode into human-readable and semantically faithful Solidity code. Our novel methodology first employs rigorous static program analysis to convert bytecode into a structured three-address code (TAC) representation. This intermediate representation then guides a Llama-3.2-3B model, specifically fine-tuned on a comprehensive dataset of 238,446 TAC-to-Solidity function pairs, to generate high-quality Solidity. This approach uniquely recovers meaningful variable names, intricate control flow, and precise function signatures. Our extensive empirical evaluation demonstrates a significant leap beyond traditional decompilers, achieving an average semantic similarity of 0.82 with original source and markedly superior readability. The practical viability and effectiveness of our research are demonstrated through its implementation in a publicly accessible system, available at https://evmdecompiler.com.

Position: Intelligent Science Laboratory Requires the Integration of Cognitive and Embodied AI

저자: Sha Zhang, Suorong Yang, Tong Xie, Xiangyuan Xue, Zixuan Hu, Rui Li, Wenxi Qu, Zhenfei Yin, Tianfan Fu, Di Hu, Andres M Bran, Nian Ran, Bram Hoex, Wangmeng Zuo, Philippe Schwaller, Wanli Ouyang, Lei Bai, Yanyong Zhang, Lingyu Duan, Shixiang Tang, Dongzhan Zhou

초록:

Scientific discovery has long been constrained by human limitations in expertise, physical capability, and sleep cycles. The recent rise of AI scientists and automated laboratories has accelerated both the cognitive and operational aspects of research. However, key limitations persist: AI systems are often confined to virtual environments, while automated laboratories lack the flexibility and autonomy to adaptively test new hypotheses in the physical world. Recent advances in embodied AI, such as generalist robot foundation models, diffusion-based action policies, fine-grained manipulation learning, and sim-to-real transfer, highlight the promise of integrating cognitive and embodied intelligence. This convergence opens the door to closed-loop systems that support iterative, autonomous experimentation and the possibility of serendipitous discovery. In this position paper, we propose the paradigm of Intelligent Science Laboratories (ISLs): a multi-layered, closed-loop framework that deeply integrates cognitive and embodied intelligence. ISLs unify foundation models for scientific reasoning, agent-based workflow orchestration, and embodied agents for robust physical experimentation. We argue that such systems are essential for overcoming the current limitations of scientific discovery and for realizing the full transformative potential of AI-driven science.

A Wireless Self-Calibrating Ultrasound Microphone Array with Sub-Microsecond Synchronization

저자: Dennis Laurijssen, Rens Baeyens, Walter Daems, Jan Steckel

초록:

We present a novel system architecture for a distributed wireless, self-calibrating ultrasound microphone network for synchronized in-air acoustic sensing. Once deployed the embedded nodes determine their position in the environment using the infrared optical tracking system found in the HTC Vive Lighthouses. After self-calibration, the nodes start sampling the ultrasound microphone while embedding a synchronization signal in the data which is established using a wireless Sub-1GHz RF link. Data transmission is handled via the Wi-Fi 6 radio that is embedded in the nodes' SoC, decoupling synchronization from payload transport. A prototype system with a limited amount of network nodes was used to verify the proposed distributed microphone array's wireless data acquisition and synchronization capabilities. This architecture lays the groundwork for scalable, deployable ultrasound arrays for sound source localization applications in bio-acoustic research and industrial acoustic monitoring.

Filters of Identity: AR Beauty and the Algorithmic Politics of the Digital Body

저자: Miriam Doh, Corinna Canali, Nuria Oliver

초록:

This position paper situates AR beauty filters within the broader debate on Body Politics in HCI. We argue that these filters are not neutral tools but technologies of governance that reinforce racialized, gendered, and ableist beauty standards. Through naming conventions, algorithmic bias, and platform governance, they impose aesthetic norms while concealing their influence. To address these challenges, we advocate for transparency-driven interventions and a critical rethinking of algorithmic aesthetics and digital embodiment.

V2T-CoT: From Vision to Text Chain-of-Thought for Medical Reasoning and Diagnosis

저자: Yuan Wang, Jiaxiang Liu, Shujian Gao, Bin Feng, Zhihang Tang, Xiaotang Gai, Jian Wu, Zuozhu Liu

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초록:	

Recent advances in multimodal techniques have led to significant progress in Medical Visual Question Answering (Med-VQA). However, most existing models focus on global image features rather than localizing disease-specific regions crucial for diagnosis. Additionally, current research tends to emphasize answer accuracy at the expense of the reasoning pathway, yet both are crucial for clinical decision-making. To address these challenges, we propose From Vision to Text Chain-of-Thought (V2T-CoT), a novel approach that automates the localization of preference areas within biomedical images and incorporates this localization into region-level pixel attention as knowledge for Vision CoT. By fine-tuning the vision language model on constructed R-Med 39K dataset, V2T-CoT provides definitive medical reasoning paths. V2T-CoT integrates visual grounding with textual rationale generation to establish precise and explainable diagnostic results. Experimental results across four Med-VQA benchmarks demonstrate state-of-the-art performance, achieving substantial improvements in both performance and interpretability.

Implementation and Analysis of Different Geomagnetic Field Models for Attitude Determination and Control System (ADCS) of a Satellite

저자: Hoor Bano, Tatiana Podladchikova, Bisma Sajid, Dmitry Ris

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초록:	

An Attitude Determination and Control System is essential for orientation stability and performance of slew maneuvers on the satellite. This research focuses on comparing two different geomagnetic field models, Direct Dipole Model and International Geomagnetic Reference Field Model, for modeling of magnetometer and magnetorquers. Both these magnetic field models are compared and analyzed for two satellite attitude cases: orientation stability and unloading of reaction wheels. Magnetometer modeling is utilized to get sensor data for attitude determination and control to attain orientation stability. Whereas, the magnetorquer model aids in reaction wheel unloading, by performing the required actuation on the satellite, upon interaction with the Earth's magnetic field. The study offers a comprehensive lookout on the impact of geomagnetic field models on the overall ADCS performance, incorporating both attitude estimation and control via the sensor and actuator modeling. Apart from this, valuable insights are gained into selecting optimal models based on specific mission requirements and available computational resources. Finally, this comparison and analysis results in unique findings for an actual future satellite mission, that is to be launched soon.

ConStellaration: A dataset of QI-like stellarator plasma boundaries and optimization benchmarks

저자: Santiago A. Cadena, Andrea Merlo, Emanuel Laude, Alexander Bauer, Atul Agrawal, Maria Pascu, Marija Savtchouk, Enrico Guiraud, Lukas Bonauer, Stuart Hudson, Markus Kaiser

초록:

Stellarators are magnetic confinement devices under active development to deliver steady-state carbon-free fusion energy. Their design involves a high-dimensional, constrained optimization problem that requires expensive physics simulations and significant domain expertise. Recent advances in plasma physics and open-source tools have made stellarator optimization more accessible. However, broader community progress is currently bottlenecked by the lack of standardized optimization problems with strong baselines and datasets that enable data-driven approaches, particularly for quasi-isodynamic (QI) stellarator configurations, considered as a promising path to commercial fusion due to their inherent resilience to current-driven disruptions. Here, we release an open dataset of diverse QI-like stellarator plasma boundary shapes, paired with their ideal magnetohydrodynamic (MHD) equilibria and performance metrics. We generated this dataset by sampling a variety of QI fields and optimizing corresponding stellarator plasma boundaries. We introduce three optimization benchmarks of increasing complexity: (1) a single-objective geometric optimization problem, (2) a "simple-to-build" QI stellarator, and (3) a multi-objective ideal-MHD stable QI stellarator that investigates trade-offs between compactness and coil simplicity. For every benchmark, we provide reference code, evaluation scripts, and strong baselines based on classical optimization techniques. Finally, we show how learned models trained on our dataset can efficiently generate novel, feasible configurations without querying expensive physics oracles. By openly releasing the dataset along with benchmark problems and baselines, we aim to lower the entry barrier for optimization and machine learning researchers to engage in stellarator design and to accelerate cross-disciplinary progress toward bringing fusion energy to the grid.

Towards an Introspective Dynamic Model of Globally Distributed Computing Infrastructures

저자: Ozgur O. Kilic, David K. Park, Yihui Ren, Tatiana Korchuganova, Sairam Sri Vatsavai, Joseph Boudreau, Tasnuva Chowdhury, Shengyu Feng, Raees Khan, Jaehyung Kim, Scott Klasky, Tadashi Maeno, Paul Nilsson, Verena Ingrid Martinez Outschoorn, Norbert Podhorszki, Frédéric Suter, Wei Yang, Yiming Yang, Shinjae Yoo, Alexei Klimentov, Adolfy Hoisie

초록:

Large-scale scientific collaborations like ATLAS, Belle II, CMS, DUNE, and others involve hundreds of research institutes and thousands of researchers spread across the globe. These experiments generate petabytes of data, with volumes soon expected to reach exabytes. Consequently, there is a growing need for computation, including structured data processing from raw data to consumer-ready derived data, extensive Monte Carlo simulation campaigns, and a wide range of end-user analysis. To manage these computational and storage demands, centralized workflow and data management systems are implemented. However, decisions regarding data placement and payload allocation are often made disjointly and via heuristic means. A significant obstacle in adopting more effective heuristic or AI-driven solutions is the absence of a quick and reliable introspective dynamic model to evaluate and refine alternative approaches. In this study, we aim to develop such an interactive system using real-world data. By examining job execution records from the PanDA workflow management system, we have pinpointed key performance indicators such as queuing time, error rate, and the extent of remote data access. The dataset includes five months of activity. Additionally, we are creating a generative AI model to simulate time series of payloads, which incorporate visible features like category, event count, and submitting group, as well as hidden features like the total computational load-derived from existing PanDA records and computing site capabilities. These hidden features, which are not visible to job allocators, whether heuristic or AI-driven, influence factors such as queuing times and data movement.

Has Machine Translation Evaluation Achieved Human Parity? The Human Reference and the Limits of Progress

저자: Lorenzo Proietti, Stefano Perrella, Roberto Navigli

초록:

In Machine Translation (MT) evaluation, metric performance is assessed based on agreement with human judgments. In recent years, automatic metrics have demonstrated increasingly high levels of agreement with humans. To gain a clearer understanding of metric performance and establish an upper bound, we incorporate human baselines in the MT meta-evaluation, that is, the assessment of MT metrics' capabilities. Our results show that human annotators are not consistently superior to automatic metrics, with state-of-the-art metrics often ranking on par with or higher than human baselines. Despite these findings suggesting human parity, we discuss several reasons for caution. Finally, we explore the broader implications of our results for the research field, asking: Can we still reliably measure improvements in MT evaluation? With this work, we aim to shed light on the limits of our ability to measure progress in the field, fostering discussion on an issue that we believe is crucial to the entire MT evaluation community.

Euclid: Quick Data Release (Q1) -- Watching ICM-selected galaxy clusters with Euclid eyes -- prospects of Euclid data in the context of large SZ and X-ray based surveys

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초록:

Galaxy clusters detected through their X-ray emission or Sunyaev--Zeldovich effect (SZE), both produced by the intra-cluster medium (ICM), are key probes in cosmological and astrophysical studies. To maximise the scientific return of such surveys, complementary data are required for cluster confirmation and redshift estimation. This is typically provided by wide-field optical and infrared surveys, which are increasingly challenged by ongoing and future ICM-selected samples. In particular, at high redshifts ($z>1$) probed by upcoming SZE-selected samples, current large surveys may be insufficient for reliable confirmation. Deep, high-resolution infrared surveys like Euclid will thus be essential for confirming most high-redshift clusters. We present an analysis of the first sizeable Euclid dataset (Q1), overlapping with several ICM-selected cluster samples. We apply an adaptation of the MCMF cluster confirmation tool to estimate key properties, including redshift and richness, and to predict Euclid's capabilities for high-redshift cluster confirmation. We find promising performance, particularly at high redshifts, while richness estimates at low redshifts ($z<0.4$) are currently limited by Q1 data quality but should improve with future releases. Using MCMF runs on random lines of sight, we predict that Euclid will confirm clusters at $1<z<2$ as effectively as current optical surveys at $z<0.6$, significantly enhancing high-redshift confirmation. SZE-selected samples will thus greatly benefit from Euclid overlap. Among five known high-z SZE clusters in Q1, we identify the highest-redshift jellyfish galaxy candidate to date, EUCLJ035330.86$-$504347.6 in SPT-CLJ0353$-$5043 ($z=1.32$), two massive star-forming galaxies near ACT-CLJ0350.0$-$4819 ($z=1.46$), and strong lensing features in SPT-CLJ0353$-$5043 and SPT-CLJ0421$-$4845.

General Methods Make Great Domain-specific Foundation Models: A Case-study on Fetal Ultrasound

저자: Jakob Ambsdorf, Asbjørn Munk, Sebastian Llambias, Anders Nymark Christensen, Kamil Mikolaj, Randall Balestriero, Martin Tolsgaard, Aasa Feragen, Mads Nielsen

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초록:

With access to large-scale, unlabeled medical datasets, researchers are confronted with two questions: Should they attempt to pretrain a custom foundation model on this medical data, or use transfer-learning from an existing generalist model? And, if a custom model is pretrained, are novel methods required? In this paper we explore these questions by conducting a case-study, in which we train a foundation model on a large regional fetal ultrasound dataset of 2M images. By selecting the well-established DINOv2 method for pretraining, we achieve state-of-the-art results on three fetal ultrasound datasets, covering data from different countries, classification, segmentation, and few-shot tasks. We compare against a series of models pretrained on natural images, ultrasound images, and supervised baselines. Our results demonstrate two key insights: (i) Pretraining on custom data is worth it, even if smaller models are trained on less data, as scaling in natural image pretraining does not translate to ultrasound performance. (ii) Well-tuned methods from computer vision are making it feasible to train custom foundation models for a given medical domain, requiring no hyperparameter tuning and little methodological adaptation. Given these findings, we argue that a bias towards methodological innovation should be avoided when developing domain specific foundation models under common computational resource constraints.

Toward the Explainability of Protein Language Models for Sequence Design

저자: Andrea Hunklinger, Noelia Ferruz

초록:

Transformer-based language models excel in a variety of protein-science tasks that range from structure prediction to the design of functional enzymes. However, these models operate as black boxes, and their underlying working principles remain unclear. Here, we survey emerging applications of explainable artificial intelligence (XAI) to protein language models (pLMs) and describe their potential in protein research. We break down the workflow of a generative decoder-only Transformer into four information contexts: (i) training sequences, (ii) input prompt, (iii) model architecture, and (iv) output sequence. For each, we describe existing methods and applications of XAI. Additionally, from published studies we distil five (potential) roles that XAI can play in protein design: Evaluator, Multitasker, Engineer, Coach, and Teacher, with the Evaluator role being the only one widely adopted so far. These roles aim to help both protein science practitioners and model developers understand the possibilities and limitations of implementing XAI for the design of sequences. Finally, we highlight the critical areas of application for the future, including risks related to security, trustworthiness, and bias, and we call for community benchmarks, open-source tooling, and domain-specific visualizations to advance explainable protein design. Overall, our analysis aims to move the discussion toward the use of XAI in protein design.

Reconfigurable Intelligent Surfaces for 6G and Beyond: A Comprehensive Survey from Theory to Deployment

저자: Prasetyo Putranto, Anis Amazigh Hamza, Sameh Mabrouki, Nasrullah Armi, Iyad Dayoub

초록:

As the wireless research community moves toward shaping the vision of sixth-generation (6G) networks, reconfigurable intelligent surfaces (RIS) have emerged as a promising technology for controlling the propagation environment. Although RIS has not yet been standardized, its versatile applications and enabling capabilities have attracted growing attention in both academia and industry. This survey presents a comprehensive review of RIS technology spanning theoretical foundations, design aspects, and practical deployment considerations. In contrast to existing surveys that focus on isolated aspects, this work offers an integrated view covering use cases, control mechanisms, channel sounding methodologies, and channel estimation strategies. Each of these topics is reviewed through the lens of recent literature, synthesizing the latest advancements to provide updated insights for both academic researchers and industry practitioners. It further addresses emerging topics such as standardization activities and industrial perspectives, which are often overlooked in prior literature. By bridging theoretical insights with practical challenges, this survey aims to provide a holistic understanding of RIS and support its evolution from a research concept toward real-world implementation.

Beyond Wellbeing Apps: Co-Designing Immersive, Embodied, and Collective Digital Wellbeing Interventions for Healthcare Professionals

저자: Zheyuan Zhang, Jingjing Sun, Dorian Peters, Rafael A. Calvo

초록:

Healthcare professionals (HCPs) face increasing levels of stress and burnout. Technological wellbeing interventions provide accessible and flexible support for HCPs. While most studies have focused on mobile- and web-based programs, alternative technologies like virtual reality (VR), augmented reality (AR), tangible interfaces, and embodied technologies are emerging as engaging and effective tools for wellbeing interventions. However, there is still a lack of research on how such technologies are perceived among HCPs. This study explored HCPs' perceptions and preferences for various types of wellbeing technologies, by conducting a 2-phase co-design study involving 26 HCPs in idea generation, concept evaluation, prototype testing, and design iteration. From our findings, HCPs highly valued the potential of technologies to support mental health with immersive, embodied, and collective experiences. Furthermore, we provided design recommendations for wellbeing technologies for HCPs that sustain user engagement by meeting their needs for autonomy, competence, and relatedness in the experiences.

Robust and Resilient Networks with Integrated Sensing, Communication and Computation

저자: Ming-Chun Lee, Christian Eckrich, Vahid Jamali, Yu-Chih Huang, Arash Asadi, Li-Chun Wang

초록:

Emerging applications such as networked robotics, intelligent transportation, smart factories, and virtual and augmented reality demand integrated perception and connectivity enabled by wireless communication. This has driven growing interests in integrated sensing, communication, and computation (ISCC) systems, with a primary focus on their efficient co-designs. However, as ISCC systems increasingly support critical applications, they must not only deliver high performance but also demonstrate robustness and resilience. In this context, robustness refers to a system's ability to maintain performance under uncertainties, while resilience denotes its capacity to sustain a minimum level of service in the face of major disruptions. To address this gap, this article presents an overview of ISCC systems from the perspectives of robustness and resilience under limited resources. First, key concepts related to these properties are introduced in the ISCC context. Subsequently, design approaches for realizing robust and resilient ISCC networks are discussed. Finally, the article concludes with the discussions of a case study and open research problems in this area.

Approximating Submodular Matroid-Constrained Partitioning

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초록:

The submodular partitioning problem asks to minimize, over all partitions P of a ground set V, the sum of a given submodular function f over the parts of P. The problem has seen considerable work in approximability, as it encompasses multiterminal cuts on graphs, k-cuts on hypergraphs, and elementary linear algebra problems such as matrix multiway partitioning. This research has been divided between the fixed terminal setting, where we are given a set of terminals that must be separated by P, and the global setting, where the only constraint is the size of the partition. We investigate a generalization that unifies these two settings: minimum submodular matroid-constrained partition. In this problem, we are additionally given a matroid over the ground set and seek to find a partition P in which there exists some basis that is separated by P. We explore the approximability of this problem and its variants, reaching the state of the art for the special case of symmetric submodular functions, and provide results for monotone and general submodular functions as well.

Physics-Informed Neural Networks for Industrial Gas Turbines: Recent Trends, Advancements and Challenges

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초록:

Physics-Informed Neural Networks (PINNs) have emerged as a promising computational framework for solving differential equations by integrating deep learning with physical constraints. However, their application in gas turbines is still in its early stages, requiring further refinement and standardization for wider adoption. This survey provides a comprehensive review of PINNs in Industrial Gas Turbines (IGTs) research, highlighting their contributions to the analysis of aerodynamic and aeromechanical phenomena, as well as their applications in flow field reconstruction, fatigue evaluation, and flutter prediction, and reviews recent advancements in accuracy, computational efficiency, and hybrid modelling strategies. In addition, it explores key research efforts, implementation challenges, and future directions aimed at improving the robustness and scalability of PINNs.

phylo2vec: a library for vector-based phylogenetic tree manipulation

저자: Neil Scheidwasser, Ayush Nag, Matthew J Penn, Anthony MV Jakob, Frederik Mølkjær Andersen, Mark P Khurana, Landung Setiawan, Madeline Gordon, David A Duchêne, Samir Bhatt

초록:

Phylogenetics is a fundamental component of many analysis frameworks in biology as well as linguistics to study the evolutionary relationships of different entities. Recently, the advent of large-scale genomics and the SARS-CoV-2 pandemic has underscored the necessity for phylogenetic software to handle large datasets of genomes or phylogenetic trees. While significant efforts have focused on scaling optimisation algorithms, visualization, and lineage identification, an emerging body of research has been dedicated to efficient representations of data for genomes and phylogenetic trees such as phylo2vec. Compared to traditional tree representations such as the Newick format, which represents trees using strings of nested parentheses, modern representations of phylogenetic trees utilize integer vectors to define the tree topology traversal. This approach offers several advantages, including easier manipulability, increased memory efficiency, and applicability to downstream tasks such as machine learning. Here, we present the latest release of phylo2vec (or Phylo2Vec), a high-performance software package for encoding, manipulating, and analysing binary phylogenetic trees. At its core, the package is based on the phylo2vec representation of binary trees, which defines a bijection from any tree topology with n leaves into an integer vector of size $n-1$. Compared to the traditional Newick format, phylo2vec is designed to enable fast sampling and comparison of binary trees. This release features a core implementation in Rust, providing significant performance improvements and memory efficiency, while remaining available in Python (superseding the release described in the original paper) and R via dedicated wrappers, making it accessible to a broad audience in the bioinformatics community.

Recalling The Forgotten Class Memberships: Unlearned Models Can Be Noisy Labelers to Leak Privacy

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초록:

Machine Unlearning (MU) technology facilitates the removal of the influence of specific data instances from trained models on request. Despite rapid advancements in MU technology, its vulnerabilities are still underexplored, posing potential risks of privacy breaches through leaks of ostensibly unlearned information. Current limited research on MU attacks requires access to original models containing privacy data, which violates the critical privacy-preserving objective of MU. To address this gap, we initiate an innovative study on recalling the forgotten class memberships from unlearned models (ULMs) without requiring access to the original one. Specifically, we implement a Membership Recall Attack (MRA) framework with a teacher-student knowledge distillation architecture, where ULMs serve as noisy labelers to transfer knowledge to student models. Then, it is translated into a Learning with Noisy Labels (LNL) problem for inferring the correct labels of the forgetting instances. Extensive experiments on state-of-the-art MU methods with multiple real datasets demonstrate that the proposed MRA strategy exhibits high efficacy in recovering class memberships of unlearned instances. As a result, our study and evaluation have established a benchmark for future research on MU vulnerabilities.

LLM-based Multi-Agent System for Intelligent Refactoring of Haskell Code

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초록:

Refactoring is a constant activity in software development and maintenance. Scale and maintain software systems are based on code refactoring. However, this process is still labor intensive, as it requires programmers to analyze the codebases in detail to avoid introducing new defects. In this research, we put forward a large language model (LLM)-based multi-agent system to automate the refactoring process on Haskell code. The objective of this research is to evaluate the effect of LLM-based agents in performing structured and semantically accurate refactoring on Haskell code. Our proposed multi-agent system based on specialized agents with distinct roles, including code analysis, refactoring execution, verification, and debugging. To test the effectiveness and practical applicability of the multi-agent system, we conducted evaluations using different open-source Haskell codebases. The results of the experiments carried out showed that the proposed LLM-based multi-agent system could average 11.03% decreased complexity in code, an improvement of 22.46% in overall code quality, and increase performance efficiency by an average of 13.27%. Furthermore, memory allocation was optimized by up to 14.57%. These results highlight the ability of LLM-based multi-agent in managing refactoring tasks targeted toward functional programming paradigms. Our findings hint that LLM-based multi-agent systems integration into the refactoring of functional programming languages can enhance maintainability and support automated development workflows.

PhishingHook: Catching Phishing Ethereum Smart Contracts leveraging EVM Opcodes

저자: Pasquale De Rosa, Simon Queyrut, Yérom-David Bromberg, Pascal Felber, Valerio Schiavoni

초록:

The Ethereum Virtual Machine (EVM) is a decentralized computing engine. It enables the Ethereum blockchain to execute smart contracts and decentralized applications (dApps). The increasing adoption of Ethereum sparked the rise of phishing activities. Phishing attacks often target users through deceptive means, e.g., fake websites, wallet scams, or malicious smart contracts, aiming to steal sensitive information or funds. A timely detection of phishing activities in the EVM is therefore crucial to preserve the user trust and network integrity. Some state-of-the art approaches to phishing detection in smart contracts rely on the online analysis of transactions and their traces. However, replaying transactions often exposes sensitive user data and interactions, with several security concerns. In this work, we present PhishingHook, a framework that applies machine learning techniques to detect phishing activities in smart contracts by directly analyzing the contract's bytecode and its constituent opcodes. We evaluate the efficacy of such techniques in identifying malicious patterns, suspicious function calls, or anomalous behaviors within the contract's code itself before it is deployed or interacted with. We experimentally compare 16 techniques, belonging to four main categories (Histogram Similarity Classifiers, Vision Models, Language Models and Vulnerability Detection Models), using 7,000 real-world malware smart contracts. Our results demonstrate the efficiency of PhishingHook in performing phishing classification systems, with about 90% average accuracy among all the models. We support experimental reproducibility, and we release our code and datasets to the research community.

USIS16K: High-Quality Dataset for Underwater Salient Instance Segmentation

저자: Lin Hong, Xin Wang, Yihao Li, Xia Wang

플랫폼: arxiv

발행일: 2025-06-24

카테고리: cs.CV, I.4.6

PDF URL: http://arxiv.org/pdf/2506.19472v1

초록:

Inspired by the biological visual system that selectively allocates attention to efficiently identify salient objects or regions, underwater salient instance segmentation (USIS) aims to jointly address the problems of where to look (saliency prediction) and what is there (instance segmentation) in underwater scenarios. However, USIS remains an underexplored challenge due to the inaccessibility and dynamic nature of underwater environments, as well as the scarcity of large-scale, high-quality annotated datasets. In this paper, we introduce USIS16K, a large-scale dataset comprising 16,151 high-resolution underwater images collected from diverse environmental settings and covering 158 categories of underwater objects. Each image is annotated with high-quality instance-level salient object masks, representing a significant advance in terms of diversity, complexity, and scalability. Furthermore, we provide benchmark evaluations on underwater object detection and USIS tasks using USIS16K. To facilitate future research in this domain, the dataset and benchmark models are publicly available.

Tagged for Direction: Pinning Down Causal Edge Directions with Precision

저자: Florian Peter Busch, Moritz Willig, Florian Guldan, Kristian Kersting, Devendra Singh Dhami

플랫폼: arxiv

발행일: 2025-06-24

카테고리: cs.LG, cs.AI

PDF URL: http://arxiv.org/pdf/2506.19459v1

초록:

Not every causal relation between variables is equal, and this can be leveraged for the task of causal discovery. Recent research shows that pairs of variables with particular type assignments induce a preference on the causal direction of other pairs of variables with the same type. Although useful, this assignment of a specific type to a variable can be tricky in practice. We propose a tag-based causal discovery approach where multiple tags are assigned to each variable in a causal graph. Existing causal discovery approaches are first applied to direct some edges, which are then used to determine edge relations between tags. Then, these edge relations are used to direct the undirected edges. Doing so improves upon purely type-based relations, where the assumption of type consistency lacks robustness and flexibility due to being restricted to single types for each variable. Our experimental evaluations show that this boosts causal discovery and that these high-level tag relations fit common knowledge.

FuncVul: An Effective Function Level Vulnerability Detection Model using LLM and Code Chunk

저자: Sajal Halder, Muhammad Ejaz Ahmed, Seyit Camtepe

플랫폼: arxiv

발행일: 2025-06-24

카테고리: cs.CR

PDF URL: http://arxiv.org/pdf/2506.19453v1

초록:

Software supply chain vulnerabilities arise when attackers exploit weaknesses by injecting vulnerable code into widely used packages or libraries within software repositories. While most existing approaches focus on identifying vulnerable packages or libraries, they often overlook the specific functions responsible for these vulnerabilities. Pinpointing vulnerable functions within packages or libraries is critical, as it can significantly reduce the risks associated with using open-source software. Identifying vulnerable patches is challenging because developers often submit code changes that are unrelated to vulnerability fixes. To address this issue, this paper introduces FuncVul, an innovative code chunk-based model for function-level vulnerability detection in C/C++ and Python, designed to identify multiple vulnerabilities within a function by focusing on smaller, critical code segments. To assess the model's effectiveness, we construct six code and generic code chunk based datasets using two approaches: (1) integrating patch information with large language models to label vulnerable samples and (2) leveraging large language models alone to detect vulnerabilities in function-level code. To design FuncVul vulnerability model, we utilise GraphCodeBERT fine tune model that captures both the syntactic and semantic aspects of code. Experimental results show that FuncVul outperforms existing state-of-the-art models, achieving an average accuracy of 87-92% and an F1 score of 86-92% across all datasets. Furthermore, we have demonstrated that our code-chunk-based FuncVul model improves 53.9% accuracy and 42.0% F1-score than the full function-based vulnerability prediction. The FuncVul code and datasets are publicly available on GitHub at https://github.com/sajalhalder/FuncVul.

A Stochastic Electric Vehicle Routing Problem under Uncertain Energy Consumption

저자: Andrea Spinelli, Dario Bezzi, Ola Jabali, Francesca Maggioni

플랫폼: arxiv

발행일: 2025-06-24

카테고리: math.OC

PDF URL: http://arxiv.org/pdf/2506.19426v1

초록:

The increasing adoption of Electric Vehicles (EVs) for service and goods distribution operations has led to the emergence of Electric Vehicle Routing Problems (EVRPs), a class of vehicle routing problems addressing the unique challenges posed by the limited driving range and recharging needs of EVs. While the majority of EVRP variants have considered deterministic energy consumption, this paper focuses on the Stochastic Electric Vehicle Routing Problem with a Threshold recourse policy (SEVRP-T), where the uncertainty in energy consumption is considered, and a recourse policy is employed to ensure that EVs recharge at Charging Stations (CSs) whenever their State of Charge (SoC) falls below a specified threshold. We formulate the SEVRP-T as a two-stage stochastic mixed-integer second-order cone model, where the first stage determines the sequences of customers to be visited, and the second stage incorporates charging activities. The objective is to minimize the expected total duration of the routes, composed by travel times and recharging operations. To cope with the computational complexity of the model, we propose a heuristic based on an Iterated Local Search (ILS) procedure coupled with a Set Partitioning problem. To further speed up the heuristic, we develop two lower bounds on the corresponding first-stage customer sequences. Furthermore, to handle a large number of energy consumption scenarios, we employ a scenario reduction technique. Extensive computational experiments are conducted to validate the effectiveness of the proposed solution strategy and to assess the importance of considering the stochastic nature of the energy consumption. The research presented in this paper contributes to the growing body of literature on EVRP and provides insights into managing the operational deployment of EVs in logistics activities under uncertainty.

Loss functions incorporating auditory spatial perception in deep learning -- a review

저자: Boaz Rafaely, Stefan Weinzierl, Or Berebi, Fabian Brinkmann

초록:

Binaural reproduction aims to deliver immersive spatial audio with high perceptual realism over headphones. Loss functions play a central role in optimizing and evaluating algorithms that generate binaural signals. However, traditional signal-related difference measures often fail to capture the perceptual properties that are essential to spatial audio quality. This review paper surveys recent loss functions that incorporate spatial perception cues relevant to binaural reproduction. It focuses on losses applied to binaural signals, which are often derived from microphone recordings or Ambisonics signals, while excluding those based on room impulse responses. Guided by the Spatial Audio Quality Inventory (SAQI), the review emphasizes perceptual dimensions related to source localization and room response, while excluding general spectral-temporal attributes. The literature survey reveals a strong focus on localization cues, such as interaural time and level differences (ITDs, ILDs), while reverberation and other room acoustic attributes remain less explored in loss function design. Recent works that estimate room acoustic parameters and develop embeddings that capture room characteristics indicate their potential for future integration into neural network training. The paper concludes by highlighting future research directions toward more perceptually grounded loss functions that better capture the listener's spatial experience.

ClearerVoice-Studio: Bridging Advanced Speech Processing Research and Practical Deployment

저자: Shengkui Zhao, Zexu Pan, Bin Ma

초록:

This paper introduces ClearerVoice-Studio, an open-source, AI-powered speech processing toolkit designed to bridge cutting-edge research and practical application. Unlike broad platforms like SpeechBrain and ESPnet, ClearerVoice-Studio focuses on interconnected speech tasks of speech enhancement, separation, super-resolution, and multimodal target speaker extraction. A key advantage is its state-of-the-art pretrained models, including FRCRN with 3 million uses and MossFormer with 2.5 million uses, optimized for real-world scenarios. It also offers model optimization tools, multi-format audio support, the SpeechScore evaluation toolkit, and user-friendly interfaces, catering to researchers, developers, and end-users. Its rapid adoption attracting 3000 GitHub stars and 239 forks highlights its academic and industrial impact. This paper details ClearerVoice-Studio's capabilities, architectures, training strategies, benchmarks, community impact, and future plan. Source code is available at https://github.com/modelscope/ClearerVoice-Studio.

Chronological lifespan extension and nucleotide salvage inhibition in yeast by isonicotinamide supplementation

저자: Kalita, A., Letai, C. T., Hesles, E. E., Power, L. N., Mishra, S., Saha, S., Dinda, M., Wang, D., Singh, P. K., Smith, J. S.

초록:

Isonicotinamide (INAM) is an isomer of the NAD+ precursor nicotinamide (NAM) that stimulates the enzymatic activity of Sir2, an NAD+-dependent histone deacetylase from the budding yeast, Saccharomyces cerevisiae. Supplementing INAM into growth media promotes the replicative lifespan (RLS) of this single cell organism by maintaining intracellular NAD+ homeostasis. INAM also extends yeast chronological lifespan (CLS), but the underlying mechanisms remain largely uncharacterized. To identify interacting genes, a chemical genomics screen of the yeast knockout (YKO) collection was performed for mutants sensitized to growth inhibition by INAM. Significant Gene Ontology (GO) terms included transcription elongation factors, metabolic pathways converging on one-carbon metabolism, and de novo purine biosynthesis, collectively suggesting that INAM may perturb nucleotide metabolism. Indeed, INAM caused dose-dependent depletion of intracellular cytidine, uridine and guanosine, ribonucleosides derived from the breakdown of nucleotide monophosphates by a set of nucleotidases (Phm8, Sdt1, Isn1) or the alkaline phosphatase Pho8. Direct inhibition of recombinant Sdt1 and Phm8 nucleotidase activity by INAM was confirmed in vitro, as was inhibition of alkaline phosphatase activity. Each of these enzymes can also convert nicotinamide mononucleotide (NMN) to nicotinamide riboside (NR), consistent with an accumulation of NMN and NAD+ upon inhibition by INAM. Taken together, the findings suggest a model whereby partial impairment of nucleotide salvage pathways can trigger a hormetic stress response that supports enhanced quiescence during chronological aging.

Spatially defined multicellular functional units in colorectal cancer revealed from single cell and spatial transcriptomics

저자: Avraham-Davidi, I., Mages, S., Klughammer, J., Moriel, N., Imada, S., Hofree, M., Murray, E., Chen, J., Pelka, K., Mehta, A., Boland, G. M., Delorey, T. M., Caplan, L., Dionne, D., Strasser, R., Lalakova, J., Niesnerova, A., Xu, H., Rouault, M., Tirosh, I., Hacohen, N., Chen, F., Yilmaz, O. H., Roper, J., Rozenblatt-Rosen, O., Nitzan, M., Regev, A.

카테고리: cancer biology

PDF URL: https://www.biorxiv.org/content/10.1101/2022.10.02.508492v1.full.pdf

초록:

While advances in single cell genomics have helped to chart the cellular components of tumor ecosystems, it has been more challenging to characterize their specific spatial organization and functional interactions. Here, we combine single cell RNA-seq, spatial transcriptomics by Slide-seq, and in situ multiplex RNA analysis, to create a detailed spatial map of healthy and dysplastic colon cellular ecosystems and their association with disease progression. We profiled inducible genetic CRC mouse models that recapitulate key features of human CRC, assigned cell types and epithelial expression programs to spatial tissue locations in tumors, and computationally used them to identify the regional features spanning different cells in the same spatial niche. We find that tumors were organized in cellular neighborhoods, each with a distinct composition of cell subtypes, expression programs, and local cellular interactions. Comparing to scRNA-seq and Slide-seq data from human CRC, we find that both cell composition and layout features were conserved between the species, with mouse neighborhoods correlating with malignancy and clinical outcome in human patient tumors, highlighting the relevance of our findings to human disease. Our work offers a comprehensive framework that is applicable across various tissues, tumors, and disease conditions, with tools for the extrapolation of findings from experimental mouse models to human diseases.

The unique synaptic circuitry of specialized olfactory glomeruli in Drosophila melanogaster

저자: Gruber, L., Cantera, R., Pleijzier, M. W., Steinert, M., Pertsch, T., Hansson, B. S., Rybak, J.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: neuroscience

PDF URL: https://www.biorxiv.org/content/10.1101/2022.09.30.510181v1.full.pdf

초록:

In the Drosophila olfactory system most odorants are encoded in the antennal lobe in a combinatory way, activating several glomerular circuits. However, odorants of particular ecological role for the fly are encoded through activation of a single specialized olfactory pathway. Comparative analyses of densely reconstructed connectomes of one broadly tuned glomerulus (DL5) and one narrowly tuned glomerulus (DA2) gained detailed insight into the variations of synaptic circuitries of glomeruli with different computational tasks. Our approach combined laser-branding of glomeruli of interest with volume based focused ion beam-scanning electron microscopy (FIB-SEM) to enable precise targeting and analysis of the two glomeruli. We discovered differences in their neuronal innervation, synaptic composition and specific circuit diagrams of their major cell types: olfactory sensory neurons (OSNs), uniglomerular projection neurons (uPNs) and multiglomerular neurons (MGNs). By comparing our data with a previously mapped narrowly tuned glomerulus (VA1v), we identified putative generic features of narrowly tuned glomerular circuits, including higher density of neuronal fibers and synapses, lower degree of OSN lateralization, stronger axo-axonic connections between OSNs, dendro-dendritic connections between many uPNs, and lower degree of presynaptic input on OSN axons. In addition, this work revealed that the dendrites of the single uPN in DL5 contain a substantial amount of autapses interconnecting distant regions of the dendritic tree. The comparative analysis of glomeruli allows to formulate synaptic motifs implemented in olfactory circuits with different computational demands.

Vehicle-mounted cameras reveal negative impact of the Fukushima Daiichi nuclear power plant accident on large bird abundance via paddy field abandonment.

저자: Kumada, N., Fukasawa, K., Yoshioka, A., Tsuda, N., Ouchi, H.

초록:

Farmland bird populations are declining due to farmland abandonment and agricultural intensification. Effective conservation strategies require appropriate monitoring approaches, including efficient and scalable survey methods. In this study, we developed a large-scale monitoring method for herons and egrets (Ardeidae) using vehicle-mounted video cameras and distance sampling models that incorporate location uncertainty. The survey was conducted in and around the evacuation zone of the Fukushima Daiichi nuclear power plant accident. A total of 7,031 km of roadside video footage was recorded, covering 24.41 km^2 of farmland. Ardeidae were observed only outside the evacuation zone and were entirely absent within it. Predicted abundance differed greatly between areas inside (0.0279 +/- 0.0307/km^2) and outside (4.57 +/- 5.36/km^2) the evacuation zone. Incorporating location uncertainty into the distance sampling model had little effect on the estimates (4.57 +/- 5.36 vs. 4.51 +/- 5.29/km^2 with and without integrating location uncertainty, respectively). This suggests that our video-based roadside survey method is robust to location uncertainty in structured landscapes such as Japanese rice paddies. The accuracy may be attributed to the study system, where levees and roads divide paddy fields, limiting potential error in observer-target distances Our method can be applied to other open habitats, such as natural grasslands and wetlands, especially in areas lacking artificial markers, by incorporating measurement uncertainty into the model. This combination of roadside surveys with vehicle-mounted cameras and distance sampling provides a practical and transferable approach for monitoring large-bodied species in open landscapes, enhancing both the efficiency and spatial coverage of biodiversity assessments.

Codon usage bias study of the Vitamin D receptor (VDR) gene of Multiple Sclerosis and Diabetes-1 patients

저자: Barik, S. K., Turuk, J., Giri, S., Pati, S.

초록:

The codon bias usage study of the 33 Vitamin D Receptor (VDR) genes of the Multiple sclerosis and Diabetes-1 patients were characterized. Various computational tools were used to find out the codon usage pattern of the VDR genes in both group of patients. The base compositions, nucleotide substation rates, codon adaptation index, hydrophobic nature of the amino acids of VDR gene of both group of patients were analysed. The analysis of the synonymous codon usage pattern of the genes would helpful in the heterologous expression of the VDR genes leads to codon optimizations in Multiple Sclerosis and Diabetes-1 patients. The codon usage bias analysis of the VDR gene of the Multiple sclerosis and Diabetes-1 patients through computational approach determined the pattern of VDR gene expression and evolution during the acquiring of the disease of the patients.

Detection and localization of conspecifics in ghost knifefish are influenced by the relationship between the spatial organization of receptors and signals.

저자: Ramachandra, K. L., Milam, O. E., Pedraja, F., Cornett, J. D., Marsat, G.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: neuroscience

PDF URL: https://www.biorxiv.org/content/10.1101/2023.07.20.549925v1.full.pdf

초록:

The detection and localization of signals rely on arrays of receptors, and their spatial organization plays a key role in determining the accuracy of the system. Weakly electric ghost knifefish rely on a distributed array of electroreceptors to detect spatially diffuse electric signals from conspecifics. While we know that spatial resolution for small objects, such as prey, is enhanced near the head due to a high receptor density, it is not clear how receptor organization influences the processing of global and diffuse signals from conspecifics. Using spatially realistic modeling, we quantified how receptor density influences detection and localization accuracy for conspecific signals across varying distances. Our main result demonstrates that receptor density markedly enhances detection accuracy in frontal regions at intermediate distances (35-50 cm) yet surprisingly contributes minimally to improving localization accuracy. This highlights a fundamental principle: receptor convergence primarily benefits signal detection when dealing with spatially diffuse stimuli, even though higher receptor density can enhance localization accuracy for spatially delineated signals. Our findings extend beyond the electrosensory modality, drawing parallels with other sensory systems, and offer broader insights into spatial processing principles.

Copy number variation shapes structural genomic diversity associated with ecological adaptation in the wild tomato Solanum chilense

저자: Wei, K., Stam, R., Tellier, A., Silva Arias, G. A.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: evolutionary biology

초록:

Copy Number Variation (CNV) is a prevalent type of variation affecting large genomic regions which contributes to both genetic diversity and ecological adaptation in plants. The target genes involved in adaptation through CNV in tomato and its wild relatives remain unexplored at the population level. Therefore, we characterized the CNV landscape of Solanum chilense, a wild tomato species adapted to dry habitats, using whole-genome short-read data of 35 individuals from seven populations. We identified 212,207 CNVs, including 160,926 deletions and 51,281 duplications. We found a higher number of CNVs in diverging populations occupying stressful habitats. CNVs and single nucleotide polymorphisms analyses concordantly revealed the known species population structure, underscoring the impact of historical demographic and recent colonization events shaping genome-wide CNVs. Furthermore, we identified 3,539 candidate genes with highly divergent CNV profiles across populations. Interestingly, these genes are functionally associated with response to abiotic stress and linked to multiple pathways of flowering time regulation. Gene CNVs in S. chilense exhibit two evolutionary trends: gene loss in ancestral lineages distributed in central and southern coast populations and gene gain in the most recent diverged lineage from the southern highland region. Environmental association of the CNVs ultimately linked the dynamics of gene copy number to six climatic variables. It suggests that natural selection has likely shaped CNV patterns in stress-response genes promoting the colonization of contrasting habitats. Our findings provide insights into the role of CNV underlying adaptation during recent range expansion.

DNA methylation insulates genic regions from CTCF loops near nuclear speckles

저자: Roseman, S. A., Siegenfeld, A. P., Lee, C., Lue, N. Z., Waterbury, A. L., Liau, B. B.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: genomics

초록:

The insulator protein CTCF is essential for mediating chromatin loops and regulating gene expression. While it is established that DNA methylation hinders CTCF binding, the impacts of this methylation-sensitive CTCF binding on chromatin architecture and transcription are poorly defined. Here, we used a selective DNMT1 inhibitor (DNMT1i) to investigate the characteristics and functions of DNMT1i-specific CTCF peaks resulting from global DNA demethylation. We found that DNMT1i-specific peaks preferentially form chromatin loops on gene bodies and interact with highly-looping partner peaks located in regions of active chromatin. Notably, both DNMT1i-specific CTCF peaks and their highly-looping partners are enriched near nuclear speckles, condensate bodies implicated in transcription and splicing. Utilizing targeted protein degradation, we specifically depleted CTCF and nuclear speckles to elucidate their functional interplay. By degrading CTCF upon DNMT1 inhibition, we revealed that CTCF is important for DNMT1i-dependent interactions between chromatin and speckle proteins. Moreover, we found that CTCF promotes the activation of genes near speckles upon DNMT1 inhibition. Conversely, acute depletion of nuclear speckles revealed that they influence RNA abundance but do not maintain CTCF binding or looping. Collectively, our study suggests a model wherein DNA methylation prevents spurious CTCF occupancy and interactions with regulatory elements near nuclear speckles, yet CTCF looping is robust towards the loss of speckles.

Chromatin activity of IκBα mediates the exit from naïve pluripotency

저자: Palma, L. G., Alvarez-Villanueva, D., Maqueda, M., Barrero, M., IGLESIAS, A., Bertran, j., ALVAREZ, D., GARCIA-PRIETO, C., BALLARE, C., RODRIGUEZ-CORTEZ, V., BUENO, C., VIDAL, A., Villanueva, A., Menendez, P., Stik, G., Di Croce, L., Payer, B., Esteller, M., Espinosa, L., Bigas, A.

초록:

Maintenance of pluripotency is a multifactorial process in which NF-{kappa}B is a negative regulator. Our previous work identified a chromatin role for I{kappa}B, the master regulator of NF-{kappa}B signaling, that is critical for the proper regulation of various tissue stem cells. Here, we found that I{kappa}B accumulates specifically in the chromatin fraction of pluripotent embryonic stem cells. I{kappa}B depletion does not affect NF-kB-dependent transcription, but causes a profound epigenetic rewiring in pluripotent stem cells, including alterations in H3K27me3, a histone mark catalyzed by Polycomb repression complex 2. Chromatin changes induced by I{kappa}B depletion affect a subset of pluripotency genes and are associated with altered gene transcription. At the cellular level, I{kappa}B-deficient embryonic stem cells are arrested in a naive pluripotency state when cultured in serum/LIF conditions and fail to exit pluripotency under differentiation conditions. By constructing separation-of-function mutants, we show that the effects of I{kappa}B in regulating stem cell pluripotency are NF-{kappa}B-independent, but mainly rely on its chromatin-related function. Taken together, our results reveal a novel mechanism by which I{kappa}B participates in the regulation of the pluripotent state of embryonic stem cells and shed light on the interplay between inflammatory signals and the regulation of pluripotency.

Associations of genetic and spectral diversity in European beech

저자: Czyz, E. A., Schmid, B., Eppinga, M. B., de La Harpe, M., Moradi, A., Li, C., Coq--Etchegaray, D., Schaepman, M. E., Schuman, M. C.

플랫폼: biorxiv

발행일: 2025-06-24

카테고리: plant biology

PDF URL: https://www.biorxiv.org/content/10.1101/2023.08.16.553487v1.full.pdf

초록:

Biodiversity loss presents a growing threat to the global environment, and systematic and spatially contiguous monitoring is needed to inform mitigation strategies. Monitoring of genetic diversity within species, a key factor when assessing biodiversity loss, is laborious and could be supported by scalable phenotypic observations allowing inferences about genetic variation. We studied genetic and phenotypic variation in one of Europe's most prevalent forest-forming trees, the common beech Fagus sylvatica L., using whole-genome sequence data and spectral phenotypes from 219 individuals at 23 sites across the species' natural range. Spectral phenotypes were collected under standardized illumination and observation conditions from the same top-of-canopy leaves used for nuclear DNA extraction. We found that spectral and environmental information accounted for 77% of the variance along the first two principal coordinates representing genetic structure among sampled individuals, where spectral phenotypes contributed 12% to the prediction of genetic structure. Further, we identified 14 SNPs (single nucleotide polymorphisms), of which two were located within annotated genes, that showed significant associations with variation in leaf reflectance. Our study demonstrates how linking spectral and genomic variation in tree species may be upscaled to the remote observations to support monitoring, understanding and mitigating loss of genetic diversity within species.

Protein functional site annotation using local structure embeddings

저자: Derry, A., Tartici, A., Altman, R. B.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: bioinformatics

PDF URL: https://www.biorxiv.org/content/10.1101/2023.10.13.562298v1.full.pdf

초록:

The rapid expansion of protein sequence and structure databases has resulted in a significant number of proteins with ambiguous or unknown function. While advances in machine learning techniques hold great potential to fill this annotation gap, current methods for function prediction are unable to associate global function reliably to the specific residues responsible for that function. We address this issue by introducing PARSE (Protein Annotation by Residue-Specific Enrichment), a knowledge-based method which combines pre-trained embeddings of local structural environments with traditional statistical techniques to identify enriched functions with residue-level explainability. For the task of predicting the catalytic function of enzymes, PARSE achieves comparable or superior global performance to state-of-the-art machine learning methods (F1 score > 85%) while simultaneously annotating the specific residues involved in each function with much greater precision. Since it does not require supervised training, our method can make one-shot predictions for very rare functions and is not limited to a particular type of functional label (e.g. Enzyme Commission numbers or Gene Ontology codes). Finally, we leverage the AlphaFold Structure Database to perform functional annotation at a proteome scale. By applying PARSE to the dark proteome--predicted structures which cannot be classified into known structural families--we predict several novel bacterial metalloproteases. Each of these proteins shares a strongly conserved catalytic site despite highly divergent sequences and global folds, illustrating the value of local structure representations for new function discovery.

Early NOTCH1 mutation is positively selected but epistatically suppresses evolution of later esophageal squamous-cell carcinoma drivers

저자: Glasmacher, K. A., Mandell, J. D., Jackson, M., Fisk, N., Cannataro, V. L., Townsend, J. P.

플랫폼: biorxiv

발행일: 2025-06-25

카테고리: cancer biology
PDF URL: https://www.biorxiv.org/content/10.1101/2023.11.03.565535v1.full.pdf
초록:

Background Somatic mutations commonly accumulate in histologically normal tissues and contribute to cancer development. However, many somatic variants found at high frequencies in normal tissues are also found at high frequencies in cancers arising from the same tissue types. Consequently, the roles of these variants in cancer development remain poorly understood. To address this, we assessed the selective pressures across steps of tumorigenesis, as well as epistasis between driver mutations. Methods We employed evolutionary modeling to quantify the strength of selection on somatic variants across two key steps of esophageal development: from organogenesis to clonal histologically normal epithelium, and from there to esophageal squamous-cell carcinoma. Analyzing sequence data from 2171 samples, our first-of-its kind model revealed the stepwise contributions of somatic mutations to increased cellular division and survival and their pairwise epistatic effects on driver mutation selection. Results NOTCH1 substitutions were strongly selected along the step from organogenesis to clonal histologically normal esophageal tissue, explaining their high prevalence in samples of this tissue. However, for the first time, we show that there is little to no positive selection for NOTCH1, NOTCH2, and FAT1 mutations during progression from clonal histologically normal esophageal tissue to esophageal squamous-cell carcinoma in humans, leading to a conclusion that these substitutions promote clonal growth in normal tissue, but do not drive tumorigenesis from extant clonal tissue growths. Moreover, we provide a somatic genetic basis for this differential role: we demonstrate for the first time that mutations in NOTCH1 exhibit antagonistic epistasis with mutations of well-known tumor suppressor genes TP53 and RB1, reducing selection for these progressive mutations in tumorigenesis. Conclusions Our findings demonstrate that early positively selected mutations in NOTCH1 and other genes can shape evolutionary trajectories in ways that ultimately constrain malignant progression. Quantification of step-specific selection and identification of antagonistic epistatic interactions with key tumor suppressors reveals that somatic evolution is often context-dependent--what promotes clonal expansion in normal tissue may later impede growth or survival in tumors. These insights underscore the need for precision strategies that account for the shifting fitness landscape across premalignant and malignant stages, informing early detection, prevention, and therapeutic prioritization.

MEM-GAN: A Pseudo Membrane Generator for Single-cell Imaging in Fluorescent Microscopy

저자: Wang, Y., Ding, J., Wu, L., Wardhani, A., Danaher, P., Wen, H., Tang, W., Lu, Q., Chang, Y., Lei, Y. L., Tang, J., Xie, Y.

플랫폼: biorxiv

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카테고리: bioinformatics

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초록:

Motivation: Fluorescent microscopy imaging is vital to capturing single-cell spatial data, characterizing tissue organization and facilitating comprehensive analysis of cellular state. Advancements in fluorescent microscopy imaging technologies have enabled precise downstream cellular analysis, particularly in cell segmentation. Accurate segmentation of individual cells allows better profiling and understanding of cell properties and behaviors. The majority of existing segmentation methods predominantly concentrate on enhancing segmentation algorithms, and their effectiveness strongly relies on the input stained image quality. Factors such as high cellular density, indistinct cell boundaries, and staining artifacts can result in uneven and low-quality staining, particularly causing missing or unclear membrane staining. These artifacts adversely impact the efficacy of the subsequent cell segmentation methods.Results: To tackle this insufficient membrane staining, we propose a novel approach, MEM-GAN, to generate high-quality membranes for cells with missing or weak membranes. Inspired by advanced style transfer techniques in computer vision, MEM-GAN styles the content of the cells with missing or weak membranes into cells with integrated membrane staining. Considering the differences in membrane morphology between epithelial/tumor cells and immune cells, MEM-GAN deals with tumor and immune cells separately, not only enhancing membrane staining for cells with partially weak membrane signals but also generating membranes for cells with only nuclear channels. The proposed MEM-GAN is evaluated using the publicly available CosMx dataset. Experimental results demonstrate significant improvements in image staining quality, more accurate representation of membrane morphology characteristics, and better performance in downstream segmentation tasks. MEM-GAN is flexibly adapted and applied to other spatially resolved transcriptomics datasets, such as MERFISH and FISHseq. Our work provides a new perspective on tackling the challenges in cell segmentation from fluorescent microscopy image restoration. Availability and implementation: The implementation of MEM-GAN is open-source and available at the github repository https://github.com/OmicsML/Mem-GAN. The interactive webserver-based demo of MEM-GAN can be accessed at https://omicsml.ai/memgan.

The second messenger c-di-AMP controls natural competence via ComFB signaling protein

저자: Samir, S., Doello, S., Zimmer, E., Haffner, M., Enkerlin, A. M., Mueller, T., Dengler, L., Lambidis, S. P., Sivabalasarma, S., Albers, S.-V., Selim, K. A.

초록:

Natural competence requires a contractile pilus system. Here, we provide evidence that the pilus biogenesis and natural competence in cyanobacteria are regulated by the second messenger c-di-AMP. Furthermore, we show that the ComFB signaling protein is a novel c-di-AMP-receptor protein, widespread in bacterial phyla, and required for pilus biogenesis and DNA uptake.

Revisiting evolutionary rate-time relationships

저자: De Lisle, S., Svensson, E. I.

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카테고리: evolutionary biology

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초록:

Rates of molecular, phenotypic, and lineage diversification typically scale negatively with time interval of measurement, raising longstanding questions about time-dependency of evolutionary processes. These patterns and their potential meaning have recently re-entered evolutionary discussions. In this Perspective we revisit the general challenges in interpreting rate-time relationships. Much apparent temporal scaling of evolutionary rate is an inescapable outcome of plotting a ratio against its denominator, either directly or indirectly. Highly unlikely relationships between timescale and accumulated evolutionary change are required to produce anything other than negative rate-time relationships. Simulations reveal that constant rate evolutionary processes readily generate negative rate-time scaling relationships under many conditions, and that a range of rate-time scaling exponents can be generated by similar evolutionary processes. Reanalysis of six empirical datasets reveals unscaled magnitudes of evolution that are either unrelated to time and/or vary in their relationship with time, with over 99% of variation in rate-time relationships across six datasets explained by time variation alone. We further evaluated a recent hypothesis that evolutionary rate-time scaling reflects three modes of change, from micro- to macroevolutionary time scales using break-point regression, but we found no strong support for this hypothesis. Taken together, negative rate-time relationships are largely inevitable and difficult to interpret. In contrast, it is more straightforward to assess how evolutionary change accumulates with time.

Age differences in functional connectivity and dedifferentiation of category representations

저자: Pauley, C., Zeithamova, D., Sander, M. C.

플랫폼: biorxiv

초록:

With advancing age, the distinctiveness of neural representations of information declines. While the finding of this so-called "age-related neural dedifferentiation" in category-selective neural regions is well-described, how neural dedifferentiation manifests at the level of large-scale functional networks is less understood. Furthermore, the relationship between age-related changes in network organization and dedifferentiation is unknown. Here, we investigated age-related neural dedifferentiation of category-selective regions as well as whole-brain functional networks. We additionally examined age differences in connectivity of category-selective regions to the rest of the brain. Younger and older adults viewed blocks of face and house stimuli while performing memory encoding and retrieval in the fMRI scanner. We found an age-related decline in neural distinctiveness for faces in the fusiform gyrus (FG) and for houses in the parahippocampal gyrus (PHG). Functional connectivity analyses revealed age-related dedifferentiation of global network structure as well as age differences in the connectivity profiles to category-selective regions. Together, our findings suggest that age-related neural dedifferentiation manifests both in regional categorical representations as well as in whole-brain functional networks.

Exploring the Human-Coronavirus protein-protein interaction network from the perspective of a novel host-virus association

저자: Acharya, D., Dutta, T. K.

초록:

Host-pathogen interaction is the best example of an evolutionary arms race where pathogen and host continuously coevolve to survive and exert negative effects on each other. The adaptability of both host and pathogen is critical for this association. In this study, we explored the association of severe acute respiratory syndrome (SARS) coronaviruses (CoVs) with their human host from the genomic and evolutionary perspectives based on a comparative analysis of SARS and MERS coronaviruses. We observed that human proteins that are part of the SARS-CoV2-human association are enriched in hubs and bottlenecks. Again, these proteins take part in more protein complexes and show slower evolutionary rates compared to the human proteins associated with the two other coronaviruses, SARS-CoV and MERS-CoV. Moreover, the human proteins involved in the interaction with SARS-CoV2 are mostly longer proteins harboring long intrinsically disordered stretches and a higher level of disordered protein binding sites. Codon usage analysis revealed that the novel coronavirus is least adapted to codons used in housekeeping and lung-specific genes, compared to the other two coronaviruses. We conclude that the signatures showed by the SARS-CoV2-human protein interaction network revealed the viral association with vital human proteins and pathways, via interactions mediated by protein complexes and intrinsically disordered protein binding sites, which may have assisted the higher infectivity of SARS-CoV2 in its human host than the other two less-virulent human coronaviruses, despite having a lower optimization to the host codons.

Testosterone-Induced Metabolic Changes in Seminal Vesicle Epithelial cells Alter Plasma Components to Enhance Sperm Motility

저자: Yamanaka, T., Xiao, Z., Tsujita, N., Awad, M., Umehara, T., Shimada, M.

초록:

Male factors account for almost half of the causes of infertility. In rodents and humans, most of the components of semen are supplied by the seminal vesicles, and they support male reproductive ability, but there are many unknown details. In this study, the metabolic changes in the seminal vesicle epithelial cells were focused on, and the mechanisms by which testosterone affected the seminal plasma composition were investigated. A factor improving the linear motility of sperm was secreted from the seminal vesicles, and it was produced in an androgen-dependent manner. Bioassays, gene expression, and flux analysis studies demonstrated that testosterone promotes glucose uptake in seminal vesicle epithelial cells via GLUT4, resulting in fatty acid synthesis. ACLY was a critical factor in this metabolic change, which produced fatty acid, especially oleic acid. In conclusion, the critical role of testosterone-induced metabolic changes in the seminal vesicles is to ensure the synthesis of fatty acid. These findings suggest that testosterone-dependent lipid remodeling may contribute to sperm straight-line motility, and further functional verification is required.

Inferring Neural Communication Dynamics from Field Potentials Using Graph Diffusion Autoregression

저자: Schwock, F., Bloch, J., Khateeb, K., Zhou, J., Atlas, L., Yazdan-Shahmorad, A.

플랫폼: biorxiv

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카테고리: neuroscience

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초록:

Estimating dynamic network communication is attracting increased attention, spurred by rapid advancements in multi-site neural recording technologies and efforts to better understand cognitive processes. Yet, traditional methods, which infer communication from statistical dependencies among distributed neural recordings, face core limitations: they do not incorporate possible mechanisms of neural communication, neglect spatial information from the recording setup, and yield predominantly static estimates that cannot capture rapid changes in the brain. To address these issues, we introduce the graph diffusion autoregressive model. Designed for distributed field potential recordings, our model combines vector autoregression with a network communication process to produce a high-resolution communication signal. We successfully validated the model on simulated neural activity and recordings from subdural and intracortical micro-electrode arrays placed in macaque sensorimotor cortex demonstrating its ability to describe rapid communication dynamics induced by optogenetic stimulation, changes in resting state communication, and neural correlates of behavior during a reach task.

Effect of spatial overdispersion on confidence intervals for population density estimated by spatial capture-recapture

저자: Efford, M. G., Fletcher, D.

플랫폼: biorxiv

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카테고리: ecology

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초록:

Spatially explicit capture-recapture models are used widely to estimate the density of animal populations. The population is represented by an inhomogeneous Poisson point process, where each point is the activity centre of an individual and density corresponds to the intensity surface. Estimates of density that assume a homogeneous model (average density) are robust to unmodelled inhomogeneity, and the coverage of confidence intervals is good when the intensity surface does not change, even if it is quite uneven. However, coverage is poor when the intensity surface differs among realisations. Practical examples include populations with dynamic social aggregation, and the population in a region sampled using small detector arrays. Poor coverage results from overdispersion of the number of detected individuals; the number is Poisson when the intensity surface is static, but stochasticity leads to extra-Poisson variation. We investigated overdispersion from three point processes with a stochastic intensity surface (Thomas cluster process, random habitat mosaic and log-Gaussian Cox process). A previously proposed correction for overdispersion performed poorly. The problem is lessened by assuming population size to be fixed, but this assumption cannot be justified for common study designs. Rigorous correction for spatial overdispersion requires either prior knowledge of the generating process or replicated and representative sampling. When the generating process is known, variation in a new scalar measure of local density predicts overdispersion. Otherwise, overdispersion may be estimated empirically from the numbers detected on independent detector arrays.

Same data, different results? Machine learning approaches in bioacoustics

저자: Wierucka, K., Murphy, D., Watson, S. K., Falk, N., Fichtel, C., Leon, J., Leu, S. T., Kappeler, P. M., Briefer, E. F., Manser, M. B., Phaniraj, N., Scheumann, M., Burkart, J. M.

초록:

Automated acoustic analysis is increasingly used in behavioural ecology, and determining caller identity is a key element for many investigations. However, variability in feature extraction and classification methods limits the comparability of results across species and studies, constraining conclusions we can draw about the ecology and evolution of the groups under study. We investigated the impact of using different feature extraction (spectro-temporal measurements, Mel-frequency cepstral coefficients, and highly comparative time-series analysis) and classification methods (discriminant function analysis, support vector machines, Gaussian mixture models, neural networks, and random forests) on the consistency of classification accuracy across 16 mammalian datasets. We found that Mel-frequency cepstral coefficients and random forests yield consistently reliable results across datasets, facilitating a standardised approach across species that generates directly comparable data. These findings remained consistent across vocalisation sample sizes and number of individuals considered. We offer guidelines for processing and analysing mammalian vocalisations, fostering greater comparability, and advancing our understanding of the evolutionary significance of acoustic communication in diverse mammalian species.

The cytoplasm of living cells can sustain transient and steady intracellular pressure gradients

저자: Malboubi, M., Esteki, M. H., Vaghela, M. B., Korsak, L. I., Petrie, R. J., Moeendarbary, E., Charras, G.

초록:

Understanding the physical basis of cellular shape change in response to both internal and external mechanical stresses requires understanding cytoplasmic rheology. At subsecond time-scales and micron length-scales, cells behave as fluid-filled sponges in which shape changes necessitate intracellular fluid redistribution. However, whether these cytoplasmic poroelastic properties play an important role in cellular mechanical response over length-scales and time-scales relevant to cell physiology remains unclear. Here, we investigated whether and how a localised deformation of the cell surface gives rise to transient intracellular flows spanning several microns and lasting seconds. Next, we show that pressure gradients induced in the cytoplasm can be sustained over several minutes. We found that stable pressure gradients can arise from the combination of cytoplasmic poroelasticity and water flows across the membrane. Overall our data indicate that intracellular cytosolic flows and pressure gradients may play a much greater role than currently appreciated, acting over time- and length-scales relevant to mechanotransduction and cell migration, signifying that poroelastic properties need to be accounted for in models and states of the cell.

Image-based profiling of healthy donor immune cells with Blood Cell Painting reveals novel genotype-phenotype associations

저자: Hogel-Starck, C., Timonen, V. A., Atarsaikhan, G., Mogollon, I., Polso, M., Hassinen, A., Honkanen, J., David Sarmento, C., Koski, J., Soini, J., Urpa, L., Ruokoranta, T., Ahlnas, T., Juvila, J., Miettinen, J. J., Rodosthenous, R., FinnGen, , Kilpivaara, O., Arvas, M., Heckman, C. A., Partanen, J., Daly, M., Palotie, A., Ollila, H. M., Paavolainen, L., Pietiainen, V., Pitkanen, E.

초록:

The morphological diversity of blood immune cells of healthy individuals, critical for recognizing disease-related phenotypes, remains largely uncharacterized. To address this gap, we developed Blood Cell Painting (BCP): a high content, high throughput fluorescence imaging assay for peripheral blood mononuclear cells. We generated a BCP Atlas with images of 50 million cells from 390 healthy blood donors, identifying 18 distinct immune cell morphology clusters. A genome-wide association study of BCP-derived imaging-based cellular features revealed 93 significant associations across 30 genetic loci. These loci include genes linked to mast cell function, inflammation, immune signaling, mitochondrial maintenance and circadian immune modulation. We also observed correlations between immune cell morphological features and clinical traits, such as respiratory conditions and healthcare visits related to contraceptive management, potentially reflecting hormonal influences on immune cell phenotypes. As a proof of concept for clinical application, acute myeloid leukemia subtypes were distinguished by BCP. Our study establishes BCP as a versatile method for immune cell profiling to uncover genetic, phenotypic and clinical determinants of immune cell morphology in health and disease.

Virulence evolution: thinking outside of the host

저자: Silva, L. M., Koella, J. C.

초록:

The main theory of the evolution of virulence relies on a trade-off between virulence and transmission rate. However, it has been difficult to measure the required trade-off. A recent transmission decomposition framework explains that this might be partly due to a lack of information about the parasite's survival in the environment outside its hosts, where the parasite finds itself during transmission to its next host. In this study, we used parasite lines of the microsporidian Vavraia culicis with varying levels of virulence upon infecting their host, the mosquito Anopheles gambiae, to explore the interaction between parasite-driven virulence within its host and its survival outside of the host. The parasite lines with greater virulence and growth within their hosts had a cost in their intrinsic ability to withstand the environment, irrespective of temperature. These results underscore the importance of considering the full context of transmission and other parasite fitness traits in studying and predicting the evolution and spread of infectious diseases.

Intracellular pH dynamics respond to extracellular matrix stiffening and mediate vasculogenic mimicry through β-catenin

저자: Lund, L. M., Marchi, A. N., Alderfer, L., Hall, E. A., Hammer, J., Moremen, R., Asilebo, I., Trull, K. J., Hanjaya-Putra, D., White, K. A.

플랫폼: biorxiv

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카테고리: cell biology

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초록:

Dysregulated intracellular pH (pHi) dynamics and an altered tumor microenvironment have emerged as drivers of cancer cell phenotypes. However, the molecular integration between the physical properties of the microenvironment and dynamic intracellular signaling responses remains unclear. Here, we identify a mechanistic link between ECM stiffness and pHi dynamics in driving vasculogenic mimicry (VM), an aggressive cancer phenotype associated with poor prognosis. We performed single-cell imaging of pHi in lung and breast metastatic cell lines cultured on tunable-stiffness hydrogel systems. We used two tunable-stiffness hydrogel systems to independently model stiffness induced by increased protein secretion (Matrigel) and increased protein crosslinking (Hyaluronic acid gels). We show that increased ECM stiffness lowers single-cell pHi in both lung and breast metastatic cell lines. We also observed that stiff ECM promotes a distinct morphological phenotype called vasculogenic mimicry (VM). Importantly, we show that low pHi is a necessary mediator of VM, as raising pHi on stiff ECM reduces VM phenotypes. We also find that lowering pHi on soft ECM was sufficient to induce VM in the absence of extracellular stiffening. We characterized {beta}-catenin as a pH-dependent molecular mediator of VM, where stiffness-driven increases in {beta}-catenin abundance can be overridden by high pHi, which destabilizes {beta}-catenin to reduce VM on stiff ECM. In contrast, the transcription factor FOXC2 is activated by ECM stiffness but is insensitive 63 to pHi, and its activity alone is insufficient to maintain VM at high pHi when {beta}-catenin is lost. We uncover a novel mechanotransduction axis in which ECM stiffness regulates intracellular pH to drive {beta}-catenin-induced. We also show pHi dynamics can override mechanosensitive cell responses to the extracellular microenvironment. Thus, our work positions pHi as an integrator of mechanotransduction in cancer, suggesting a new framework for therapeutically targeting pHi in cancer and perhaps in other diseases driven by ECM remodeling.

mTORC2-mediated cell-cell interactions promote BMP4-induced WNT activation and mesoderm differentiation

저자: Tong, L., Batool, F., Chiu, Y.-H., Wu, P. D., Zhou, Y., Ma, X., Atanur, S., Cui, W.

초록:

The mechanistic target of rapamycin complex 2 (mTORC2) is essential for embryonic development but its underlying molecular mechanisms remain unclear. Here we show that disruption of mTORC2 in human embryonic stem cells (hESCs) considerably alters the Rho/Rac signaling dynamics and reduces cell adhesion. Despite this, mTORC2-deficient hESCs maintain self-renewal and expression of pluripotent markers when cultured in mouse-embryonic fibroblast conditioned medium supplemented with bFGF (MEF-CM). However, these hESCs exhibit significantly impaired mesoderm and endoderm differentiation in response to BMP4 and Activin, respectively, due to reduced WNT activation mediated by cell-cell interactions. Direct activation of the WNT pathway by a GSK3 inhibitor restores mesendoderm differentiation in mTORC2-deficient hESCs. Our study uncovers a novel mechanism by which mTORC2 regulates cell fate determination and highlights a critical link between the intercellular adhesion and the activation of canonical WNT genes.

Studying time-resolved functional connectivity via communication theory: on the complementary nature of phase synchronization and sliding window Pearson correlation.

저자: Wiafe, S.-L., Asante, N., Calhoun, V., Faghiri, A.

초록:

Time-resolved functional connectivity (trFC) assesses the time-resolved coupling between brain regions using functional magnetic resonance imaging (fMRI) data. This study aims to compare two techniques used to estimate trFC, to investigate their similarities and differences when applied to fMRI data. These techniques are the sliding window Pearson correlation (SWPC), an amplitude-based approach, and phase synchronization (PS), a phase-based technique. To accomplish our objective, we used resting-state fMRI data from the Human Connectome Project (HCP) with 827 subjects (repetition time: 0.7s) and the Function Biomedical Informatics Research Network (fBIRN) with 311 subjects (repetition time: 2s), which included 151 schizophrenia patients and 160 controls. Our simulations reveal distinct strengths in two connectivity methods: SWPC captures high-magnitude, low-frequency connectivity, while PS detects low-magnitude, high-frequency connectivity. Stronger correlations between SWPC and PS align with pronounced fMRI oscillations. For fMRI data, higher correlations between SWPC and PS occur with matched frequencies and smaller SWPC window sizes (~30s), but larger windows (~88s) sacrifice clinically relevant information. Both methods identify a schizophrenia-associated brain network state but show different patterns: SWPC highlights low anti-correlations between visual, subcortical, auditory, and sensory-motor networks, while PS shows reduced positive synchronization among these networks. Our findings underscore the complementary nature of SWPC and PS, elucidating their respective strengths and limitations without implying the superiority of one over the other.

Is subjective perceptual similarity metacognitive?

저자: Moharramipour, A., Zhou, W., Rahnev, D., Lau, H.

초록:

Perceptual similarity is a cornerstone for human learning and generalization. However, in assessing the similarity between two stimuli differing in multiple dimensions, it is not well-defined which feature(s) one should focus on. The problem has accordingly been considered ill-posed. We hypothesize that similarity judgments may be, in a sense, metacognitive: The stimuli rated as subjectively similar are those that are in fact more challenging for oneself to discern in practice, in near-threshold settings (e.g., psychophysics experiments). This self-knowledge about one's own perceptual capacities provides a quasi-objective ground truth as to whether two stimuli should be judged as similar. To test this idea, we measured perceptual discrimination capacity between face pairs, and asked subjects to rank the similarity between them. We found a positive association between perceptual discrimination capacity and subjective perceptual dissimilarity, with this association being importantly specific to each individual. The results indicate that perceptual similarity judgment reflects and predicts one's own perceptual capacities, supporting our hypothesis that perceptual similarity judgment is metacognitive.

Lacticaseibacillus rhamnosus P118 enhances host tolerance to Salmonella infection by promoting microbe-derived indole metabolites

저자: Wang, B., Peng, X., Zhou, X., Jin, X., Siddique, A., Yao, J., Zhang, H., Li, W., Li, Y., Yue, M.

초록:

Salmonella is one of the most common foodborne pathogens, resulting in inflammatory gastroenteritis and frequently accompanied by dysbiosis. Gut commensals, such as Lactobacillus species, have been proven to exhibit broad anti-bacterial activities and protect hosts against pathogenic infections. Here, Lacticaseibacillus rhamnosus strain P118, screened from 290 isolates recovered from fermented yoghurts and healthy piglet intestines using traditional and Caenorhabditis elegans-infection screening strategies, exerts great probiotic properties. Notably, P118 and its supernatant exhibited great antibacterial activities and attenuated C. elegans susceptibility to Salmonella infection. We found that P118 protected mice against Salmonella lethal infections by enhancing colonization resistance, reducing pathogen invasion, alleviating intestinal pro-inflammatory response, and improving microbial dysbiosis and fecal metabolite changes. Microbiota and fecal metabolome analyses suggested P118 administration significantly decreased the relative abundances of potentially harmful microbes (e.g., Salmonella, Anaeroplasma, Klebsiella) and increased the fecal levels of tryptophan and its derivatives (indole, indole-3-acrylic acid, 5-hydroxytryptophan, 5-methoxyindoleacetate). Deterministic processes determined the gut microbial community assembly of P118-pretreated mice. Integrated omics further demonstrated that P118 probiotic activities in enhancing host tolerance to Salmonella infection were mediated by microbe-derived tryptophan/indole metabolites (e.g., indole-3-acrylic acid, indole, tryptophan, 5-methoxyindoleacetic acid, and 5-hydroxytryptophan). Collective results demonstrate that L. rhamnosus P118 could enhance host tolerance to Salmonella infections via various pathways, including direct antibacterial actions, inhibiting Salmonella colonization and invasion, attenuating pro-inflammatory responses of intestinal macrophages, and modulating gut microbiota mediated by microbe-derived indole metabolites.

Toward improved uncertainty quantification in predictions of forest dynamics: A dynamical model of forest change

저자: Itter, M. S., Finley, A. O.

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카테고리: ecology

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초록:

Models of forest dynamics are an important tool to understand and predict forest responses to global change. Despite recent model development, predictions of forest dynamics under global change remain highly variable reflecting uncertainty in future conditions, forest demographic processes, and the data used to parameterize and validate models. Quantifying this uncertainty and accounting for it when making adaptive management decisions is critical to our ability to conserve forest ecosystems in the face of rapidly changing conditions. Dynamical spatio-temporal models (DSTMs) are a particularly powerful tool in this setting given they quantify uncertainty associated with process-based models of forest demography, the parameters upon which those models depend, and the forest data used to inform them. Further, DSTMs propagate this uncertainty to predictions of forest dynamics allowing for its formal integration within adaptive management decision frameworks. A major challenge to the application of DSTMs in applied forest ecology has been the lack of a scalable, theoretical model of forest dynamics that generates predictions at the stand level---the scale at which management decisions are made. We address this challenge by integrating a matrix projection model motivated by the McKendrick-von Foerster partial differential equation for size-structured population dynamics within a Bayesian hierarchical DSTM informed by forest inventory data. The model provides probabilistic predictions of species-specific demographic rates and changes in the size-species distribution over time. The model is applied to predict long-term dynamics (60+ years) within the Penobscot Experimental Forest in Maine, USA, accounting for uncertainty in inventory observations, process-based predictions, and model parameters for nine Acadian Forest species. We find that variability in inventory observations associated with heterogeneous stand conditions drives uncertainty in predictions of forest dynamics. We conclude with a discussion of how the initial DSTM can be refined and extended to better represent forest dynamics under global change and inform adaptive management.

Three Open Questions in Polygenic Score Portability

저자: Wang, J. Y., Lin, N., Zietz, M., Mares, J., Rathouz, P. J., Harpak, A.

초록:

A major obstacle hindering the broad adoption of polygenic scores (PGS) is their lack of ''portability'' to people that differ--in genetic ancestry or other characteristics--from the GWAS samples in which genetic effects were estimated. Here, we use the UK Biobank to measure the change in PGS prediction accuracy as a continuous function of individuals' genome-wide genetic dissimilarity to the GWAS sample (''genetic distance''). Our results highlight three gaps in our understanding of PGS portability. First, prediction accuracy is extremely noisy at the individual level and not well predicted by genetic distance. In fact, variance in prediction accuracy is explained comparably well by socioeconomic measures. Second, trends of portability vary across traits. For several immunity-related traits, prediction accuracy drops near zero quickly even at intermediate levels of genetic distance. This quick drop may reflect GWAS associations being more ancestry-specific in immunity-related traits than in other traits. Third, we show that even qualitative trends of portability can depend on the measure of prediction accuracy used. For instance, for white blood cell count, a measure of prediction accuracy at the individual level (reduction in mean squared error) increases with genetic distance. Together, our results show that portability cannot be understood through global ancestry groupings alone. There are other, understudied factors influencing portability, such as the specifics of the evolution of the trait and its genetic architecture, social context, and the construction of the polygenic score. Addressing these gaps can aid in the development and application of PGS and inform more equitable genomic research.

MLL1 directs gut-associated antibody responses to helminth and bacterial infections

저자: Zhang, Y., Chakma, C., Kirn, A., Chisanga, D., Polmear, J., Zaini, A., Farighi, R., Xie, L., Lopez-Urena, D., Mileto, S., Lyras, D., Zaph, C., Groom, J. R., Good-Jacobson, K.

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카테고리: immunology

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초록:

Soil-transmitted helminths are one of the most common infections globally, yet how to promote effective gut-associated humoral responses is not well understood. We identify the histone methyltransferase MLL1 as a key target to promote IgA-driven responses. Mll1 was increased in germinal center B cells in gut-associated lymphoid tissues, and Mll1-deficiency led to changes in the histone modification H3K4me3 on key B cell and immune-regulatory genes. Correspondingly, MLL1-deficient B cells had defective germinal centers and IgG1 in response to the helminth Trichuris muris. Yet, Mll1f/fCd23cre/+ mice expelled worms more rapidly compared to control mice. Accelerated worm clearance correlated with elevated IgA+ plasma cells, as well as both serum and fecal IgA. RNA-sequencing identified CCR9 as a key MLL1-regulated molecule. As such, Mll1f/fCd23cre/+ mice infected with T. muris had increased IgA+CCR9+ PC localized in the large intestine. Regulation of IgA by MLL1 was confirmed beyond T. muris infection. In vitro cultures confirmed Mll1-deficiency increased IgA+ plasma cells in a B cell-intrinsic manner, and IgA production was also increased in Mll1f/fCd23cre/+ mice infected with the bacterium C. rodentium. This study reveals MLL1 as a key target to promote IgA responses to gut-associated infections.

Polo-Like Kinase 1 phosphorylation tunes the functional viscoelastic properties of the centrosome scaffold

저자: Amato, M., Hwang, J. H., Rios, M. U., Familiari, N. E., Rosen, M. K., Woodruff, J. B.

초록:

Centrosomes are membranelles organelles containing centrioles encapsulated by pericentriolar material (PCM). PCM nucleates microtubules that help position and segregate chromosomes during mitosis, yet how PCM resists microtubule-mediated forces is poorly understood at the material level. Here, we show that PLK-1 phosphorylation of SPD-5 tunes the dynamics and material properties of the PCM scaffold in C. elegans embryos. Microrheology of reconstituted PCM condensates reveals that PLK-1 phosphorylation decreases SPD-5 dynamics and increases condensate viscoelasticity. Similarly, in embryos, phospho-mimetic SPD-5 is less dynamic than wild-type SPD-5, which itself is less dynamic than phospho-null SPD-5. PCM built with phospho-null SPD-5 is smaller than normal, but its assembly can be partially rescued by reducing microtubule-dependent forces. The same is true for PCM built with phospho-mimetic SPD-5, yet the underlying causes are distinct: under force, phospho-null SPD-5 fails to assemble, while phospho-mimetic SPD-5 forms hyper-stable foci that fail to cohere into a uniform, spherical mass. Both mutants have defects with chromosome segregation and viability. Thus, tuning of SPD-5 phosphorylation optimizes PCM material properties to achieve correct PCM size, integrity, and function. Our results demonstrate how regulated chemical modification of a scaffolding protein modulates the material properties and function of a membraneless organelle.

LexicMap: efficient sequence alignment against millions of prokaryotic genomes

저자: Shen, W., Lees, J., Iqbal, Z.

플랫폼: biorxiv

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카테고리: bioinformatics

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초록:

Alignment against a database of genomes is a fundamental operation in bioinformatics, popularized by BLAST. However, the rate at which microbial genomes are sequenced has continued to increase, and there are now datasets in the millions, far beyond the abilities of existing alignment tools. We introduce LexicMap, a nucleotide sequence alignment tool for efficiently querying moderate length sequences (>250 bp) such as a gene, plasmid or long read against up to millions of prokaryotic genomes. A key innovation is to construct a small set of probe k-mers (e.g. n = 20,000) which are selected to efficiently sample the entire database to be indexed, such that every 250 bp window of each database genome contains multiple seed k-mers each with a shared prefix with one of the probes. Storing these seeds in a hierarchical index enables fast and low-memory alignment. We benchmark both accuracy as the query diverges from the match in the database, and potential to scale to databases of millions of bacterial genomes, showing that LexicMap achieves comparable accuracy with state-of-the-art, but with greater speed and lower memory use. We then benchmark LexicMap on small/diverse (GTDB) and large/redundant (AllTheBacteria and GenBank+RefSeq) databases. Alignment of a single gene against 2.34 million prokaryotic genomes from GenBank and RefSeq takes 3 (rare gene) to 33 (16S rRNA gene) minutes. Full alignment against all bacterial genomes is now possible in minutes with modest resources, supporting querying at scale which will be useful for many biological applications across epidemiology, ecology and evolution. LexicMap produces output in standard formats including that of BLAST and is available under MIT license at https://github.com/shenwei356/LexicMap.

Nanoparticle-Supported, Rapid, and Electronic Detection of SARS-CoV-2 Antibodies and Antigens at Sub-Femtomolar Level

저자: Choi, Y., Mirjalili, S., Ikbal, M. A., McClure, S., Kalatehmohammadi, M., Clemens, S., Solano, J., Heggland, J., Zhang, T., Zuo, J., Wang, C.

플랫폼: biorxiv

발행일: 2025-06-24

초록:

Major challenges remain to precisely detect low-abundance proteins from diverse biofluids in a rapid and cost-effective manner. Here we present a gold nanoparticle (AuNP)-supported, rapid electronic detection (NasRED) platform with sub-femtomolar sensitivity and high specificity. Surface-functionalized AuNPs act as multivalent detectors to recognize target antigens and antibodies through high-affinity binding, subsequently forming aggregates precipitated in a microcentrifuge tube and producing a solution color change. The optical extinction of residual floating AuNPs is digitized using a customized circuitry incorporating inexpensive optoelectronic elements and feedback mechanisms for stabilized readout. Uniquely, NasRED introduces active fluidic forces through engineered centrifugation and vortex agitation, effectively promoting protein detection at low concentrations and accelerating signal generation. Using SARS-CoV-2 as a demonstration, NasRED enables detection of both antibodies and antigens from a small sample volume (6 uL), distinguishes the viral antigens from those of human coronaviruses, and delivers test results in a short time (as fast as 3,000 times more sensitive than Enzyme-Linked Immunosorbent Assay (ELISA), ~76 aM (11 fg/mL) in human pooled serum and in the femtomolar range in diluted whole blood. For nucleocapsid protein detection, NasRED LoDs are ~190 aM (10 fg/mL) in human saliva and ~2 fM (100 fg/mL) in nasal fluid. Unlike laboratory-based ELISA platforms, NasRED is a one-pot, in-solution assay that eliminates the needs for washing, labeling, expensive instrumentation or highly trained operators. With low reagent costs and a compact system footprint, this modular digital platform is well-suited for accurate, near-patient diagnosis and screening of a wide range of infectious and chronic diseases.

Towards site-specific information on PET degrading enzymesusing NMR near operational temperature

저자: Gabrielli, V., Grga, J., Gavalda, S., Perrot, L., Cantrelle, F.-X., Boll, E., Lippens, G., Charlier, C.

초록:

PETases are enzymes that can break down the poly-ethylene terephthalate (PET) polymer in its constituent building blocks. This enzymatic recycling process offers a sustainable solution for producing new, high-quality plastics from previously used materials. NMR spectroscopy can help in understanding and ultimately improving these enzymes but is always confronted with the lengthy step of acquisition and interpretation of triple resonance spectra for the spectral assignment. Here, we explore whether this step can be made more efficient by recording the spectra directly at high temperature, which simultaneously corresponds to more realistic working conditions for the enzyme. Taking the inactive variant of LCCICCG as an example, we compare spectral quality at 30C and 50C, and find that the latter condition greatly improves the Signal-to-Noise (S/N) ratio of the standard triple resonance spectra. Going up to 60C, we show that pulse sequences mainly used for the assignment of intrinsically disordered proteins (IDPs) also become feasible. As a result, we present a methodology enabling exhaustive backbone assignment based on a minimal set of triple resonance spectra acquired and analysed in less than two weeks. The assignment process hence can be completed on a time scale comparable to crystallography, bringing NMR in a favourable position to contribute to bio-structural studies on this family of highly thermostable PETases.

Ablation of hematopoietic stem cell derived adipocytes reduces tumor burden in syngeneic mouse models of high-grade serous carcinoma

저자: Woodruff, E. R., Bailey, C. A., To, F., Manda, V., Maltzahn, J. K., Sullivan, T. M., Boorgula, M. P., Recouvreux, M. S., Vianzon, R., Conrad, B., Gavin, K. M., Jordan, K. R., Klemm, D. J., Orsulic, S., Bitler, B. G., Watson, Z. L.

플랫폼: biorxiv

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카테고리: cancer biology

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초록:

Hematopoietic stem cell-derived adipocytes (HSCDAs) are an adipose subtype derived from myeloid precursors that are distinct from conventional mesenchymal adipocytes (CMAs). We hypothesized that HSCDAs promote high grade serous carcinoma (HGSC), the most common form of ovarian cancer. Despite similar rates of differentiation, primary human HSCDAs from female donors showed marked transcriptional differences from CMAs, including downregulation of cell cycle and upregulation of lipid metabolic pathways. HSCDAs secreted greater amounts of inflammatory cytokines than CMAs. We also conducted two independent tumor studies using ID8 and SO syngeneic HGSC murine models in immunocompetent mice that were either HSCDA Proficient (HSCDA-Pro; can make both adipocyte subtypes) or Deficient (HSCDA-Def; can only make CMAs). Tumor burden trended lower in HSCDA-Def mice in both models. Relative to HSCDA-Pro mice, omental ID8 tumors from HSCDA-Def mice downregulated transcription of multiple metabolic pathways that were enriched in human HSCDA cells in vitro, suggesting that ablation of HSCDAs altered the tumor metabolic environment. Compared to HSCDA-Pro mice, tumors from HSCDA-Def mice had lower densities of dendritic cells (DC) and natural killer (NK) cells, as well as fewer DCs, NKs, and B-cells in proximity to tumor cells. Our data suggest that HSCDAs alter the peritoneal immune and metabolic environment to support HGSC progression. ONE SENTENCE SUMMARYHematopoietic stem cell derived adipocytes may alter the peritoneal metabolic and immune environment to establish a metastatic niche and support ovarian cancer progression.

Comparative proteomic analysis of the composition of decellularized extracellular matrix (dECM) and dECM-based inks as compared to the native tissue

저자: Irastorza, A., Vazquez Aristizabal, P., Zumeta Olaskoaga, L., Mateo Abad, M., Guerrero, P., de la Caba, K., Izeta, A.

초록:

Regenerative medicine and tissue engineering approaches based on the use of 3D-bioprinted decellularized extracellular matrix (dECM) present the advantage of a relatively biomolecule-rich matrix, which directs cell growth and differentiation in a tissue-specific manner. However, little is known about the composition changes that occur with standard processing of dECM-based inks. To characterize this process, six porcine tissues/tissue layers (artery, breast, dermis, epidermis, muscle and nerve) were independently decellularized via chemical, mechanical and enzymatic processes and the resulting dECMs formulated into biocompatible inks, to serve as source biomaterials for 3D printing. A comparative liquid chromatography-tandem mass spectrometry (LC-MS/MS)-based proteomic analysis was carried out for native tissue, decellularized and formulated ECMs, and the resulting complexity of the matrisome analyzed. A core matrisome was found to overlap in all decellularized tissues, as well as tissue-specific components that correlated with predicted functional (gene ontology-based) definitions. The proportion of collagens (mostly the 1 chains of collagen type I and III) increased in the final processing step (inks) as compared to the native ECM and dECM stages. Overall, a median of 55 matrisomal proteins (range 45-126) was detected in the dECM-derived inks. This complexity is far superior in terms of mimicking the composition of native tissue to non-dECMbased inks. Our results support the use of dECM-based inks and biomaterials in mimicking native tissue ECM complexity, demonstrating tissue specific composition, which can improve future therapeutic approximations.

Human-specific gene expansions contribute to brain evolution

저자: Soto, D. C., Uribe-Salazar, J. M., Kaya, G., Valdarrago, R., Sekar, A., Haghani, N. K., Hino, K., La, G. N., Mariano, N. A. F., Ingamells, C., Baraban, A. E., Jamal, Z., Turner, T. N., Green, E. D., Simo, S., Quon, G., Andres, A., Dennis, M. Y.

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카테고리: genomics

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초록:

Duplicated genes expanded in the human lineage likely contributed to brain evolution, yet challenges exist in their discovery due to sequence-assembly errors. We used a complete telomere-to-telomere genome sequence to identify 213 human-specific gene families. From these, 362 paralogs were found in all modern human genomes tested and brain transcriptomes, making them top candidates contributing to human-universal brain features. Choosing a subset of paralogs, long-read DNA sequencing of hundreds of modern humans revealed previously hidden signatures of selection, including for T-cell marker CD8B. To understand roles in brain development, we generated zebrafish CRISPR "knockout" models of nine orthologs and introduced mRNA-encoding paralogs, effectively "humanizing" larvae. Our findings implicate two genes in possibly contributing to hallmark features of the human brain: GPR89B in dosage-mediated brain expansion and FRMPD2B in altered synapse signaling. Our holistic approach provides insights and a comprehensive resource for studying gene expansion drivers of human brain evolution.

A new iterative framework for simulation-based population genetic inference with improved coverage properties of confidence intervals

저자: Rousset, F., Leblois, R., Estoup, A., Marin, J.-M.

플랫폼: biorxiv

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카테고리: bioinformatics

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초록:

Simulation-based methods such as approximate Bayesian computation (ABC) are widely used to infer the evolutionary history of populations from molecular genetic data. We describe and evaluate a new iterative method of statistical inference about model parameters, which revisits the idea of inferring a likelihood surface using simulation when the likelihood function cannot be evaluated. In addition to the traditional assessment of precision in terms of bias and mean square error, we also evaluate the coverage of confidence intervals. It is based on combining the random forest machine learning method, and multivariate Gaussian mixture (MGM) models, in an effective inference workflow, here used to fit models with up to 15 variable parameters. Masked autoregressive flows, a deep learning technique, is also tested as an alternative to MGM models. The method is compared to that of approximate Bayesian computation (ABC) with random forests, with which it shares some technical features, on scenarios of inference of historical demography from population genetic data. These comparisons highlight the importance of an iterative workflow for exploring the parameter space efficiently. For equivalent simulation effort of the data-generating process, the new summary-likelihood method provides intervals whose coverage is better controlled than the marginal coverage of intervals provided by ABC with random forests, and than generally reported for ABC methods. The iterative workflow can also yield greater improvements in estimator precision when larger datasets are used.

Assessment of high-efficacy agonism in synthetic cannabinoid receptor agonists containing l-tert-leucinate

저자: Lucaj, C., Oh, S. J., Pitha, C., Davis, J., Yano, H.

플랫폼: biorxiv

발행일: 2025-06-25

초록:

Synthetic cannabinoid receptor agonists (SCRAs) represent a class of new psychoactive substances that pose great health risks attributed to their wide-ranging and severe adverse effects. Recent evidence has shown that SCRAs with key moieties can confer superagonism, yet this phenomenon is still not well understood. Here we report structure-activity relationships (SARs) of modular SCRAs contributing to superagonism by comparing eight compounds differing by their head moiety (l-valinate vs. l-tert-leucinate), core moiety (indole vs. indazole), and tail moiety (5-fluoropentyl vs. 4-fluorobenzyl) through different modes of bioluminescence resonance energy transfer (BRET) assays. We found that the l-tert-leucinate head moiety and indazole core moiety conferred superagonism across multiple Gi/o proteins and {beta}-arrestin-2. After generating the cannabinoid type 1 receptor (CB1R) mutant constructs, we found that transmembrane 2 (TM2) interactions to the head moiety of tested SCRAs at F170, F174, F177, and H178 are key to eliciting activity. Finally, we found that l-tert-leucinate SCRAs confer a high-efficacy response in ex vivo slice electrophysiology.

Neutralizing human monoclonal antibodies that target the PcrV component of the Type III Secretion System of Pseudomonas aeruginosa act through distinct mechanisms

저자: Desveaux, J.-M., Faudry, E., Contreras-Martel, C., Cretin, F., Dergan-Dylon, L. S., Amen, A., Bally, I., Tardivy-Casemajor, V., Chenavier, F., Fouquenet, D., Caspar, Y., Attree, I., Dessen, A., Poignard, P.

초록:

Pseudomonas aeruginosa is a major human opportunistic pathogen associated with a high incidence of multi-drug resistance. The antibody-based blockade of P. aeruginosa virulence factors represents a promising alternative strategy to mitigate its infectivity. In this study, we employed single B cell sorting to isolate, from cystic fibrosis patients, human monoclonal antibodies (mAbs) targeting proteins from the P. aeruginosa Type 3 Secretion System (T3SS) and characterized a panel of mAbs directed at PscF and PcrV. Among those, two mAbs, P5B3 and P3D6, that bind to the injectisome tip protein PcrV, exhibited T3SS blocking activity. We solved the crystal structure of the P3D6 Fab-PcrV complex, which revealed that the Ab binds to the C-terminal region of PcrV. Further, we compared the T3SS-blocking activity of three PcrV-targeting mAbs, including two from previous independent studies, using two distinct assays to evaluate pore formation and toxin injection. We conducted a mechanistic and structural analysis of their modes of action through modeling based on the known structure of a functional homolog, SipD from Salmonella typhimurium. The analysis suggests that anti-PcrV mAbs may act through different mechanisms, ranging from preventing PcrV oligomerization to disrupting PcrV's scaffolding function, thereby inhibiting the assembly and function of the translocon pore. Our findings provide additional evidence that T3SS-targeting Abs, some capable of inhibiting virulence, are elicited in P. aeruginosa-infected patients. The results offer deeper insights into PcrV recognition by mAbs and their associated mechanisms of action, helping to identify which Abs are more likely to be therapeutically useful based on their mode of action and potency. This paves the way for developing effective alternatives to traditional antibiotics in the fight against this resilient pathogen.

Oxytocin neurons signal state-dependent transitions from rest to thermogenesis and behavioral arousal in social and non-social settings

저자: Vandendoren, M., Landen, J. G., Rogers, J. F., Killmer, S., Alimiri, B., Pohlman, C., Tattersall, G. J., Bedford, N. L., Nelson, A. C.

초록:

Core body temperature (Tb) is defended within narrow limits through thermoregulatory behaviors like huddling, nesting, and physical activity as well as autonomic responses like brown fat thermogenesis and peripheral vasodilation. While Tb displays regulated fluctuations across different behavioral states and rest/arousal cycles, the neural control of these transitions is poorly understood. Here, we investigate the relationship between oxytocin neurons of the paraventricular hypothalamus ((PVNOT)) and behavioral and autonomic thermoeffector pathways across physiological states in mice. First, we show that (PVNOT) neurons are activated during social thermoregulation. We then demonstrate that, in both social and nonsocial contexts, in vivo (PVNOT) calcium dynamics align with transitions from rest to thermogenesis and behavioral arousal. Using a computer vision model to track thermoeffector pathways, we demonstrate that precisely timed stimulation of (PVNOT) during low-Tb resting states increases thermogenesis and behavioral arousal. We therefore suggest a model in which (PVNOT) neurons facilitate state-dependent transitions in thermo-behavioral states.

A Chaperonin Complex Regulates Organelle Proteostasis in Malaria Parasites

저자: Tissawak, A., Rosin, Y., Katz Galay, S., Qasem, A., Shahar, M., Trabelsi, N., Schueler-Furman, O., Johnson, S. M., Florentin, A.

초록:

The apicoplast of Plasmodium parasites serves as a metabolic hub that synthesize essential biomolecules. Like other endosymbiotic organelles, 90% of the apicoplast proteome is encoded by the cell nucleus and transported to the organelle. Evidence suggests that the apicoplast has minimal control over the synthesis of its proteome and therefore it is unclear how organelle proteostasis is regulated. Here, we identified and investigated a large and conserved chaperonin (CPN) complex with a previously unknown function. Using genetic tools, we demonstrated that ablation of the apicoplast CPN60 subunit leads to parasite death due to organellar damage, immediately within its first replication cycle, deviating from the delayed death phenotype commonly observed for apicoplast translation inhibitors. Unlike its close orthologues in other prokaryotic and eukaryotic cells, CPN60 is not upregulated during heat shock (HS) and does not affect HS response in the parasite. Instead, we found that it is directly involved in proteostasis through interaction with the Clp (caseinolytic protease) proteolytic complex. We showed that CPN60 physically binds both the active and inactive forms of the Clp complex, and manipulates its stability. A computational structural model of a possible interaction between these two large complexes suggests a stable interface. Finally, we screened a panel of inhibitors for the bacterial CPN60 orthologue GroEL, to test the potential of chaperonin inhibition as antimalarial. These inhibitors demonstrated an anti-Plasmodium activity that was not restricted to apicoplast function, with additional targets outsides of this organelle. Taken together, this work reveals how balanced activities of proteolysis and refolding safeguard the apicoplast proteome, and is essential for organelle biogenesis.

The Synergy between Topography and Lipid Domains in the Plasma Membrane of Mast Cells Controls the Localization of Signaling Proteins and Facilitates their Coordinated Activation

저자: Ghosh, S., Wagenknecht-Wiesner, A., Desai, S., Vyphuis, J., Ramos, M. S., Grazul, J. L., Baird, B.

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카테고리: immunology

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초록:

Similar to T cells and B cells, mast cell surfaces are dominated by microvilli, and like these other immune cells we showed with microvillar cartography (MC) that key signaling proteins for RBL mast cells localize to these topographical features. Although stabilization of ordered lipid nanodomains around antigen-crosslinked IgE-Fc{varepsilon}RI is known to facilitate necessary coupling with Lyn tyrosine kinase to initiate transmembrane signaling in these mast cells, the relationship of ordered-lipid nanodomains to membrane topography had not been determined. With nanoscale resolution provided by MC, SEM and co-localization probability (CP) analysis, we found that Fc{varepsilon}RI and Lyn kinase are positioned exclusively on the microvilli of resting mast cells in separate nano-assemblies, and upon antigen-activation they merge into overlapping populations together with the LAT scaffold protein, accompanied by elongation and merger of microvilli into ridge-like ruffles. With selective lipid probes, we further found that ordered-lipid nanodomains preferentially occupy microvillar membranes, contrasting with localization of disordered lipids to flatter regions. With this proximity of signaling proteins and ordered lipid nanodomains in microvilli, the mast cells are poised to respond sensitively and efficiently to antigen but only in the presence of this stimulus. Use of a short chain ceramide to disrupt ordered-lipid regions of the plasma membrane and evaluation with MC, CP, and flow cytometry provided strong evidence that the microvillar selective localization of signaling proteins and lipid environments is facilitated by the interplay between ordered-lipid nanodomains and actin attachment proteins, ERM (ezrin, radixin, moesin) and cofilin.

Global Neuron Shape Reasoning with Point Affinity Transformers

저자: Troidl, J., Knittel, J., Li, W., Zhan, F., Pfister, H., Turaga, S. C.

플랫폼: biorxiv

발행일: 2025-06-25

초록:

Connectomics is a subfield of neuroscience that aims to map the brains intricate wiring diagram. Accurate neuron segmentation from microscopy volumes is essential for automating connectome reconstruction. However, current state-of-the-art algorithms use image-based convolutional neural networks that are limited to local neuron shape context. Thus, we introduce a new framework that reasons over global neuron shape with a novel point affinity transformer. Our framework embeds a (multi-)neuron point cloud into a fixed-length feature set from which we can decode any point pair affinities, enabling clustering neuron point clouds for automatic proofreading. We also show that the learned feature set can easily be mapped to a contrastive embedding space that enables neuron type classification using a simple KNN classifier. Our approach excels in two demanding connectomics tasks: proofreading segmentation errors and classifying neuron types. Evaluated on three benchmark datasets derived from state-of-the-art connectomes, our method outperforms point transformers, graph neural networks, and unsupervised clustering baselines.

Codon decoding by split-tRNA: revisiting the tRNA selection mechanism

저자: Mureev, S., Wu, Y., Cui, Z., Alexandrov, K.

초록:

The translation machinery is required to process all codon triplets without exception while maintaining high speed and accuracy, despite orders-of-magnitude differences in cognate pairing stability. For stability-based selection to be efficient, the range of pairing stabilities must be narrowed by raising the lower bound and lowering the upper bound. The constrained structure and intramolecular cooperativity of tRNA complicate understanding of how it modulates codon-anticodon stability and whether it affects selection kinetics beyond codon recognition. To address these questions, we engineered functional split-tRNAs bearing a dangling anticodon in place of the anticodon loop. Our results demonstrate that split-tRNA supports in vitro translation nearly as efficiently as intact synthetic tRNA, challenging the notion that tRNA strain is essential for triggering GTP hydrolysis in response to codon recognition. Using split-tRNA architecture, we found that codon- anticodon stability is likely modulated by the dipole moments of adjacent nucleobases. Our kinetic modeling aligns with a conformational selection mechanism, where the decoding site fluctuates between open and closed states, and the correct codon-anticodon minihelix acts as an allosteric effector that permits its spontaneous closure and stabilizes the closed state. Overall, our data challenge the notion that tRNA is an active player in the selection process.

Stranded short nascent strand sequencing reveals the topology of DNA replication origins in Trypanosoma brucei.

저자: STANOJCIC, S., BARCKMANN, B., MONSIEURS, P., CROBU, L., GEORGE, S., Sterkers, Y.

초록:

The universal features that define genomic regions acting as replication origins remain unclear. In this study, we mapped a set of origins in Trypanosoma brucei using stranded short nascent strand sequencing method. Our results showed that DNA replication predominantly initiates in intergenic regions between poly(dA)- and poly(dT)-enriched sequences. G4 structures were detected in the vicinity of some origins and were embedded in poly(dA)-enriched sequences in a strand-specific manner: G4s on the plus strand were located upstream, while those on the minus strand were located downstream of the centre. The origins centres were found to be areas of low nucleosome occupancy, surrounded by regions of high nucleosome occupancy. Furthermore, our results demonstrate that 90% of replication origins overlap with a minor proportion of the previously reported R-loops. These findings shed new light on the sequence and structural features that define the topology of replication origins in T. brucei. To further characterize replication dynamics at the single-molecule level, we employed DNA combing analysis.

Vocal species are more central in Eastern Himalayan Mixed-Species bird flocks

저자: Gupta, S., Bharadwaj, A., Bhat, A., Thapa, A., Biswakarma, A., Tamang, B., Munda, B., Biswakarma, B., Pradhan, D., Tamang, D., Rai, M., Rai, R., Rai, S., Srinivasan, U.

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카테고리: ecology

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초록:

Mixed-species flocks (MSF) represent an important form of social organisation in bird communities worldwide. Despite its likely importance in flock formation and cohesion, the role of vocal communication in the formation and maintenance of MSF in birds is hitherto understudied. In this study, we examine if a species centrality within a mixed-species flock is influenced by its vocal behaviour during the dawn chorus, i.e., the time of MSF formation. Using acoustic sampling and field observation, we studied bird species found in MSF in the Eastern Himalayas. Our results show differential vocal activity patterns among MSF-forming bird species and suggest a positive correlation between calling rates and closeness centrality in understory MSFs. We also found a more synchronised vocalisation pattern in the understory MSFs, with a consistent peak in vocal activity in the early morning hours, whereas no consistent vocal pattern was found for canopy flocks. Overall, our results suggest a potential mechanism that drives MSF formation wherein the vocal activity of central species precedes and likely attracts participation from other attendant species.

Cancer Screening Progress and Non-invasive Screening Opportunities Since Onset of the COVID-19 Pandemic

저자: John M. Carethers

플랫폼: pmc

발행일: 2025-06-02

카테고리: Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187480/pdf/

초록:

Cancer screening lowers morbidity and mortality from cancer, and is cost-effective. The COVID-19 pandemic upended cancer screening utilization in 2020 with data showing a deficit in screened patients in 2020 and 2021 as compared to 2019, with return to 2019 baseline screening levels by December 2022. The cumulative shortfall in screenings, lasting nearly three years into the pandemic, are predicted by models to generate an incremental population cancer burden in the out years of the models. Recovery of screening rates may vary based on the racial or ethnic population, and time will tell if there is an uneven burden of future cancers that worsen cancer incidence and mortality in those populations, some even after years of gains of reducing disparities for cancer screening. For some cancer screenings, particularly cervical and colorectal cancer, use of at-home non-invasive tests may increase screening participation overall across multiple populations, and may help mitigate some of the screening shortfalls from 2020 to 2022 by elevating numbers of the population screened. For colorectal cancer, new additional comparably sensitive or ease-of-use non-invasive screening tests are being added for utilization.

Male and female pattern hair loss

저자: Laxmi Iyengar, Jane Li

플랫폼: pmc

발행일: 2025-06-10

카테고리: Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187474/pdf/

초록:

Androgenetic alopecia, commonly referred to as male or female pattern hair loss, is a prevalent condition encountered in clinical practice. It is important to identify potential underlying causes and differentiate it from other forms of hair loss, which may require referral to a dermatologist for management.

Periprosthetic Joint Infection: A Multifaceted Burden Undermining Arthroplasty Success

저자: Mohammad H.S. Aftab, Troye Joseph, Richard Almeida, Nkhodiseni Sikhauli, Jurek R.T. Pietrzak

플랫폼: pmc

초록:

Despite advancements in surgical techniques and implant designs, Periprosthetic joint infection (PJI) continues to be one of the commonest and most devastating causes of failure in total joint arthroplasty. PJIs are associated with significant morbidity and mortality, placing a multifactorial burden on patients, caregivers, surgeons, hospitals, health systems, and economies. The incidence of PJI ranges from 0.5% to 2.3% based on current literature. Mortality rates in PJI subsequent to a primary total hip arthroplasty (THA) range from 4% to 8% after one year. The common treatment for PJI is a two-stage revision THA, which itself is associated with significant morbidity and mortality. The economic burden of PJI is substantial, with treatment costs 3 to 5.6 times higher than primary THA. Patients with PJI experience inferior hip function, lower health-related quality of life scores, and higher odds of developing new onset depression. PJI's negatively impacts on a patient's capacity to work and conduct everyday activities. Orthopaedic surgeons also face significant psychological stress due to the challenges in managing PJI, including feelings of incompetence, insecurity, and frustration. Continued research and innovation are essential to optimize THA outcomes and reduce the need for revision surgeries. Improved prevention strategies, multidisciplinary cooperation, and comprehensive care and support for both patients and surgeons are crucial. It is paramount that every orthopaedic surgeon remains cognisant of this complication to institute better prevention strategies, promote better multi-disciplinary cooperation and enhance patient pre-operative care.

The role of mobile DNA elements in the dynamics of plant genome plasticity

초록:

Plants host a range of DNA elements capable of self-replication. These molecules, usually associated with the activity of transposable elements or viruses, are found integrated in the genome or in the form of extrachromosomal DNA. The activity of these elements can impact genome plasticity by a variety of mechanisms, including the generation of structural variants, the shuffling of regulatory or coding DNA sequences across the genome, and DNA endoduplication. This plasticity can dynamically alter gene expression and genome stability, ultimately affecting plant development or the response to environmental changes. While the activation of these elements is often considered deleterious to the genome, their role in creating variation is important in adaptation and evolution. Moreover, the mechanisms by which mobile DNA proliferates have been exploited for plant engineering, or contributed to understand how desirable traits can be generated in crops. In this review, we discuss the origins and the roles of mobile DNA element activity on genome plasticity and plant biology, as well as their potential function and current application in plant biotechnology.

Syringomyelia Associated with Magendie's Foramen Obstruction Due to Probably Congenital Gliomesenchymal Anomaly

저자: Shunsuke KUMAGAI, Ryosuke OGURA, Kohei SHIBUYA, Jotaro ON, Shoji SAITO, Masakazu SANO, Akiyoshi KAKITA, Makoto OISHI

초록:

We report a case of syringomyelia in a 55-year-old man with a unique obstruction of Magendie's foramen. Spinal magnetic resonance imaging revealed a large syrinx extending from C1 to C3, with intermittent syringomyelia extending down to Th11. While the obstruction was not clearly evident on T2-weighted imaging, three-dimensional constructive interference in steady-state imaging demonstrated a thickened membranous tissue blocking the cerebrospinal fluid outlet, leading to syrinx formation.

Genetic ancestry superpopulations show distinct prevalence and outcomes across pediatric central nervous system tumors from the Pediatric Brain Tumor Atlas and Pediatric Neuro-Oncology Consortium

저자: Ryan J Corbett, Cricket C Gullickson, Zhuangzhuang Geng, Miguel A Brown, Bo Zhang, Chuwei Zhong, Nicholas Van Kuren, Antonia Chroni, Christopher Blackden, Ammar S Naqvi, Alexa Plisiewicz, Sean McHugh, Emmett Drake, Kaitlin Lehmann, Tom B Davidson, Michael Prados, Phillip B Storm, Adam C Resnick, Angela J Waanders, Sebastian M Waszak, Sabine Mueller, Jo Lynne Rokita, Cassie Kline

플랫폼: pmc

발행일: 2025-01-23

카테고리: Pediatric Neuro-Oncology, AcademicSubjects/MED00300, AcademicSubjects/MED00310

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187462/pdf/

초록:

High prevalence of unrecognized chronic kidney disease in the Lolland-Falster Health Study: a population-based study in a rural provincial area of Denmark

저자: Ebba Mannheimer, Morten Buus Jørgensen, Kristine Hommel, Anne-Lise Kamper, Randi Jepsen, Knud Rasmussen, Lau Caspar Thygesen, Bo Feldt-Rasmussen, Mads Hornum

플랫폼: pmc

발행일: 2025-01-22

카테고리: Non Communicable Diseases, AcademicSubjects/MED00860, AcademicSubjects/SOC01210, AcademicSubjects/SOC02610

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187459/pdf/

초록:

Chronic kidney disease (CKD) affects 10–15% globally and is a marked independent risk factor for cardiovascular disease. Prevalence estimations are essential for public health planning and implementation of CKD treatment strategies. This study aimed to estimate the prevalence and stages of CKD in the population-based Lolland-Falster Health Study, set in a rural provincial area with the lowest socioeconomic status in Denmark. Additionally, the study characterized participants with CKD, evaluated the overall disease recognition, including the awareness of CKD and compared it with other common conditions. Cross-sectional data were obtained from clinical examinations, biochemical analyses, and questionnaires. CKD was defined as albuminuria (urine albumin–creatinine ratio ≥30 mg/g), estimated glomerular filtration rate (eGFR) 50% for hypertension and >80% for diabetes, and the overall CKD recognition (self-reported or registered diagnosis) was 7.1%. Thus, in this population-based study, CKD was highly prevalent but poorly recognized, indicating great potential for preventing CKD progression and related complications.

Increasing incidence and prevalence of Hodgkin's lymphoma in Finland: a population-based registry study

저자: Tessa Antikainen, Noora Hannuksela, Anna Anttalainen, Anu Partanen, Aino Rönkä, Hanne Kuitunen, Liisa Ukkola-Vuoti, Iiro Toppila, Tatu Miettinen, Outi Kuittinen

플랫폼: pmc

발행일: 2025-01-20

카테고리: Non Communicable Diseases, AcademicSubjects/MED00860, AcademicSubjects/SOC01210, AcademicSubjects/SOC02610

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187456/pdf/

초록:

Hodgkin's lymphoma (HL) is a lymphoid malignancy with an emphasized incidence in developed countries. This study aimed to assess the changes in the epidemiology of HL in Finland at the population level by utilizing data from six nationwide healthcare registries. A total of 2912 patients with HL, diagnosed and treated between 2000 and 2019 were matched by controls and divided into younger (<50 years) and older cohorts (≥50 years) for analysis. A slightly increasing trend in incidence per age group was observed. For the younger patients, the mean annual incidence was 3.19 for males and 2.89 for females. For the older patients, it was 3.07 and 1.59, respectively. Finland has higher incidence rates than other Scandinavian countries possibly due to unique human leucocyte antigen allele distribution. There was a notable increase in prevalence. For females, this was particularly emphasized between the ages of 30–50 years, while among males, it was more evenly distributed across all ages. As a result of improved disease management, the proportion of HL survivors is increasing.

Nanoparticle encapsulation enables systemic IGF-Trap delivery to inhibit intracerebral glioma growth

저자: Yinhsuan Michely Chen, Julien Chambon, Alexandre Moquin, Masakazu Hashimoto, Stephanie Perrino, Matthew Leibovitch, Yasmine Benslimane, Orçun Haçariz, Qin Yang, Ichiro Nakano, Brian Meehan, Janusz Rak, Stéphane Gagné, Pnina Brodt

플랫폼: pmc

발행일: 2025-01-29

카테고리: Basic and Translational Investigations, AcademicSubjects/MED00300, AcademicSubjects/MED00310

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187454/pdf/

초록:

Development and validation of a molecular classifier of meningiomas

저자: Alexander P Landry, Justin Z Wang, Jeff Liu, Vikas Patil, Chloe Gui, Zeel Patel, Andrew Ajisebutu, Yosef Ellenbogen, Qingxia Wei, Olivia Singh, Julio Sosa, Sheila Mansouri, Christopher Wilson, Aaron A Cohen-Gadol, Mohamed A Zaazoue, Ghazaleh Tabatabai, Marcos Tatagiba, Felix Behling, Jill S Barnholtz-Sloan, Andrew E Sloan, Silky Chotai, Lola B Chambless, Alexander D Rebchuk, Serge Makarenko, Stephen Yip, Alireza Mansouri, Derek S Tsang, Kenneth Aldape, Andrew Gao, Farshad Nassiri, Gelareh Zadeh

플랫폼: pmc

발행일: 2025-01-08

카테고리: Clinical Investigations, AcademicSubjects/MED00300, AcademicSubjects/MED00310

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187452/pdf/

초록:

Using Rasch analysis to assess the latent construct of the Capacity to Work Index in a Swedish working population sample

저자: Agneta Blomberg, Gunnel Hensing, Monica Bertilsson, Emina Hadžibajramovi

초록:

Measurements of capacity to work (CTW) in relation to common mental disorders (CMD) are needed to improve research on determinants for maintained work participation (WP). The aim of this study was to assess the construct validity of the Capacity to Work Index (C2WI) in a heterogenous sample of the Swedish working population. Cross-sectional web survey data among Swedish employees (

A Review of the Role of Paraprobiotics in the Formulation of High-Protein Ice Cream as an Advanced Functional Food

저자: Seyed Ali Issazadeh, Samaneh Hatami

초록:

Paraprobiotics are nonvital bacteria that have health benefits. Recently, they have been incorporated into dairy products as supplements to probiotics. The advantages of using paraprobiotics mainly include superior resistance to processing conditions, extended shelf-life, and safer consumption by people with weaker immune systems. In high-protein ice cream, paraprobiotics enhance freezing stability and eliminate the risks of microbial overgrowth and rare adverse effects. They also promote gut health, regulate immune responses, and have anti-inflammatory properties, which are important for children. Moreover, paraprobiotics enhance the functional value of high-protein ice cream by promoting gut health and immune support, making it an ideal functional supplement for athletes and bodybuilders. This review discusses recent developments in high-protein ice cream fortified with paraprobiotics, focusing on product stability, texture, and consumer acceptance while addressing challenges in the sensory quality of the final product.

The Role of Servant Leadership in Fostering Psychological Safety Among Nurses in Jordanian Hospitals

저자: Luma Asfour, Ali Moh'd Saleh, Yousef Abu-Wardeh

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187444/pdf/

초록:

Exploring the Nutritional and Antimicrobial Properties of Wild Fruit,

저자: Hmingremhlua Sailo, Laldinliana Khiangte, Laldinfeli Ralte, Sagolshem Priyokumar Singh, Y. Tunginba Singh

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187442/pdf/

초록:

A wild edible fruit

The Effectiveness of Low-Level LED Light Therapy for Sleep Problems, Psychological Symptoms, and Heart Rate Variability in Shift-Work Nurses: A Randomized Controlled Trial

저자: Yung-Hsuan Liao, Chen-Jei Tai, Jin-Lain Ming, Li-Hwa Lin, Li-Yin Chien

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187440/pdf/

초록:

The Relationship Between Social Media Use Purposes, Healthy Lifestyle Behaviors, and Metabolic Parameters in Adolescents With Type 1 Diabetes

저자: Hakan Avan, Nimet Barna

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187438/pdf/

초록:

The Epidemiology and Determinants of Opportunistic Intestinal Parasites Among HIV-Positive Patients Attending Care and Treatment Centers in Northcentral Ethiopia

저자: Yitbarek Mulie, Sissay Menkir, Abayeneh Girma

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187436/pdf/

초록:

The Effect of Nutrient Deprivation on Markers of Oxidative Stress, Inflammation, and Transcriptome in Normal and Type-2 Diabetic Human Skeletal Muscle Myoblasts

저자: Lael Ceriani, Daniel E. Newmire, Xavier F. Gonzales, Jean Sparks, Jose Guardiola, Felix O. Omoruyi

플랫폼: pmc

발행일: 2025-06-10

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187435/pdf/

초록:

Natural Progression of Rheumatic Aortic Valve Disease Following Mitral Valve Intervention: A 16-Year Single-Center Experience

저자: Seok Hyun Kim, Ji Hoon Lim, Sang Hyun Lee, Mi Hee Lim, Chee-Hoon Lee, Min Ho Ju, Hyung Gon Je, Yong Hyun Park

플랫폼: pmc

발행일: 2025-06-17

카테고리: Research Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187430/pdf/

초록:

Six-legged-bound: a newly described insect gait

저자: Avi Amir, O. Yuval, Amir Ayali

플랫폼: pmc

발행일: 2025-06-01

카테고리: Organismal and Evolutionary Biology, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187426/pdf/

초록:

Locomotor behaviour is a hallmark of animal biology and ecology. Mole crickets constitute a unique group of subterranean insects that present extreme morphological and behavioural adaptations. They therefore present a valuable model for locomotion-related research. Despite their remarkable leg-morphology adaptations, mole crickets mostly demonstrate the common insect double-tripod gait for locomotion. Here we report, however, that in response to an aversive stimulus from the front, the mole cricket will consistently adopt a unique backwards gait that we have termed 'backward-bound'. Our temporal and spatial analysis shows that this previously unreported six-legged gait comprises a cyclic alternation between the middle and hind-leg pairs with rarely observed (in insects) left–right in-phase synchronization, while the front legs display noisy and less-consistent phase dynamics. This exceptional gait is transient and is replaced by regular backwards walking after several cycles. It is employed to distance the animal quickly from danger. A gait that can be characterized as 'forward-bound' is also displayed by the mole cricket, albeit for a much shorter duration (up to two cycles).

A feasibility study on non-invasive and non-contact jugular venous pulse measurement using 60 GHz FMCW radar

저자: Shatabdi Das, Hadi Afsharan, Girish Dwivedi, Coen Arrow, Omid Kavehei

플랫폼: pmc

발행일: 2025-06-01

카테고리: Engineering, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187424/pdf/

초록:

The jugular venous pulse (JVP) reflects right atrial pressure and provides diagnostic insight into cardiovascular and pulmonary health. However, reliable assessment remains difficult due to neck adiposity, anatomical variability and suboptimal positioning. Although central venous catheterization is the gold standard, its invasive nature restricts routine or long-term use. This study introduces a non-invasive method for JVP estimation using a 60 GHz frequency-modulated continuous wave (FMCW) radar. The system captures venous pulsations at the skin surface and applies eigenbeamforming to enhance signal-to-noise ratio and pulse clarity. Radar parameters were optimized for signal fidelity and validated through morphological comparison with simultaneously recorded photoplethysmography (PPG) signals. Additionally, we compared radar-derived JVP signals with previously recorded catheterization data from a patient with early-stage heart failure to assess clinical relevance. Signal localization was successfully achieved within a direction-of-arrival (DoA) range of

Foraging and thermally induced phenotypic plasticity interact in the most northerly distributed freshwater fish

저자: Colin E. Adams, Colin Bean, Kevin Parsons

플랫폼: pmc

발행일: 2025-06-01

카테고리: Evolutionary Biology, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187422/pdf/

초록:

Elevated temperatures from climate change are predicted to be more extreme at higher latitudes. This could require phenotypic plasticity to generate variation that allows organisms to persist in these regions. However, climate change will provide a multifactorial change in environmental cues, making an understanding of how they interact essential for predicting persistence and future evolutionary potential. Here, the impacts of temperature on ecologically relevant phenotypic plasticity (foraging environment) in Arctic charr (

Big team science reveals promises and limitations of machine learning efforts to model physiological markers of affective experience

저자: Nicholas A. Coles, Bartosz Perz, Maciej Behnke, Johannes C. Eichstaedt, Soo Hyung Kim, Tu N. Vu, Chirag Raman, Julian Tejada, Van-Thong Huynh, Guangyi Zhang, Tanming Cui, Sharanyak Podder, Rushi Chavda, Shubham Pandey, Arpit Upadhyay, Jorge I. Padilla-Buritica, Carlos J. Barrera Causil, Linying Ji, Felix Dollack, Kiyoshi Kiyokawa, Huakun Liu, Monica Perusquia-Hernandez, Hideaki Uchiyama, Xin Wei, Houwei Cao, Ziqing Yang, Alessia Iancarelli, Kieran McVeigh, Yiyu Wang, Isabel M. Berwian, Jamie C. Chiu, Dan-Mircea Mirea, Erik C. Nook, Henna I. Vartiainen, Claire Whiting, Young Won Cho, Sy-Miin Chow, Zachary F. Fisher, Yanling Li, Xiaoyue Xiong, Yuqi Shen, Enzo Tagliazucchi, Leandro A. Bugnon, Raydonal Ospina, Nicolas M. Bruno, Tomas A. D'Amelio, Federico Zamberlan, Luis R. Mercado Diaz, Javier O. Pinzon-Arenas, Hugo F. Posada-Quintero, Maneesh Bilalpur, Saurabh Hinduja, Fernando Marmolejo-Ramos, Shaun Canavan, Liza Jivnani, Stanisław Saganowski

플랫폼: pmc

발행일: 2025-06-01

카테고리: Psychology and Cognitive Neuroscience, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187420/pdf/

초록:

Researchers are increasingly using machine learning to study physiological markers of emotion. We evaluated the promises and limitations of this approach via a big team science competition. Twelve teams competed to predict self-reported affective experiences using a multi-modal set of peripheral nervous system measures. Models were trained and tested in multiple ways: with data divided by participants, targeted emotion, inductions, and time. In 100% of tests, teams outperformed baseline models that made random predictions. In 46% of tests, teams also outperformed baseline models that relied on the simple average of ratings from training datasets. More notably, results uncovered a methodological challenge: multiplicative constraints on generalizability. Inferences about the accuracy and theoretical implications of machine learning efforts depended not only on their architecture, but also how they were trained, tested, and evaluated. For example, some teams performed better when tested on observations from the same (vs. different) subjects seen during training. Such results could be interpreted as evidence against claims of universality. However, such conclusions would be premature because other teams exhibited the opposite pattern. Taken together, results illustrate how big team science can be leveraged to understand the promises and limitations of machine learning methods in affective science and beyond.

Why collective behaviours self-organize to criticality: a primer on information-theoretic and thermodynamic utility measures

저자: Qianyang Chen, Mikhail Prokopenko

플랫폼: pmc

발행일: 2025-06-01

카테고리: Physics and Biophysics, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187418/pdf/

초록:

Collective behaviours are frequently observed to self-organize to criticality. Existing proposals to explain these phenomena are fragmented across disciplines and only partially answer the question. This primer compares the underlying,

Life history and nesting traits reflect urban tolerance in coastal birds

저자: Sarah L. Jennings, Emma M. Garrison, Clinton D. Francis

초록:

Rapid urbanization has prompted considerable interest in understanding which species thrive or fail in these novel environments. Because half of the human population resides in coastal areas, studies that explicitly examine urban tolerances among coastal species are needed. Here, we sought to explain variation in coastal bird tolerances to urban habitats with species life history, diet, nest, social, sensory and sexual selection traits using phylogenetically informed models and three urban-tolerance indexes. We found that nest site height was the strongest predictor, with species nesting in elevated locations exhibiting greater urban tolerance, probably due to reduced anthropogenic disturbances and risk of predation. Life-history traits, including larger clutch sizes and lower brood value, reflecting more lifetime breeding attempts, also predicted urban tolerance, suggesting that fast reproductive strategies buffer against urban-associated risks. Contrary to our prediction, species with altricial young displayed higher urban tolerance, potentially due to shorter incubation and fledging times. Collectively, our results suggest that many of the predictors related to urban tolerance in songbirds also predict tolerances among a broader swath of avian diversity. Such knowledge should help researchers forecast the composition of coastal, urban bird communities in the future and will inform efforts to conserve functionally diverse coastal ecosystems.

Morphometric characterization of Holocene mandibles expands the ecological baseline for understanding gibbon extinction dynamics

저자: Samuel T. Turvey, Alejandra Ortiz, Matthew Granger, Selina Brace, Rasmus Amund Henriksen, Qingping Yang, Tu n Anh Nguy n, Laura T. Buck, Heidi Ma, James P. Hansford, Thomas Booth, Helen J. Chatterjee, Pengfei Fan, Xi Chen

초록:

Human activities have driven biodiversity loss for millennia, and conservation of 'refugee species' that survive as remnant populations requires insights from historical baselines. However, reconstructing the past distribution and ecology of such species is challenging due to data limitations with specimen-based archives. Here, we assess the taxonomic identity of two gibbon mandibles from the Wumingshan Neolithic site in Guangxi, China. Although ancient DNA extraction was unsuccessful, a suite of linear and geometric morphometric analyses using dental and mandibular characters reveals that these mandibles fall within or close to variation shown by extant Chinese

Physiological consequences of nitrogen enrichment for corals in the Caribbean

저자: Jonathan Jung, Ryanne Ardisana, Mark J. A. Vermeij, Erin L. Murphy

플랫폼: pmc

발행일: 2025-06-01

카테고리: Ecology, Conservation, and Global Change Biology, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187412/pdf/

초록:

Nutrient pollution has been a major contributor to coral decline throughout the Caribbean. Coral physiological responses to excess nutrients vary with nutrient forms (e.g. nitrate or ammonia), concentrations and nitrogen-to-phosphate (N : P) ratios. However, how these responses differ across nutrient contexts remains understudied. We show that

Avoidance of reproductive conflict and the evolution of menopause in chimpanzees

저자: Lauren C. White, Dieter Lukas, Kevin E. Langergraber, Linda Vigilant

플랫폼: pmc

발행일: 2025-06-01

카테고리: Organismal and Evolutionary Biology, Research Articles

초록:

The reproductive conflict hypothesis suggests menopause is rare in nature because it is only evolutionarily favoured in specific dispersal and mating systems. In social groups with local mating, shared resource competition and female-biased dispersal, an increase in a breeding female's relatedness to her fellow community members with age is expected to favour late-life reproductive cessation as a response to intergenerational reproductive competition. Here, we use observational and genomic data from the Ngogo chimpanzee community to characterize kinship dynamics and investigate the potential role of reproductive conflict in explaining a recent report of menopause in this community. We first find that, as predicted by simple models, the combination of female dispersal and local breeding leads to age-specific increases in relatedness between female and male community members. Next, we use the observed kinship dynamics in inclusive fitness formulae to test whether reproductive cessation might have been selected for in chimpanzee females. We find that kinship dynamics measured within subgroups of the community, where competition is presumably most intense, favour the evolution of menopause beginning around age 40. This is consistent with patterns of age-related fertility declines observed in Ngogo, suggesting reproductive conflict may have contributed to the evolution of chimpanzee post-reproductive lifespans.

Efficient approximations of transcriptional bursting effects on the dynamics of a gene regulatory network

저자: Jochen Kursawe, Antoine Moneyron, Tobias Galla

초록:

Mathematical models of gene regulatory networks are widely used to study cell fate changes and transcriptional regulation. When designing such models, it is important to accurately account for sources of stochasticity. However, doing so can be computationally expensive and analytically untractable, posing limits on the extent of our explorations and on parameter inference. Here, we explore this challenge using the example of a simple auto-negative feedback motif, in which we incorporate stochastic variation due to transcriptional bursting and noise from finite copy numbers. We find that transcriptional bursting may change the qualitative dynamics of the system by inducing oscillations when they would not otherwise be present, or by magnifying existing oscillations. We describe multiple levels of approximation for the model in the form of differential equations, piecewise-deterministic processes and stochastic differential equations. Importantly, we derive how the classical chemical Langevin equation can be extended to include a noise term representing transcriptional bursting. This approximation drastically decreases computation times and allows us to analytically calculate properties of the dynamics, such as their power spectrum. We explore when these approximations break down and provide recommendations for their use. Our analysis illustrates the importance of accounting for transcriptional bursting when simulating gene regulatory network dynamics and provides recommendations to do so with computationally efficient methods.

The microarchitectural variability in the echinoid skeleton: a 3D geometrical and stiffness characterization of

저자: Valentina Perricone, Pasquale Cesarano, Mainak Deb, Derek Lublin, Mirko Mutalipassi, Lucia Pappalardo, David Kisailus, Francesco Marmo

초록:

The sea urchin skeleton is a lightweight yet load-bearing hierarchical structure composed of calcitic plates with a species-specific three-dimensional (3D) trabecular meshwork known as stereom. Interestingly, the stereom architecture is extremely complex and variable in different basic types, each one characterized by a unique geometry and structural behaviours. The present study provides an in-depth analysis of the microarchitectural variability in the sea urchin

The challenge of measuring mosquito flight performance: going beyond sterile insect technique and into transgenic and gene drive-based approaches

저자: Paola Najera, Christian E. Ogaugwu, Tyler F. Chan, Raja Babu Singh Kushwah, Zach Adelman

플랫폼: pmc

발행일: 2025-06-01

카테고리: Review Articles, Review Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187402/pdf/

초록:

Invasive insects inflict global costs of more than 70 billion USD annually by destroying crops and spreading disease-causing pathogens. Sterile insect technique (SIT), an insect population control method, involves the irradiation or chemical sterilization of insects to produce sterile males that are mass-released. SIT has proven effective in reducing populations of the Mediterranean fruit fly, Mexican fruit fly and screwworm fly. In the past decade, efforts to improve SIT with transgenic approaches have increased, including the development of potentially highly invasive gene drive transgenes. Determining flight capability is vital to the success of any insect control programme, and various flight assays can be used to analyse insect dispersal, flight behaviour and the mechanics behind flight. However, traditional flight assays such as mark–release–recapture become more challenging with transgenic or gene drive arthropods due to ecological concerns, while assays such as wind tunnels or flight mills/arenas may not capture the full range of flight abilities. This review seeks to cover current flight assays and their limitations as well as the requirements for flight assays to establish comparative flight ability for genetically modified insects to better prioritize strains prior to any potential field-based releases.

Reinventing the spermatheca: unveiling a novel sperm storage organ in Epilachninae ladybirds

저자: Paulo Henrique Rezende, Glenda Dias, Mauricio da Silva Paulo, Dayvson Ayala-Costa, Ana Clara Pereira Teixeira, José Lino-Neto

플랫폼: pmc

발행일: 2025-06-01

카테고리: Research Articles, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187400/pdf/

초록:

This study investigates the reproductive apparatus of

Revisiting the link between true-self and morality: Replication and extension Registered Report of Newman, Bloom, and Knobe (2014) Studies 1 and 2

저자: Shuk Ching Lee, Gilad Feldman

플랫폼: pmc

발행일: 2025-06-01

카테고리: Psychology and Cognitive Neuroscience, Registered Report

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187398/pdf/

초록:

Newman

Good, bad, different or something else? A scoping review of the convictions, conventions and developments around quality in qualitative research

저자: Xavier Salet, John Gelissen, Guy Moors, Jelte Wicherts

플랫폼: pmc

발행일: 2025-06-01

카테고리: Science, Society and Policy, Research Articles

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187396/pdf/

초록:

We present a scoping review of methodological papers in the social science literature covered in Scopus from 2017 to 2022. In this review, we document the shared norms, ideals and practices regarding the quality of qualitative research methodology. More specifically, we examined the regularly proposed idea that qualitative methodology is so diverse that it is unfeasible to establish shared quality standards. Coding of 111 articles yielded 17 categories that relate to key topics discussed in publications on research quality in qualitative research, such as the quality of the research process, integrity, reflexivity, ethics and transparency. These codes reflect both established ideals and new developments. We conclude that articles in our sample have many shared values in common, but that these values at this point do not yet translate into shared research practices or a common core for quality evaluation.

Empirical evidence that diversionary feeding increases productivity in ground-nesting birds

저자: Jack Anthony Bamber, Chris Sutherland, Kenny Kortland, Xavier Lambin

초록:

The recovery of predator populations may negatively impact other species of conservation concern, leading to conservation conflicts. Evidence-based solutions are needed to resolve such conflicts. Robust, large-scale field experiments provide the most rigorous evidence to justify new forms of intervention. Still, they are hard to implement and often call for indirect and non-invasive monitoring. In this study, we used camera traps to experimentally evaluate diversionary feeding to reduce conservation conflict and non-invasively monitor capercaillie hen productivity over 3 years under a randomized control (unfed) and treatment (fed) design. Diversionary feeding significantly increased the probability that a detected hen would have a brood. Brood size decreased over time, but the change did not differ between fed and unfed treatments. Importantly, the increased chance of having a brood with diversionary feeding substantially increases overall productivity at the end of the sampling season. This was just 0.82 (0.35–1.29) chicks per hen without diversionary feeding, and more than doubled to 1.90 (1.24–2.55) with diversionary feeding. This study provides compelling empirical evidence that diversionary feeding positively affects productivity, offering an effective non-lethal solution to the increasingly common conservation conflict where both predator and prey are afforded protection.

A remarkable beak morphology in a bird skull from the Eocene of Messel (Germany) signifies unusual feeding specializations

저자: Gerald Mayr, Krister Smith
플랫폼: pmc
발행일: 2025-06-01
카테고리: Earth and Environmental Science, Research Articles
PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187392/pdf/

초록:

We report the skull of a new avian species from the latest early or earliest middle Eocene fossil site Messel in Germany.

Scaly-tail organ enhances static stability during Pel's scaly-tailed flying squirrels' arboreal locomotion

저자: Andrew K. Schulz, Mrudul Chellapurath, Pranav C. Khandelwal, SeyedReza Rezaei, Stefan Merker, Ardian Jusufi

플랫폼: pmc
발행일: 2025-06-01
카테고리: Life Sciences–Engineering interface, Research Articles
PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187390/pdf/

초록:

Scaly-tailed squirrels (Anomaluridae) are one of the least studied mammalian families. Their name is due to a peculiar and unique scaly-tail organ extruding from the caudal vertebra that has been predicted to help reduce skidding. This study investigates the function of the scaly-tail organ found in

Remote Monitoring of Amyotrophic Lateral Sclerosis Using Digital Health Technologies

저자: Jordi W.J. van Unnik, Leslie Ing, Miguel Oliveira Santos, Christopher J. McDermott, Mamede de Carvalho, Ruben P.A. van Eijk

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187388/pdf/

초록:

Current care and research pathways for amyotrophic lateral sclerosis (ALS) primarily rely on regularly scheduled visits to specialized centers. These visits provide intermittent clinical information to health care professionals and require patients to travel to the clinic. Digital health technologies enable continuous data collection directly from the patient's home, bringing new opportunities for personalized, timely care and a refined assessment of disease severity in clinical trials. In this review, we summarize the state of the art in digital health technologies for remote monitoring of patients with ALS, ranging from televisits through videoconferencing to sensor-based wearable devices. We explore how these technologies can benefit clinical care and advance treatment development. Despite significant progress, real-world adoption of these technologies remains limited. An overview is provided of the key barriers hindering their widespread implementation and the opportunities to advance the field. Significantly, there is an urgent need for harmonization across stakeholders through consensus guidelines and consortia. These efforts are essential to accelerate progress and harness the full potential of digital health technologies to better meet the needs of patients.

CGRP-Targeted Migraine Therapies in Patients With Vascular Risk Factors or Stroke

저자: Michael Thomas Eller, Katarína Schwarzová, Lena Gufler, Anel Karisik, Katharina Kaltseis, Florian Frank, Gregor Broessner

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187386/pdf/

초록:

Calcitonin gene-related peptide (CGRP)–targeted therapies, including monoclonal antibodies (mAbs) and gepants, represent a major advancement in migraine prevention, offering greater efficacy and improved tolerability compared with traditional treatments. These agents selectively inhibit the CGRP pathway, a key mediator in migraine pathophysiology, and are increasingly used even as first-line options in selected patients. While clinical trials and real-world data suggest a favorable cardiovascular (CV) safety profile, particularly in patients without major risk factors, evidence remains limited for those with established vascular disease or recent vascular events. Concerns persist regarding long-term effects and the safety of CGRP blockade in high-risk populations. This narrative review focuses on the CV and cerebrovascular safety of CGRP-targeted migraine treatments—an area of growing clinical relevance. We compare these newer agents with traditional migraine preventives and highlight the paucity of data in patients with previous stroke, subarachnoid hemorrhage, myocardial infarction, or significant CV comorbidities. In addition, we discuss the emerging topic of dual CGRP pathway blockade (mAbs plus gepants), which has not previously been reviewed in the context of vascular risk. Based on currently available scientific evidence, we offer structured clinical considerations to guide the use of CGRP-targeted therapies in patients with vascular risk or cerebrovascular disease. Our aim is to support informed decision making in a population that has often been excluded from clinical trials but is becoming increasingly important in clinical practice.

Estimated Glomerular Filtration Rate Decline is Causally Associated with Acute Pulmonary Embolism: A Nested Case–Control and Mendelian Randomization Study

저자: Yanshuang Lyu, Haobo Li, Xin Liu, Xiaomeng Zhang, Yinong Chen, Guohui Fan, Hong Zhang, Zhifa Han, Zhuangjie Guo, Haoyi Weng, Huiyuan Hu, Xincheng Li, Zhu Zhang, Yu Zhang, Feiya Xu, Chen Wang, Dingyi Wang, Peiran Yang, Zhenguo Zhai

플랫폼: pmc

발행일: 2025-03-28

카테고리: Stroke, Systemic or Venous Thromboembolism

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187385/pdf/

초록:

Environmental health risk analysis of microplastics due to consumption of squid and mussels at coastal area

저자: Muhammad Addin Rizaldi, R Azizah, Lilis Sulistyorini, Khaidar Ali

초록:

Microplastic in marine environment represent a global issue, originating from both land-based and ocean-based activities. The microplastic contamination in marine biota can lead to the ingestion of microplastics by human through the consumption. This study aims to investigates the abundance of microplastic in marine biota and to assess human health risk among community in coastal area of Muncar District – Banyuwangi Regency. This study was conducted in the coastal area of Muncar district in 2023. The sample of mussels and squid was collected 100 gr, respectively, used to measure the abundance of microplastics. Additionally, 130 respondents were recruited to assess the health risk among community. Partial Least Square Structural Equation Modeling (PLS-SEM) with was used to examine the influence of microplastic concentration, the intake rate, and human health risk with Smart PLS 3. The total abundance of microplastic in mussels and squid was found 23 particles or 0.23 particle per gram. The microplastics identified were primarily fiber, with colors including transparent, purple, red and black. The microplastics consisted of polyethylene (PE), polypropylene (PP), Polyethylene terephthalate (PET), polyester terephthalic acid and Polyvinyl acetate ethylene. The indirect effect between microplastics concentration, intake rate and hazard quotient are significant (p-value < 0.05). Therefore, microplastic concentrations in marine biota can influence carcinogenic intake, which in turn becomes an indirect factor affecting hazard quotient associated with microplastic consumption. Prolonged or excessive consumption of marine biota with high levels of microplastics can lead to increased carcinogenic intake, thereby elevating the potential health risks to humans.

Spatial and temporal distribution of

저자: Dahae Park, Sungjin Jung, Hekap Kim

초록:

This study aimed to analyze the spatial and temporal distribution of

Tobacco Smoking in Early Adulthood and Labor Market Performance: The Cardiovascular Risk in Young Finns Study

저자: Jutta Viinikainen, Petri Böckerman, Christian Hakulinen, Jaana T Kari, Terho Lehtimäki, Katja Pahkala, Jaakko Pehkonen, Jorma Viikari, Olli T Raitakari

플랫폼: pmc

발행일: 2025-01-14

카테고리: Brief Reports, AcademicSubjects/MED00010, AcademicSubjects/SOC02541

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187365/pdf/

초록:

Confocal imaging of the cell cycle and cytokinin signaling during gynoecium development in Arabidopsis

저자: Juan Ramos Pulido, Stefan de Folter

플랫폼: pmc

발행일: 2025-06-24

카테고리: Original Article, Original Article

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187362/pdf/

초록:

In angiosperms, the gynoecium is the female reproductive structure, whose function is to contain the ovules and promote their fertilization. In Arabidopsis, the gynoecium develops from a small primordium with meristematic properties to a complex structure with internal and external specialized tissues. Due to its anatomical and developmental complexity, it is challenging to study

Severe Anemia With Intraosseous-Intramuscular Hemorrhage in a Patient With Kit-C-Negative Systemic Mastocytosis

저자: Natalia Fongrat, Anjali Davichan, Christopher Vaughn, Sagah Ahmed, Andrew Mangano

초록:

Systemic mastocytosis (SM) is a rare hematologic disorder characterized by clonal proliferation of mast cells in various tissues, often presenting with skin lesions, gastrointestinal symptoms, or anaphylaxis. However, atypical presentations lacking these classical features may delay diagnosis and complicate management. We report the case of a 42-year-old woman who presented with progressive anemia, recurrent spontaneous intramuscular and intraosseous hemorrhages, and severe, unexplained pain. Notably, she lacked cutaneous signs or known allergic triggers. Extensive laboratory and imaging workups ruled out common hematologic and autoimmune causes. Bone marrow biopsy ultimately revealed multifocal clusters of atypical mast cells consistent with SM, despite the absence of the KIT D816V mutation. This case underscores the protean manifestations of SM and the need to maintain a high index of suspicion in patients with unexplained cytopenia and bleeding. It also highlights the role of bone marrow evaluation in the diagnostic pathway, even when classic clinical features are absent. Timely recognition of atypical SM can guide appropriate management and improve patient outcomes.

Research on mammary gland hyperplasia compound patents' herbal combination rules based on complex system entropy clustering: A review

저자: Xujie Yang, Xiaohua Pei, Hong Zhang, Wanyue Zhang

초록:

The aim of this study was to investigate the combination rules of herbal compound patents for the treatment of mammary gland hyperplasia (MGH). Herbal compound patents (oral drugs) for the treatment of MGH from the past 31 years were collected, and a database was created. Complex system entropy clustering was used to analyze the prescription rule of herbal compound patents for the treatment of MGH. In total, 765 MGH herbal compound authorized patents, including 136 Chinese herbs, were identified. High-frequency herbs, herbal pairs, and core associations were obtained by complex system entropy clustering. MGH herbal compound patents are known to activate blood circulation, remove stasis, soothe the liver, regulate

Revisiting Treatment Strategies: Addressing Epithelial-to-Mesenchymal Transition-Induced Resistance in Hepatocellular Carcinoma

저자: Roghayeh Naserkhaki, Bahare Shokouhian, Yaser Tahamtani, Arezoo Khosravi, Siavash Iravani, Ali Zarrabi, Massoud Vosough

초록:

One of the major therapeutic challenges for hepatocellular carcinoma (HCC), the most form of primary liver cancer, is how to overcome drug resistance. Due to the high failure rate of systemic therapy in treating advanced HCC patients and the increasing recurrence rate, HCC is a highly lethal malignancy. Primary and acquired drug resistance are major contributing factors to the patients with advanced HCC who do not respond effectively to long-term systemic therapy. Therefore, it is essential to look into the molecular processes that lead to drug resistance. Different studies have indicated that epithelial-to-mesenchymal transition (EMT) plays a critical part in the emergence of drug resistance. Several signaling pathways regulate this phenomenon. This review primarily concentrates on drug resistance triggered by EMT, especially in the context of HCC. The key signaling pathways that cause drug resistance in HCC, including transforming growth factor-β and epidermal growth factor receptor signaling, liver cancer stem cells, and noncoding RNAs, are highlighted in the present study, along with the most recent molecular targets discovered to prevent drug resistance. These targets could help develop novel and combinatory HCC therapy approaches. Therefore, this review aims to provide both the latest findings on molecular basis and potential solutions for HCC drug resistance.

Ulcerative colitis-associated diffuse enteritis without prior colectomy: A case report

저자: Qiuming He, Wanhui Wei, Jie Li, Zhitao Chen, Heng Zhang

플랫폼: pmc

발행일: 2025-06-20

카테고리: 4500, Research Article, Clinical Case Report

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187356/pdf/

초록:

Laparoscopic treatment of giant ovarian cystic tumors in children: Case report

저자: Huashan Zhao, Shumin Zhao, Shisong Zhang, Rui Guo, Hongxiu Xu, Sai Huang, Gang Shen, Yunpeng Zhai

플랫폼: pmc

발행일: 2025-06-20

카테고리: 6200, Research Article, Clinical Case Report

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187354/pdf/

초록:

Correlations between serum cytokines and gut microbiota in patients with Graves' disease: A case–control study

저자: Hong Chao, Jie Shan, Li Qun Che, Yu Cheng, Hong Jie Li, Xue Yan Qian

플랫폼: pmc	

발행일: 2025-06-20

카테고리: 4300, Research Article, Observational Study

PDF URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC12187351/pdf/

초록:

Graves' disease (GD) is the most prevalent autoimmune thyroid disorder. Gut microbiome as a critical modulator of autoimmune pathogenesis through its bidirectional communication with host immunity. To elucidate the pathophysiological interplay between cellular immunity and gut microbiome composition in GD through systematic analysis of associations between peripheral blood cytokine profiles and microbial community dynamics. This case–control study enrolled 30 untreated GD patients consecutively admitted to the Department of Endocrinology at the Third Affiliated Hospital of Qiqihar Medical University between January and July 2023, along with 30 age/sex-matched healthy controls (HC). Comprehensive evaluations included: electrochemiluminescence immunoassay quantification of thyroid function parameters, high-resolution Illumina HiSeq 2000 platform-based 16S rRNA gene sequencing for fecal microbial community profiling, multiplex cytokine array analysis of peripheral blood immune markers. Spearman correlation analyses were conducted to delineate relationships among cytokines, thyroid function index and gut microbial taxa alterations in GD pathogenesis. Alpha diversity analysis revealed that the abundance and diversity of certain microbiota in the GD group decreased. Beta diversity analysis revealed that the intestinal microbiome composition of GD patients was significantly different from that of HC. The proportion of

Signal Use and Emergent Cooperation

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.18920.pdf

초록:

In this work, we investigate how autonomous agents, organized into tribes, learn to use communication signals to coordinate their activities and enhance their collective efficiency. Using the NEC-DAC (Neurally Encoded Culture - Distributed Autonomous Communicators) system, where each agent is equipped with its own neural network for decision-making, we demonstrate how these agents develop a shared behavioral system -- akin to a culture -- through learning and signalling. Our research focuses on the self-organization of culture within these tribes of agents and how varying communication strategies impact their fitness and cooperation. By analyzing different social structures, such as authority hierarchies, we show that the culture of cooperation significantly influences the tribe's performance. Furthermore, we explore how signals not only facilitate the emergence of culture but also enable its transmission across generations of agents. Additionally, we examine the benefits of coordinating behavior and signaling within individual agents' neural networks.

Do LLMs Know When to Flip a Coin? Strategic Randomization through Reasoning and Experience

초록:

Strategic randomization is a key principle in game theory, yet it remains underexplored in large language models (LLMs). Prior work often conflates the cognitive decision to randomize with the mechanical generation of randomness, leading to incomplete evaluations. To address this, we propose a novel zero-sum game inspired by the Tian Ji Horse Race, where the Nash equilibrium corresponds to a maximal entropy strategy. The game's complexity masks this property from untrained humans and underdeveloped LLMs. We evaluate five LLMs across prompt styles -- framed, neutral, and hinted -- using competitive multi-tournament gameplay with system-provided random choices, isolating the decision to randomize. Results show that weaker models remain deterministic regardless of prompts, while stronger models exhibit increased randomization under explicit hints. When facing weaker models, strong LLMs adopt deterministic strategies to exploit biases, but converge toward equilibrium play when facing peers. Through win/loss outcomes and Bayes factor analysis, we demonstrate meaningful variation in LLMs' strategic reasoning capabilities, highlighting opportunities for improvement in abstract reasoning and adaptive learning. We make our implementation publicly available at https://github.com/ocelopus/llm-when-to-throw-coin to ensure full reproducibility.

A Comment On "The Illusion of Thinking": Reframing the Reasoning Cliff as an Agentic Gap

초록:

The recent work by Shojaee et al. (2025), titled The Illusion of Thinking: Understanding the Strengths and Limitations of Reasoning Models via the Lens of Problem Complexity, presents a compelling empirical finding, a reasoning cliff, where the performance of Large Reasoning Models (LRMs) collapses beyond a specific complexity threshold, which the authors posit as an intrinsic scaling limitation of Chain-of-Thought (CoT) reasoning. This commentary, while acknowledging the study's methodological rigor, contends that this conclusion is confounded by experimental artifacts. We argue that the observed failure is not evidence of a fundamental cognitive boundary, but rather a predictable outcome of system-level constraints in the static, text-only evaluation paradigm, including tool use restrictions, context window recall issues, the absence of crucial cognitive baselines, inadequate statistical reporting, and output generation limits. We reframe this performance collapse through the lens of an agentic gap, asserting that the models are not failing at reasoning, but at execution within a profoundly restrictive interface. We empirically substantiate this critique by demonstrating a striking reversal. A model, initially declaring a puzzle impossible when confined to text-only generation, now employs agentic tools to not only solve it but also master variations of complexity far beyond the reasoning cliff it previously failed to surmount. Additionally, our empirical analysis of tool-enabled models like o4-mini and GPT-4o reveals a hierarchy of agentic reasoning, from simple procedural execution to complex meta-cognitive self-correction, which has significant implications for how we define and measure machine intelligence. The illusion of thinking attributed to LRMs is less a reasoning deficit and more a consequence of an otherwise capable mind lacking the tools for action.

From Rows to Yields: How Foundation Models for Tabular Data Simplify Crop Yield Prediction

초록:

We present an application of a foundation model for small- to medium-sized tabular data (TabPFN), to sub-national yield forecasting task in South Africa. TabPFN has recently demonstrated superior performance compared to traditional machine learning (ML) models in various regression and classification tasks. We used the dekadal (10-days) time series of Earth Observation (EO; FAPAR and soil moisture) and gridded weather data (air temperature, precipitation and radiation) to forecast the yield of summer crops at the sub-national level. The crop yield data was available for 23 years and for up to 8 provinces. Covariate variables for TabPFN (i.e., EO and weather) were extracted by region and aggregated at a monthly scale. We benchmarked the results of the TabPFN against six ML models and three baseline models. Leave-one-year-out cross-validation experiment setting was used in order to ensure the assessment of the models capacity to forecast an unseen year. Results showed that TabPFN and ML models exhibit comparable accuracy, outperforming the baselines. Nonetheless, TabPFN demonstrated superior practical utility due to its significantly faster tuning time and reduced requirement for feature engineering. This renders TabPFN a more viable option for real-world operation yield forecasting applications, where efficiency and ease of implementation are paramount.

Baba is LLM: Reasoning in a Game with Dynamic Rules

저자: Unknown

초록:

Large language models (LLMs) are known to perform well on language tasks, but struggle with reasoning tasks. This paper explores the ability of LLMs to play the 2D puzzle game Baba is You, in which players manipulate rules by rearranging text blocks that define object properties. Given that this rule-manipulation relies on language abilities and reasoning, it is a compelling challenge for LLMs. Six LLMs are evaluated using different prompt types, including (1) simple, (2) rule-extended and (3) action-extended prompts. In addition, two models (Mistral, OLMo) are finetuned using textual and structural data from the game. Results show that while larger models (particularly GPT-4o) perform better in reasoning and puzzle solving, smaller unadapted models struggle to recognize game mechanics or apply rule changes. Finetuning improves the ability to analyze the game levels, but does not significantly improve solution formulation. We conclude that even for state-of-the-art and finetuned LLMs, reasoning about dynamic rule changes is difficult (specifically, understanding the use-mention distinction). The results provide insights into the applicability of LLMs to complex problem-solving tasks and highlight the suitability of games with dynamically changing rules for testing reasoning and reflection by LLMs.

Spiritual-LLM : Gita Inspired Mental Health Therapy In the Era of LLMs

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19185.pdf

초록:

Traditional mental health support systems often generate responses based solely on the user's current emotion and situations, resulting in superficial interventions that fail to address deeper emotional needs. This study introduces a novel framework by integrating spiritual wisdom from the Bhagavad Gita with advanced large language model GPT-4o to enhance emotional well-being. We present the GITes (Gita Integrated Therapy for Emotional Support) dataset, which enhances the existing ExTES mental health dataset by including 10,729 spiritually guided responses generated by GPT-4o and evaluated by domain experts. We benchmark GITes against 12 state-of-the-art LLMs, including both mental health specific and general purpose models. To evaluate spiritual relevance in generated responses beyond what conventional n-gram based metrics capture, we propose a novel Spiritual Insight metric and automate assessment via an LLM as jury framework using chain-of-thought prompting. Integrating spiritual guidance into AI driven support enhances both NLP and spiritual metrics for the best performing LLM Phi3-Mini 3.2B Instruct, achieving improvements of 122.71% in ROUGE, 126.53% in METEOR, 8.15% in BERT score, 15.92% in Spiritual Insight, 18.61% in Sufficiency and 13.22% in Relevance compared to its zero-shot counterpart. While these results reflect substantial improvements across automated empathy and spirituality metrics, further validation in real world patient populations remains a necessary step. Our findings indicate a strong potential for AI systems enriched with spiritual guidance to enhance user satisfaction and perceived support outcomes. The code and dataset will be publicly available to advance further research in this emerging area.

Bayesian Evolutionary Swarm Architecture: A Formal Epistemic System Grounded in Truth-Based Competition

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

초록:

We introduce a mathematically rigorous framework for an artificial intelligence system composed of probabilistic agents evolving through structured competition and belief revision. The architecture, grounded in Bayesian inference, measure theory, and population dynamics, defines agent fitness as a function of alignment with a fixed external oracle representing ground truth. Agents compete in a discrete-time environment, adjusting posterior beliefs through observed outcomes, with higher-rated agents reproducing and lower-rated agents undergoing extinction. Ratings are updated via pairwise truth-aligned utility comparisons, and belief updates preserve measurable consistency and stochastic convergence. We introduce hash-based cryptographic identity commitments to ensure traceability, alongside causal inference operators using do-calculus. Formal theorems on convergence, robustness, and evolutionary stability are provided. The system establishes truth as an evolutionary attractor, demonstrating that verifiable knowledge arises from adversarial epistemic pressure within a computable, self-regulating swarm.

GBGC: Efficient and Adaptive Graph Coarsening via Granular-ball Computing

초록:

The objective of graph coarsening is to generate smaller, more manageable graphs while preserving key information of the original graph. Previous work were mainly based on the perspective of spectrum-preserving, using some predefined coarsening rules to make the eigenvalues of the Laplacian matrix of the original graph and the coarsened graph match as much as possible. However, they largely overlooked the fact that the original graph is composed of subregions at different levels of granularity, where highly connected and similar nodes should be more inclined to be aggregated together as nodes in the coarsened graph. By combining the multi-granularity characteristics of the graph structure, we can generate coarsened graph at the optimal granularity. To this end, inspired by the application of granular-ball computing in multi-granularity, we propose a new multi-granularity, efficient, and adaptive coarsening method via granular-ball (GBGC), which significantly improves the coarsening results and efficiency. Specifically, GBGC introduces an adaptive granular-ball graph refinement mechanism, which adaptively splits the original graph from coarse to fine into granular-balls of different sizes and optimal granularity, and constructs the coarsened graph using these granular-balls as supernodes. In addition, compared with other state-of-the-art graph coarsening methods, the processing speed of this method can be increased by tens to hundreds of times and has lower time complexity. The accuracy of GBGC is almost always higher than that of the original graph due to the good robustness and generalization of the granular-ball computing, so it has the potential to become a standard graph data preprocessing method.

RecLLM-R1: A Two-Stage Training Paradigm with Reinforcement Learning and Chain-of-Thought v1

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19235.pdf

초록:

Traditional recommendation systems often grapple with "filter bubbles", underutilization of external knowledge, and a disconnect between model optimization and business policy iteration. To address these limitations, this paper introduces RecLLM-R1, a novel recommendation framework leveraging Large Language Models (LLMs) and drawing inspiration from the DeepSeek R1 methodology. The framework initiates by transforming user profiles, historical interactions, and multi-faceted item attributes into LLM-interpretable natural language prompts through a carefully engineered data construction process. Subsequently, a two-stage training paradigm is employed: the initial stage involves Supervised Fine-Tuning (SFT) to imbue the LLM with fundamental recommendation capabilities. The subsequent stage utilizes Group Relative Policy Optimization (GRPO), a reinforcement learning technique, augmented with a Chain-of-Thought (CoT) mechanism. This stage guides the model through multi-step reasoning and holistic decision-making via a flexibly defined reward function, aiming to concurrently optimize recommendation accuracy, diversity, and other bespoke business objectives. Empirical evaluations on a real-world user behavior dataset from a large-scale social media platform demonstrate that RecLLM-R1 significantly surpasses existing baseline methods across a spectrum of evaluation metrics, including accuracy, diversity, and novelty. It effectively mitigates the filter bubble effect and presents a promising avenue for the integrated optimization of recommendation models and policies under intricate business goals.

Emotion Detection on User Front-Facing App Interfaces for Enhanced Schedule Optimization: A Machine Learning Approach

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19280.pdf

초록:

Human-Computer Interaction (HCI) has evolved significantly to incorporate emotion recognition capabilities, creating unprecedented opportunities for adaptive and personalized user experiences. This paper explores the integration of emotion detection into calendar applications, enabling user interfaces to dynamically respond to users' emotional states and stress levels, thereby enhancing both productivity and engagement. We present and evaluate two complementary approaches to emotion detection: a biometric-based method utilizing heart rate (HR) data extracted from electrocardiogram (ECG) signals processed through Long Short-Term Memory (LSTM) and Gated Recurrent Unit (GRU) neural networks to predict the emotional dimensions of Valence, Arousal, and Dominance; and a behavioral method analyzing computer activity through multiple machine learning models to classify emotions based on fine-grained user interactions such as mouse movements, clicks, and keystroke patterns. Our comparative analysis, from real-world datasets, reveals that while both approaches demonstrate effectiveness, the computer activity-based method delivers superior consistency and accuracy, particularly for mouse-related interactions, which achieved approximately 90₩% accuracy. Furthermore, GRU networks outperformed LSTM models in the biometric approach, with Valence prediction reaching 84.38₩% accuracy.

Skywork-SWE: Unveiling Data Scaling Laws for Software Engineering in LLMs

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19290.pdf

초록:

Software engineering (SWE) has recently emerged as a crucial testbed for next-generation LLM agents, demanding inherent capabilities in two critical dimensions: sustained iterative problem-solving (e.g., >50 interaction rounds) and long-context dependency resolution (e.g., >32k tokens). However, the data curation process in SWE remains notoriously time-consuming, as it heavily relies on manual annotation for code file filtering and the setup of dedicated runtime environments to execute and validate unit tests. Consequently, most existing datasets are limited to only a few thousand GitHub-sourced instances. To this end, we propose an incremental, automated data-curation pipeline that systematically scales both the volume and diversity of SWE datasets. Our dataset comprises 10,169 real-world Python task instances from 2,531 distinct GitHub repositories, each accompanied by a task specified in natural language and a dedicated runtime-environment image for automated unit-test validation. We have carefully curated over 8,000 successfully runtime-validated training trajectories from our proposed SWE dataset. When fine-tuning the Skywork-SWE model on these trajectories, we uncover a striking data scaling phenomenon: the trained model's performance for software engineering capabilities in LLMs continues to improve as the data size increases, showing no signs of saturation. Notably, our Skywork-SWE model achieves 38.0% pass@1 accuracy on the SWE-bench Verified benchmark without using verifiers or multiple rollouts, establishing a new state-of-the-art (SOTA) among the Qwen2.5-Coder-32B-based LLMs built on the OpenHands agent framework. Furthermore, with the incorporation of test-time scaling techniques, the performance further improves to 47.0% accuracy, surpassing the previous SOTA results for sub-32B parameter models. We release the Skywork-SWE-32B model checkpoint to accelerate future research.

FEAT: A Preference Feedback Dataset through a Cost-Effective Auto-Generation and Labeling Framework for English AI Tutoring

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19325.pdf

초록:

In English education tutoring, teacher feedback is essential for guiding students. Recently, AI-based tutoring systems have emerged to assist teachers; however, these systems require high-quality and large-scale teacher feedback data, which is both time-consuming and costly to generate manually. In this study, we propose FEAT, a cost-effective framework for generating teacher feedback, and have constructed three complementary datasets: (1) DIRECT-Manual (DM), where both humans and large language models (LLMs) collaboratively generate high-quality teacher feedback, albeit at a higher cost; (2) DIRECT-Generated (DG), an LLM-only generated, cost-effective dataset with lower quality;, and (3) DIRECT-Augmented (DA), primarily based on DG with a small portion of DM added to enhance quality while maintaining cost-efficiency. Experimental results showed that incorporating a small portion of DM (5-10%) into DG leads to superior performance compared to using 100% DM alone.

Evolutionary Level Repair

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19359.pdf

초록:

We address the problem of game level repair, which consists of taking a designed but non-functional game level and making it functional. This might consist of ensuring the completeness of the level, reachability of objects, or other performance characteristics. The repair problem may also be constrained in that it can only make a small number of changes to the level. We investigate search-based solutions to the level repair problem, particularly using evolutionary and quality-diversity algorithms, with good results. This level repair method is applied to levels generated using a machine learning-based procedural content generation (PCGML) method that generates stylistically appropriate but frequently broken levels. This combination of PCGML for generation and search-based methods for repair shows great promise as a hybrid procedural content generation (PCG) method.

Conversational Intent-Driven GraphRAG: Enhancing Multi-Turn Dialogue Systems through Adaptive Dual-Retrieval of Flow Patterns and Context Semantics

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19385.pdf

초록:

We present CID-GraphRAG (Conversational Intent-Driven Graph Retrieval Augmented Generation), a novel framework that addresses the limitations of existing dialogue systems in maintaining both contextual coherence and goal-oriented progression in multi-turn customer service conversations. Unlike traditional RAG systems that rely solely on semantic similarity (Conversation RAG) or standard knowledge graphs (GraphRAG), CID-GraphRAG constructs dynamic intent transition graphs from goal achieved historical dialogues and implements a dual-retrieval mechanism that adaptively balances intent-based graph traversal with semantic search. This approach enables the system to simultaneously leverage both conversional intent flow patterns and contextual semantics, significantly improving retrieval quality and response quality. In extensive experiments on real-world customer service dialogues, we employ both automatic metrics and LLM-as-judge assessments, demonstrating that CID-GraphRAG significantly outperforms both semantic-based Conversation RAG and intent-based GraphRAG baselines across all evaluation criteria. Quantitatively, CID-GraphRAG demonstrates substantial improvements over Conversation RAG across automatic metrics, with relative gains of 11% in BLEU, 5% in ROUGE-L, 6% in METEOR, and most notably, a 58% improvement in response quality according to LLM-as-judge evaluations. These results demonstrate that the integration of intent transition structures with semantic retrieval creates a synergistic effect that neither approach achieves independently, establishing CID-GraphRAG as an effective framework for addressing the challenges of maintaining contextual coherence and goal-oriented progression in knowledge-intensive multi-turn dialogues.

Is an object-centric representation beneficial for robotic manipulation ?

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

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초록:

Object-centric representation (OCR) has recently become a subject of interest in the computer vision community for learning a structured representation of images and videos. It has been several times presented as a potential way to improve data-efficiency and generalization capabilities to learn an agent on downstream tasks. However, most existing work only evaluates such models on scene decomposition, without any notion of reasoning over the learned representation. Robotic manipulation tasks generally involve multi-object environments with potential inter-object interaction. We thus argue that they are a very interesting playground to really evaluate the potential of existing object-centric work. To do so, we create several robotic manipulation tasks in simulated environments involving multiple objects (several distractors, the robot, etc.) and a high-level of randomization (object positions, colors, shapes, background, initial positions, etc.). We then evaluate one classical object-centric method across several generalization scenarios and compare its results against several state-of-the-art hollistic representations. Our results exhibit that existing methods are prone to failure in difficult scenarios involving complex scene structures, whereas object-centric methods help overcome these challenges.

Unsupervised Dataset Dictionary Learning for domain shift robust clustering: application to sitting posture identification

저자: Unknown

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19410.pdf

초록:

This paper introduces a novel approach, Unsupervised Dataset Dictionary Learning (U-DaDiL), for totally unsupervised robust clustering applied to sitting posture identification. Traditional methods often lack adaptability to diverse datasets and suffer from domain shift issues. U-DaDiL addresses these challenges by aligning distributions from different datasets using Wasserstein barycenter based representation. Experimental evaluations on the Office31 dataset demonstrate significant improvements in cluster alignment accuracy. This work also presents a promising step for addressing domain shift and robust clustering for unsupervised sitting posture identification

Commander-GPT: Dividing and Routing for Multimodal Sarcasm Detection

저자: Unknown

플랫폼: arxiv

초록:

Multimodal sarcasm understanding is a high-order cognitive task. Although large language models (LLMs) have shown impressive performance on many downstream NLP tasks, growing evidence suggests that they struggle with sarcasm understanding. In this paper, we propose Commander-GPT, a modular decision routing framework inspired by military command theory. Rather than relying on a single LLM's capability, Commander-GPT orchestrates a team of specialized LLM agents where each agent will be selectively assigned to a focused sub-task such as context modeling, sentiment analysis, etc. Their outputs are then routed back to the commander, which integrates the information and performs the final sarcasm judgment. To coordinate these agents, we introduce three types of centralized commanders: (1) a trained lightweight encoder-based commander (e.g., multi-modal BERT); (2) four small autoregressive language models, serving as moderately capable commanders (e.g., DeepSeek-VL); (3) two large LLM-based commander (Gemini Pro and GPT-4o) that performs task routing, output aggregation, and sarcasm decision-making in a zero-shot fashion. We evaluate Commander-GPT on the MMSD and MMSD 2.0 benchmarks, comparing five prompting strategies. Experimental results show that our framework achieves 4.4% and 11.7% improvement in F1 score over state-of-the-art (SoTA) baselines on average, demonstrating its effectiveness.

KunLunBaizeRAG: Reinforcement Learning Driven Inference Performance Leap for Large Language Models

초록:

This paper introduces KunLunBaizeRAG, a reinforcement learning-driven reasoning framework designed to enhance the reasoning capabilities of large language models (LLMs) in complex multi-hop question-answering tasks. The framework addresses key limitations of traditional RAG, such as retrieval drift, information redundancy, and strategy rigidity. Key innovations include the RAG-driven Reasoning Alignment (RDRA) mechanism, the Search-Think Iterative Enhancement (STIE) mechanism, the Network-Local Intelligent Routing (NLR) mechanism, and a progressive hybrid training strategy. Experimental results demonstrate significant improvements in exact match (EM) and LLM-judged score (LJ) across four benchmarks, highlighting the framework's robustness and effectiveness in complex reasoning scenarios.

NaviAgent: Bilevel Planning on Tool Dependency Graphs for Function Calling

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19500.pdf

초록:

LLMs' reliance on static knowledge and fragile tool invocation severely hinders the orchestration of complex, heterogeneous toolchains, particularly at large scales. Existing methods typically use rigid single-path execution, resulting in poor error recovery and exponentially growing search spaces. We introduce NaviAgent, a graph-navigated bilevel planning architecture for robust function calling, comprising a Multi-Path Decider and Graph-Encoded Navigator. As an LLM-powered agent, the Multi-Path Decider defines a four-dimensional decision space and continuously perceives environmental states, dynamically selecting the optimal action to fully cover all tool invocation scenarios. The Graph-Encoded Navigator constructs a Tool Dependency Heterogeneous Graph (TDHG), where node embeddings explicitly fuse API schema structure with historical invocation behavior. It also integrates a novel heuristic search strategy that guides the Decider toward efficient and highly successful toolchains, even for unseen tool combinations. Experiments show that NaviAgent consistently achieves the highest task success rate (TSR) across all foundation models and task complexities, outperforming the average baselines (ReAct, ToolLLM, {₩alpha}-UMI) by 13.5%, 16.4%, and 19.0% on Qwen2.5-14B, Qwen2.5-32B, and Deepseek-V3, respectively. Its execution steps are typically within one step of the most efficient baseline, ensuring a strong balance between quality and efficiency. Notably, a fine-tuned Qwen2.5-14B model achieves a TSR of 49.5%, surpassing the much larger 32B model (44.9%) under our architecture. Incorporating the Graph-Encoded Navigator further boosts TSR by an average of 2.4 points, with gains up over 9 points on complex tasks for larger models (Deepseek-V3 and GPT-4o), highlighting its essential role in toolchain orchestration.

NTRL: Encounter Generation via Reinforcement Learning for Dynamic Difficulty Adjustment in Dungeons and Dragons

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19530.pdf

초록:

Balancing combat encounters in Dungeons & Dragons (D&D) is a complex task that requires Dungeon Masters (DM) to manually assess party strength, enemy composition, and dynamic player interactions while avoiding interruption of the narrative flow. In this paper, we propose Encounter Generation via Reinforcement Learning (NTRL), a novel approach that automates Dynamic Difficulty Adjustment (DDA) in D&D via combat encounter design. By framing the problem as a contextual bandit, NTRL generates encounters based on real-time party members attributes. In comparison with classic DM heuristics, NTRL iteratively optimizes encounters to extend combat longevity (+200%), increases damage dealt to party members, reducing post-combat hit points (-16.67%), and raises the number of player deaths while maintaining low total party kills (TPK). The intensification of combat forces players to act wisely and engage in tactical maneuvers, even though the generated encounters guarantee high win rates (70%). Even in comparison with encounters designed by human Dungeon Masters, NTRL demonstrates superior performance by enhancing the strategic depth of combat while increasing difficulty in a manner that preserves overall game fairness.

Interpretable Hybrid Machine Learning Models Using FOLD-R++ and Answer Set Programming

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19573.pdf

초록:

Machine learning (ML) techniques play a pivotal role in high-stakes domains such as healthcare, where accurate predictions can greatly enhance decision-making. However, most high-performing methods such as neural networks and ensemble methods are often opaque, limiting trust and broader adoption. In parallel, symbolic methods like Answer Set Programming (ASP) offer the possibility of interpretable logical rules but do not always match the predictive power of ML models. This paper proposes a hybrid approach that integrates ASP-derived rules from the FOLD-R++ algorithm with black-box ML classifiers to selectively correct uncertain predictions and provide human-readable explanations. Experiments on five medical datasets reveal statistically significant performance gains in accuracy and F1 score. This study underscores the potential of combining symbolic reasoning with conventional ML to achieve high interpretability without sacrificing accuracy.

Adaptive Domain Modeling with Language Models: A Multi-Agent Approach to Task Planning

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19592.pdf

초록:

We introduce TAPAS (Task-based Adaptation and Planning using AgentS), a multi-agent framework that integrates Large Language Models (LLMs) with symbolic planning to solve complex tasks without the need for manually defined environment models. TAPAS employs specialized LLM-based agents that collaboratively generate and adapt domain models, initial states, and goal specifications as needed using structured tool-calling mechanisms. Through this tool-based interaction, downstream agents can request modifications from upstream agents, enabling adaptation to novel attributes and constraints without manual domain redefinition. A ReAct (Reason+Act)-style execution agent, coupled with natural language plan translation, bridges the gap between dynamically generated plans and real-world robot capabilities. TAPAS demonstrates strong performance in benchmark planning domains and in the VirtualHome simulated real-world environment.

ChordPrompt: Orchestrating Cross-Modal Prompt Synergy for Multi-Domain Incremental Learning in CLIP

초록:

Continual learning (CL) empowers pre-trained vision-language models to adapt effectively to novel or previously underrepresented data distributions without comprehensive retraining, enhancing their adaptability and efficiency. While vision-language models like CLIP show great promise, they struggle to maintain performance across domains in incremental learning scenarios. Existing prompt learning methods face two main limitations: 1) they primarily focus on class-incremental learning scenarios, lacking specific strategies for multi-domain task incremental learning; 2) most current approaches employ single-modal prompts, neglecting the potential benefits of cross-modal information exchange. To address these challenges, we propose the ₩ChordPrompt framework, which facilitates a harmonious interplay between visual and textual prompts. ₩ChordPrompt introduces cross-modal prompts to leverage interactions between visual and textual information. Our approach also employs domain-adaptive text prompts to select appropriate prompts for continual adaptation across multiple domains. Comprehensive experiments on multi-domain incremental learning benchmarks demonstrate that ₩ChordPrompt outperforms state-of-the-art methods in zero-shot generalization and downstream task performance.

Position: Intelligent Science Laboratory Requires the Integration of Cognitive and Embodied AI

초록:

Scientific discovery has long been constrained by human limitations in expertise, physical capability, and sleep cycles. The recent rise of AI scientists and automated laboratories has accelerated both the cognitive and operational aspects of research. However, key limitations persist: AI systems are often confined to virtual environments, while automated laboratories lack the flexibility and autonomy to adaptively test new hypotheses in the physical world. Recent advances in embodied AI, such as generalist robot foundation models, diffusion-based action policies, fine-grained manipulation learning, and sim-to-real transfer, highlight the promise of integrating cognitive and embodied intelligence. This convergence opens the door to closed-loop systems that support iterative, autonomous experimentation and the possibility of serendipitous discovery. In this position paper, we propose the paradigm of Intelligent Science Laboratories (ISLs): a multi-layered, closed-loop framework that deeply integrates cognitive and embodied intelligence. ISLs unify foundation models for scientific reasoning, agent-based workflow orchestration, and embodied agents for robust physical experimentation. We argue that such systems are essential for overcoming the current limitations of scientific discovery and for realizing the full transformative potential of AI-driven science.

On the efficacy of old features for the detection of new bots

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19635.pdf

초록:

For more than a decade now, academicians and online platform administrators have been studying solutions to the problem of bot detection. Bots are computer algorithms whose use is far from being benign: malicious bots are purposely created to distribute spam, sponsor public characters and, ultimately, induce a bias within the public opinion. To fight the bot invasion on our online ecosystem, several approaches have been implemented, mostly based on (supervised and unsupervised) classifiers, which adopt the most varied account features, from the simplest to the most expensive ones to be extracted from the raw data obtainable through the Twitter public APIs. In this exploratory study, using Twitter as a benchmark, we compare the performances of four state-of-art feature sets in detecting novel bots: one of the output scores of the popular bot detector Botometer, which considers more than 1,000 features of an account to take a decision; two feature sets based on the account profile and timeline; and the information about the Twitter client from which the user tweets. The results of our analysis, conducted on six recently released datasets of Twitter accounts, hint at the possible use of general-purpose classifiers and cheap-to-compute account features for the detection of evolved bots.

Identifying Macro Causal Effects in C-DMGs over DMGs

초록:

The do-calculus is a sound and complete tool for identifying causal effects in acyclic directed mixed graphs (ADMGs) induced by structural causal models (SCMs). However, in many real-world applications, especially in high-dimensional setting, constructing a fully specified ADMG is often infeasible. This limitation has led to growing interest in partially specified causal representations, particularly through cluster-directed mixed graphs (C-DMGs), which group variables into clusters and offer a more abstract yet practical view of causal dependencies. While these representations can include cycles, recent work has shown that the do-calculus remains sound and complete for identifying macro-level causal effects in C-DMGs over ADMGs under the assumption that all clusters size are greater than 1. Nevertheless, real-world systems often exhibit cyclic causal dynamics at the structural level. To account for this, input-output structural causal models (ioSCMs) have been introduced as a generalization of SCMs that allow for cycles. ioSCMs induce another type of graph structure known as a directed mixed graph (DMG). Analogous to the ADMG setting, one can define C-DMGs over DMGs as high-level representations of causal relations among clusters of variables. In this paper, we prove that, unlike in the ADMG setting, the do-calculus is unconditionally sound and complete for identifying macro causal effects in C-DMGs over DMGs. Furthermore, we show that the graphical criteria for non-identifiability of macro causal effects previously established C-DMGs over ADMGs naturally extends to a subset of C-DMGs over DMGs.

From memories to maps: Mechanisms of in context reinforcement learning in transformers

초록:

Humans and animals show remarkable learning efficiency, adapting to new environments with minimal experience. This capability is not well captured by standard reinforcement learning algorithms that rely on incremental value updates. Rapid adaptation likely depends on episodic memory -- the ability to retrieve specific past experiences to guide decisions in novel contexts. Transformers provide a useful setting for studying these questions because of their ability to learn rapidly in-context and because their key-value architecture resembles episodic memory systems in the brain. We train a transformer to in-context reinforcement learn in a distribution of planning tasks inspired by rodent behavior. We then characterize the learning algorithms that emerge in the model. We first find that representation learning is supported by in-context structure learning and cross-context alignment, where representations are aligned across environments with different sensory stimuli. We next demonstrate that the reinforcement learning strategies developed by the model are not interpretable as standard model-free or model-based planning. Instead, we show that in-context reinforcement learning is supported by caching intermediate computations within the model's memory tokens, which are then accessed at decision time. Overall, we find that memory may serve as a computational resource, storing both raw experience and cached computations to support flexible behavior. Furthermore, the representations developed in the model resemble computations associated with the hippocampal-entorhinal system in the brain, suggesting that our findings may be relevant for natural cognition. Taken together, our work offers a mechanistic hypothesis for the rapid adaptation that underlies in-context learning in artificial and natural settings.

Toward Decision-Oriented Prognostics: An Integrated Estimate-Optimize Framework for Predictive Maintenance

저자: Unknown

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19698.pdf

초록:

Recent research increasingly integrates machine learning (ML) into predictive maintenance (PdM) to reduce operational and maintenance costs in data-rich operational settings. However, uncertainty due to model misspecification continues to limit widespread industrial adoption. This paper proposes a PdM framework in which sensor-driven prognostics inform decision-making under economic trade-offs within a finite decision space. We investigate two key questions: (1) Does higher predictive accuracy necessarily lead to better maintenance decisions? (2) If not, how can the impact of prediction errors on downstream maintenance decisions be mitigated? We first demonstrate that in the traditional estimate-then-optimize (ETO) framework, errors in probabilistic prediction can result in inconsistent and suboptimal maintenance decisions. To address this, we propose an integrated estimate-optimize (IEO) framework that jointly tunes predictive models while directly optimizing for maintenance outcomes. We establish theoretical finite-sample guarantees on decision consistency under standard assumptions. Specifically, we develop a stochastic perturbation gradient descent algorithm suitable for small run-to-failure datasets. Empirical evaluations on a turbofan maintenance case study show that the IEO framework reduces average maintenance regret up to 22% compared to ETO. This study provides a principled approach to managing prediction errors in data-driven PdM. By aligning prognostic model training with maintenance objectives, the IEO framework improves robustness under model misspecification and improves decision quality. The improvement is particularly pronounced when the decision-making policy is misaligned with the decision-maker's target. These findings support more reliable maintenance planning in uncertain operational environments.

LLM-Driven Medical Document Analysis: Enhancing Trustworthy Pathology and Differential Diagnosis

초록:

Medical document analysis plays a crucial role in extracting essential clinical insights from unstructured healthcare records, supporting critical tasks such as differential diagnosis. Determining the most probable condition among overlapping symptoms requires precise evaluation and deep medical expertise. While recent advancements in large language models (LLMs) have significantly enhanced performance in medical document analysis, privacy concerns related to sensitive patient data limit the use of online LLMs services in clinical settings. To address these challenges, we propose a trustworthy medical document analysis platform that fine-tunes a LLaMA-v3 using low-rank adaptation, specifically optimized for differential diagnosis tasks. Our approach utilizes DDXPlus, the largest benchmark dataset for differential diagnosis, and demonstrates superior performance in pathology prediction and variable-length differential diagnosis compared to existing methods. The developed web-based platform allows users to submit their own unstructured medical documents and receive accurate, explainable diagnostic results. By incorporating advanced explainability techniques, the system ensures transparent and reliable predictions, fostering user trust and confidence. Extensive evaluations confirm that the proposed method surpasses current state-of-the-art models in predictive accuracy while offering practical utility in clinical settings. This work addresses the urgent need for reliable, explainable, and privacy-preserving artificial intelligence solutions, representing a significant advancement in intelligent medical document analysis for real-world healthcare applications. The code can be found at ₩href{https://github.com/leitro/Differential-Diagnosis-LoRA}{https://github.com/leitro/Differential-Diagnosis-LoRA}.

From Reproduction to Replication: Evaluating Research Agents with Progressive Code Masking

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19724.pdf

초록:

Recent progress in autonomous code generation has fueled excitement around AI agents capable of accelerating scientific discovery by running experiments. However, there is currently no benchmark that evaluates whether such agents can implement scientific ideas when given varied amounts of code as a starting point, interpolating between reproduction (running code) and from-scratch replication (fully re-implementing and running code). We introduce AutoExperiment, a benchmark that evaluates AI agents' ability to implement and run machine learning experiments based on natural language descriptions in research papers. In each task, agents are given a research paper, a codebase with key functions masked out, and a command to run the experiment. The goal is to generate the missing code, execute the experiment in a sandboxed environment, and reproduce the results. AutoExperiment scales in difficulty by varying the number of missing functions n, ranging from partial reproduction to full replication. We evaluate state-of-the-art agents and find that performance degrades rapidly as n increases. Agents that can dynamically interact with the environment (e.g. to debug their code) can outperform agents in fixed "agentless" harnesses, and there exists a significant gap between single-shot and multi-trial success rates (Pass@1 vs. Pass@5), motivating verifier approaches to our benchmark. Our findings highlight critical challenges in long-horizon code generation, context retrieval, and autonomous experiment execution, establishing AutoExperiment as a new benchmark for evaluating progress in AI-driven scientific experimentation. Our data and code are open-sourced at https://github.com/j1mk1m/AutoExperiment .

Automatic Prompt Optimization for Knowledge Graph Construction: Insights from an Empirical Study

저자: Unknown

플랫폼: arxiv

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카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19773.pdf

초록:

A KG represents a network of entities and illustrates relationships between them. KGs are used for various applications, including semantic search and discovery, reasoning, decision-making, natural language processing, machine learning, and recommendation systems. Triple (subject-relation-object) extraction from text is the fundamental building block of KG construction and has been widely studied, for example, in early benchmarks such as ACE 2002 to more recent ones, such as WebNLG 2020, REBEL and SynthIE. While the use of LLMs is explored for KG construction, handcrafting reasonable task-specific prompts for LLMs is a labour-intensive exercise and can be brittle due to subtle changes in the LLM models employed. Recent work in NLP tasks (e.g. autonomy generation) uses automatic prompt optimization/engineering to address this challenge by generating optimal or near-optimal task-specific prompts given input-output examples. This empirical study explores the application of automatic prompt optimization for the triple extraction task using experimental benchmarking. We evaluate different settings by changing (a) the prompting strategy, (b) the LLM being used for prompt optimization and task execution, (c) the number of canonical relations in the schema (schema complexity), (d) the length and diversity of input text, (e) the metric used to drive the prompt optimization, and (f) the dataset being used for training and testing. We evaluate three different automatic prompt optimizers, namely, DSPy, APE, and TextGrad and use two different triple extraction datasets, SynthIE and REBEL. Through rigorous empirical evaluation, our main contribution highlights that automatic prompt optimization techniques can generate reasonable prompts similar to humans for triple extraction. In turn, these optimized prompts achieve improved results, particularly with increasing schema complexity and text size.

SAGE: Strategy-Adaptive Generation Engine for Query Rewriting

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19783.pdf

초록:

Query rewriting is pivotal for enhancing dense retrieval, yet current methods demand large-scale supervised data or suffer from inefficient reinforcement learning (RL) exploration. In this work, we first establish that guiding Large Language Models (LLMs) with a concise set of expert-crafted strategies, such as semantic expansion and entity disambiguation, substantially improves retrieval effectiveness on challenging benchmarks, including HotpotQA, FEVER, NFCorpus, and SciFact. Building on this insight, we introduce the Strategy-Adaptive Generation Engine (SAGE), which operationalizes these strategies in an RL framework. SAGE introduces two novel reward shaping mechanisms-Strategic Credit Shaping (SCS) and Contrastive Reward Shaping (CRS)-to deliver more informative learning signals. This strategy-guided approach not only achieves new state-of-the-art NDCG@10 results, but also uncovers a compelling emergent behavior: the agent learns to select optimal strategies, reduces unnecessary exploration, and generates concise rewrites, lowering inference cost without sacrificing performance. Our findings demonstrate that strategy-guided RL, enhanced with nuanced reward shaping, offers a scalable, efficient, and more interpretable paradigm for developing the next generation of robust information retrieval systems.

Learning Task Belief Similarity with Latent Dynamics for Meta-Reinforcement Learning

초록:

Meta-reinforcement learning requires utilizing prior task distribution information obtained during exploration to rapidly adapt to unknown tasks. The efficiency of an agent's exploration hinges on accurately identifying the current task. Recent Bayes-Adaptive Deep RL approaches often rely on reconstructing the environment's reward signal, which is challenging in sparse reward settings, leading to suboptimal exploitation. Inspired by bisimulation metrics, which robustly extracts behavioral similarity in continuous MDPs, we propose SimBelief-a novel meta-RL framework via measuring similarity of task belief in Bayes-Adaptive MDP (BAMDP). SimBelief effectively extracts common features of similar task distributions, enabling efficient task identification and exploration in sparse reward environments. We introduce latent task belief metric to learn the common structure of similar tasks and incorporate it into the specific task belief. By learning the latent dynamics across task distributions, we connect shared latent task belief features with specific task features, facilitating rapid task identification and adaptation. Our method outperforms state-of-the-art baselines on sparse reward MuJoCo and panda-gym tasks.

KnowRL: Exploring Knowledgeable Reinforcement Learning for Factuality

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19807.pdf

초록:

Large Language Models (LLMs), particularly slow-thinking models, often exhibit severe hallucination, outputting incorrect content due to an inability to accurately recognize knowledge boundaries during reasoning. While Reinforcement Learning (RL) can enhance complex reasoning abilities, its outcome-oriented reward mechanism often lacks factual supervision over the thinking process, further exacerbating the hallucination problem. To address the high hallucination in slow-thinking models, we propose Knowledge-enhanced RL, KnowRL. KnowRL guides models to perform fact-based slow thinking by integrating a factuality reward, based on knowledge verification, into the RL training process, helping them recognize their knowledge boundaries. KnowRL guides models to perform fact-based slow thinking by integrating a factuality reward, based on knowledge verification, into the RL training process, helping them recognize their knowledge boundaries. This targeted factual input during RL training enables the model to learn and internalize fact-based reasoning strategies. By directly rewarding adherence to facts within the reasoning steps, KnowRL fosters a more reliable thinking process. Experimental results on three hallucination evaluation datasets and two reasoning evaluation datasets demonstrate that KnowRL effectively mitigates hallucinations in slow-thinking models while maintaining their original strong reasoning capabilities. Our code is available at https://github.com/zjunlp/KnowRL.

Evaluating Compliance with Visualization Guidelines in Diagrams for Scientific Publications Using Large Vision Language Models

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.AI

PDF URL: https://arxiv.org/pdf/2506.19825.pdf

초록:

Diagrams are widely used to visualize data in publications. The research field of data visualization deals with defining principles and guidelines for the creation and use of these diagrams, which are often not known or adhered to by researchers, leading to misinformation caused by providing inaccurate or incomplete information. In this work, large Vision Language Models (VLMs) are used to analyze diagrams in order to identify potential problems in regards to selected data visualization principles and guidelines. To determine the suitability of VLMs for these tasks, five open source VLMs and five prompting strategies are compared using a set of questions derived from selected data visualization guidelines. The results show that the employed VLMs work well to accurately analyze diagram types (F1-score 82.49 %), 3D effects (F1-score 98.55 %), axes labels (F1-score 76.74 %), lines (RMSE 1.16), colors (RMSE 1.60) and legends (F1-score 96.64 %, RMSE 0.70), while they cannot reliably provide feedback about the image quality (F1-score 0.74 %) and tick marks/labels (F1-score 46.13 %). Among the employed VLMs, Qwen2.5VL performs best, and the summarizing prompting strategy performs best for most of the experimental questions. It is shown that VLMs can be used to automatically identify a number of potential issues in diagrams, such as missing axes labels, missing legends, and unnecessary 3D effects. The approach laid out in this work can be extended for further aspects of data visualization.

Temporal-IRL: Modeling Port Congestion and Berth Scheduling with Inverse Reinforcement Learning

저자: Unknown

초록:

Predicting port congestion is crucial for maintaining reliable global supply chains. Accurate forecasts enableimprovedshipment planning, reducedelaysand costs, and optimizeinventoryanddistributionstrategies, thereby ensuring timely deliveries and enhancing supply chain resilience. To achieve accurate predictions, analyzing vessel behavior and their stay times at specific port terminals is essential, focusing particularly on berth scheduling under various conditions. Crucially, the model must capture and learn the underlying priorities and patterns of berth scheduling. Berth scheduling and planning are influenced by a range of factors, including incoming vessel size, waiting times, and the status of vessels within the port terminal. By observing historical Automatic Identification System (AIS) positions of vessels, we reconstruct berth schedules, which are subsequently utilized to determine the reward function via Inverse Reinforcement Learning (IRL). For this purpose, we modeled a specific terminal at the Port of New York/New Jersey and developed Temporal-IRL. This Temporal-IRL model learns berth scheduling to predict vessel sequencing at the terminal and estimate vessel port stay, encompassing both waiting and berthing times, to forecast port congestion. Utilizing data from Maher Terminal spanning January 2015 to September 2023, we trained and tested the model, achieving demonstrably excellent results.

JoyAgents-R1: Joint Evolution Dynamics for Versatile Multi-LLM Agents with Reinforcement Learning

초록:

Multi-agent reinforcement learning (MARL) has emerged as a prominent paradigm for increasingly complex tasks. However, joint evolution across heterogeneous agents remains challenging due to cooperative inefficiency and training instability. In this paper, we propose the joint evolution dynamics for MARL called JoyAgents-R1, which first applies Group Relative Policy Optimization (GRPO) to the joint training of heterogeneous multi-agents. By iteratively refining agents' large language models (LLMs) and memories, the method achieves holistic equilibrium with optimal decision-making and memory capabilities. Specifically, JoyAgents-R1 first implements node-wise Monte Carlo sampling on the behavior of each agent across entire reasoning trajectories to enhance GRPO sampling efficiency while maintaining policy diversity. Then, our marginal benefit-driven selection strategy identifies top-K sampling groups with maximal reward fluctuations, enabling targeted agent model updates that improve training stability and maximize joint benefits through cost-effective parameter adjustments. Meanwhile, JoyAgents-R1 introduces an adaptive memory evolution mechanism that repurposes GRPO rewards as cost-free supervisory signals to eliminate repetitive reasoning and accelerate convergence. Experiments across general and domain-specific scenarios demonstrate that JoyAgents-R1 achieves performance comparable to that of larger LLMs while built on smaller open-source models.

Recycling the Web: A Method to Enhance Pre-training Data Quality and Quantity for Language Models

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카테고리: cs.CL

PDF URL: https://arxiv.org/pdf/2506.04689.pdf

초록:

Scaling laws predict that the performance of large language models improves with increasing model size and data size. In practice, pre-training has been relying on massive web crawls, using almost all data sources publicly available on the internet so far. However, this pool of natural data does not grow at the same rate as the compute supply. Furthermore, the availability of high-quality texts is even more limited: data filtering pipelines often remove up to 99% of the initial web scrapes to achieve state-of-the-art. To address the "data wall" of pre-training scaling, our work explores ways to transform and recycle data discarded in existing filtering processes. We propose REWIRE, REcycling the Web with guIded REwrite, a method to enrich low-quality documents so that they could become useful for training. This in turn allows us to increase the representation of synthetic data in the final pre-training set. Experiments at 1B, 3B and 7B scales of the DCLM benchmark show that mixing high-quality raw texts and our rewritten texts lead to 1.0, 1.3 and 2.5 percentage points improvement respectively across 22 diverse tasks, compared to training on only filtered web data. Training on the raw-synthetic data mix is also more effective than having access to 2x web data. Through further analysis, we demonstrate that about 82% of the mixed in texts come from transforming lower-quality documents that would otherwise be discarded. REWIRE also outperforms related approaches of generating synthetic data, including Wikipedia-style paraphrasing, question-answer synthesizing and knowledge extraction. These results suggest that recycling web texts holds the potential for being a simple and effective approach for scaling pre-training data.

Neural Cellular Automata for ARC-AGI

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.NE

초록:

Cellular automata and their differentiable counterparts, Neural Cellular Automata (NCA), are highly expressive and capable of surprisingly complex behaviors. This paper explores how NCAs perform when applied to tasks requiring precise transformations and few-shot generalization, using the Abstraction and Reasoning Corpus for Artificial General Intelligence (ARC-AGI) as a domain that challenges their capabilities in ways not previously explored. Specifically, this paper uses gradient-based training to learn iterative update rules that transform input grids into their outputs from the training examples and apply them to the test inputs. Results suggest that gradient-trained NCA models are a promising and efficient approach to a range of abstract grid-based tasks from ARC. Along with discussing the impacts of various design modifications and training constraints, this work examines the behavior and properties of NCAs applied to ARC to give insights for broader applications of self-organizing systems.

Privacy-Preserving LLM Interaction with Socratic Chain-of-Thought Reasoning and Homomorphically Encrypted Vector Databases

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.CR

초록:

Large language models (LLMs) are increasingly used as personal agents, accessing sensitive user data such as calendars, emails, and medical records. Users currently face a trade-off: They can send private records, many of which are stored in remote databases, to powerful but untrusted LLM providers, increasing their exposure risk. Alternatively, they can run less powerful models locally on trusted devices. We bridge this gap. Our Socratic Chain-of-Thought Reasoning first sends a generic, non-private user query to a powerful, untrusted LLM, which generates a Chain-of-Thought (CoT) prompt and detailed sub-queries without accessing user data. Next, we embed these sub-queries and perform encrypted sub-second semantic search using our Homomorphically Encrypted Vector Database across one million entries of a single user's private data. This represents a realistic scale of personal documents, emails, and records accumulated over years of digital activity. Finally, we feed the CoT prompt and the decrypted records to a local language model and generate the final response. On the LoCoMo long-context QA benchmark, our hybrid framework, combining GPT-4o with a local Llama-3.2-1B model, outperforms using GPT-4o alone by up to 7.1 percentage points. This demonstrates a first step toward systems where tasks are decomposed and split between untrusted strong LLMs and weak local ones, preserving user privacy.

Automatic Depression Assessment using Machine Learning: A Comprehensive Survey

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: q-bio.NC

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초록:

Depression is a common mental illness across current human society. Traditional depression assessment relying on inventories and interviews with psychologists frequently suffer from subjective diagnosis results, slow and expensive diagnosis process as well as lack of human resources. Since there is a solid evidence that depression is reflected by various human internal brain activities and external expressive behaviours, early traditional machine learning (ML) and advanced deep learning (DL) models have been widely explored for human behaviour-based automatic depression assessment (ADA) since 2012. However, recent ADA surveys typically only focus on a limited number of human behaviour modalities. Despite being used as a theoretical basis for developing ADA approaches, existing ADA surveys lack a comprehensive review and summary of multi-modal depression-related human behaviours. To bridge this gap, this paper specifically summarises depression-related human behaviours across a range of modalities (e.g. the human brain, verbal language and non-verbal audio/facial/body behaviours). We focus on conducting an up-to-date and comprehensive survey of ML-based ADA approaches for learning depression cues from these behaviours as well as discussing and comparing their distinctive features and limitations. In addition, we also review existing ADA competitions and datasets, identify and discuss the main challenges and opportunities to provide further research directions for future ADA researchers.

MemeMind: A Large-Scale Multimodal Dataset with Chain-of-Thought Reasoning for Harmful Meme Detection

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.CL

PDF URL: https://arxiv.org/pdf/2506.18919.pdf

초록:

The rapid development of social media has intensified the spread of harmful content. Harmful memes, which integrate both images and text, pose significant challenges for automated detection due to their implicit semantics and complex multimodal interactions. Although existing research has made progress in detection accuracy and interpretability, the lack of a systematic, large-scale, diverse, and highly explainable dataset continues to hinder further advancement in this field. To address this gap, we introduce MemeMind, a novel dataset featuring scientifically rigorous standards, large scale, diversity, bilingual support (Chinese and English), and detailed Chain-of-Thought (CoT) annotations. MemeMind fills critical gaps in current datasets by offering comprehensive labeling and explicit reasoning traces, thereby providing a solid foundation for enhancing harmful meme detection. In addition, we propose an innovative detection framework, MemeGuard, which effectively integrates multimodal information with reasoning process modeling, significantly improving models' ability to understand and identify harmful memes. Extensive experiments conducted on the MemeMind dataset demonstrate that MemeGuard consistently outperforms existing state-of-the-art methods in harmful meme detection tasks.

Connecting Vision and Emissions: A Behavioural AI Approach to Carbon Estimation in Road Design

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.CV

PDF URL: https://arxiv.org/pdf/2506.18924.pdf

초록:

We present an enhanced YOLOv8 real time vehicle detection and classification framework, for estimating carbon emissions in urban environments. The system enhances YOLOv8 architecture to detect, segment, and track vehicles from live traffic video streams. Once a vehicle is localized, a dedicated deep learning-based identification module is employed to recognize license plates and classify vehicle types. Since YOLOv8 lacks the built-in capacity for fine grained recognition tasks such as reading license plates or determining vehicle attributes beyond class labels, our framework incorporates a hybrid pipeline where each detected vehicle is tracked and its bounding box is cropped and passed to a deep Optical Character Recognition (OCR) module. This OCR system, composed of multiple convolutional neural network (CNN) layers, is trained specifically for character-level detection and license plate decoding under varied conditions such as motion blur, occlusion, and diverse font styles. Additionally, the recognized plate information is validated using a real time API that cross references with an external vehicle registration database to ensure accurate classification and emission estimation. This multi-stage approach enables precise, automated calculation of per vehicle carbon emissions. Extensive evaluation was conducted using a diverse vehicle dataset enriched with segmentation masks and annotated license plates. The YOLOv8 detector achieved a mean Average Precision (mAP@0.5) of approximately 71% for bounding boxes and 70% for segmentation masks. Character level OCR accuracy reached up to 99% with the best performing CNN model. These results affirm the feasibility of combining real time object detection with deep OCR for practical deployment in smart transportation systems, offering a scalable solution for automated, vehicle specific carbon emission monitoring.

Interpretable and Granular Video-Based Quantification of Motor Characteristics from the Finger Tapping Test in Parkinson Disease

저자: Unknown

플랫폼: arxiv

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카테고리: cs.CV

PDF URL: https://arxiv.org/pdf/2506.18925.pdf

초록:

Accurately quantifying motor characteristics in Parkinson disease (PD) is crucial for monitoring disease progression and optimizing treatment strategies. The finger-tapping test is a standard motor assessment. Clinicians visually evaluate a patient's tapping performance and assign an overall severity score based on tapping amplitude, speed, and irregularity. However, this subjective evaluation is prone to inter- and intra-rater variability, and does not offer insights into individual motor characteristics captured during this test. This paper introduces a granular computer vision-based method for quantifying PD motor characteristics from video recordings. Four sets of clinically relevant features are proposed to characterize hypokinesia, bradykinesia, sequence effect, and hesitation-halts. We evaluate our approach on video recordings and clinical evaluations of 74 PD patients from the Personalized Parkinson Project. Principal component analysis with varimax rotation shows that the video-based features corresponded to the four deficits. Additionally, video-based analysis has allowed us to identify further granular distinctions within sequence effect and hesitation-halts deficits. In the following, we have used these features to train machine learning classifiers to estimate the Movement Disorder Society Unified Parkinson Disease Rating Scale (MDS-UPDRS) finger-tapping score. Compared to state-of-the-art approaches, our method achieves a higher accuracy in MDS-UPDRS score prediction, while still providing an interpretable quantification of individual finger-tapping motor characteristics. In summary, the proposed framework provides a practical solution for the objective assessment of PD motor characteristics, that can potentially be applied in both clinical and remote settings. Future work is needed to assess its responsiveness to symptomatic treatment and disease progression.

AI-based Approach in Early Warning Systems: Focus on Emergency Communication Ecosystem and Citizen Participation in Nordic Countries

저자: Unknown

초록:

Climate change and natural disasters are recognized as worldwide challenges requiring complex and efficient ecosystems to deal with social, economic, and environmental effects. This chapter advocates a holistic approach, distinguishing preparedness, emergency responses, and postcrisis phases. The role of the Early Warning System (EWS), Risk modeling and mitigation measures are particularly emphasized. The chapter reviews the various Artificial Intelligence (AI)-enabler technologies that can be leveraged at each phase, focusing on the INFORM risk framework and EWSs. Emergency communication and psychological risk perception have been emphasized in emergency response times. Finally, a set of case studies from Nordic countries has been highlighted.

Reinforcement Learning-Based Dynamic Grouping for Tubular Structure Tracking

저자: Unknown

플랫폼: arxiv

발행일: 2025-06-25

카테고리: cs.CV

PDF URL: https://arxiv.org/pdf/2506.18930.pdf

초록:

The computation of minimal paths for the applications in tracking tubular structures such as blood vessels and roads is challenged by complex morphologies and environmental variations. Existing approaches can be roughly categorized into two research lines: the point-wise based models and the segment-wise based models. Although segment-wise approaches have obtained promising results in many scenarios, they often suffer from computational inefficiency and heavily rely on a prescribed prior to fit the target elongated shapes. We propose a novel framework that casts segment-wise tracking as a Markov Decision Process (MDP), enabling a reinforcement learning approach. Our method leverages Q-Learning to dynamically explore a graph of segments, computing edge weights on-demand and adaptively expanding the search space. This strategy avoids the high cost of a pre-computed graph and proves robust to incomplete initial information. Experimental reuslts on typical tubular structure datasets demonstrate that our method significantly outperforms state-of-the-art point-wise and segment-wise approaches. The proposed method effectively handles complex topologies and maintains global path coherence without depending on extensive prior structural knowledge.

Safe Pruning LoRA: Robust Distance-Guided Pruning for Safety Alignment in Adaptation of LLMs

저자: Unknown

플랫폼: arxiv

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카테고리: cs.LG

PDF URL: https://arxiv.org/pdf/2506.18931.pdf

초록:

Fine-tuning Large Language Models (LLMs) with Low-Rank Adaptation (LoRA) enhances adaptability while reducing computational costs. However, fine-tuning can compromise safety alignment, even with benign data, increasing susceptibility to harmful outputs. Existing safety alignment methods struggle to capture complex parameter shifts, leading to suboptimal safety-utility trade-offs. To address this issue, we propose Safe Pruning LoRA (SPLoRA), a novel pruning-based approach that selectively removes LoRA layers that weaken safety alignment, improving safety while preserving performance. At its core, we introduce Empirical-DIEM (E-DIEM), a dimension-insensitive similarity metric that effectively detects safety misalignment in LoRA-adapted models. We conduct extensive experiments on LLMs fine-tuned with mixed of benign and malicious data, and purely benign datasets, evaluating SPLoRA across utility, safety, and reliability metrics. Results demonstrate that SPLoRA outperforms state-of-the-art safety alignment techniques, significantly reducing safety risks while maintaining or improving model performance and reliability. Additionally, SPLoRA reduces inference overhead, making it a scalable and efficient solution for deploying safer and more reliable LLMs. The code is available at https://github.com/AoShuang92/SPLoRA.

AI Safety vs. AI Security: Demystifying the Distinction and Boundaries

저자: Unknown

플랫폼: arxiv

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카테고리: cs.CY

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초록:

Artificial Intelligence (AI) is rapidly being integrated into critical systems across various domains, from healthcare to autonomous vehicles. While its integration brings immense benefits, it also introduces significant risks, including those arising from AI misuse. Within the discourse on managing these risks, the terms "AI Safety" and "AI Security" are often used, sometimes interchangeably, resulting in conceptual confusion. This paper aims to demystify the distinction and delineate the precise research boundaries between AI Safety and AI Security. We provide rigorous definitions, outline their respective research focuses, and explore their interdependency, including how security breaches can precipitate safety failures and vice versa. Using clear analogies from message transmission and building construction, we illustrate these distinctions. Clarifying these boundaries is crucial for guiding precise research directions, fostering effective cross-disciplinary collaboration, enhancing policy effectiveness, and ultimately, promoting the deployment of trustworthy AI systems.

Which Consciousness Can Be Artificialized? Local Percept-Perceiver Phenomenon for the Existence of Machine Consciousness

저자: Unknown

플랫폼: arxiv

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카테고리: q-bio.NC

PDF URL: https://arxiv.org/pdf/2506.18935.pdf

초록:

This paper presents a novel paradigm of the local percept-perceiver phenomenon to formalize certain observations in neuroscientific theories of consciousness. Using this model, a set-theoretic formalism is developed for artificial systems, and the existence of machine consciousness is proved by invoking Zermelo-Fraenkel set theory. The article argues for the possibility of a reductionist form of epistemic consciousness within machines.

Damba-ST: Domain-Adaptive Mamba for Efficient Urban Spatio-Temporal Prediction

저자: Unknown

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카테고리: cs.CV

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초록:

Training urban spatio-temporal foundation models that generalize well across diverse regions and cities is critical for deploying urban services in unseen or data-scarce regions. Recent studies have typically focused on fusing cross-domain spatio-temporal data to train unified Transformer-based models. However, these models suffer from quadratic computational complexity and high memory overhead, limiting their scalability and practical deployment. Inspired by the efficiency of Mamba, a state space model with linear time complexity, we explore its potential for efficient urban spatio-temporal prediction. However, directly applying Mamba as a spatio-temporal backbone leads to negative transfer and severe performance degradation. This is primarily due to spatio-temporal heterogeneity and the recursive mechanism of Mamba's hidden state updates, which limit cross-domain generalization. To overcome these challenges, we propose Damba-ST, a novel domain-adaptive Mamba-based model for efficient urban spatio-temporal prediction. Damba-ST retains Mamba's linear complexity advantage while significantly enhancing its adaptability to heterogeneous domains. Specifically, we introduce two core innovations: (1) a domain-adaptive state space model that partitions the latent representation space into a shared subspace for learning cross-domain commonalities and independent, domain-specific subspaces for capturing intra-domain discriminative features; (2) three distinct Domain Adapters, which serve as domain-aware proxies to bridge disparate domain distributions and facilitate the alignment of cross-domain commonalities. Extensive experiments demonstrate the generalization and efficiency of Damba-ST. It achieves state-of-the-art performance on prediction tasks and demonstrates strong zero-shot generalization, enabling seamless deployment in new urban environments without extensive retraining or fine-tuning.

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