



University of Georgia
School of Science and Technologies
Institute of Informatics, Department of Informatics

საქართველოს უნივერსიტეტი
მეცნიერებისა და ტექნოლოგიების სკოლა
ინფორმატიკის ინსტიტუტი, ინფორმატიკის დეპარტამენტი

International Conference on Informatics and Computer Science

**ინფორმატიკისა და კომპიუტერული მეცნიერების
საერთაშორისო კონფერენცია**

Program - პროგრამა

77a Merab Kostava Street, Tbilisi, 0171, Georgia, June 18-20, 2026
მერაბ კოსტავას 77ა, თბილისი, 0171, საქართველო, 18-20 ივნისი, 2026

University of Georgia (UG), ICICS-2026, Tbilisi, June 18 – 20, 2026

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ICICS 2026

International Conference on Informatics and Computer Science

It is our great honor and pleasure to welcome you to Tbilisi for the opening of the First International Conference on Informatics and Computer Science (ICICS 2026). We are confident that this conference, taking place from June 18 to June 20, will establish a strong and lasting presence within the scientific community, bringing together leading scientists, engineers, and young researchers from around the world.

ICICS 2026 aims to foster the free exchange of scientific ideas, facilitate discussions on current trends in Computer Science, Informatics, Applied Mathematics, Bioinformatics, and Artificial Intelligence, and promote the development of new international collaborations.

About 50 reports were presented at this conference from Armenia, Azerbaijan, Croatia, France, Georgia, Germany, Iran, Iraq, Kazakhstan, Lithuania, Poland, Russia, Turkey, Ukraine, USA. The reports are categorized into the following sections: “Machine Learning and Cognitive Modeling”, “Blockchain and Distributed Ledger Technologies”, “Cybersecurity and Privacy”, “Computational Mathematics and Modeling”, “Bioinformatics and Computational Biology”, “Interdisciplinary Applications Across Science, Engineering, Economics”.

ICICS 2026 includes a dedicated Doctoral Symposium aimed at PhD students and early-stage researchers with Presentation of ongoing research, Feedback from senior experts, Best Doctoral Paper Award, Opportunity for further publication.

The plenary reports focus on ensuring trust and bridging data spaces with continuous growth in the volume, complexity, and speed of information generation.

The plenary reports focus on problems of Exascale Computing and New Computing Paradigms, Cybersecurity, Monotone Boolean Reconstruction, Modelling of Shell Equation on a Hypersurface With Γ -Convergence, Bioinformatics, and Logical-Combinatorial Modeling of Reconfigurable Organizational Systems with Multifunctional Elements.

In addition to the scientific agenda, ICICS-2026 also offers a chance for cultural exchange. Participants will have the opportunity to get acquainted with the rich cultural heritage of ancient city Mtskheta, combining scientific pursuits with friendly interactions.

We are grateful to all the conference participants who responded to our invitation. The conference was organized by the institute of Informatics, and Department of Informatics of School of Science and Technologies at University of Georgia.

We wish you a productive and inspiring conference, as well as a pleasant stay in Tbilisi.

ინფორმატიკისა და კომპიუტერული მეცნიერების საერთაშორისო კონფერენცია

ჩვენთვის დიდი პატივია მოგესალმოდეთ თბილისში ინფორმატიკისა და კომპიუტერული მეცნიერების პირველი საერთაშორისო კონფერენციის (ICICS 2026) გახსნაზე. გვჯერა, რომ ეს კონფერენცია, რომელიც გაიმართება 18–20 ივნისს, ღირსეულ ადგილს დაიმკვიდრებს სამეცნიერო საზოგადოებაში და გააერთიანებს მეცნიერებსა და ახალგაზრდა მკვლევრებს მსოფლიოს სხვადასხვა ქვეყნიდან.

ICICS 2026 მიზნად ისახავს სამეცნიერო იდეების თავისუფალი გაცვლის ხელშეწყობას, თანამედროვე ტენდენციების განხილვას კომპიუტერულ მეცნიერებაში, ინფორმატიკაში, გამოყენებით მათემატიკაში, ბიოინფორმატიკასა და ხელოვნურ ინტელექტში, ასევე საერთაშორისო თანამშრომლობის გაძლიერებას.

კონფერენციაზე წარმოდგენილია დაახლოებით 50 მოხსენება მსოფლიოს 17 ქვეყნიდან, რომლებიც გაერთიანებულია შემდეგ სექციებში: მანქანური სწავლება და კოგნიტური მოდელირება; ბლოკჩეინი და დეცენტრალიზებული ტექნოლოგიები; კიბერუსაფრთხოება და კონფიდენციალურობა; გამოთვლითი მათემატიკა და მოდელირება; ბიოინფორმატიკა და გამოთვლითი ბიოლოგია; ინტერდისციპლინური გამოყენებები მეცნიერებაში, ინჟინერიაში და ეკონომიკაში.

კონფერენციის ფარგლებში გაიმართება სადოქტორო სიმპოზიუმი, რომელიც დოქტორანტებს აძლევს შესაძლებლობას წარმოადგინონ თავიანთი კვლევები, მიიღონ ექსპერტების შეფასება და მონაწილეობა მიიღონ საუკეთესო ნაშრომის კონკურსში.

პლენარული მოხსენებები შეეხება თანამედროვე მეცნიერებისა და ტექნოლოგიების მნიშვნელოვან მიმართულებებს, მათ შორის ეგზომასშტაბურ გამოთვლებს, კიბერუსაფრთხოებას, ბიოინფორმატიკასა და მათემატიკური მოდელირების თანამედროვე მეთოდებს.

სამეცნიერო პროგრამასთან ერთად, მონაწილეებს ექნებათ შესაძლებლობა გაეცნონ მცხეთის მდიდარ კულტურულ მემკვიდრეობას.

გმადლობთ მონაწილეობისთვის. კონფერენცია ორგანიზებულია საქართველოს უნივერსიტეტის მეცნიერებისა და ტექნოლოგიების სკოლის ინფორმატიკის ინსტიტუტისა და ინფორმატიკის დეპარტამენტის მიერ.

გისურვებთ ნაყოფიერ და შთამაგონებელ კონფერენციას, ასევე სასიამოვნო ყოფნას თბილისში.

Conference Program

Thursday, June 18, 2026

09⁰⁰ – 14⁰⁰ Registration

09⁰⁰ – 10⁰⁰ Welcome Coffee Break

10⁰⁰ – 10¹⁵ Opening of ICICS-2026 (UG, 519)

Welcome Messages:

Sulkhan Sulkhanishvili – Head of Department of Informatics

Sergo Tsiramua – Director of Institute of Informatics

Konstantine Topuria – Rector of University of Georgia

10¹⁵ – 13⁰⁰ Plenari Session (UG, 519)

Moderators: Tinatin Endeladze, Michel Dayde

10¹⁵ Michel Daydé (France) – 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.

10⁴⁵ **Kim W. Tracy** (USA) 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.



11¹⁵ **Dr. Levon Aslanyan** (Armenia) - 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.

11⁴⁵ **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 Lipshitz boundary $\Gamma := \partial \mathbb{C}$, governed by the Lamé equation $L = -\mu \Delta \Omega h - (\lambda + \mu) \nabla \Omega h \operatorname{div} \Omega h$. 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

$\mathbf{U} := (U_1, U_2, U_3)^{\top}$ is the displacement vector, λ, μ are the Lamé constants, $\mathcal{D}_j := \partial_j - \nu_j \mathcal{D}_4$, $j = 1, 2, 3$ are the Günter's derivatives, $\nu = (\nu_1, \nu_2, \nu_3)^{\top}$ is the normal vector

field, H_c is the mean curvature of the surface $D_4 := \partial_v = v_1 \partial_1 + v_2 \partial_2 + v_3 \partial_3$ is the normal derivative and $\Delta_c = D_1^2 + D_2^2 + D_3^2$ 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 $U \in L_2(C)$.

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

¹⁶¹⁵ **Dr. Paul de Souza** (USA, Online) 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) Försvarshögskolan; 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.

13⁰⁰ – 14⁰⁰ Lunch/Free Time

14⁰⁰ – 16³⁰ Session 1 (UG, 519) “Machine Learning and Cognitive Modeling” Moderators: Davit Bitmalkishev, Oleksii Mints

- 14⁰⁰ Esmira Ahmadova (Online, Azerbaijan) “Comparing Machine Learning And Classical Time-Series Models For Forecasting Digital Activity”
- 14¹⁵ Erol Eğrioglu, Eren Bas (Turkey) “Percentage Artificial Neural Network with Laplace Activation Function for Forecasting”
- 14³⁰ Tigran Shahinyan, Sedrak Grigoryan, Edward Pogossian (Online, Armenia) “From Numeric Constraints to Semantic Relations in Processing of Meanings”
- 14⁴⁵ Boris Karapetyan (Online, Armenia) “Adaptive Learning System: Integrating Experiential Design Across Educational Stages”
- 15⁰⁰ Oleksii Mints (Lithuania) “Detecting low-level manipulation on YouTube through comment relevance anomalies”
- 15¹⁵ Dariusz Ruciński (Online, Poland) “Hybrid LSTM Model with Solar Impact Feature for Day-Ahead Electricity Price Forecasting on the Polish Power Exchange”
- 15³⁰ Rati Skhirtladze (Georgia) “AI-Powered Speech-to-Text for Georgian Broadcast Media Monitoring: A Case Study”
- 15⁴⁵ Elnara Kadyrgali, Nuray Togan, Muragul Muratbekova, Pakizar Shamo (Kazakhstan) “Perceptual Asymmetry Between Hue Categories: Evidence from Human Color Categorization”

14⁰⁰ – 16⁰⁰ Session 2 (UG, 319) “Information and Communication Technologies”, “Blockchain and Distributed Ledger Technologies”, “Cybersecurity and Privacy”

Moderator: Nikoloz Katsitadze

- 14⁰⁰ Nikoloz Katsitadze, Sulkhan Sulkhanishvili (Georgia) “AI-Based Quantitative Risk Assessment of Fraudulent Activities in Decentralized Finance”
- 14¹⁵ Merab Pkhovelishvili, Natela Archvadze, Lia Shetsiruli, Giorgi Patsatsia (Georgia) “Blockchain Hybrid Consensus Models: A Critical Analysis of PoW and PoS Synthesis
- 14³⁰ Natalia Grigoreva (Russia) “Single Machine Scheduling Problem with Delayed Precedence Constraints”
- 14⁴⁵ Pavlo Sidelov (Online, Ukraine) “A Multi-Algorithm Approach to Proactive Phishing Website Detection”
- 15⁰⁰ Arsenii Likhachev, Elena Zamyatina (Online, Russia) “Study of reinforcement learning algorithm for routing in wireless networks using simulation methods”
- 15¹⁵ Arthur Petrosyan, Gurgen Petrosyan, Vladimir Sahakyan, Hrachya Astsatryan, Arusyak Manasyan, Robert Tadevosyan (Armenia) “Holistic Defense-in-Depth for Defeating Automated Threats in Self-Hosted Academic Infrastructure”
- 15³⁰ Aleksandre Benashvili, Sergo Tsirumua (Georgia) “Enhancing Processor Performance Based on VLIW Architecture”

19⁰⁰ – 21⁰⁰ Welcome Reception (UG, 519)

Friday, June 19, 2026

09⁰⁰ – 10⁰⁰ Welcome Coffee Break

10⁰⁰ - 13⁰⁰ Plenari Session (UG, 519)

Moderator: Yana Bromberg

10⁰⁰ 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.

10³⁰ **Andrey Bzikadze** (USA) 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



Lessons 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 of downstream tasks including molecular-level tasks such as protein-protein interaction prediction.

11⁰⁰ Dr., Professor, **Dmitrij Frishman** (Germany) - 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.

11³⁰ **Mark Borodovsky** (USA) 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>).

12⁰⁰ **Sergo Tsiramua** (Georgia) – 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.

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.



12⁰⁰ **George Tsiramua** (Georgia) - Head of Business Technology Department, Toyota Caucasus; Founder, OptiCrew



“Logical-Combinatorial Modeling of Reconfigurable Organizational Systems with Multifunctional Elements”

Abstract: Opticrew is built on logical-combinatorial and logical-probabilistic mathematical 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.

13⁰⁰ – 14⁰⁰ Lunch/Free Time

14⁰⁰ – 17¹⁵ Session 3 (UG, 519) “Computational Mathematics and Modeling” Moderators: Tinatin Davitashvili, Hasmik Sahakyan

- 14⁰⁰ Vladimir Sahakyan, Artur Vardanyan (Armenia) “Multi-server Queueing Model with Simultaneous Service and Abandonments”
- 14¹⁵ Tatyana Kosovskaya (Russia) “On the isomorphism of hypergraphs of relations”
- 14³⁰ Stanisław Ambroszkiewicz (Poland) “On reliable computing on the real numbers”
- 14⁴⁵ Hasmik Sahakyan, Levon Aslanyan (Armenia) “Identification of Monotone Binary Functions on a Specific Multi-valued Grid¹”
- 15⁰⁰ Nana Odishelidze (Georgia) “On One Mixed Problem of Plate Bending”
- 15¹⁵ Irakli Bashesheishvili, Sergo Tsiramua (Online, Georgia) “Design and Development of an Expert Assessment Based Decision Support System”
- 15³⁰ Vakhtang Kvaratskhelia, Marina Menteshashvili (Georgia) “Application of a characteristic of the Walsh matrix in digital image processing”
- 15⁴⁵ George Baghaturia, Marina Menteshashvili (Georgia) “Analytical and numerical methods to solve the Cauchy and Inverse problems”
- 16⁰⁰ Hamlet Meladze, Tinatin Davitashvili, Sergo Tsiramua, Mamuli Zakradze (Georgia) “A Regularized Difference Scheme for a Nonstationary Problem in the Theory of Elasticity with Periodic Initial Conditions”
- 16¹⁵ Iskandar Karapetyan, Karen Karapetyan (Armenia) “New Method for Constructing Complete Cap Sets”
- 16³⁰ Merab Pkhovelishvili, Natela Archvadze, Elisabed Asabashvili (Georgia) “A Formal Framework for Constructing Hybrid Necessary Forecasting Models from Nearly Necessary Models”
- 16⁴⁵ Ketevan Kutkhashvili, Elisabed Asabashvili (Georgia) “The problem of packing circles in a rectangular area”
- 17⁰⁰ Elisabed Asabashvili, Natela Archvadze, Ketevan Kutkhashvili (Georgia) “A Stochastic Risk Model for Cybersecurity Analysis of Input Validation and Sanitization”

14⁰⁰ – 16⁰⁰ Session 4 (UG, 319) “Interdisciplinary Applications Across Science, Engineering, Economics”

Moderator: Roya Anvari

- 14⁰⁰ Martina Maté, Marija Opačak Eror, Marijana Jerić (Croatia) “Digital Tax Infrastructure and Productivity Dynamics: Evidence from European Revenue Administrations”
- 14¹⁵ Murad Taghiev (Azerbaijan) “Some Aspects of the Theory of Complex Variables in Economic Modeling”
- 14³⁰ Ali Kadhim Saddam, Roya Anvari, Rokhsareh Mobarhan (Iraq, Georgia, Iran) “A strategic evaluation of digital components for consumer engagement in Iraq’s online market”
- 14⁴⁵ Ali Kadhim Saddam, Roya Anvari, Rokhsareh Mobarhan (Iraq, Georgia, Iran) “Analyzing digital marketing strategies and consumer behaviour in Iraq using data analytics”
- 15⁰⁰ Hrachya Stepanyan (Online, Armenia) “A Decentralized Mission Engineering Platform with Inter-UAV LoRa Communication for Self-Organizing UAV Swarms”

- 15¹⁵ Davit Hayrapetyan (Online, Armenia) “Inverse Rotor-Router Reconstruction of Eulerian Mission Structures From Self-Organizing UAV Swarms Trajectories”
- 15³⁰ Tigran Shahinyan, Sedrak Grigoryan, Edward Pogossian (Online, Armenia) "From Numeric Constraints to Semantic Relations in Processing of Meanings"

Saturday, June 20, 2026

09⁰⁰ – 10⁰⁰ Welcome Coffee Break

10⁰⁰ - 13⁰⁰ Session 5 (UG, 519) “Special Symposium for Doctoral Students”

Moderators: Tamar Tevzadze, Nikoloz Katsitadze

- 10⁰⁰ Giorgi Dolenjishvili (UG, Georgia) “AI-Based Failure Minimization in Mobile Application Test Automation Systems”
- 10¹⁵ Michael Gigauri (UG, Georgia) “Precision Enhancement of Human and Face Verification from UAV Using RGB–Thermal Sensor Fusion and Liveness Detection”
- 10³⁰ Luka Z. Tabagari, Ioseb Kachiashvili (GTU, Georgia) “Forced Align”ment and Offline ASR for Georgian Sensitive Speech Data”
- 10⁴⁵ Levan Lomsadze, Davit Bitmalkishev, Sergo Tsiramua (UG, Georgia) “Universal AutoByte: Evolutionary AutoML for Byte-Level NLP in Low-Resource Languages”
- 11⁰⁰ Grigol Mikadze (TSU, Georgia) “Privacy-Preserving Event Monitoring in Biometric Access Control Systems”
- 11¹⁵ Tornike Razmadze (UG, Georgia) “Evaluating Binet’s Test Results Using the Set Ordering Method of Computerized Adaptive Testing”
- 11³⁰ Artem Sologhashvili (GTU, Georgia) “The Evolution and Multifaceted Achievements of Robotic Technology”
- 11⁴⁵ Tamar Tevzadze, Sergo Tsiramua, Anastasia Bajiashvili (UG, Georgia) “Risk Assessment of the Project for Implementing an IT Strategy in the Banking System”
- 12⁰⁰ Zurab Chachava (UG, Georgia) “Methodology of Large Language Model Integration in Banking Products Using the MCP Standard”
- 12¹⁵ Lazare Kvirtia, Sergo Tsiramua (UG, Georgia) “Comparative analysis of logical-probabilistic methods”
- 12³⁰ Aleko Khomasuridze, Sergo Tsiramua, Davit Bitmalkishev (UG, Georgia) “Intelligent Topology Selection in Dynamic Wireless Mesh Networks”
- 12⁴⁵ Sarko Zakarya, Burhan Ergen (Online, Turkey) “Early Brain Tumour Detection Using Deep Learning and MRI Image Similarity Analysis”

13⁰⁰ – 13³⁰ Closing meeting (UG, 519)

13³⁰ – 14³⁰ Lunch

15⁰⁰ – 18⁰⁰ Mtskheta tour

19⁰⁰ – 22⁰⁰ Farewell Banquet