

ICICS 2026

International Conference on Informatics and Computer Science

The International Conference on Informatics and Computer Science (ICICS 2026) will bring together leading researchers, academicians, and industry experts to present the latest innovations, trends, and challenges in computer science, informatics, and interdisciplinary applications. The conference provides an international forum for exchanging ideas, fostering collaboration, and advancing knowledge in emerging domains of digital transformation, artificial intelligence, and computational sciences.

As part of the ICICS-2026 Conference, a **special symposium** will be held for doctoral students to present and discuss their research.

We invite high-quality submissions of original research papers, case studies, and review articles addressing theoretical foundations, innovative methodologies, and real-world applications.

Venue - [University of Georgia \(UG\)](#), Tbilisi, Georgia

See news about the conference on the [ICICS-2026 website](#)

Social Program & Cultural Heritage

The ICICS 2026 conference offers a rich social program including a welcome reception, gala dinner, and guided tours of the ancient city of Mtskheta cultural heritage sites.



Topics of Interest

Machine Learning and Cognitive Modeling
Information and Communication Technologies
Blockchain and Distributed Ledger Technologies
Computational Mathematics and Modeling
Logic and Combinatorial Methods
Adaptive and Reconfigurable Systems

Reliability, Risk Analysis and Fault-Tolerant Design
Bioinformatics and Computational Biology
Cybersecurity and Privacy
Interdisciplinary Applications Across Science,
Engineering, Economics, Health Informatics
Special Symposium for Doctoral Students

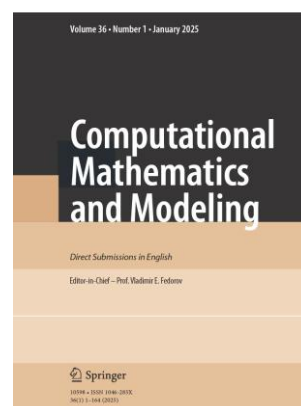
Conference Proceedings

Accepted articles will be published after conference with Digital Object Identifiers (DOIs) by The **University of Georgia Publishing House**, in the **Conference Section**.



High-quality papers presented at the ICICS 2026 after the conference will be selected for publication in the **Springer Nature** journal **“Computational Mathematics and Modeling”**, which is a research journal focusing on numerical and analytical methods of computational mathematics, mathematical modeling. Authors of selected papers will be invited to submit extended versions to the journal after the conference, accompanied by detailed publication guidelines.

Articles will be indexed in: Scopus, Google Scholar, Research Gate. Metrics of Journal: artificial h-index 18, SCImago Journal Rank (SJR) 0.168, Impact Score 0.49, ISSN 1046283X, Best Quartile Q4.



Paper Submission Guidelines

Full papers must present original and unpublished work. Submissions should be written in English and formatted according to the conference template. Authors are encouraged to use LaTeX to format their papers, using the style file and template below, you can also use MS Word. The formatted paper must be converted to PDF file and the number of pages should not exceed 4, please be careful that the paper size is set to A4. The template is based on the [IEEE style](#).

Important dates

Conference Dates	June 18-20, 2026
Papers Submission	March 2, 2026
Notification of acceptance	March 23, 2026
Final Papers due	April 24, 2026
Registration Dates	May 29, 2026
Final Program Publication	June 5, 2026

Registration Fees

	Until May 1, 2026	After May 1, 2026
Regular (International/Local)	170€/170₾	200€/200₾
Student (Certificate required)	50€/50₾	75€/75₾
Online Participants	100€/100₾	150€/150₾
Accompanying person	70€/70₾	100€/100₾
Tour in ancient city of Mtskheta		50€/50₾

Registration fee includes: The possibility of submitting one presentation, access to all sessions of the conference program, documentation, lunches, coffee breaks, and Banquet.

Accompanying Person Registration fee includes: Lunches, coffee breaks, Banquet.

Participation in the conference is free for members of the program committee and plenary speakers.

Registration

[ICICS-2026 Registration form](#)

All participants are kindly requested to fill the Registration Form before May 29, 2026

Transfer type: *

Bank transfer (Requisites: GEL | EURO)

Committees

Conference Chair:

Konstantine Topuria — Rector, University of Georgia

Co-Chairs:

Merab Topuria — Director, School of Science and Technology, University of Georgia

Sergo Tsiramua — Director, Institute of Informatics, University of Georgia

Zurab Tskiria — Vice Rector for Academic and IT Affairs, University of Georgia

Sulkhan Sulkhanishvili — Head, Department of Informatics, University of Georgia

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Plenary Speakers



Dr. Paul de Souza is the founder of the Cyber Security Forum Initiative (CSFI). Dr. de Souza has over 25 years of cybersecurity experience. He is faculty at George Washington University; designed AT&T's Managed Security Services networks as Chief Security Engineer; engineered solutions for CSC and U.S. Robotics; consults for governments, militaries, and corporations worldwide; and served as Federal Director of Training and Education for Norman Data Defense Systems.

Dr. de Souza serves as a CENTRIC (Centre of Excellence in Terrorism, Resilience, Intelligence & Organized Crime Research) Visiting Researcher at Sheffield Hallam University, U.K., and as a Guest Lecturer at the Swedish Defence University (SEDU) Försvarshögskolanand; former Institute of World Politics Board of Advisors for the Cyber Intelligence Initiative (Ci2) in Washington, D.C.; and served as an Advisor for the

MCPA (Military Cyber Professionals Association). He is a Cyber SME NATO Instructor and an Order of Thor Medal recipient.

He is a Negev Hi-Tech Faculty Startup Accelerator Advisor for Ben-Gurion University of the Negev, Israel, and an Advisory Board member at IntellCorp (Lisbon, Portugal – Counter-Terrorism / Counter-Intelligence / Cyber). He has been a Visiting Research Fellow at the National Security Studies, Tel Aviv University, Israel (INSS) – Cyber Security and Military & Strategic Affairs Programs. He has completed the Executive Program in Counter-Terrorism Studies from the Interdisciplinary Center (IDC) Herzliya in Israel. He is also a Cybersecurity Exec Ed alum at Harvard Kennedy School. He serves as an American Public University Ambassador, a Cybersecurity Programs Advisory Board Member at Capitol Technology University, a Cybersecurity Advisory Committee member for the Cybersecurity Risk Management Master's program at Georgetown University, Washington, D.C., a Professor of Cyber Threat Intelligence at The University of Georgia, Tbilisi, and an Executive in Residence at the Geneva Centre for Security Policy (GCSP), Geneva, Switzerland (CTI Information Sharing Policy Project Lead). Cyber Warfare Documentary Research Advisor for the documentary "Dawn of Cyber Warfare."

Dr. de Souza has a master's degree in National Security Studies (M.A.) with a concentration in Terrorism from American Military University, West Virginia, and a Ph.D. in Critical Infrastructure from Capitol Technology University, Maryland. Dr. de Souza is pursuing an LL.M. in Digital Law and Technology at Université catholique de Lyon, focused on European Cyber Law.



Mark Borodovsky is a Regents' Professor in the Georgia Tech and Emory Department of Biomedical Engineering in Atlanta, Georgia. His research focuses on computational genome analysis, particularly on developing accurate algorithms for whole-genome gene prediction — the fundamental first step in deciphering the multilayered functional information encoded in DNA sequences. This work led to the development of the GeneMark family of gene finders, widely used for the annotation of prokaryotic and eukaryotic genomes as well as metagenomes. He is the founder of the Georgia Tech graduate programs in Bioinformatics and an elected Fellow of the International Society for Computational Biology.

Efficient Gene Prediction Algorithms Employing Probabilistic Models of Genome Organization

Abstract: Over the past four decades, bioinformatics has emerged as a new field of applied mathematics dedicated to developing efficient methods for analyzing the rapidly growing volumes of biological sequences - DNA, RNA and proteins.

A central challenge in bioinformatics is the functional interpretation of genomes, particularly the prediction of protein-coding regions. Modeling genomic sequences using Markov chains and hidden Markov models (HMMs) has allowed the gene prediction problem to be framed as one of pattern recognition and optimization. Notably, representing genome through hidden semi-Markov model (HSMM), parameterized through either supervised or unsupervised training has proven highly effective. Within this framework, gene prediction is achieved by applying dynamic programming optimization algorithms to produce the most likely parse of a genomic sequence into segments with distinct functional roles.

In recent years, data on RNA transcripts and protein sequences have become increasingly abundant. Integrating this additional information into the optimization algorithms has significantly constrained the space of possible genome parses (gene annotations) and improved prediction accuracy.

In this talk, we present several gene prediction methods developed in our lab (<https://genemark.bme.gatech.edu>).



Michel Daydé – CNRS/IRIT - Toulouse Institute for Research in Computer Science, University of Toulouse, Toulouse INP - National Polytechnic Institute of Toulouse.

Exascale Computing and New Computing Paradigms

Abstract: The importance of calculus does not appear clearly to the general public, even though it is at the heart of changes in our societies for example with artificial intelligence that benefits from the huge data volumes and computing resources available nowadays. The talk is an attempt to cover the main topics related to exascale computing consequence of the growing application requirements. We enumerate some of the main exascale applications, and actually not only scientific, since they have a considerable impact at the societal (e.g. energy, health, environment, defense and security), economic

and financial (e.g. industrial competitiveness) and ethical (e.g. biology) levels. Modeling, simulation and artificial intelligence are increasingly appearing as decision support tools for a number of critical situations such as natural disasters and climate change. We will also cover major issues such as energy consumption of supercomputers and have a look to some of the emerging computing paradigms: quantum, neuromorphic and molecular/DNA computing.



Kim W. Tracy has extensive and varied experience with many different aspects of software development and in computing education. He's worked on a wide variety of software ranging from system software (UNIX[®] and network systems at Bell Labs) to database systems and expert systems during his over 30-year career. While at Bell Labs, he worked on a number of different products including the 5ESS[®] Telephone Switch as well as consulting for clients around the world. He also served as Northeastern Illinois University's Chief Information Officer for a decade and oversaw all aspects of the technology used by the university. He's taught many courses in computer science that include traditional computer science, software engineering, cybersecurity, and

information technology for many different universities, beginning part-time over 30 years ago. He currently is a professor of practice for the Computer Science and Software Engineering department at Rose-Hulman Institute of Technology. He's also been heavily involved in ABET computing program accreditation and in volunteer leadership roles in other professional societies. He's recently authored a textbook on software history for ACM Books and co-authored another book on object-oriented AI. He's a senior member of ACM and IEEE, a member of SHOT and currently serves as chair for the ACM History Committee.



Dr. Levon Aslanyan began his scientific career in 1961 at the Institute of Energetics of the Armenian SSR Academy of Sciences, later studying at Yerevan State University and graduating with honors from Novosibirsk State University in 1968. From 1969 to 1972 he pursued postgraduate studies at the Computer Center of the USSR Academy of Sciences in Moscow. He earned his PhD in Physics and Mathematics in 1976 and his Doctoral degree in 1997. He was awarded the titles of Senior Researcher (1983) and Professor (2008), and in 2014 was elected a Corresponding Member of the National Academy of Sciences of Armenia. He leads the Department of Discrete Mathematics at the Institute of Informatics and Automation of the NAS RA.

His research spans discrete analysis, including local algorithm efficiency, complexity of weakly defined Boolean functions, logic-separation methods in pattern recognition,

discrete isoperimetric problems, and associative rule mining. He has supervised the development of practical systems such as best-match search algorithms, cluster analysis software, seismic data preprocessing tools, enterprise information systems, the ArmReader OCR for Armenian characters, and a network intrusion detection system. Dr. Aslanyan has been active in scientific organization: co-founder of the Bulgarian Institute for Information Theories and Applications (2003), member of editorial boards of international journals, and participant in numerous international conference program committees. Since 1997, he has served as Armenia's National Contact Point for EU information and telecommunication research programs.

He is the author of about 200 scientific publications and has lectured at universities across Europe.

Monotone Boolean Reconstruction

Abstract. Monotone Boolean reconstruction refers to a process in the field of combinatorial optimization and information theory, where the goal is to recover a hidden binary function (a function that takes as input the values 0 or 1) based on limited information obtained from observations. The term "monotone" indicates that the function maintains the non-decreasing property: if one of the inputs is changed from 0 to 1, the output will not decrease. In applications such as data mining and network analysis, reconstructing the structure of monotone Boolean functions can help in understanding underlying relationships or dependencies within data. This reconstruction problem is significant in various fields including economics, bioinformatics, and machine learning. Key components of monotone Boolean reconstruction involve:

Observations: Limited data or samples that provide insights into the behavior of a Boolean function.

Reconstruction: The process of inferring the original function from the available observations, often requiring algorithms and techniques from combinatorial and optimization theory.

Applications: Implications for various practical scenarios where understanding monotonic relationships between variables is crucial.

The complexity of this problem can vary, and often involves algorithmic challenges, in particular, to determining the minimum set of observations required for accurate reconstruction. Researchers use different structural methods and mathematical frameworks to efficiently tackle such reconstruction tasks. Boolean functions form a descriptive model of compatibility of sets of independent constraints, but the class of all functions is unambiguously complex and it is of interest to find also relatively simple subclasses of monotone functions. In this survey, we summarize existing results in the area of monotone Boolean recognition, including those related to special classes of monotone Boolean functions. Results related to the multivalued domain are also briefly presented.



Dr. Yana Bromberg - Professor, Departments of Biology and Computer Science, Emory University, Hans Fischer Fellow, Institute for Advanced Study, Technical University of Munich, Principal Fellow, Center for AI Learning, Emory University, Director and Fellow of the International Society for Computational Biology.

The primary focus of Dr. Yana Bromberg's research is the concept of biological function as encoded in the DNA "blueprints" of life. Specifically, she is interested in understanding the origins and mechanisms of the molecular machinery that underpins life. She believes that machine learning (ML), and the more recent Artificial Intelligence (AI), tools hold great promise in deciphering these functional details. Accordingly, her long-term goal is to use these advances, and other computational techniques, to gain a

deeper understanding of how biological functionality is encoded in genomic data, whether on the level of individual genes, whole genomes, or metagenomes. The lab is currently working on implementing machine learning-based models for understanding what function aspects (if any) are captured by protein language models, how genome variants impact molecular function in association with disease, and whether metagenome functionality can be inferred from sequencing reads (it can be!). <http://www.bromberglab.org/>

Quantifying Uncertainty of Biological Molecule Representations

Abstract. Latent space embeddings, derived by language models, are widely used as numeric proxies for human language sentences and structured data. In the realm of biomolecules, embeddings serve as efficient sequence and/or structure representations, enabling similarity searches, structure and function prediction, and estimation of biophysical and biological properties. However, relying on computed embeddings without assessing the model's confidence in its ability to accurately represent molecular properties is a critical flaw—akin to using a scalpel in surgery without verifying its sharpness.

We propose a means to evaluate the ability of protein language models to represent proteins, assessing their capacity to encode biologically relevant information. Our findings reveal that low-quality embeddings fail to capture meaningful biology, displaying vector properties indistinguishable from those of randomly generated sequences. A key contributor to this performance issue is the models' failure to learn the underlying biology from unevenly distributed sequence spaces in the training data. Our novel, model-agnostic scoring framework is the first to quantify protein sequence embedding quality. We believe that our robust approach to screening embeddings prior to making biological inferences, stands to significantly enhance the reliability of downstream applications.



The group of **Professor Dr. Dmitrij Frishman** - (b. 1961) develops bioinformatics algorithms and software to support high-throughput biological research at the intersection of structural genomics and proteomics. He is particularly interested in the evolution, structural diversity, and interactions of transmembrane proteins. Other research directions include bioinformatics of viruses, evolution of mRNAs, and cancer informatics.

Professor Frishman studied Biomedical Electronics at the Saint Petersburg Electrotechnical University (1984) and received a PhD in Biochemistry from the Russian Academy of Sciences (1991). Supported by a Humboldt Fellowship, he pursued postdoctoral research at the Biocomputing Department of EMBL in Heidelberg (1991–

1996). He subsequently joined the Munich Information Center for Protein Sequences as a senior scientist and later became Deputy Director of the Institute for Bioinformatics at the German Research Center for Health and Environment. In 1997, he co-founded Biomax Informatics AG. Professor Frishman was appointed to TUM in 2003.

AI Is All You Need ... to Study Alzheimer's Disease

Abstract: Artificial intelligence has become an integral part of modern bioinformatics and is now routinely applied to problems ranging from protein structure prediction to the analysis of large-scale omics data. In this talk, I will present several examples from our recent work that illustrate how machine learning can help address biological questions related to neurodegenerative disease.

The first part of the talk focuses on the use of explainable machine learning to identify the molecular features that determine protein processing and to predict previously unknown disease-relevant targets. The second part explores the integration of heterogeneous neuroproteomics datasets and the application of machine learning approaches to the analysis of Alzheimer's disease.

Using these examples, I will discuss both the potential and the limitations of current AI methods in biomedical research, and argue that successful applications still depend as much on biological understanding and data quality as on the choice of machine learning algorithms.



Andrey Bzikadze is an Applied Scientist and a Technical Lead at Amazon, working on projects that utilize machine learning for life science applications (Amazon Special Projects, San Francisco, CA).

In 2022, Andrey graduated from Pavel Pevzner's lab in University of California, San Diego where his research was focused on computational methods for genome assembly, human centromere biology, and immunoinformatics.

Andrey is a member of the international Telomere-to-Telomere (T2T) Consortium. During his doctorate, Andrey presented the first algorithm for automated assembly of a human centromere.

Andrey used this workflow to generate and validate the first complete assembly of a human genome developed by the T2T Consortium.

From Training Protein Language Models

Abstract: Protein language models have moved quickly from research prototypes to widely used tools across drug design. Scaling has carried us a long way: it yields representations that implicitly capture fitness and structural properties. As these capabilities have matured, the natural next question is what additional ingredients can compound with scale to extend that trajectory.

In this talk, we will focus on one such ingredient: molecular interactions. Proteins function through their engagements with binding partners, and specificity emerges from the geometry and chemistry of contact interfaces. Recent multimodal foundation models have begun to reach beyond sequence and fold — incorporating secondary structure, solvent accessibility, and per-residue functional annotations — but they continue to be informed by only coarse descriptors of the surfaces and interfaces through which proteins actually engage their partners. Bringing richer interaction signal directly into pre-training — through new input modalities, pair-level training objectives, and carefully curated interaction data — opens a direction that scale alone does not reach.

We present BioFM, a multimodal protein foundation model built around this idea. BioFM extends the multimodal recipe on three fronts — interaction-aware tasks, modalities and trillion-token data scale. We present a novel interaction-aware in-painting task and masking that directly rehearses partner-aware protein design. BioFM models detailed molecular surface chemistry, and integrates binding-site and antibody-region labels derived from co-folded complex structures rather than from single-protein annotations alone. A unified framework supports masked reconstruction, indel-aware editing, interaction-conditioned design, and controllable generation across a broad set of biophysical properties, all within a single architecture. This framework appears to be especially useful for a wide range downstream tasks including molecular-level tasks such as protein-protein interaction prediction.



Roland Duduchava - (Georgia) Professor, Director of the V. Kupradze Institute of Mathematics, The University of Georgia, Head of a Department at A. Razmadze Mathematical Institute Ivane Javakhishvili Tbilisi State University, Former stipendiant of Humboldt Foundation and Professor-Merkator of DFG (Germany).

Modelling of Shell Equation on a Hypersurface With Γ -Convergence

Abstract: We consider boundary value problems (BVPs) of bending elastic isotropic thin media $\Omega h: \mathbb{C} \times [-h, h]$ around a surface $\mathbb{C}$ with the Lipschitz boundary $\Gamma := \partial \mathbb{C}$, governed by the Lamé equation $\mathcal{L} = -\mu \Delta \Omega h - (\lambda + \mu) \nabla \cdot \nabla \Omega h \operatorname{div} \Omega h$. The object of the investigation is what happens with the boundary value problems when the thickness of the layer diminishes to

zero $h \rightarrow 0$.

Using the Γ -convergence, which maintains infimum of energy potential, is derived a new equation of shell on the mid-surface $\mathbb{C}$ of the form

$$\begin{aligned} & \mu [\Delta_{\mathbb{C}} U_{\alpha} + \mathcal{D}_{\beta} \mathcal{D}_{\alpha} U_{\beta} - 2\mathcal{H}_{\mathbb{C}} \nu_{\beta} \mathcal{D}_{\alpha} U_{\beta} - \mathcal{D}_{\gamma} (\nu_{\alpha} \nu_{\beta} \mathcal{D}_{\gamma} U_{\beta})] \\ & + \frac{4\lambda\mu}{\lambda + 2\mu} [\mathcal{D}_{\alpha} \mathcal{D}_{\beta} U_{\beta} - 2\mathcal{H}_{\mathbb{C}} \nu_{\alpha} \mathcal{D}_{\beta} U_{\beta}] = \frac{1}{2} F_{\alpha} + H_{\alpha}^{(1)} \quad \text{on } \mathbb{C}, \\ & \mathbf{U}(t) = 0 \quad \text{on } \Gamma = \partial \mathbb{C}. \end{aligned} \quad (1)$$

where $\mathbf{U} := (U_1, U_2, U_3)^T$ is the displacement vector, λ, μ are the Lamé constants, $\mathcal{D}_j := \partial_j - \nu_j D_4$, $j = 1, 2, 3$ are the Günther's derivatives, $\nu = (\nu_1, \nu_2, \nu_3)^T$ is the normal vector field, $\mathcal{H}_{\mathbb{C}}$ is the mean curvature of the surface $D_4 := \partial_{\nu} = \nu_1 \partial_1 + \nu_2 \partial_2 + \nu_3 \partial_3$ is the normal derivative and $\Delta_{\mathbb{C}} = D_1^2 + D_2^2 + D_3^2$ is the Laplace-Beltrami operator on the surface.

The shell equation (1) is positive definite and the boundary value problem is uniquely solvable in the classical setting $\mathbf{U} \in L_2(\mathbb{C})$.

The investigation is carried out in collaboration with T. Buchukuri (Tbilisi)



Sergo Tsiramua – Professor, Dr. at the University of Georgia, School of Science and Technology; Director of the Institute of Informatics; Head of the Doctoral Program in Computer Science, s.tsiramua@ug.edu.ge

Sergo Tsiramua's research interests include reliability theory, logical-probabilistic and logical-combinatorial methods, risk and safety analysis, structural analysis and optimization of complex systems, machine learning, and computational modeling.

His research focuses on the modeling, analysis, and optimal control of complex reconfigurable systems composed of multifunctional elements. In particular, he studies the reliability,

fault tolerance, and risk assessment of reconfigurable systems, including their functional degradation and recovery through the use of functional redundancy and the interchangeability of multifunctional elements.



George Tsiramua – Head of Business Technology Department, Toyota Caucasus; Founder, OptiCrew, georgetsimua@opticrew.ai

Logical-Combinatorial Modeling of Reconfigurable Organizational Systems with Multifunctional Elements

Abstract. Organizations often focus on hiring highly skilled specialists – top engineers, designers, and project managers – assuming that individual expertise will naturally lead to project success. But in practice, such teams can become rigid and difficult to adapt.

McKinsey studies show that over 75% of teams without proper structural integration fail to meet key delivery goals – not due to a lack of talent, but due to fragile team design.

To challenge that we created OptiCrew – a platform that helps organizations build flexible, balanced and resilient teams based on multifunctional personnel.

Opticrew is built on logical-combinatorial and logical-probabilistic models, which helps in creating structurally reconfigurable teams. Structural reconfiguration is achieved through the multifunctionality of system elements, enabling interchangeability and replacement in cases of partial or complete failure.

Each team member is assessed across all potential roles, and optimization algorithms identify the best team configuration and role allocation.

Scenario-based simulations – unavailability, performance drops, and scope changes – evaluate team robustness under stress. Teams with interchangeable personnel demonstrate higher reliability and reduced need for external replacements. Additionally, AI and natural language processing convert behavioral data into quantitative indicators, while Generative AI identifies skill gaps and provides targeted recommendations to improve team adaptability and performance.

Contact Us

For any inquiries, please contact the organizing committee at: icics2026@ug.edu.ge

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Supporting organizations



SPRINGER NATURE



Recommended Hotels:

Holiday Inn, 1, 26 May Square, Tbilisi 0171 Georgia

Ameri Plaza Tbilisi, Kostava st. 76A, Tbilisi 0171 Georgia

Ibis budget Tbilisi Center, 22 Giorgiy Akhvediani st, 0108 Tbilisi, Georgia