Science Newsletter

Contents

Introduction:

There are 3 main elements in the Science Newsletter is composed. In the first part, we provide articles about central issues for each discipline in this university, and they are provided with one subject for a time. In the second part, we select articles from the top journals in the whole science research. In the third part, we post information about calling papers for international conferences. Hopefully, some of the information in this manuscript may be useful for those who are dedicating to scientific career. Besides, the journals are also posted on the website of our library, and they are available to be accessed any time at http://lib.jsut.edu.cn/2018/1015/c5474a113860/page.htm. If there are any questions or suggestions, please send e-mails to 289595883@qq.com in no hesitate.

Ⅰ Topics

The key word of this month is **Computational Intelligence.** We list several articles which are related to the top concerned topics of computer science researches. The articles are classified in 5 categories, and they are: **Bioinformatics, Computational Biology, Genetics and Genomics, Systems Biology** and **Cloud computing**. Also, the listed articles are all arranged in a descending sort of impact factor in order to make it convenient to read. There are also links to both official site and full text for each article.

BIOINFORMATICS

Nature (impact factor: 64.84) 1 ⊠

Highly accurate protein structure prediction with AlphaFold

John Jumper · Richard Evans · Alexander Pritzel et.al

Abstract:
Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort1,2,3,4, the structures of around 100,000 unique proteins have been determined5, but this represents a small fraction of the billions of known protein sequences6,7. Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are

needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence—the structure prediction component of the 'protein folding problem'8—has been an important open research problem for more than 50 years9. Despite recent progress10,11,12,13,14, existing methods fall far short of atomic accuracy, especially when no homologous structure is available. Here we provide the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated an entirely redesigned version of our neural network-based model, AlphaFold, in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14)15, demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm.

Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition

Kevin Litchfield · James L Reading · Clare Puttick et.al

Abstract:

Checkpoint inhibitors (CPIs) augment adaptive immunity. Systematic pan-tumor analyses may reveal the relative importance of tumor-cell-intrinsic and microenvironmental features underpinning CPI sensitization. Here, we collated whole-exome and transcriptomic data for >1,000 CPI-treated patients across seven tumor types, utilizing standardized bioinformatics workflows and clinical outcome criteria to validate multivariable predictors of CPI sensitization. Clonal tumor mutation burden (TMB) was the strongest predictor of CPI response, followed by total TMB and CXCL9 expression. Subclonal TMB, somatic copy alteration burden, and histocompatibility leukocyte antigen (HLA) evolutionary divergence failed to attain pan-cancer significance. Dinucleotide variants were identified as a source of immunogenic epitopes associated with radical amino acid substitutions and enhanced peptide hydrophobicity/immunogenicity. Copy-number analysis revealed two additional determinants of CPI outcome supported by prior functional evidence: 9q34 (TRAF2) loss associated with response and CCND1 amplification associated with resistance. Finally, single-cell RNA sequencing (RNA-seq) of clonal neoantigen-reactive CD8 tumor-infiltrating lymphocytes (TILs), combined with bulk RNA-seq analysis of CPI-responding tumors, identified CCR5 and CXCL13 as T-cell-intrinsic markers of CPI sensitivity.

Advances in the development of personalized neoantigen-based therapeutic cancer vaccines

Eryn Blass · Patrick A. Ott

Abstract:

Within the past decade, the field of immunotherapy has revolutionized the treatment of many cancers with the development and regulatory approval of various immune-checkpoint inhibitors and chimeric antigen receptor T cell therapies in diverse indications. Another promising approach to cancer immunotherapy involves the use of personalized vaccines designed to trigger de novo T cell responses against neoantigens, which are highly specific to tumours of individual patients, in order to amplify and broaden the endogenous repertoire of tumour-specific T cells. Results from initial clinical studies of personalized neoantigen-based vaccines, enabled by the availability of rapid and cost-effective sequencing and bioinformatics technologies, have demonstrated robust tumour-specific immunogenicity and preliminary evidence of antitumour activity in patients with melanoma and other cancers. Herein, we provide an overview of the complex process that is necessary to generate a personalized neoantigen vaccine, review the types of vaccine-induced T cells that are found within tumours and outline strategies to enhance the T cell responses. In addition, we discuss the current status of clinical studies testing personalized neoantigen vaccines in patients with cancer and considerations for future clinical investigation of this novel, individualized approach to immunotherapy.

Epigenetics, fragmentomics, and topology of cell-free DNA in liquid biopsies

Y. M. Dennis Lo · Diana S. C. Han · Peiyong Jiang, et. Al

Abstract:

Liquid biopsies that analyze cell-free DNA in blood plasma are used for noninvasive prenatal testing, oncology, and monitoring of organ transplant recipients. DNA molecules are released into the plasma from various bodily tissues. Physical and molecular features of cell-free DNA fragments and their distribution over the genome bear information about their tissues of origin. Moreover, patterns of DNA methylation of these molecules reflect those of their tissue sources. The nucleosomal organization and nuclease content of the tissue of origin affect the fragmentation profile of plasma DNA molecules, such as fragment size and end motifs. Besides double-stranded linear fragments, other topological forms of cell-free DNA also exist—namely circular and single-stranded molecules. Enhanced by these features, liquid biopsies hold promise for the noninvasive detection of tissue-specific pathologies with a range of clinical applications.

Computational Biology

A Systems Biology Approach To Disentangle the Direct and Indirect Effects of Global Transcription Factors on Gene Expression in Escherichia coli

Mahesh S. Iyer · Ankita Pal · K. V. Venkatesh

Abstract:

Delineating the pleiotropic effects of global transcriptional factors (TFs) is critical for understanding the system-wide regulatory response in a particular environment. Currently, with the availability of genome-wide TF binding and gene expression data for Escherichia coli, several gene targets can be assigned to the global TFs, albeit inconsistently. Here, using a systematic integrated approach with emphasis on metabolism, we characterized and quantified the direct effects as well as the growth rate-mediated indirect effects of global TFs using deletion mutants of FNR, ArcA, and IHF regulators (focal TFs) under glucose fermentative conditions. This categorization enabled us to disentangle the dense connections seen within the transcriptional regulatory network (TRN) and determine the exact nature of focal TF-driven epistatic interactions with other global and pathway-specific local regulators (iTFs). We extended our analysis to combinatorial deletions of these focal TFs to determine their cross talk effects as well as conserved patterns of regulatory interactions. Moreover, we predicted with high confidence several novel metabolite-iTF interactions using inferred iTF activity changes arising from the allosteric effects of the intracellular metabolites perturbed as a result of the absence of focal TFs. Further, using compendium level computational analyses, we revealed not only the coexpressed genes regulated by these focal TFs but also the coordination of the direct and indirect target expression in the context of the economy of intracellular metabolites. Overall, this study leverages the fundamentals of TF-driven regulation, which could serve as a better template for deciphering mechanisms underlying complex phenotypes.

Remembering the Work of Phillip L. Geissler: A Coda to His Scientific Trajectory

Gregory R Bowman · Stephen J Cox · Christoph Dellago et. all

Abstract:

Phillip L. Geissler made important contributions to the statistical mechanics of biological polymers, heterogeneous materials, and chemical dynamics in aqueous environments. He devised analytical and computational methods that revealed the underlying organization of complex systems at the frontiers of biology, chemistry, and materials science. In this retrospective we celebrate his work at these frontiers.

Simulation of Complex Biomolecular Systems: The Ribosome Challenge

Lars V Bock · Sara Gabrielli · Michal H Kolář et.al

Abstract:

Large biomolecular systems are at the heart of many essential cellular processes. The dynamics and energetics of an increasing number of these systems are being studied by computer simulations. Pushing the limits of length- and timescales that can be accessed by current hard- and software has expanded the ability to describe biomolecules at different levels of detail. We focus in this review on the ribosome, which exemplifies the close interplay between experiment and various simulation approaches, as a particularly challenging and prototypic nanomachine that is pivotal to cellular biology due to its central role in translation. We sketch widely used simulation methods and demonstrate how the combination of simulations and experiments advances our understanding of the function of the translation apparatus based on fundamental physics.

Dispersion-less Kerr solitons in spectrally confined optical cavities

Xiaoxiao Xue · Philippe Grelu · Bofan Yang, et. al

Abstract:

Solitons are self-reinforcing localized wave packets that manifest in the major areas of nonlinear science, from optics to biology and Bose–Einstein condensates. Recently, optically driven dissipative solitons have attracted great attention for the implementation of the chip-scale frequency combs that are decisive for communications, spectroscopy, neural computing, and quantum information processing. In the current understanding, the generation of temporal solitons involves the chromatic dispersion as a key enabling physical effect, acting either globally or locally on the cavity dynamics in a decisive way. Here, we report on a novel class of solitons, both theoretically and experimentally, which builds up in spectrally confined optical cavities when dispersion is practically absent, both globally and locally. Precisely, the interplay between the Kerr nonlinearity and spectral filtering results in an infinite hierarchy of eigenfunctions which, combined with optical gain, allow for the generation of stable dispersion-less dissipative solitons in a previously unexplored regime. When the filter order tends to infinity, we find an unexpected link between dissipative and conservative solitons, in the form of Nyquist-pulse-like solitons endowed with an ultra-flat spectrum. In contrast to the conventional dispersion-enabled nonlinear Schrödinger solitons, these dispersion-less Nyquist solitons build on a fully confined spectrum and their energy scaling is not constrained by the pulse duration. Dispersion-less soliton molecules and

their deterministic transitioning to single solitons are also evidenced. These findings broaden the fundamental scope of the dissipative soliton paradigm and open new avenues for generating soliton pulses and frequency combs endowed with unprecedented temporal and spectral features.

GENETICS AND GENOMICS

SARS-CoV-2 variants, spike mutations and immune escape

William T. Harvey · Alessandro M. Carabelli · Ben Jackson, et. al

Abstract:

Although most mutations in the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) genome are expected to be either deleterious and swiftly purged or relatively neutral, a small proportion will affect functional properties and may alter infectivity, disease severity or interactions with host immunity. The emergence of SARS-CoV-2 in late 2019 was followed by a period of relative evolutionary stasis lasting about 11 months. Since late 2020, however, SARS-CoV-2 evolution has been characterized by the emergence of sets of mutations, in the context of 'variants of concern', that impact virus characteristics, including transmissibility and antigenicity, probably in response to the changing immune profile of the human population. There is emerging evidence of reduced neutralization of some SARS-CoV-2 variants by postvaccination serum; however, a greater understanding of correlates of protection is required to evaluate how this may impact vaccine effectiveness. Nonetheless, manufacturers are preparing platforms for a possible update of vaccine sequences, and it is crucial that surveillance of genetic and antigenic changes in the global virus population is done alongside experiments to elucidate the phenotypic impacts of mutations. In this Review, we summarize the literature on mutations of the SARS-CoV-2 spike protein, the primary antigen, focusing on their impacts on antigenicity and contextualizing them in the protein structure, and discuss them in the context of observed mutation frequencies in global sequence datasets.

Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England

Erik Volz · Swapnil Mishra · Meera Chand et.al

Abstract:

The SARS-CoV-2 lineage B.1.1.7, designated variant of concern (VOC) 202012/01 by Public Health England1, was first identified in the UK in late summer to early

autumn 20202. Whole-genome SARS-CoV-2 sequence data collected from community-based diagnostic testing for COVID-19 show an extremely rapid expansion of the B.1.1.7 lineage during autumn 2020, suggesting that it has a selective advantage. Here we show that changes in VOC frequency inferred from genetic data correspond closely to changes inferred by S gene target failures (SGTF) in community-based diagnostic PCR testing. Analysis of trends in SGTF and non-SGTF case numbers in local areas across England shows that B.1.1.7 has higher transmissibility than non-VOC lineages, even if it has a different latent period or generation time. The SGTF data indicate a transient shift in the age composition of reported cases, with cases of B.1.1.7 including a larger share of under 20-year-olds than non-VOC cases. We estimated time-varying reproduction numbers for B.1.1.7 and co-circulating lineages using SGTF and genomic data. The best-supported models did not indicate a substantial difference in VOC transmissibility among different age groups, but all analyses agreed that B.1.1.7 has a substantial transmission advantage over other lineages, with a 50% to 100% higher reproduction number.

Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program

Daniel Taliun · Daniel N. Harris · Michael D, et.al

Abstract:

The Trans-Omics for Precision Medicine (TOPMed) programme seeks to elucidate the genetic architecture and biology of heart, lung, blood and sleep disorders, with the ultimate goal of improving diagnosis, treatment and prevention of these diseases. The initial phases of the programme focused on whole-genome sequencing of individuals with rich phenotypic data and diverse backgrounds. Here we describe the TOPMed goals and design as well as the available resources and early insights obtained from the sequence data. The resources include a variant browser, a genotype imputation server, and genomic and phenotypic data that are available through dbGaP (Database of Genotypes and Phenotypes)1. In the first 53,831 TOPMed samples, we detected more than 400 million single-nucleotide and insertion or deletion variants after alignment with the reference genome. Additional previously undescribed variants were detected through assembly of unmapped reads and customized analysis in highly variable loci. Among the more than 400 million detected variants, 97% have frequencies of less than 1% and 46% are singletons that are present in only one individual (53% among unrelated individuals). These rare variants provide insights into mutational processes and recent human evolutionary history. The extensive catalogue of genetic variation in TOPMed studies provides unique opportunities for exploring the contributions of rare and noncoding sequence variants to phenotypic variation. Furthermore, combining TOPMed haplotypes with modern imputation methods improves the power and reach of genome-wide association studies to include variants down to a frequency of approximately 0.01%.

Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape

Karolina Matuszek · Mega Kar · Jennifer M, et.al

Abstract

Zoonotic pandemics, such as that caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), can follow the spillover of animal viruses into highly susceptible human populations. The descendants of these viruses have adapted to the human host and evolved to evade immune pressure. Coronaviruses acquire substitutions more slowly than other RNA viruses. In the spike glycoprotein, we found that recurrent deletions overcome this slow substitution rate. Deletion variants arise in diverse genetic and geographic backgrounds, transmit efficiently, and are present in novel lineages, including those of current global concern. They frequently occupy recurrent deletion regions (RDRs), which map to defined antibody epitopes. Deletions in RDRs confer resistance to neutralizing antibodies. By altering stretches of amino acids, deletions appear to accelerate SARS-CoV-2 antigenic evolution and may, more generally, drive adaptive evolution.

Systems Biology

Perturbed iron biology in the prefrontal cortex of people with schizophrenia

Amit Lotan · Sandra Luza · Carlos M, et.al

Abstract

Despite loss of grey matter volume and emergence of distinct cognitive deficits in young adults diagnosed with schizophrenia, current treatments for schizophrenia do not target disruptions in late maturational reshaping of the prefrontal cortex. Iron, the most abundant transition metal in the brain, is essential to brain development and function, but in excess, it can impair major neurotransmission systems and lead to lipid peroxidation, neuroinflammation and accelerated aging. However, analysis of cortical iron biology in schizophrenia has not been reported in modern literature. Using a combination of inductively coupled plasma-mass spectrometry and western blots, we quantified iron and its major-storage protein, ferritin, in post-mortem prefrontal cortex specimens obtained from three independent, well-characterised brain tissue resources. Compared to matched controls (n = 85), among schizophrenia cases (n = 86) we found elevated tissue iron, unlikely to be confounded by demographic and lifestyle variables, by duration, dose and type of antipsychotic medications used or by copper and zinc levels. We further observed a loss of physiologic age-dependent iron accumulation

among people with schizophrenia, in that the iron level among cases was already high in young adulthood. Ferritin, which stores iron in a redox-inactive form, was paradoxically decreased in individuals with the disorder. Such iron-ferritin uncoupling could alter free, chemically reactive, tissue iron in key reasoning and planning areas of the young-adult schizophrenia cortex. Using a prediction model based on iron and ferritin, our data provide a pathophysiologic link between perturbed cortical iron biology and schizophrenia and indicate that achievement of optimal cortical iron homeostasis could offer a new therapeutic target.

Broadening horizons: the role of ferroptosis in cancer

Xin Chen · Rui Kang · Guido Kroemer, et.al

Abstract

The discovery of regulated cell death processes has enabled advances in cancer treatment. In the past decade, ferroptosis, an iron-dependent form of regulated cell death driven by excessive lipid peroxidation, has been implicated in the development and therapeutic responses of various types of tumours. Experimental reagents (such as erastin and RSL3), approved drugs (for example, sorafenib, sulfasalazine, statins and artemisinin), ionizing radiation and cytokines (such as IFNγ and TGFβ1) can induce ferroptosis and suppress tumour growth. However, ferroptotic damage can trigger inflammation-associated immunosuppression in the tumour microenvironment, thus favouring tumour growth. The extent to which ferroptosis affects tumour biology is unclear, although several studies have found important correlations between mutations in cancer-relevant genes (for example, RAS and TP53), in genes encoding proteins involved in stress response pathways (such as NFE2L2 signalling, autophagy and hypoxia) and the epithelial-to-mesenchymal transition, and responses to treatments that activate ferroptosis. Herein, we present the key molecular mechanisms of ferroptosis, describe the crosstalk between ferroptosis and tumour-associated signalling pathways, and discuss the potential applications of ferroptosis in the context of systemic therapy, radiotherapy and immunotherapy.

Emerging concepts in the science of vaccine adjuvants

Shun Yong · Hanqing Wang · Zenan Lin, et.al

Abstract

Adjuvants are vaccine components that enhance the magnitude, breadth and durability of the immune response. Following its introduction in the 1920s, alum remained the only adjuvant licensed for human use for the next 70 years. Since the 1990s, a further

five adjuvants have been included in licensed vaccines, but the molecular mechanisms by which these adjuvants work remain only partially understood. However, a revolution in our understanding of the activation of the innate immune system through pattern recognition receptors (PRRs) is improving the mechanistic understanding of adjuvants, and recent conceptual advances highlight the notion that tissue damage, different forms of cell death, and metabolic and nutrient sensors can all modulate the innate immune system to activate adaptive immunity. Furthermore, recent advances in the use of systems biology to probe the molecular networks driving immune response to vaccines ('systems vaccinology') are revealing mechanistic insights and providing a new paradigm for the vaccine discovery and development process. Here, we review the 'known knowns' and 'known unknowns' of adjuvants, discuss these emerging concepts and highlight how our expanding knowledge about innate immunity and systems vaccinology are revitalizing the science and development of novel adjuvants for use in vaccines against COVID-19 and future pandemics.

Liquid biopsy enters the clinic — implementation issues and future challenges

Michail Ignatiadis · George W. Sledge · Stefanie S. Jeffrey

Abstract

Historically, studies of disseminated tumour cells in bone marrow and circulating tumour cells in peripheral blood have provided crucial insights into cancer biology and the metastatic process. More recently, advances in the detection and characterization of circulating tumour DNA (ctDNA) have finally enabled the introduction of liquid biopsy assays into clinical practice. The FDA has already approved several single-gene assays and, more recently, multigene assays to detect genetic alterations in plasma cell-free DNA (cfDNA) for use as companion diagnostics matched to specific molecularly targeted therapies for cancer. These approvals mark a tipping point for the widespread use of liquid biopsy in the clinic, and mostly in patients with advanced-stage cancer. The next frontier for the clinical application of liquid biopsy is likely to be the systemic treatment of patients with 'ctDNA relapse', a term we introduce for ctDNA detection prior to imaging-detected relapse after curative-intent therapy for early stage disease. Cancer screening and diagnosis are other potential future applications. In this Perspective, we discuss key issues and gaps in technology, clinical trial methodologies and logistics for the eventual integration of liquid biopsy into the clinical workflow.

Engineering organoids

Moritz Hofer · Matthias P. Lutolf

Abstract

Organoids are in vitro miniaturized and simplified model systems of organs that have gained enormous interest for modelling tissue development and disease, and for personalized medicine, drug screening and cell therapy. Despite considerable success in culturing physiologically relevant organoids, challenges remain to achieve real-life applications. In particular, the high variability of self-organizing growth and restricted experimental and analytical access hamper the translatability of organoid systems. In this Review, we argue that many limitations of traditional organoid culture can be addressed by engineering approaches at all levels of organoid systems. We investigate cell surface and genetic engineering approaches, and discuss stem cell niche engineering based on the design of matrices that allow spatiotemporal control of organoid growth and shape-guided morphogenesis. We examine how microfluidic approaches and lessons learnt from organs-on-a-chip enable the integration of mechano-physiological parameters and increase accessibility of organoids to improve functional readouts. Applying engineering principles to organoids increases reproducibility and provides experimental control, which will, ultimately, be required to enable clinical translation.

CLOUD COMPUTING

Parallel convolutional processing using an integrated photonic tensor core

J. Feldmann · N. Youngblood · M. Karpov, et.al

Abstract

With the proliferation of ultrahigh-speed mobile networks and internet-connected devices, along with the rise of artificial intelligence (AI)1, the world is generating exponentially increasing amounts of data that need to be processed in a fast and efficient way. Highly parallelized, fast and scalable hardware is therefore becoming progressively more important2. Here we demonstrate a computationally specific integrated photonic hardware accelerator (tensor core) that is capable of operating at speeds of trillions of multiply-accumulate operations per second (1012 MAC operations per second or tera-MACs per second). The tensor core can be considered as the optical analogue of an application-specific integrated circuit (ASIC). It achieves parallelized photonic in-memory computing using phase-change-material memory arrays and photonic chip-based optical frequency combs (soliton microcombs3). The computation is reduced to measuring the optical transmission of reconfigurable and non-resonant passive components and can operate at a bandwidth exceeding 14 gigahertz, limited only by the speed of the modulators and photodetectors. Given recent advances in hybrid integration of soliton microcombs at microwave line rates3,4,5, ultralow-loss silicon nitride waveguides6,7, and high-speed on-chip detectors and modulators, our approach provides a path towards full complementary

metal–oxide–semiconductor (CMOS) wafer-scale integration of the photonic tensor core. Although we focus on convolutional processing, more generally our results indicate the potential of integrated photonics for parallel, fast, and efficient computational hardware in data-heavy AI applications such as autonomous driving, live video processing, and next-generation cloud computing services.

Molecular imaging in oncology: Current impact and future directions

Steven P. Rowe · Martin G. Pomper

Abstract:

With the rapid growth and development of proton-exchange membrane fuel cell (PEMFC) technology, there has been increasing demand for clean and sustainable global energy applications. Of the many device-level and infrastructure challenges that need to be overcome before wide commercialization can be realized, one of the most critical ones is increasing the PEMFC power density, and ambitious goals have been proposed globally. For example, the short- and long-term power density goals of Japan's New Energy and Industrial Technology Development Organization are 6 kilowatts per litre by 2030 and 9 kilowatts per litre by 2040, respectively. To this end, here we propose technical development directions for next-generation high-power-density PEMFCs. We present the latest ideas for improvements in the membrane electrode assembly and its components with regard to water and thermal management and materials. These concepts are expected to be implemented in next-generation PEMFCs to achieve high power density.

A global inventory of photovoltaic solar energy generating units

L. Kruitwagen · K. T. Story · J. Friedrich，et.al

Abstract:

Photovoltaic (PV) solar energy generating capacity has grown by 41 per cent per year since 20091. Energy system projections that mitigate climate change and aid universal energy access show a nearly ten-fold increase in PV solar energy generating capacity by 20402,3. Geospatial data describing the energy system are required to manage generation intermittency, mitigate climate change risks, and identify trade-offs with biodiversity, conservation and land protection priorities caused by the land-use and land-cover change necessary for PV deployment. Currently available inventories of solar generating capacity cannot fully address these needs1,2,3,4,5,6,7,8,9. Here we provide a global inventory of commercial-, industrial- and utility-scale PV installations (that is, PV generating stations in excess of 10 kilowatts nameplate capacity) by using

a longitudinal corpus of remote sensing imagery, machine learning and a large cloud computation infrastructure. We locate and verify 68,661 facilities, an increase of 432 per cent (in number of facilities) on previously available asset-level data. With the help of a hand-labelled test set, we estimate global installed generating capacity to be 423 gigawatts (−75/+77 gigawatts) at the end of 2018. Enrichment of our dataset with estimates of facility installation date, historic land-cover classification and proximity to vulnerable areas allows us to show that most of the PV solar energy facilities are sited on cropland, followed by aridlands and grassland. Our inventory could aid PV delivery aligned with the Sustainable Development Goals.

Direct radiative effects of airborne microplastics

Laura E. Revell · Peter Kuma · Eric C. Le Ru, et.al

Abstract:

Microplastics are now recognized as widespread contaminants in the atmosphere, where, due to their small size and low density, they can be transported with winds around the Earth[1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25]. Atmospheric aerosols, such as mineral dust and other types of airborne particulate matter, influence Earth's climate by absorbing and scattering radiation (direct radiative effects) and their impacts are commonly quantified with the effective radiative forcing (ERF) metric[26]. However, the radiative effects of airborne microplastics and associated implications for global climate are unknown. Here we present calculations of the optical properties and direct radiative effects of airborne microplastics (excluding aerosol–cloud interactions). The ERF of airborne microplastics is computed to be 0.044 ± 0.399 milliwatts per square metre in the present-day atmosphere assuming a uniform surface concentration of 1 microplastic particle per cubic metre and a vertical distribution up to 10 kilometres altitude. However, there are large uncertainties in the geographical and vertical distribution of microplastics. Assuming that they are confined to the boundary layer, shortwave effects dominate and the microplastic ERF is approximately -0.746 ± 0.553 milliwatts per square metre. Compared with the total ERF due to aerosol–radiation interactions[27] (−0.71 to −0.14 watts per square metre), the microplastic ERF is small. However, plastic production has increased rapidly over the past 70 years[28]; without serious attempts to overhaul plastic production and waste-management practices, the abundance and ERF of airborne microplastics will continue to increase.

Aerosol invigoration of atmospheric convection through increases in humidity

Tristan H Abbott · Timothy W Cronin

Abstract:

Cloud-aerosol interactions remain a major obstacle to understanding climate and severe weather. Observations suggest that aerosols enhance tropical thunderstorm activity; past research, motivated by the importance of understanding aerosol impacts on clouds, has proposed several mechanisms that could explain that observed link. We find that high-resolution atmospheric simulations can reproduce the observed link between aerosols and convection. However, we also show that previously proposed mechanisms are unable to explain the invigoration. Examining underlying processes reveals that, in our simulations, high aerosol concentrations increase environmental humidity by producing clouds that mix more condensed water into the surrounding air. In turn, higher humidity favors large-scale ascent and stronger convection. Our results provide a physical reason to expect invigorated thunderstorms in high-aerosol regions of the tropics.

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Ⅱ Concentration

Physics

Metalearning Generalizable Dynamics from Trajectories

Qiaofeng Li, Tianyi Wang, Vwani Roychowdhury, et.al.

Abstract

We present the interpretable meta neural ordinary differential equation (iMODE) method to rapidly learn generalizable (i.e., not parameter-specific) dynamics from trajectories of multiple dynamical systems that vary in their physical parameters. The iMODE method learns metaknowledge, the functional variations of the force field of dynamical system instances without knowing the physical parameters, by adopting a bilevel optimization framework: an outer level capturing the common force field form among studied dynamical system instances and an inner level adapting to individual system instances. A priori physical knowledge can be conveniently embedded in the neural network architecture as inductive bias, such as conservative force field and Euclidean symmetry. With the learned metaknowledge, iMODE can model an unseen system within seconds, and inversely reveal knowledge on the physical parameters of a system, or as a neural gauge to "measure" the physical parameters of an unseen system with observed trajectories. iMODE can be generally applied to a dynamical system of an arbitrary type or number of physical parameters and is validated on bistable, double pendulum, Van der Pol, Slinky, and reaction-diffusion systems.

Brain criticality predicts individual levels of inter-areal synchronization in human electrophysiological data

Fuscà, Marco, Siebenhühner, Felix, et.al.

Abstract

Neuronal oscillations and their synchronization between brain areas are fundamental for healthy brain function. Yet, synchronization levels exhibit large inter-individual variability that is associated with behavioral variability. We test whether individual synchronization levels are predicted by individual brain states along an extended regime of critical-like dynamics – the Griffiths phase (GP). We use computational modelling to assess how synchronization is dependent on brain criticality indexed by long-range temporal correlations (LRTCs). We analyze LRTCs and synchronization of oscillations

from resting-state magnetoencephalography and stereo-electroencephalography data. Synchronization and LRTCs are both positively linearly and quadratically correlated among healthy subjects, while in epileptogenic areas they are negatively linearly correlated. These results show that variability in synchronization levels is explained by the individual position along the GP with healthy brain areas operating in its subcritical and epileptogenic areas in its supercritical side. We suggest that the GP is fundamental for brain function allowing individual variability while retaining functional advantages of criticality.

Emergent structure and dynamics of tropical forest-grassland landscapes

Wuyts, Bert, Sieber, Jan

Abstract

Previous work indicates that tropical forest can exist as an alternative stable state to savanna. Therefore, perturbation by climate change or human impact may lead to crossing of a tipping point beyond which there is rapid forest dieback that is not easily reversed. A hypothesized mechanism for such bistability is feedback between fire and vegetation, where fire spreads as a contagion process on grass patches. Theoretical models have largely implemented this mechanism implicitly, by assuming a threshold dependence of fire spread on flammable vegetation. Here, we show how the nonlinear dynamics and bistability emerge spontaneously, without assuming equations or thresholds for fire spread. We find that the forest geometry causes the nonlinearity that induces bistability. We demonstrate this in three steps. First, we model forest and fire as interacting contagion processes on grass patches, showing that spatial structure emerges due to two counteracting effects on the forest perimeter: forest expansion by dispersal and forest erosion by fires originating in adjacent grassland. Then, we derive a landscape-scale balance equation in which these two effects link forest geometry and dynamics: Forest expands proportionally to its perimeter, while it shrinks proportionally to its perimeter weighted by adjacent grassland area. Finally, we show that these perimeter quantities introduce nonlinearity in our balance equation and lead to bistability. Relying on the link between structure and dynamics, we propose a forest resilience indicator that could be used for targeted conservation or restoration.

MATERIALS

2D quasi-layered material with domino structure

Lan, Haihui, Wang, et.al.

Abstract

Interlayer coupling strength dichotomizes two-dimensional (2D) materials into layered

and non-layered types. Traditionally, they can be regarded as atomic layers intrinsically linked via van der Waals (vdW) forces or covalent bonds, oriented orthogonally to their growth plane. In our work, we report a material system that differentiates from layered and non-layered materials, termed quasi-layered domino-structured (QLDS) materials, effectively bridging the gap between these two typical categories. Considering the skewed structure, the force orthogonal to the 2D QLDS-GaTe growth plane constitutes a synergistic blend of vdW forces and covalent bonds, with neither of them being perpendicular to the 2D growth plane. This unique amalgamation results in a force that surpasses that in layered materials, yet is weaker than that in non-layered materials. Therefore, the lattice constant contraction along this unique orientation can be as much as 7.7%, tantalizingly close to the theoretical prediction of 10.8%. Meanwhile, this feature endows remarkable anisotropy, second harmonic generation enhancement with a staggering susceptibility of 394.3 pm V−1. These findings endow further applications arranged in nonlinear optics, sensors, and catalysis.

Large area inkjet-printed OLED fabrication with solution-processed TADF ink

Kant, Chandra, Shukla, et.al.

Abstract

This work demonstrates successful large area inkjet printing of a thermally activated delayed fluorescence (TADF) material as the emitting layer of organic light-emitting diodes (OLEDs). TADF materials enable efficient light emission without relying on heavy metals such as platinum or iridium. However, low-cost manufacturing of large-scale TADF OLEDs has been restricted due to their incompatibility with solution processing techniques. In this study, we develop ink formulation for a TADF material and show successful ink jet printing of intricate patterns over a large area (6400 mm2) without the use of any lithography. The stable ink is successfully achieved using a non-chlorinated binary solvent mixture for a solution processable TADF material, 3‐(9,9‐dimethylacridin‐10(9H)‐yl)‐9H‐xanthen‐9‐one dispersed in 4,4'-bis-(N-carbazolyl)-1,1'-biphenyl host. Using this ink, large area ink jet printed OLEDs with performance comparable to the control spin coated OLEDs are successfully achieved. In this work, we also show the impact of ink viscosity, density, and surface tension on the droplet formation and film quality as well as its potential for large-area roll-to-roll printing on a flexible substrate. The results represent a major step towards the use of TADF materials for large-area OLEDs without employing any lithography.

Design of a trigonal halide superionic conductor by regulating cation order-disorder

Seungju Yu, Joohyeon Noh, Byunghoon Kim, et.al.

Abstract

Lithium-metal-halides have emerged as a class of solid electrolytes that can deliver superionic conductivity comparable to that of state-of-the-art sulfide electrolytes, as well as electrochemical stability that is suitable for high-voltage (>4 volt) operations. We show that the superionic conduction in a trigonal halide, such as Li_3MCl_6 [where metal (M) is Y or Er], is governed by the in-plane lithium percolation paths and stacking interlayer distance. These two factors are inversely correlated with each other by the partial occupancy of M, serving as both a diffusion inhibitor and pillar for maintaining interlayer distance. These findings suggest that a critical range or ordering of M exists in trigonal halides, and we showcase the achievement of high ionic conductivity by adjusting the simple M ratio (per Cl or Li). We provide general design criteria for superionic trigonal halide electrolytes.

CHEMISTRY

Parallel Nanosheet Arrays for Industrial Oxygen Production

Jianxin Kang, Gui Liu, Qi Hu, et al.

Abstract

According to the traditional nucleation theory, crystals in solution nucleate under thermal fluctuations with random crystal orientation. Thus, nanosheet arrays grown on a substrate always exhibit disordered arrangements, which impede mass transfer during catalysis. To overcome this limitation, here, we demonstrate stress-induced, oriented nucleation and growth of nanosheet arrays. A regularly self-growing parallel nanosheet array is realized on a curved growth substrate. During electrochemical oxygen production, the ordered array maintains a steady flow of liquids in the microchannels, suppressing the detrimental production of flow-blocking oxygen bubbles typical of randomly oriented nanosheet arrays. Controllable parallel arrays, fully covered fluffy-like ultrathin nanosheets, and amorphous disordered structures altogether enable full-scale design of hierarchical interfaces from the micro- to the atomic scale, significantly improving the otherwise sluggish kinetics of oxygen evolution toward industrial ultrafast production. Record-high ultrafast oxygen production of 135 L·min–1·m–2 with high working current of 4000 mA·cm–2 is steadily achieved at a competitively low cell voltage of 2.862 V. These results and related insights lay the basis for further developments in oriented nucleation and growth of crystals beyond classical nucleation approaches, with benefits for large-scale, industrial electrochemical processes as shown here for ultrafast oxygen production.

Electrocatalytic valorization of lignocellulose-derived aromatics at industrial-scale current densities

Peng, Tao, Zhang, et al.

Abstract

Electrocatalytic hydrogenation of lignocellulosic bio-oil to value-added chemicals offers an attractive avenue to use the increasing intermittent renewable electricity and biomass-derived feedstocks. However, to date the partial current densities to target products of these reactions are lower than those needed for industrial-scale productivity, which limits its prospects. Here we report a flow-cell system equipped with a Rh diffusion electrode to hydrogenate lignocellulose-derived aromatic monomers, such as furans and lignin monomers, to value-added chemicals. We achieve high faradaic efficiencies up to 64% at industrial-scale current densities of $300–500\,\mathrm{mA\,cm^{-2}}$, representing high productivities to target products. A screening of electrocatalysts indicates that only by highly-electrolyte-permeable Rh diffusion electrodes are we able to unite current density with faradaic efficiency. We apply in-situ infrared reflection–absorption spectroscopy to investigate the electrode-potential-dependent reaction pathways and intermediates, confirming a wide potential window for efficient electrocatalytic hydrogenation of lignocellulose-derived aromatics to target products.

Improving the photovoltage of Cu2O photocathodes with dual buffer layers

Wangwang Xu, Jiantao Li, Xiaobin Liao, et al.

Abstract

Cuprous oxide (Cu2O) is a promising oxide material for photoelectrochemical water splitting (PEC), and increasing its photovoltage is the key to creating efficient overall PEC water-splitting devices. Previous reports are mostly focused on optimizing the energy band alignment between Cu2O and the n-type buffer layer to improve the photovoltage of Cu2O photocathodes. However, the band alignment between the n-type buffer layer and the protective layer is often ignored. In this work, Cu2O photocathodes with a single buffer layer (Ga2O3) and dual buffer layers (Ga2O3/ZnGeOx) are fabricated, and their PEC performances are compared. Results show that after inserting the second buffer layer (ZnGeOx), the onset potential of the Cu2O photocathode increases by 0.16 V. Operando electrochemical impedance spectroscopy measurements and analysis of the energy-level diagrams of each layer show that an energy level gradient between Ga2O3 and TiO2 is created when ZnGeOx is introduced, which eliminates the potential barrier at the interface of Ga2O3/TiO2 and improves the photovoltage of the Cu2O photocathode. Our work provides an effective approach to improve the photovoltage of photoelectrodes for solar water splitting by introducing dual buffer layers.

Morphologic alterations of the fear circuitry: the role of sex hormones and oral contraceptives AMORIS cohort

Brouillard, Alexandra, Davignon, et al.

Abstract

Background: Endogenous sex hormones and oral contraceptives (OCs) have been shown to influence key regions implicated in fear processing. While OC use has been found to impact brain morphology, methodological challenges remain to be addressed, such as avoiding selection bias between OC users and non-users, as well as examining potential lasting effects of OC intake.Objective: We investigated the current and lasting effects of OC use, as well as the interplay between the current hormonal milieu and history of hormonal contraception use on structural correlates of the fear circuitry. We also examined the role of endogenous and exogenous sex hormones within this network.We recruited healthy adults aged 23-35 who identified as women currently using (n=62) or having used (n=37) solely combined OCs, women who never used any hormonal contraceptives (n=40), or men (n=41). Salivary endogenous sex hormones and current users' salivary ethinyl estradiol (EE) were assessed using liquid chromatography -tandem mass spectrometry. Using structural magnetic resonance imaging, we extracted surface-based gray matter volumes (GMVs) and cortical thickness (CT) for regions of interest of the fear circuitry. Exploratory whole-brain analyses were conducted with surface-based and voxel-based morphometry methods.Results: Compared to men, all three groups of women exhibited a larger GMV of the dorsal anterior cingulate cortex, while only current users showed a thinner ventromedial prefrontal cortex. Irrespective of the menstrual cycle phase, never users exhibited a thicker right anterior insular cortex than past users. While associations with endogenous sex hormones remain unclear, we showed that EE dosage in current users had a greater influence on brain anatomy compared to salivary EE levels and progestin androgenicity, with lower doses being associated with smaller cortical GMVs. Discussion: Our results highlight a sex difference for the dorsal anterior cingulate cortex GMV (a fearpromoting region), as well as a reduced CT of the ventromedial prefrontal cortex (a fear-inhibiting region) specific to current OC use. Precisely, this finding was driven by lower EE doses. These findings may represent structural vulnerabilities to anxiety and stress-related disorders. We showed little evidence of durable anatomical effects, suggesting that OC intake can (reversibly) affect fear-related brain morphology.

The transformative power of transformers in protein structure prediction

Moussad, Bernard, Roche, et al.

Abstract

Transformer neural networks have revolutionized structural biology with the ability to predict protein structures at unprecedented high accuracy. Here, we report the predictive modeling performance of the state-of-the-art protein structure prediction methods built on transformers for 69 protein targets from the recently concluded 15th Critical Assessment of Structure Prediction (CASP15) challenge. Our study shows the power of transformers in protein structure modeling and highlights future areas of improvement.

Brain criticality predicts individual levels of inter-areal synchronization in human electrophysiological data

Fuscà, Marco, Siebenhühner, et al.

Abstract

Neuronal oscillations and their synchronization between brain areas are fundamental for healthy brain function. Yet, synchronization levels exhibit large inter-individual variability that is associated with behavioral variability. We test whether individual synchronization levels are predicted by individual brain states along an extended regime of critical-like dynamics – the Griffiths phase (GP). We use computational modelling to assess how synchronization is dependent on brain criticality indexed by long-range temporal correlations (LRTCs). We analyze LRTCs and synchronization of oscillations from resting-state magnetoencephalography and stereo-electroencephalography data. Synchronization and LRTCs are both positively linearly and quadratically correlated among healthy subjects, while in epileptogenic areas they are negatively linearly correlated. These results show that variability in synchronization levels is explained by the individual position along the GP with healthy brain areas operating in its subcritical and epileptogenic areas in its supercritical side. We suggest that the GP is fundamental for brain function allowing individual variability while retaining functional advantages of criticality.

Ⅲ   Calling for papers

ISAI--Eɪ 2024

Submission deadline: **Dec 1, 2023**
Conference date: **Apr 25, 2024 - Apr 27, 2024**
Full name: **2024 the 4th International Symposium on AI (ISAI 2024)**
Location: **Chengdu, China**
Website: http://www.isai.org/

I ISAI 2024, 2024 the 4th International Symposium on AI. It's event on research related to learning and reasoning in the presence of AI. ISAI 2024 will be held in Chengdu, China, on April 25-27, 2024. It's organized by Sichuan Institute of Electronics, and hosted by Xihua University, co-organized by Southwest Jiaotong University and Sichuan University, China; technically supported by Key Lab of Cloud Computing & Intelligent Technology, Sichuan Province, and Chongqing University of Posts and Telecommunications, ect...

ISAI 2024 keeps working on itself as an event whose aim is to provide this chance and platform for the researchers from academia, industry, and government institutions to exchange and present the novel research on artificial intelligence.

We sincerely invite you to participate in ISAI 2024 in Chengdu!

*ISAI 2024 provides online session for whom can't attend the conference in person.

Topics include, but not limited to:
- Topics of interest include, but are not limited to:
- AI and Creativity
- Deep Learning
- Evolutionary Computing
- Fuzzy Systems
- Hybrid Intelligent Systems
- Industrial Applications of AI
- Intelligence and Cybersecurity
- Intelligent User Interfaces
- Knowledge Representation and Reasoning
- Knowledge-Based Systems
- Ambient Intelligence
- Machine Learning
- Model-Based Reasoning
- Natural Language Processing
- Neural Networks
- Ontologies

ICSCA 2024

Submission deadline: **Dec 5, 2023**

Conference date: **Feb 1, 2024 - Feb 3, 2024**

Full name: **2024 13th International Conference on Software and Computer Applications**

Location: **Bali Island, Indonesia**

Website: http://www.icsca.org/

We are proud to bring you to Bali, Indonesia to attend 2024 13th International Conference on Software and Computer Applications (ICSCA 2024) during 1-3 February, 2024.

The success story of ICSCA includes the organization of 12 conferences taking part worldwide. The history of ICSCA started in 2012 in Singapore, next it was hosted in quite a number of countries and regions including France and Great Britain, Hong Kong, Thailand, Brunei, and last 4 years it was organized in Malaysia.

We invites you to publish an extended version of ICSCA 2024 paper. Please make sure you have added at least 30% of a new contents.

■ Journal of Advances in Information Technology

Indexing: ESCI (Web of Science), Scopus, CNKI, etc. http://www.jait.us/

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■ International Journal of Software Engineering and Computer Systems

The IJSECS is reviewed by international and local researchers and is published by UMP Publisher https://ijsecs.ump.edu.my/index.php/en/

★ Speakers ★

Prof. Witold Pedrycz, IEEE Life Fellow, University of Alberta, Edmonton, Canada

Agung Trisetyarso, Bina Nusantara University, Indonesia

Sergei Gorlatch, University of Muenster, Germany

Mohammad Akour, Prince Sultan University, Saudi Arabia

Hoshang Kolivand, Liverpool John Moores University, UK

Mohamed Bahaj, University Hassan 1st Faculty of Sciences & Technologies Settat Morocco, Morocco

Topics of interest for submission include, but are not limited to:

Track 1. Software Engineering

Requirements Engineering

Software Architecture and Design

Software Quality Assurance and Usability Issues

Empirical Software Engineering

Formal Methods

Modern Programming Techniques

Software Applications for I4.0

Mobile Applications

Augmented Reality

Distributed and parallel software systems
Embedded and real-time software systems

Track 2. Computer Applications
Operating Systems
Cyber-Physical Systems
IoT and Cloud Computing
Information Systems
Blockchain Technology
Information Security and Forensics
Computer-based Educational Technologies
Social Networks
Bio-informatics
Economic and Financial Systems

Track 3. Computational Intelligence and AI techniques
Algorithms and Protocols
Big Data
Meta-heuristics Algorithms
High Performance Computing
Natural Language Processing
Image Processing
Intelligent Human Computer Interaction
Robotics
Scientific Computing
Cost Modeling and analysis
More Topics, please visit at http://www.icsca.org/cfp.html

ICIAI--Eɪ 2024

Submission deadline: Dec 10, 2023

Conference date: Mar 16, 2024 - Mar 18, 2024

Full name: 2024 the 8th International Conference on Innovation in Artificial Intelligence (ICIAI 2024)

Location: Tokyo, Japan

Website: http://www.iciai.org

2024 the 8th International Conference on Innovation in Artificial Intelligence (ICIAI 2024) will be held in Tokyo, Japan during March 16-18, 2024. ICIAI 2024 will bring together an international community of experts to discuss the state-of-the-art for new research results, perspectives of future developments, and innovative applications relevant to Artificial Intelligence, mechatronics, robotics, control, and automation.

ICIAI2024 is co-sponsored by Waseda University, Japan and Research Institute of Big Data Analytics, Xi'an Jiaotong-Liverpool University, China. Prof. Steven Guan (Xi'an Jiaotong-Liverpool University, China) and Prof. Hayato YAMANA (Waseda University, Japan) take charge of the Conference Co-chairs.

Artificial intelligence (AI) is wide-ranging branch of computer science concerned with building smart machines capable of performing tasks that typically require human intelligence. AI is an interdisciplinary science with multiple approaches, but advancements in machine learning and deep learning are creating a paradigm shift in virtually every sector of the tech industry.

Topics of interest include, but are not limited to:

- Artificial Intelligence and Technology
- Natural Language Processing
- Computer Vision
- Bioinformatics
- Robotics and Related Fields
- Expert Systems
- Multi-agent Systems
- Speech Understanding
- Knowledge Engineering
- Distributed Intelligent Processing
- Concurrent and Parallel Processing
- Intelligent Database Systems
- Supervised and Unsupervised Learning
- Neural Network Theory and Architectures
- Hardware Implementations
- Fuzzy Logic
- Fuzzy Optimisation

- Fuzzy Control
- Fuzzy Computing with Words
- Theory of Evolutionary Algorithms
- Evolutionary Design
- Evolutionary Scheduling and Optimisation
- Rough Sets Theory: Foundations and Applications
- Data Mining
- Artificial Intelligence in Scheduling and Optimization
- Artificial Intelligence in Modelling and Simulation
- Various Applications

ACEE 2024

Submission deadline:	**Dec 10, 2023**
Conference date:	**Mar 15, 2024 - Mar 17, 2024**
Full name:	**2024 The 2nd Asia Pacific Computer Systems Conference (APCS 2024)**
Location:	**Honolulu, Hawaii, USA**
Website:	http://apcs.net/

The 2nd Asia Pacific Computer Systems Conference (APCS 2024) will be held at Honolulu, Hawaii, USA during March 15-17, 2024.

APCS is premier research conference that emphasis on design, implement and manage computer systems which are present in every aspect of human activities, such as manufacturing, communications, defense, transportation, aerospace, hazardous environments, energy, and health care. The computer systems are frequently distributed over heterogeneous networks and processing large amount data. Computer systems arises from many factors, including the dynamic environments and scenarios these systems operate in; demanding and sometimes conflicting requirements in functionality, efficiency, scalability, security, dependability and adaptability; as well as the large variation in development methodology, programming languages and implementation details. The key issues in these systems include performance, real-time behavior, fault tolerance, security, adaptability, development time and cost, and long life concerns.

The goal of this conference is to bring together industrial, academic, and government experts, from a variety of application domains and software disciplines, to discuss how the disciplines' problems and solution techniques interact within the whole system. Researchers, practitioners, tool developers and users, and technology transfer experts are all welcome.

* The organizing committee will not ask delegates to provide credit card information for any purpose. The registration will be completed only via conference system. Please be alert. Considering the on-going Covid-19 pandemic, there is currently uncertainty in the format of the Conference. However, the safety of our speakers and attendees will remain of paramount concern. Thus, we will be fully prepared to deliver a virtual conference.

Topics of interest for submission include, but are not limited to:

- Language support and runtime systems
- Verification, validation, and testing
- Systems security and privacy
- Database systems and data analytics frameworks
- Virtualization and virtualized systems
- Mobile and pervasive systems
- Bio-inspired AI
- Communication, electronics and power systems

- Tracing, analysis, transformation of systems
- Model-driven development
- Cognitive computing
- Parallelism, concurrency, and multicore systems
- Human-Robot interactions
- Reverse engineering and refactoring
- Big data management
- Ambient intelligence, pervasive computing
- Ubiquitous computing, context awareness, sensor networks
- Safety-critical and fault-tolerant architectures
- Adaptive, self-managing and multi-agent systems
- Real-time, hybrid and embedded systems
- Cloud computing and AI
- Mining software repositories
- Operating and distributed systems
- File, storage, and non-volatile memory systems