2025 ANNUAL REPORT

ARMENIAN BIOINFORMATICS INSTITUTE

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THE ARMENIAN BIOINFORMATICS INSTITUTE (ABI) IS A NON-PROFIT PRIVATE SCIENTIFIC-EDUCATIONAL FOUNDATION, LAUNCHED IN FEBRUARY OF 2021 TO SUPPORT BIOINFORMATICS CAPACITY BUILDING AND THE DEVELOPMENT OF PRECISION MEDICINE AND MODERN BIOTECHNOLOGIES.

THIS REPORT SUMMARIZES THE FIFTH YEAR OF OUR ACTIVITIES.

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HANS BINDER (CONTENT)
RUZAN ADYAN (DESIGN)

ARMENIAN BIOINFORMATICS INSTITUTE
SCIENTIFIC EDUCATIONAL FOUNDATION

2025

7 EZRAS HASRATYAN STR., 0014, YEREVAN, ARMENIA

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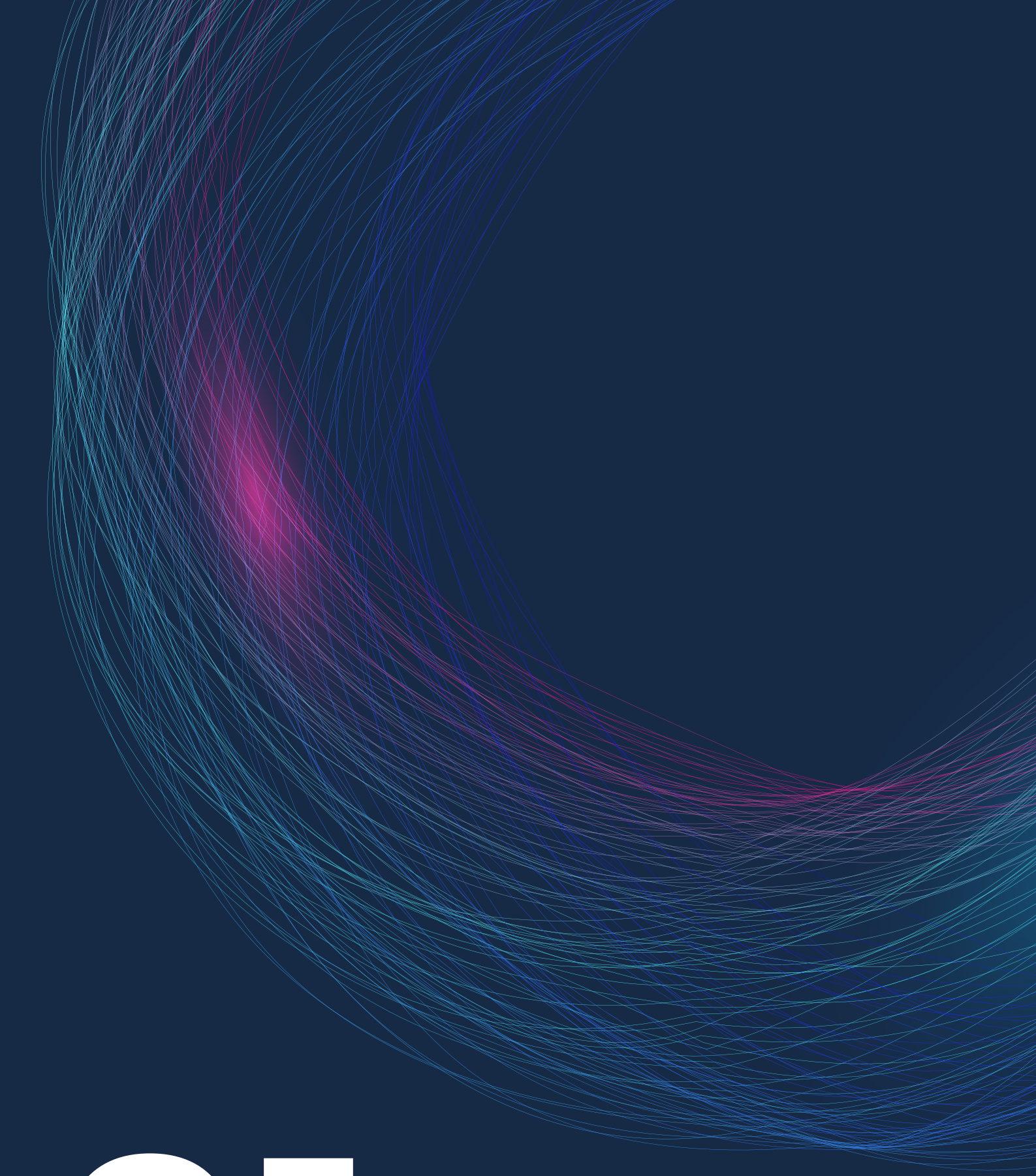


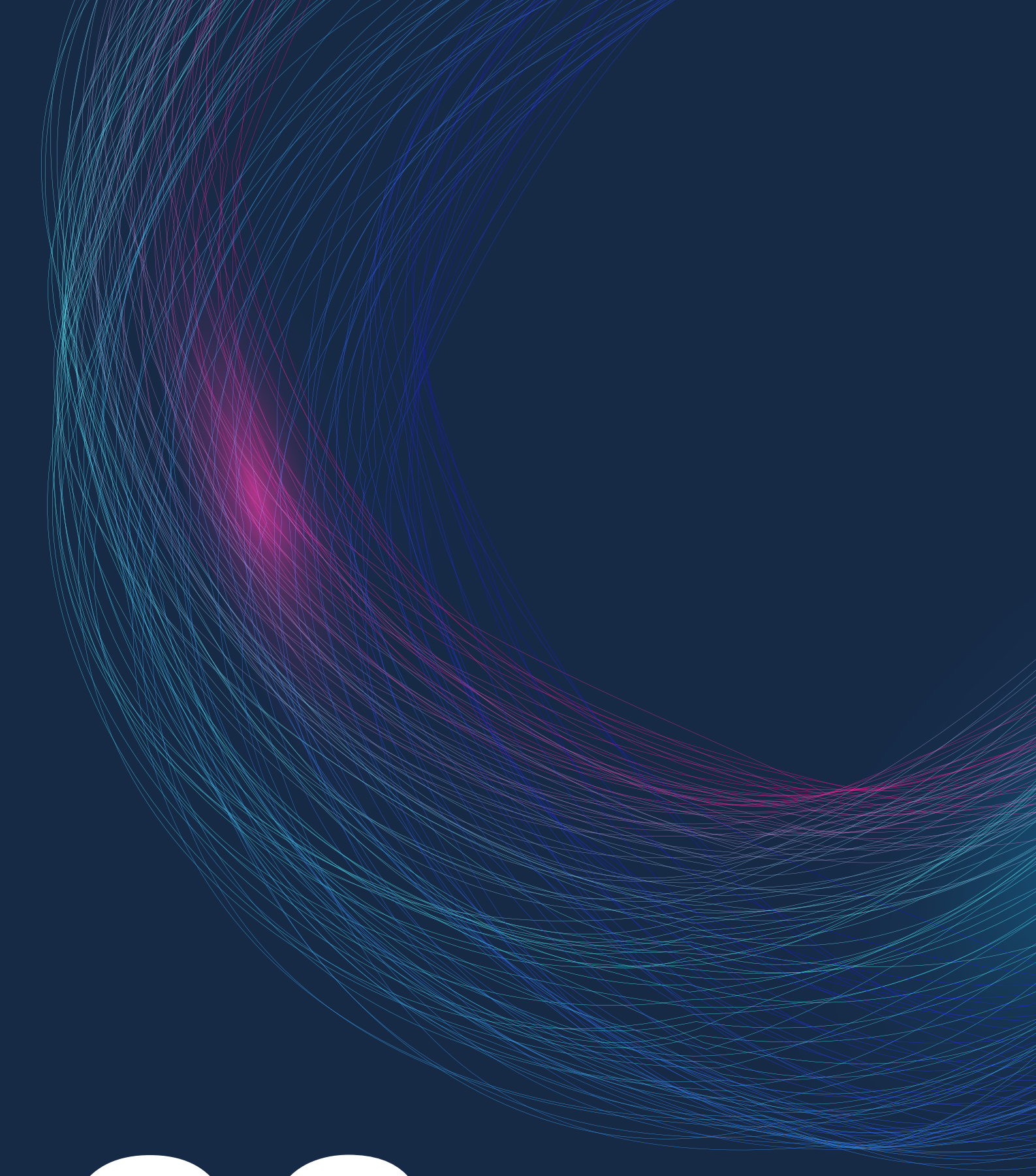
01 INTRODUCTION

INTRODUCTION

Bioinformatics plays a central role in modern life sciences by transforming large-scale biological data into interpretable knowledge that informs research, medicine, and biotechnology. By integrating computation, statistics, and biological domain expertise, the field enables the analysis of complex genomic and multi-omics datasets that cannot be understood through experimental approaches alone.

In 2025, bioinformatics is entering a phase of consolidation and refinement. Integrative analyses across multiple data modalities, longitudinal and real-world datasets, and the growing use of AI-assisted tools are reshaping how research is conducted. Developments such as domain-specific foundational models, AI-supported coding environments, and agent-based analytical workflows improve efficiency and accessibility, but do not replace scientific judgment. Instead, they shift the emphasis toward strong statistical reasoning, and deep biological understanding to guide analyses toward meaningful interpretation.

The mission and training philosophy of ABI are closely aligned with these developments. ABI focuses on developing scientists who combine (i) strong quantitative and statistical foundations, (ii) biological insight and interpretability, (iii) reproducible and well-documented analytical practice, and (iv) leadership and initiative. Equal emphasis is placed on scientific independence and responsibility, preparing researchers to take proactive roles in shaping research questions, guiding analyses, and contributing effectively to interdisciplinary teams across academia and industry.



02 2025 IN NUMBERS

2025 IN NUMBERS

27
RESEARCH TEAM

ACTIVE RESEARCHERS: 22

INTERNS: 2

ALUMNI: 3

9
PUBLICATIONS

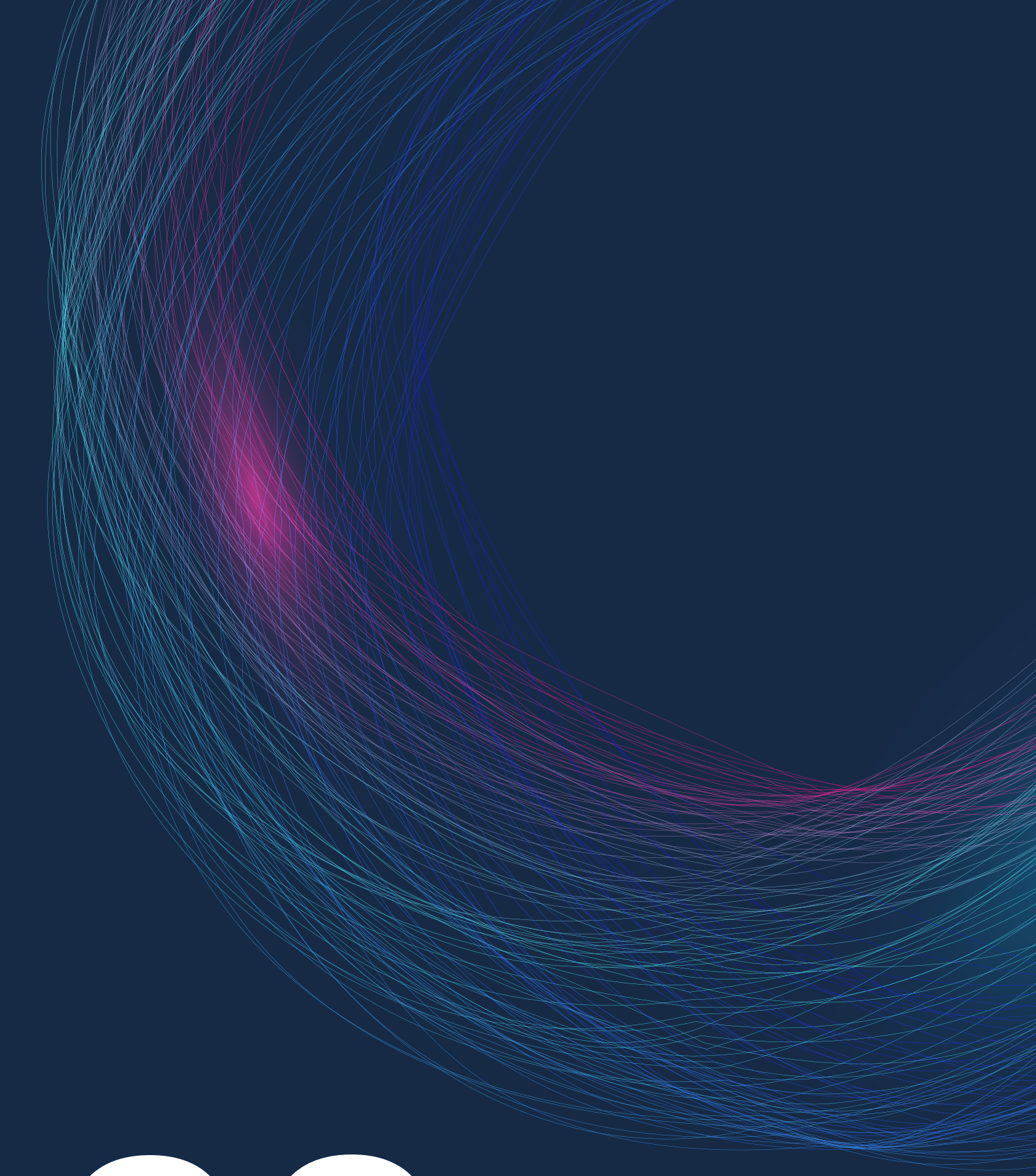
4
SERVICES DELIVERED

6
COURSES

69
STUDENTS TRAINED

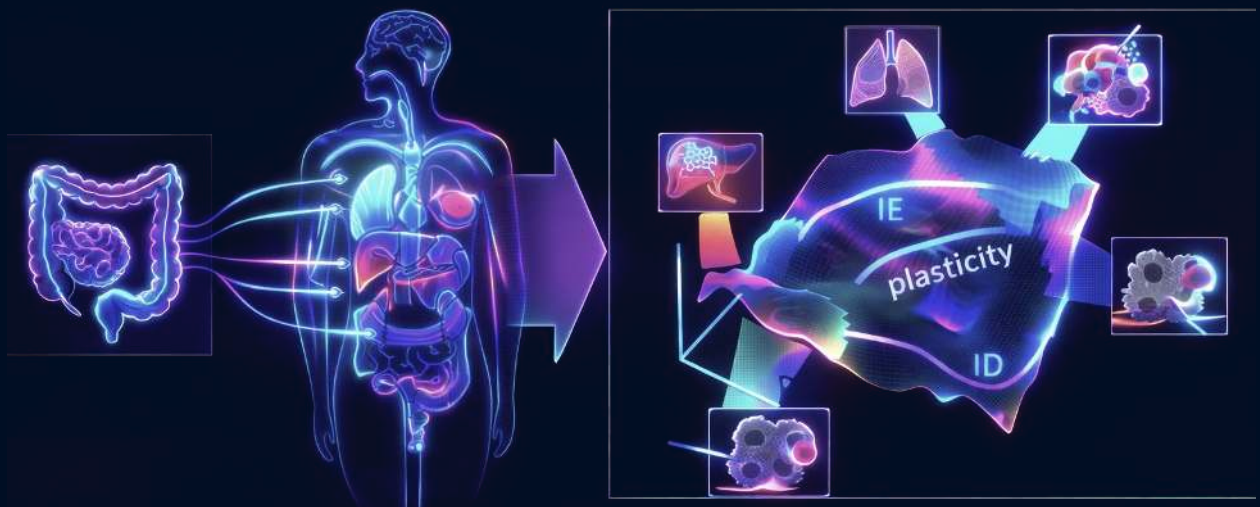
6
GRANTS

3
RESEARCH UNITS



03 RESEARCH

BIOINFORMATICS FOR PRECISION ONCOLOGY: MECHANISMS OF METASTASIS AND TREATMENT RESISTANCE



Bioinformatics in oncology has expanded rapidly in recent years, shifting from foundational method development toward integration into translational and clinical research. Technological and computational advances now enable high-dimensional analyses for subtype classification, precision oncology, and therapeutic target discovery for major challenges, such as metastasis, immuno-oncology, and treatment resistance. In collaboration with Agenus, we investigate the efficacy of immune checkpoint inhibitors (ICIs), which remain largely ineffective in microsatellite-stable metastatic colorectal cancer (MSS mCRC). Here, low tumor immunogenicity and molecular heterogeneity across metastatic sites are major drivers of therapeutic resistance. We performed comprehensive transcriptomic analyses of primary and metastatic tumor biopsies from MSS mCRC patients treated with botensilimab (BOT), an Fc-enhanced anti-CTLA-4 antibody, alone or in combination with balstilimab (BAL), an anti-PD-1 antibody, as part of a clinical study conducted by Agenus. We revealed that ICI treatment was associated with transcriptomic shifts toward immune-enriched tumor states, characterized by upregulation of antigen presentation, T cell recruitment, and cytotoxicity pathways. We identified distinct tumor microenvironment states, as well as APOBEC3 gene activity, as correlates of immunotherapy response in MSS mCRC. In 2026, we will extend this work to single-cell transcriptomics and ATAC-seq analyses of cutaneous melanoma and gastric cancer datasets. Alongside this primary focus, additional cancer research activities were carried in collaboration with the Institute of Molecular Biology (IMB), including spatial transcriptomics of melanoma, telomere maintenance mechanisms in lower-grade gliomas, and Nanopore sequencing-based transcriptomic approaches in hematological malignancies.

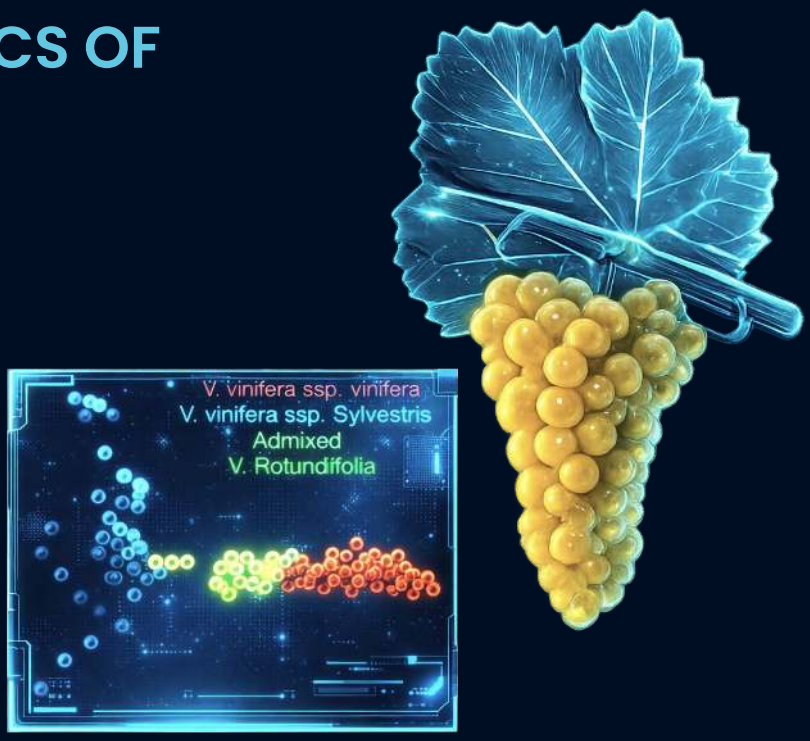
Konecny T, Zadirako N, Grigoryan A, Tamazyan M, Mnatsakanyan S, Stepanyan L, Loeffler-Wirth H, Bourdelais S, Mednick G, Delepine C, Chand D, Binder H.
Transcriptomic profiling identifies immunotherapy-responsive phenotypes in microsatellite-stable metastatic colorectal cancer. *Manuscript under review.*

Hakobyan S, Schmidt M, Binder H, Arakelyan A.
Topology-aware pathway analysis of spatial transcriptomics. *PeerJ,* 2025.

Hakobyan M, Binder H, Arakelyan A.
Telomere maintenance pathways in lower-grade gliomas: insights from genetic subtypes and telomere length dynamics. *International Journal of Molecular Sciences,* 2025.

Arakelyan A, Sirunyan T, Khachatryan G, Hakobyan S, Minasyan A, Nikoghosyan M, Hakobyan M, Chavushyan A, Martirosyan G, Hakobyan Y, Binder H.
Assigning transcriptomic subtypes to chronic lymphocytic leukemia samples using Nanopore RNA sequencing and self-organizing maps. *Cancers,* 2025.

PAN-GENOMICS OF CAUCASIAN GRAPEVINES



The South Caucasus region, including Armenia, is recognized as a center of early viticulture, hosting the oldest known winery and a long-standing winemaking tradition. Armenia's diverse topography has contributed to the preservation of genetically rich grapevine populations. Both cultivated grapevines (Vitis vinifera ssp. vinifera) and their wild ancestor (V. vinifera ssp. sylvestris) exhibit high genetic diversity, providing valuable resources for studying domestication, adaptation, and breeding.

Despite Armenia's historical and economic significance in viticulture, the genomic diversity of its wild and cultivated grapevines remains insufficiently characterized.

In 2025, and for the first time in Armenia, we performed whole-genome analyses of wild and cultivated grapevine populations to characterize genetic diversity and identify candidate genes and domestication-related genomic regions associated with agronomic traits. These results highlight the importance of conserving local grapevine diversity in a historically significant and genetically rich viticultural region.

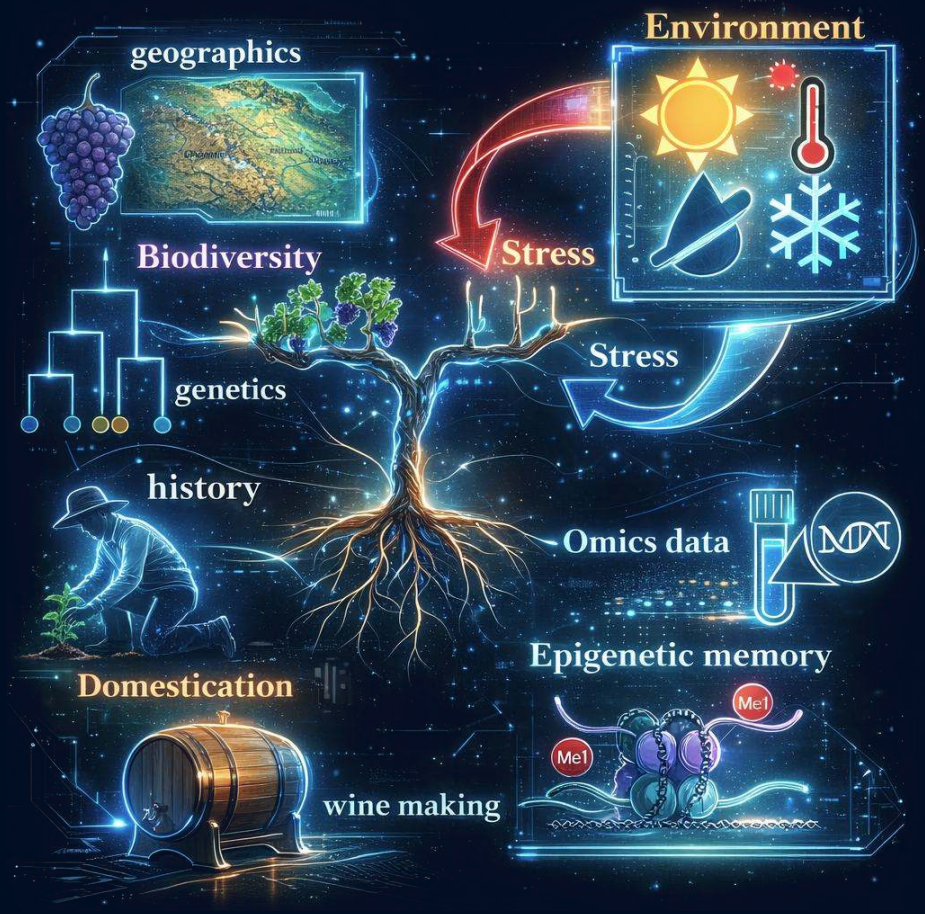
We further applied machine learning–based approaches to analyze genetic patterns across worldwide grapevine accessions, enabling characterization of genomic diversity, population structure, and domestication history.

Current work focuses on the construction of a pangenome of Armenian grapevine accessions and the development of a comprehensive whole-genome atlas of wild and cultivated grapevines from the South Caucasus, including Armenia, Georgia, Azerbaijan, and Turkey.

Baloyan A, Konecny T, Hovhannisyan E, Zadirako N, Nikoghosyan M, Binder H.
A topological map of the genetic components of grapevine: admixture meets SOMmelier machine learning. *Manuscript under review.*

Nikoghosyan M, Hovhannisyan E, Zadirako N, Duan S, Asataryan A, Arakelyan A, Margaryan K, Baloyan A, Konecny T, Binder H.
The genetic richness of wild and cultivated grapevine in Armenia. *Manuscript under review.*

FUNCTIONAL GENOMICS OF GRAPEVINE IN A CHANGING CLIMATE



Climate change, including altered precipitation patterns and increasing temperature extremes, poses a significant challenge to global viticulture by affecting grapevine growth, yield, and fruit quality. Understanding the molecular basis of grapevine resilience is essential for developing adaptive strategies.

We apply multi-omics approaches, integrating genomics, transcriptomics, proteomics, metabolomics, and epigenetic analyses, to investigate grapevine stress responses.

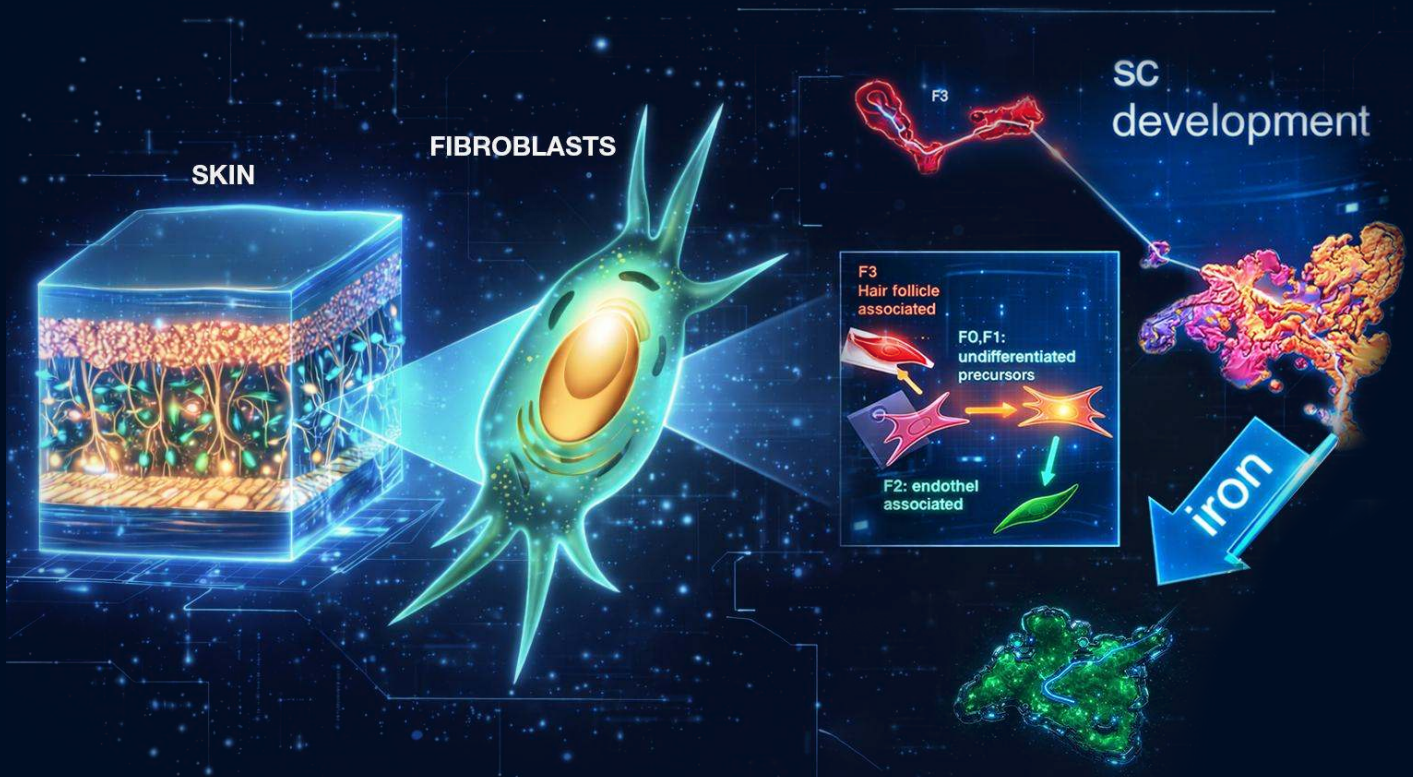
Recent advances in these technologies have enabled the identification of key stress-response genes, metabolic pathways, and regulatory networks underlying tolerance to water deficit and temperature extremes. The extensive genetic diversity of grapevines represents an important resource for improving stress resilience.

Current work focuses on epigenetic memory mechanisms and seasonal transcriptomic programs governing grapevine bud development across the annual cycle.

Konecny T, Asatryan A, Binder H.
Responding to stress: diversity and resilience of grapevine in a changing climate under the perspective of omics research. *International Journal of Molecular Sciences,* 2025.

Konecny T, Asatryan A, Binder H.
Annual transcriptomic trajectory of grapevine buds reveals the coordinated regulation of thiamine and stilbenoid biosynthesis during winter dormancy. *Manuscript under review.*

FIBROBLASTS UNDER STRESS AS SEEN BY SINGLE-CELL TRANSCRIPTOMICS



Dermal fibroblasts are the "construction workers" of the skin. These cells help keep it strong, flexible, and healthy. They produce and maintain the supportive framework of the dermis, including collagen and other fibers that give the skin its structure and elasticity. Dermal fibroblasts also communicate with surrounding cells, helping to regulate skin renewal, immune defense, and blood vessel function. They play a central role in wound healing by repairing damaged tissue, but can also contribute to scarring and skin diseases when their activity is dysregulated.

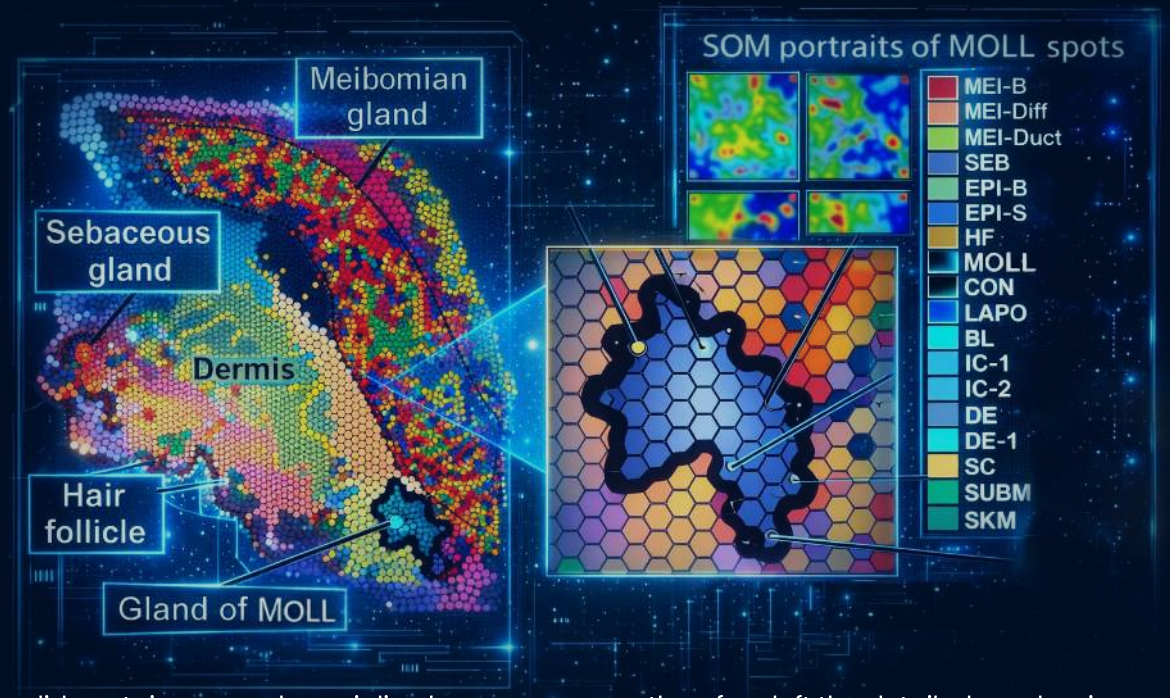
We studied skin samples of mice in cooperation with Leipzig University to better understand fibroblast development under iron overload conditions as an experimental model of scleroderma disease.

Under conditions of iron overload, fibroblasts undergo profound functional and metabolic changes, such as oxidative stress, DNA damage, and altered mitochondrial function. In response, fibroblasts may shift their gene expression programs toward stress adaptation, inflammation, and extracellular matrix remodeling.

Chronic iron overload can drive fibroblast activation, excessive collagen deposition, and tissue fibrosis, while in severe cases it may induce cellular senescence or ferroptotic cell death. These iron-induced alterations in fibroblast behavior are increasingly recognized as important contributors to impaired wound healing and the progression of fibrotic and inflammatory diseases.

M Torregrossa, A Grigoryan, M Tamazyan, M Schmidt, H Loeffler-Wirth, H Binder, S Franz.
Iron overload and WNT signalling dysregulation drive lipodermatosclerosis progression. *Experimental Dermatology,* 2025

SPATIAL TRANSCRIPTOMICS OF UNICORNS: GLANDS IN THE EYELID



The eyelid contains several specialized glands that are essential for maintaining the health and function of the ocular surface. The glands of Moll are modified sweat glands located at the eyelid margin and contribute to local moisture and antimicrobial defense. Sebaceous glands, associated with eyelash follicles, secrete lipids that lubricate the lashes and skin and help protect against microbial invasion. Meibomian glands are large, specialized sebaceous glands embedded within the tarsal plate of the eyelid; they produce meibum, a lipid-rich secretion that forms the outer layer of the tear film, reduces tear evaporation, and ensures tear film stability.

Together, these glands play a crucial role in eyelid integrity, tear film homeostasis, and ocular surface protection. All these glands are micro-organs composed of only a few cell layers, which makes them inaccessible to standard bulk omics methods and has therefore left the detailed mechanisms of their function largely unexplored. The combination of modern spatial transcriptomics at single-cell resolution with comprehensive bioinformatics has opened new avenues for their study. Our spatial transcriptome browser [Schmidt et al, Curr. Issues Mol. Biol. 2024] was mentioned among the Bioinformatics Breakthroughs in 2024–2025.

In cooperation with Leipzig University, which provided the omics samples, we develop and apply these computational approaches to elucidate the microphysiology of meibum and sebum production in the Meibomian and sebaceous glands, respectively, as well as the previously enigmatic function of the Moll gland. These results will advance our understanding of ocular surface diseases and inform the development of potential treatments.

Binder H, Hampel U, Loeffler-Wirth H, Hansmann F, Pfannkuche H, Schmidt M, Schneider MR.
Spatial transcriptome analysis of the human eyelid depicts meibomian gland cell differentiation: a pilot study. *Physiological Reports,* 2025.

Schmidt M, Binder H, Schneider MR.
The metabolic underpinnings of sebaceous lipogenesis. *Communications Biology,* 2025.

Konecny T, Binder H, Hampel U, Hansmann F, Pfannkuche H, Schneider MR.
Spotting a unicorn: spatial transcriptome analysis of the eyelid reveals gene regulatory networks enriched in Moll glands. *Manuscript under review.*

FUNDING

GaBioMed: German Program of Cooperation with the countries of the South Caucasus

Spatial and Single-Cell Genome Bioinformatics for Precision Medicine (2026-2029)

We were awarded a project grant under the German Program of Cooperation with the countries of the South Caucasus. The GaBioMed project aims to establish single-cell genomics, including spatial gene expression profiling, as a modern and sustainable technology for molecular biomedicine in Armenia, with a strong emphasis on bioinformatics. The project is implemented by the International Center for Bioinformatics at Leipzig University, ABI in Yerevan, and IMB, building on more than ten years of collaboration in genomic bioinformatics.

GaBioMed will develop and apply novel bioinformatic methods for single-cell and spatial omics analyses in pilot studies addressing cancer progression, metastasis, therapy resistance, wound healing, and pathological skin processes at single-cell resolution in space and time. The project includes hands-on training of early-career Armenian scientists through joint research activities, alongside the establishment of the required computational and experimental infrastructure at IMB and ABI. The project is scheduled to start in 2026.

Adjunct Research Professorship Program of the Higher Education and Science Committee, MoESCS RA (2025–2030)

From Spatial Single-Cell Omics to Computational Precision Oncology : Unraveling Mechanisms of Metastasis and Treatment Resistance in Solid Tumors

In 2025, we secured a project under the SCS Adjunct Research Professorship Program, formally awarded to IMB and implemented through a shared research framework with the ABI. The project is led by Dr. Hans Binder as the remote Principal Investigator, with Maria Nikoghosyan, PhD, serving as the local co-Principal Investigator. We address key challenges in molecular cancer biomedicine by applying advanced bioinformatics, biodata science, and machine learning approaches to precision oncology, utilizing unique and original datasets.

The project focuses on the analysis of spatial and single-cell omics data to investigate mechanisms of metastasis and treatment resistance in solid tumors.

Through this project, we strengthen advanced computational oncology expertise across ABI and IMB, while training early-career researchers through integrated, hands-on research activities within a unified team. The project started in July 2025.

FUNDING

ADVANCE 2025 Program of the Higher Education and Science Committee (2023–2026)

Vine Bioinformatics: Grape Genomics for Innovative Viticulture

The Vine Bioinformatics project develops sequencing-based methods built around a machine learning framework and applies them to grape genomics for innovative viticulture. It integrates advances in genomic bioinformatics and data science with viticulture research in Armenia, focusing on grapevine genomic diversity and molecular regulatory mechanisms associated with environmental stress, derived from large and complex omics datasets.

We develop machine learning-based bioinformatics methods for plant genomics to enable genome-wide screening of cultivated and wild grape accessions, identifying genotypes linked to pathogen resistance, pest tolerance, and climate adaptation.

The project aims to generate a comprehensive genetic map of wild grapes and cultivars from the South Caucasus, contributing to international studies on grapevine biodiversity and evolution.

The project was previously awarded to ABI by the FAST Foundation and is now formally awarded to IMB, with the same core research team continuing the work. Dr. Hans Binder serves as the remote Principal Investigator, with Maria Nikoghosyan, PhD, as the local co-Principal Investigator.

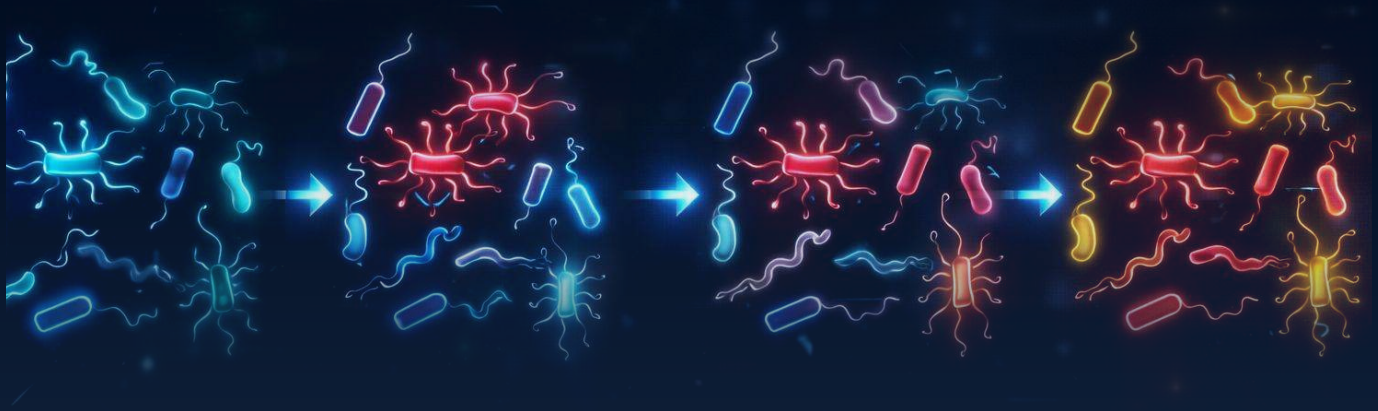
MICROBIOME DYNAMICS: HOW MICROORGANISMS SHAPE OUR HEALTH

Humans and animals host diverse microbial communities, collectively referred to as the microbiome, which play a central role in maintaining health and modulating disease. Different microorganisms perform distinct functions and interact within complex ecosystems through cooperation and competition. These interactions take place across multiple body sites, including the gut, oral cavity, skin, and reproductive tract, where microbial composition is often relatively stable over time. External stressors, such as diet, antibiotics, medications, and disease, can disrupt this balance. While some perturbations are transient, others can induce long-lasting or irreversible shifts in microbial composition that may contribute to chronic disease.

Our team develops bioinformatics algorithms to investigate the temporal sequence of events that lead to such irreversible microbiome changes. We aim to identify microbial taxa directly affected by external stressors and to track how changes in their abundance propagate through the microbial network, ultimately resulting in a new, stable but disease-associated state.

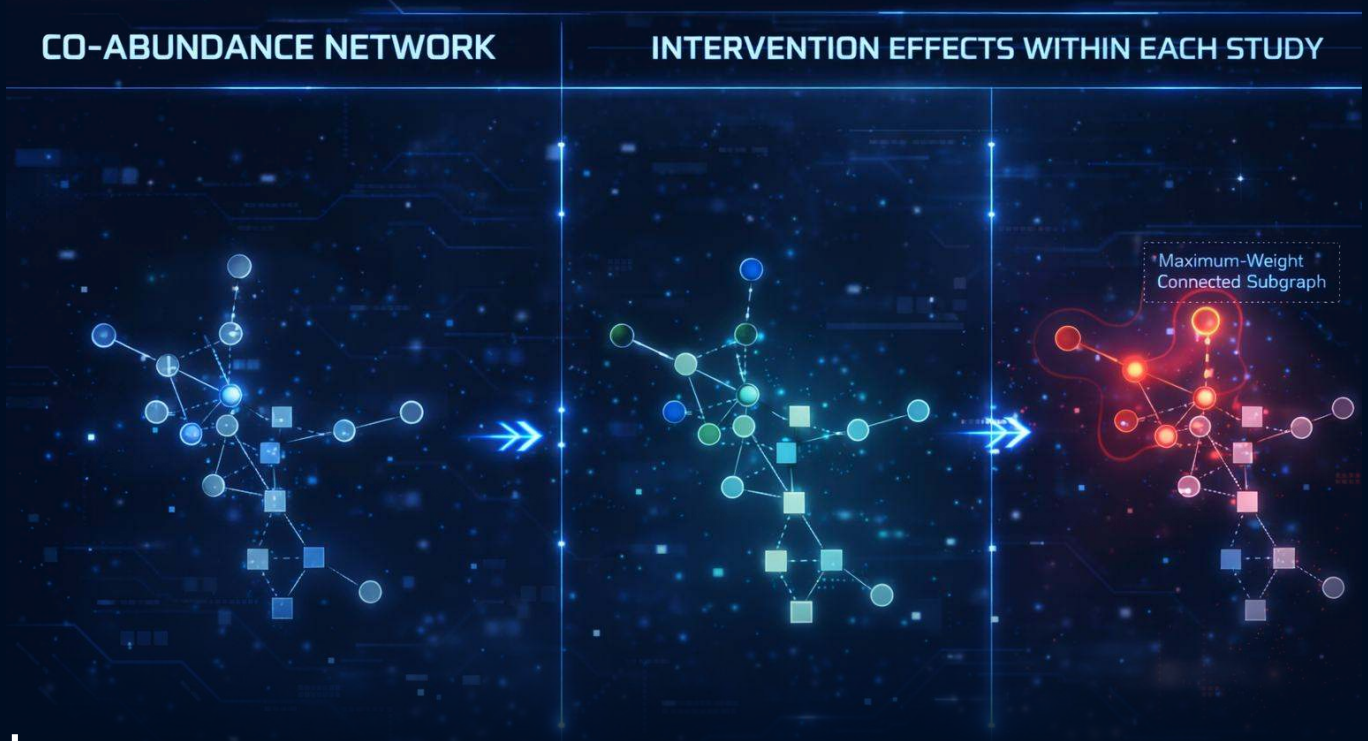
Understanding these dynamics is essential for the rational design of targeted pro- and prebiotic interventions to prevent harmful long-term alterations.

To complement our computational work, we have established a joint laboratory with the Institute of Molecular Biology, NAS RA, enabling experimental perturbation of microbial communities and time-resolved monitoring of compositional changes. As an initial step, we are advancing bioinformatics methods to estimate growth rates of individual bacterial taxa from shotgun metagenomic sequencing data, providing quantitative insight into microbial responses to environmental stress.



Poster presentation: Razmik Sargsyan, Magdalina Zakharyan, Davit Hakobyan, Nelli Vardazaryan, Honglian Liu, Vicent Pelechano, Lilit Nersisyan.
mRNA decay informs about antibiotic response in clinical strains of Staphylococcus aureus. *FEMS Microbiology,* 2025.

INVESTIGATING ENVIRONMENTAL IMPACTS ON THE BEE GUT MICROBIOME THROUGH A NOVEL NETWORK-BASED APPROACH



Like humans, the honeybee gut is home to a diverse community of microorganisms that play a critical role in health and resilience. In recent years, there has been a concerning decline in honeybee colonies, which threatens global agriculture due to their vital role in pollination. One potential contributor to this decline is agricultural practices, particularly pesticide use, which can directly impact honeybee physiology or indirectly affect their health by altering the gut microbiome.

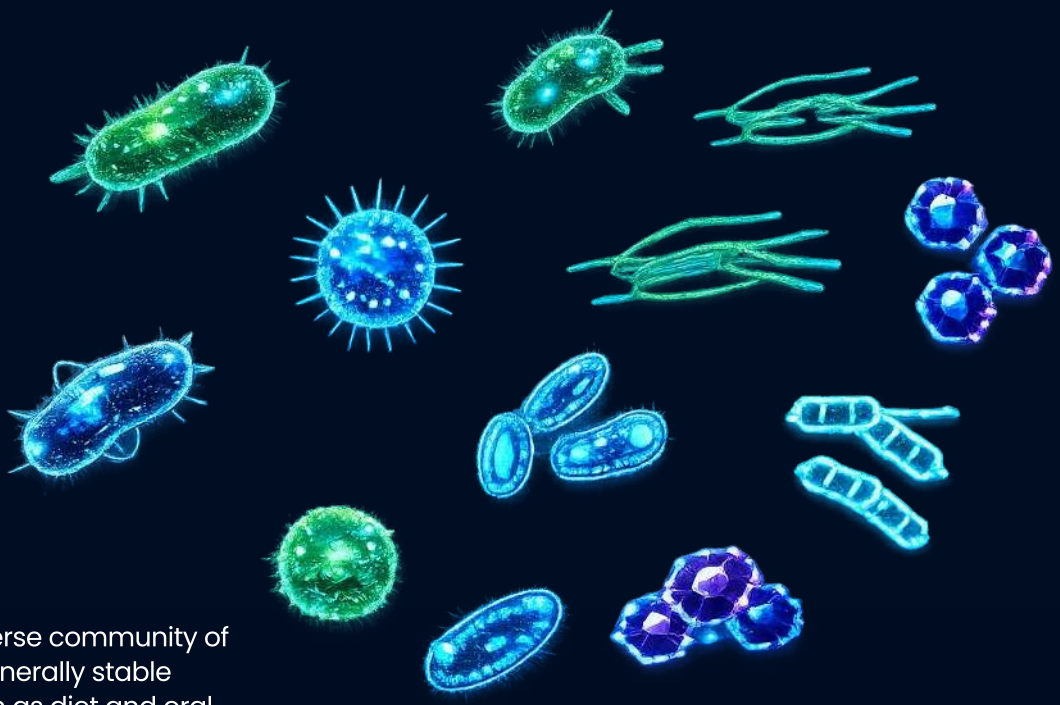
Our team conducted a comprehensive meta-analysis of the honeybee gut microbiome, incorporating data from diverse ecosystems, including data from Armenia generated at Yerevan State University.

This study evaluates the effects of pesticides and dietary supplements on microbial composition, and expands the current understanding of the bee gut microbiome by including samples from various regions of Armenia alongside reanalyzed datasets from other parts of the world.

To assess pesticide impacts, we employed an innovative graph-based algorithm to identify networks of bacterial species significantly affected by treatments, including glyphosate—the most widely used herbicide—along with various insecticides and sugar-based supplements. These analyses enabled the identification of potential adaptive microbial responses to pesticide exposure.

Poster presentation: Nelli Vardazaryan, Lusine Adunts, Inga Bazukyan, Magdalina Zakharyan, Honglian Liu, Chrats Melkonian, Lilit Nersisyan.
Network-Based Meta-Analysis Reveals Pesticide-Associated Shifts in the Honeybee Gut Microbiome. *FEMS Microbiology Congress, 2025. Manuscript under review.*

ORAL MICROBIOME ANALYSIS USING MACHINE LEARNING AND NETWORK-BASED METHODS



The oral cavity hosts a diverse community of bacteria and fungi that is generally stable despite daily influences such as diet and oral hygiene. However, factors including smoking, dietary patterns, and chronic health conditions can disrupt this balance, contributing to oral diseases such as gingivitis, periodontitis, dental caries, and halitosis.

Our team is developing a global co-abundance network of the oral microbiome to comprehensively characterize microbial communities, their interactions, and their associations with disease. This network-based analysis is implemented in tsantsR, a bioinformatics package for multi-condition microbial network analysis, and is used to identify functionally coherent microbial subcommunities and to examine how these clusters change in oral diseases, such as periodontitis and caries.

Extensions of this work to systemic conditions, specifically head and neck cancers, are carried out in collaboration with the Karolinska Institute.

In a complementary line of work, we evaluate machine-learning and statistical approaches to identify microbial features associated with disease. This includes the development of a curated database of microbe–disease associations, which provides feature-level insight and complements the system-level network analyses.

Poster presentation: Adunts L, Vardazaryan N, Hakobyan D, Aydinyan G, Melkonian C, Nersisyan L.
tsantsR: a package for multi-condition microbial network analysis. *FEMS Microbiology,* 2025.

Poster presentation: Hakobyan D, Adunts L, Vardazaryan N, Sargsyan R, Nersisyan L.
Differences in oral microbial communities between smokers and non-smokers. *FEMS Microbiology,* 2025.

TELOMERES IN BLOOD CIRCULATION: UNLOCKING NEW INSIGHTS FOR CANCER DETECTION

Our bodies continuously release genetic material into the bloodstream, either through active secretion or following cell death, resulting in fragments of DNA known as cell-free DNA (cfDNA). In cancer patients, cfDNA originates from both healthy and tumor cells, providing a non-invasive means to detect and monitor cancer through blood sampling, an approach known as liquid biopsy. This strategy has gained increasing attention for its potential in early cancer detection and real-time monitoring of disease progression and treatment response.

Our research focuses on identifying cancer-specific biomarkers within cfDNA to improve diagnostic precision and treatment monitoring, with particular emphasis on telomere-derived cfDNA. Telomeres, the protective ends of chromosomes, play a central role in maintaining genomic stability, and their length and sequence composition are frequently altered in cancer. These telomeric changes vary across cancer types and reflect tumor-specific telomere maintenance mechanisms.

To capture this information, we are developing advanced bioinformatics methods to detect and characterize telomeric DNA fragments circulating in the blood. As part of this effort, we are extending our work on Computel 2.0, a computational framework for accurate estimation of mean telomere length and telomeric repeat variants from whole-genome sequencing data. By applying Computel 2.0 to cfDNA and tumor sequencing datasets, we aim to systematically identify cancer-associated telomeric alterations, improve liquid biopsy–based cancer diagnostics, and gain deeper insight into tumor biology and telomere dynamics.

Poster presentation: Tarverdyan D, Yeghiazaryan A, Jalatyan T, Nersisyan L.
Computel 2.0: An accurate approach for calculating mean telomere length and telomeric repeat variants from whole-genome sequencing data. ISMB/ECCB, 2025. *Manuscript in preparation.*

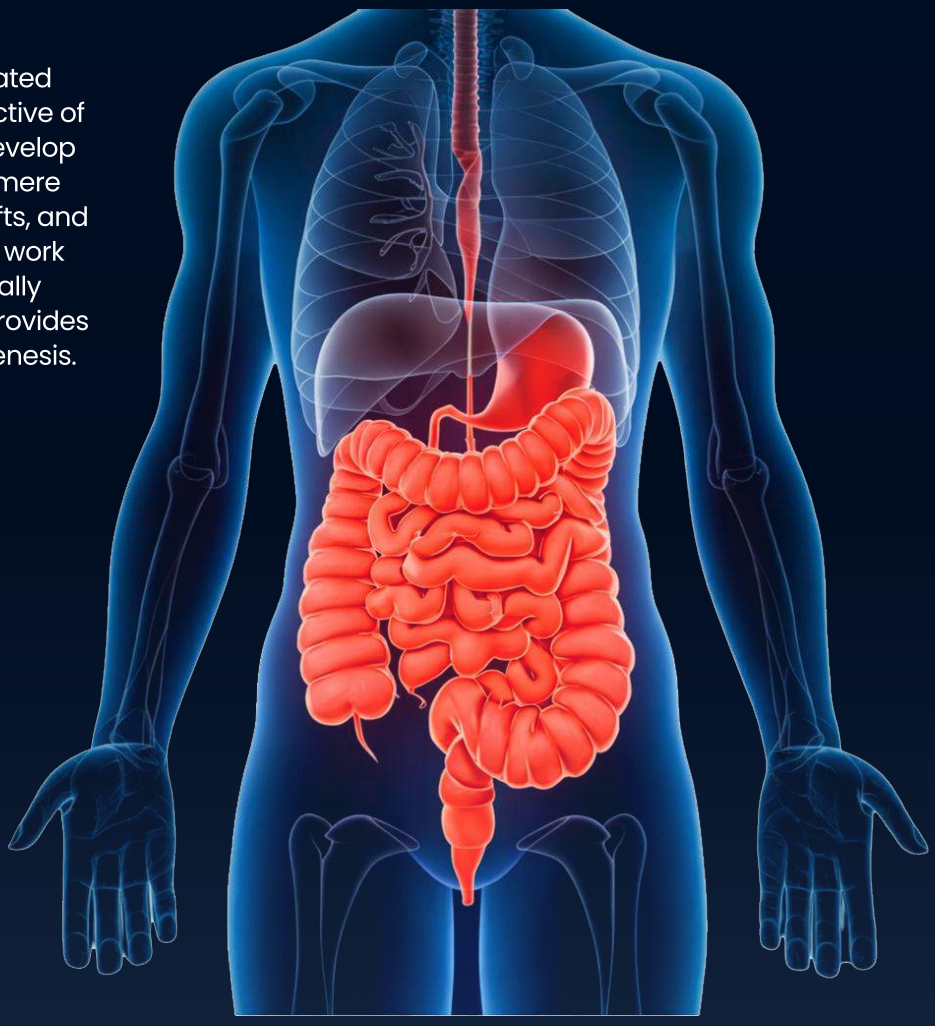
TELOMERES, MICROBIOME, AND INFLAMMATION IN INFLAMMATORY BOWEL DISEASE

Our research in inflammatory bowel disease (IBD) focuses on understanding how telomere dysfunction, intestinal tissue senescence, and gut microbiome dynamics jointly contribute to chronic inflammation and disease progression. IBD is characterized by recurrent inflammatory flares and substantial heterogeneity in clinical course, underscoring the need for molecular biomarkers that capture disease state and trajectory beyond clinical symptoms alone.

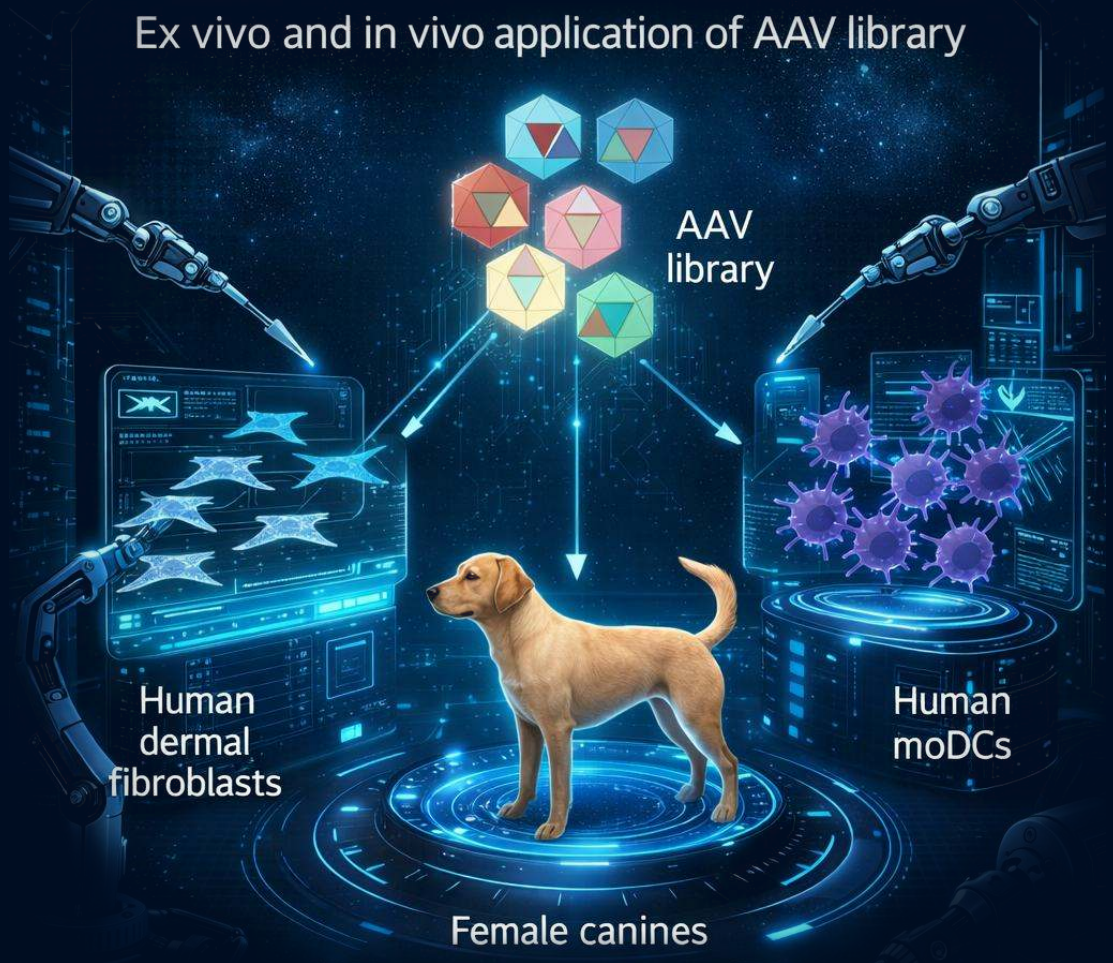
We combine longitudinal multi-omics profiling of IBD patients with advanced bioinformatics analyses to study telomere length and telomeric repeat variants in cell-free DNA and stool-derived DNA, alongside microbiome composition and functional changes.

Our work explores how telomere-derived cfDNA reflects intestinal epithelial damage and immune activation, and how microbial perturbations and microbial extracellular factors may interact with host senescence pathways to sustain inflammation. This work is conducted using a shared research infrastructure with IMB.

Current efforts aim to identify integrated host–microbiome biomarkers predictive of disease activity and flares, and to develop computational models that link telomere dynamics, microbial community shifts, and inflammatory signals over time. This work supports the development of minimally invasive biomarker strategies and provides mechanistic insight into IBD pathogenesis.



GENE THERAPIES: DESIGNING VIRAL VECTORS FOR DISEASE TREATMENT



Certain diseases result from the absence of a functional gene in specific tissues, leading to impaired biological function. Gene therapies address this by delivering a functional gene copy to target cells using viral vectors, most commonly adeno-associated viruses (AAVs). However, the high cost and complexity of viral vector manufacturing remain major barriers to broad clinical application, highlighting the need for improved vector design, delivery efficiency, and scalability.

This year, we completed a study conducted within a shared research effort with the Wyss Institute at Harvard University and Rejuvenate Bio, focused on the rational design of more efficient and cost-effective viral vectors for age-related diseases.

Through targeted genetic modifications, our collaborators generated diverse libraries of chimeric AAV vectors and experimentally identified variants with enhanced gene delivery performance.

To address the analytical challenges posed by these highly diverse libraries, we developed hafoe, a computational tool for the analysis and prioritization of chimeric AAV variants following random mutagenesis. Using novel experimental datasets, hafoe enabled the identification of new AAV variants with enhanced tropism toward specific cell types and tissues, including immune cells, skin, and muscle, in both human and animal systems. The software is openly available at: https://github.com/abi-am/hafoe

Jalatyan T, Aznauryan E, Hasan R, Vardanyan V, Nersisyan S, Thompson D, Davidsohn N, van Haren S, Tam J, Milanova D, Church G, Nersisyan L.
***hafoe*: an interactive tool for the analysis of chimeric AAV libraries after random mutagenesis.** *Gene Therapy,* 2025. This work was also presented at ISMB/ECCB 2025.

FUNDING

RESEARCH GRANT PROGRAM OF THE HIGHER EDUCATION AND SCIENCE COMMITTEE, MOESCS RA (2024–2028)

The Interplay Between Telomere Dysfunction, Gut Microbiome, and Inflammation in Inflammatory Bowel Disease

In 2024, we secured a project under the Research Grant Program of the Higher Education and Science Committee, MoESCS RA, formally awarded to IMB and implemented through shared research infrastructure with ABI. The project investigates how telomere dysfunction, intestinal tissue senescence, and gut microbiome alterations jointly contribute to chronic inflammation and disease progression in inflammatory bowel disease (IBD).

We combine longitudinal multi-omics profiling of IBD patients with advanced bioinformatics analyses to study telomere length and telomeric repeat variants in cell-free DNA and stool-derived DNA, alongside microbiome composition and functional dynamics.

The project aims to identify integrated host–microbiome biomarkers associated with disease activity and flare dynamics, providing mechanistic insight into IBD pathogenesis and supporting the development of minimally invasive monitoring strategies.

RESEARCH GRANT PROGRAM OF THE HIGHER EDUCATION AND SCIENCE COMMITTEE, MOESCS RA (2024–2026)

Deciphering the Fine-Scaled Temporal Changes in Microbiome Communities Following Antibiotic Exposure

In 2024, we secured a second project under the Research Grant Program of the Higher Education and Science Committee, MoESCS RA, formally awarded to IMB and carried out using shared research infrastructure with ABI.

This project focuses on understanding how antibiotic exposure perturbs microbiome communities over time and why certain perturbations result in long-lasting or irreversible community shifts. Using dense longitudinal sampling and shotgun metagenomic sequencing, we analyze fine-scaled temporal changes in microbial composition, growth dynamics, and interaction networks following antibiotic treatment.

By developing and applying time-resolved and network-based bioinformatics methods, the project aims to identify early microbial indicators of resilience versus collapse, contributing to a mechanistic understanding of microbiome recovery and informing strategies for microbiome-preserving interventions.

PHD SUPPORT PROGRAM OF EARLY-CAREER RESEARCHERS, HIGHER EDUCATION AND SCIENCE COMMITTEE, MOESCS RA (2024–2027)

Longitudinal Analysis of Antibiotic Response in Microbiome Communities

In 2024, we secured a project under the Support Program for Research of PhD Students and Early-Career Researchers of the Higher Education and Science Committee, MoESCS RA, formally awarded to IMB and carried out using shared research infrastructure with ABI. The project, led by PhD student Nelli Vardazaryan under the supervision of Lilit Nersisyan, investigates longitudinal changes in microbiome communities following antibiotic exposure.

The work focuses on understanding how antibiotic treatments induce compositional shifts and promote the emergence of antibiotic resistance in microbial communities.

Using time-resolved metagenomic and transcriptomic sequencing of bacterial and fecal cultures, the project aims to develop bioinformatics methods for analyzing longitudinal microbiome data and tracking the rapid evolution of resistance. This research addresses a critical gap in current microbiome analysis methodologies and contributes to a mechanistic understanding of microbiome response and recovery following antibiotic perturbations.

ARPA FELLOWSHIP PROGRAM (2025)

Development of Telomere-Based Cancer Biomarkers from Liquid Biopsies

In 2025, we secured an ARPA Fellowship awarded to Tatevik Jalatyan to develop telomere-based biomarkers for cancer detection using liquid biopsy data. The fellowship supports research on the analysis of telomeric features in cell-free DNA, including telomere length and telomeric repeat variants, as indicators of tumor-specific genomic instability. The work builds on our computational frameworks for telomere analysis and focuses on identifying robust, cancer-associated telomeric signatures across sequencing datasets.

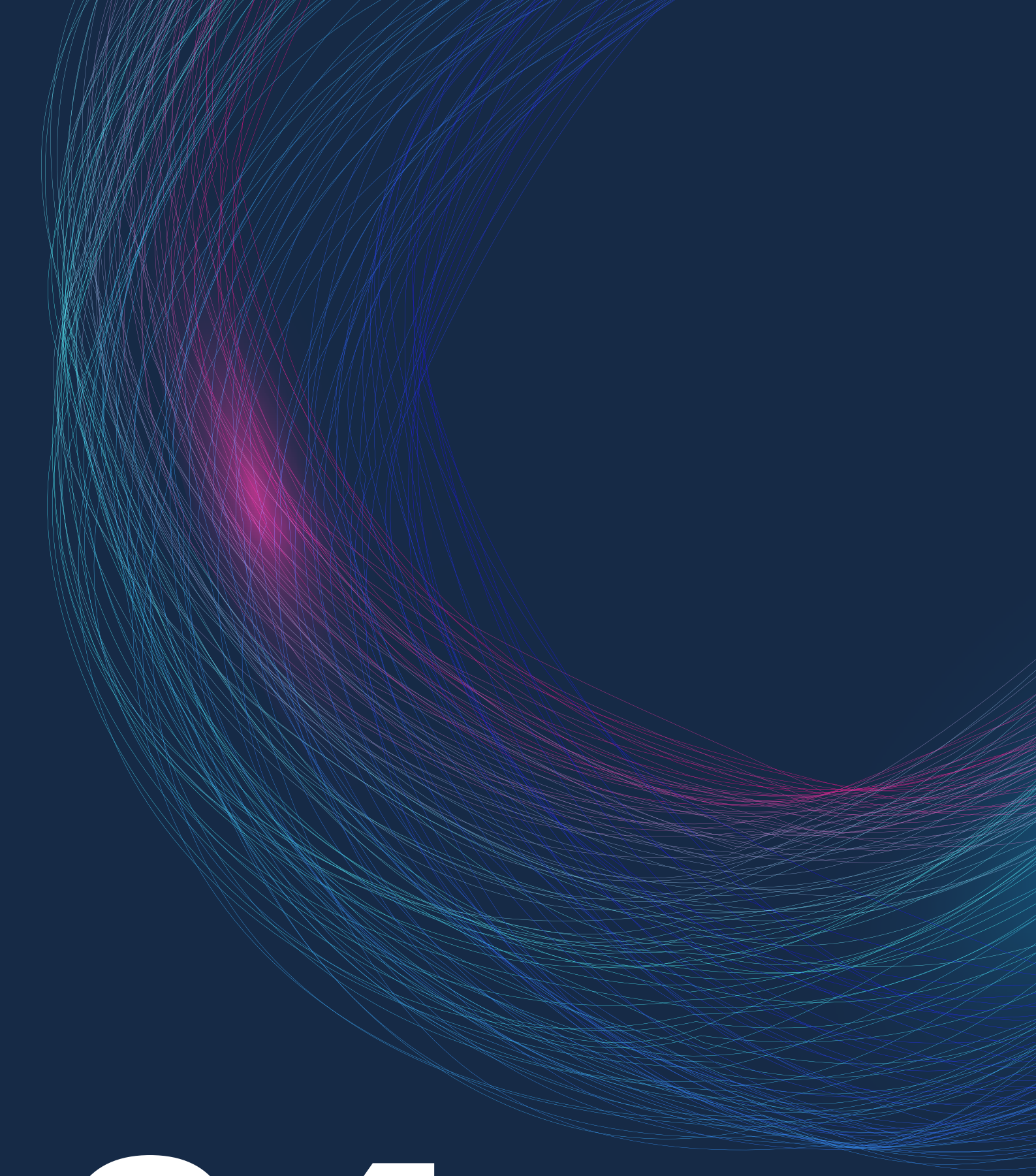
This project contributes to the development of minimally invasive cancer biomarkers and strengthens methodological links between telomere biology, computational genomics, and precision oncology.

PUBLICATIONS IN 2025

1. Jalatyan T, Aznauryan E, Hasan R, Vardanyan V, Nersisyan S, Thompson DB, Davidsohn N, Thomas S, van Haren S, Tam J, Milanova D, Church GM, Nersisyan L. **hafoe: an interactive tool for the analysis of chimeric AAV libraries after random mutagenesis.** *Gene Therapy,* 2025.
2. Borisov N, Ilnytsky Y, Byeon B, Kovalchuk O, Kovalchuk I. **Multi-omics data integration for topology-based pathway activation assessment and personalized drug ranking**. *Molecular Omics*, 2025.
3. Zhang Y, Nersisyan L, Fürst E, Alexopoulos I, Santolaria C, Huch S, Bassot C, Garre E, Sunnerhagen P, Piazza I, Pelechano V. **Ribosomes modulate transcriptome abundance via generalized frameshift and out-of-frame mRNA decay.** *Molecular Cell,* 2025.
4. Binder H, Hampel U, Loeffler-Wirth H, Hansmann F, Pfannkuche H, Schmidt M, Schneider MR. **Spatial transcriptome analysis of the human eyelid depicts meibomian gland cell differentiation: A pilot study.** *Physiological Reports,* 2025.
5. Schmidt M, Binder H, Schneider MR. **The metabolic underpinnings of sebaceous lipogenesis.** *Communications Biology,* 2025.
6. Konecny T, Asatryan A, Binder H. **Responding to stress: diversity and resilience of grapevine in a changing climate under the perspective of -omics research.** *International Journal of Molecular Sciences,* 2025.
7. Hakobyan S, Schmidt M, Binder H, Arakelyan A. **Topology-aware pathway analysis of spatial transcriptomics.** *PeerJ,* 2025.
8. Hakobyan M, Binder H, Arakelyan A. **Telomere maintenance pathways in lower-grade gliomas: insights from genetic subtypes and telomere length dynamics.** *International Journal of Molecular Sciences,* 2025.
9. Arakelyan A, Sirunyan T, Khachatryan G, Hakobyan S, Minasyan A, Nikoghosyan M, Hakobyan M, Chavushyan A, Martirosyan G, Hakobyan Y, Binder H. **Assigning transcriptomic subtypes to chronic lymphocytic leukemia samples using Nanopore RNA-sequencing and Self-Organizing Maps.** *Cancers (Basel),* 2025.

PREPRINTS

1. Vardazaryan N, Adunts L, Bazukyan I, Zakharyan M, Liu H, Melkonian Ch, Nersisyan L. **Global distribution of honeybee gut microbiome and pesticide-driven adaptations in opportunistic microbial species.** *BioRxiv*, 2025.



04 TRAINING

OMICSS-25 SUMMER SCHOOL IN GENOME BIOINFORMATICS

The fourth edition of the OMICSS Genome Bioinformatics Summer School took place from July 28 to August 24, 2025. Organized by the Armenian Bioinformatics Institute (ABI) in partnership with the Institute of Molecular Biology (IMB) and Leipzig University, this year's program brought together 17 participants from Armenia and Europe for four intensive weeks of learning and collaboration.

The curriculum covered a wide range of fundamental and applied topics, including sequencing technologies, bioinformatics algorithms, and genomics data analysis. A defining feature of OMICSS-25 was the early integration of practical research: project work began from the first day of the program, allowing participants to immediately apply newly learned concepts as they progressed through the course. Throughout the program, students engaged in hands-on sessions and group projects spanning cancer genomics, microbiome research, and plant genomics, connecting theoretical concepts with real-world research challenges in real time.

Prior to the start of the main program, ABI organized three preparatory training sessions covering Introduction to Molecular Biology, Programming, and Statistics.

These bridge courses were designed to bring participants with diverse educational backgrounds to a common starting level, ensuring that all participants could fully benefit from the intensive Summer School curriculum.

A total of 13 lecturers and 18 mentors guided students throughout the program. Mentors, lecturers and invited speakers represented a broad range of institutions, including ABI (Armenia), Leipzig University (Germany), IMB (Armenia), Stanford University (USA), Johns Hopkins University (USA), Muna Therapeutics (Belgium), St. Anna Children's Cancer Research Institute (Austria), Boehringer Ingelheim (USA), EPFL (Switzerland), Thomas Jefferson University (USA), the National University of Singapore, the Arctic University of Norway, PMI Science, Utrecht University (The Netherlands), and the Julius Kühn-Institut (Germany). Participants came from universities including Yerevan State University, Yerevan State Medical University, Russian-Armenian University, the American University of Armenia, the University of Trieste (Italy), the University of Rhein-Waal (Germany), Tallinn University (Estonia), the University of L'Aquila (Italy), the University of Groningen (The Netherlands), the National Polytechnic University of Armenia, as well as specialists from Armenian technology companies and medical institutions.

OMICSS-25 SUMMER SCHOOL IN GENOME BIOINFORMATICS

The program culminated in a four-day BootCamp in Yeghegis, structured in two complementary parts. In the first part, students finalized their research projects, engaged in discussions with invited scientists, and presented their work during the final presentation and closing day of the Summer School. These activities were guided by their mentors from the ABI team and reflected the full research cycle, from question formulation and data analysis to interpretation and presentation. Student projects addressed diverse topics, including identification of bacterial biomarkers for disease classification, discovery of telomeric biomarkers for cancer detection in cell-free DNA, genomic characterization of population structure in Caucasian grape varieties using whole-genome sequencing, and dissection of lung cancer heterogeneity using single-cell transcriptomic profiling.

The second part of the BootCamp was the German-Armenian Workshop Day, organized within the scope of the DigitalLife project. DigitalLife aims to advance collaboration between ABI, the Interdisciplinary Center for Bioinformatics (IZBI) at Leipzig University, and IMB in Yerevan, addressing the growing convergence of digital and life sciences driven by large-scale biological and molecular medical data. The workshop featured presentations and discussions by Armenian and German researchers on ongoing collaborative work, covering topics ranging from bioinformatics methods development to applications in machine learning, cancer genomics, telomere biology, microbiome research, plant science, immunology, skin wound healing, and Caucasian grapevine genomics.

All OMICSS-25 activities, including the Summer School, and the BootCamp, were supported by a network of academic and industry partners, including the Institute of Molecular Biology, Leipzig University, the DigitalLife project, Deep Origin, and BostonGene.

BRIDGE COURSES FOR OMICSS-25

Introduction to Molecular Biology

Held from February 25 to March 21 at ABI, this bridge course provided participants with a comprehensive overview of fundamental molecular biology concepts, including cell structure, DNA, RNA, and gene expression. The course was taught by Alexey Kurnosov, PhD, and aimed to establish a solid theoretical foundation for participants with diverse educational backgrounds.

Python for Genomic Data Science

The Python for Genomic Data Science bridge course took place from March 25 to April 18 at ABI, introducing participants to essential programming skills for genomic research. Led by Alisa Davtyan, the course covered core Python concepts and their application to biological datasets, including DNA and RNA sequence analysis and basic genomics workflows.

Introduction to Statistics

Held from April 22 to May 9 at ABI, the Introduction to Statistics bridge course provided participants with fundamental concepts and tools for data analysis in the life sciences. Taught by Alisa Davtyan, the course covered descriptive and inferential statistics, probability theory, and practical data analysis using Python libraries such as Pandas and Statsmodels. Designed for beginners, it offered a clear and accessible introduction to statistical reasoning and data analysis in biological research.

COURSES

Mathematical Modeling in the Life Sciences

ABI hosted the Mathematical Modeling in the Life Sciences course led by Nicola Vassena, PhD (Leipzig University). Over five intensive days, participants explored how mathematical tools can describe and predict biological phenomena, including dynamical systems, evolutionary models, reaction networks, and pattern formation. The course was specifically designed for bioinformatics students with limited formal mathematical training, making complex concepts accessible and directly relevant to biological applications.

Introduction to Machine Learning

The seven-week Introduction to Machine Learning course, led by Simon Steshin, introduced participants to fundamental machine learning algorithms, including linear models, decision trees, neural networks, and dimensionality reduction techniques. With a strong emphasis on real world biological applications, the course provided hands-on experience in analyzing biological datasets using modern machine-learning methods.

CAPSTONES

Undergraduate Theses

Davit Tarverdyan

Davit Tarverdyan completed his Bachelor's degree in Informatics and Applied Mathematics at the National Polytechnic University of Armenia. His thesis focused on clustering-based analysis of telomeric repeat patterns in cell-free DNA as potential cancer biomarkers. The work was supervised by Dr. Lilit Nersisyan (ABI) and Dr. Parandzem Hakobyan (IIAP NAS RA, NPUA).

Luiza Stepanyan

Luiza Stepanyan completed her Bachelor's degree in Data Science at the American University of Armenia. Her thesis addressed cell-state deconvolution of the tumor microenvironment in microsatellite-stable metastatic colorectal cancer, under the supervision of Dr. Hans Binder.

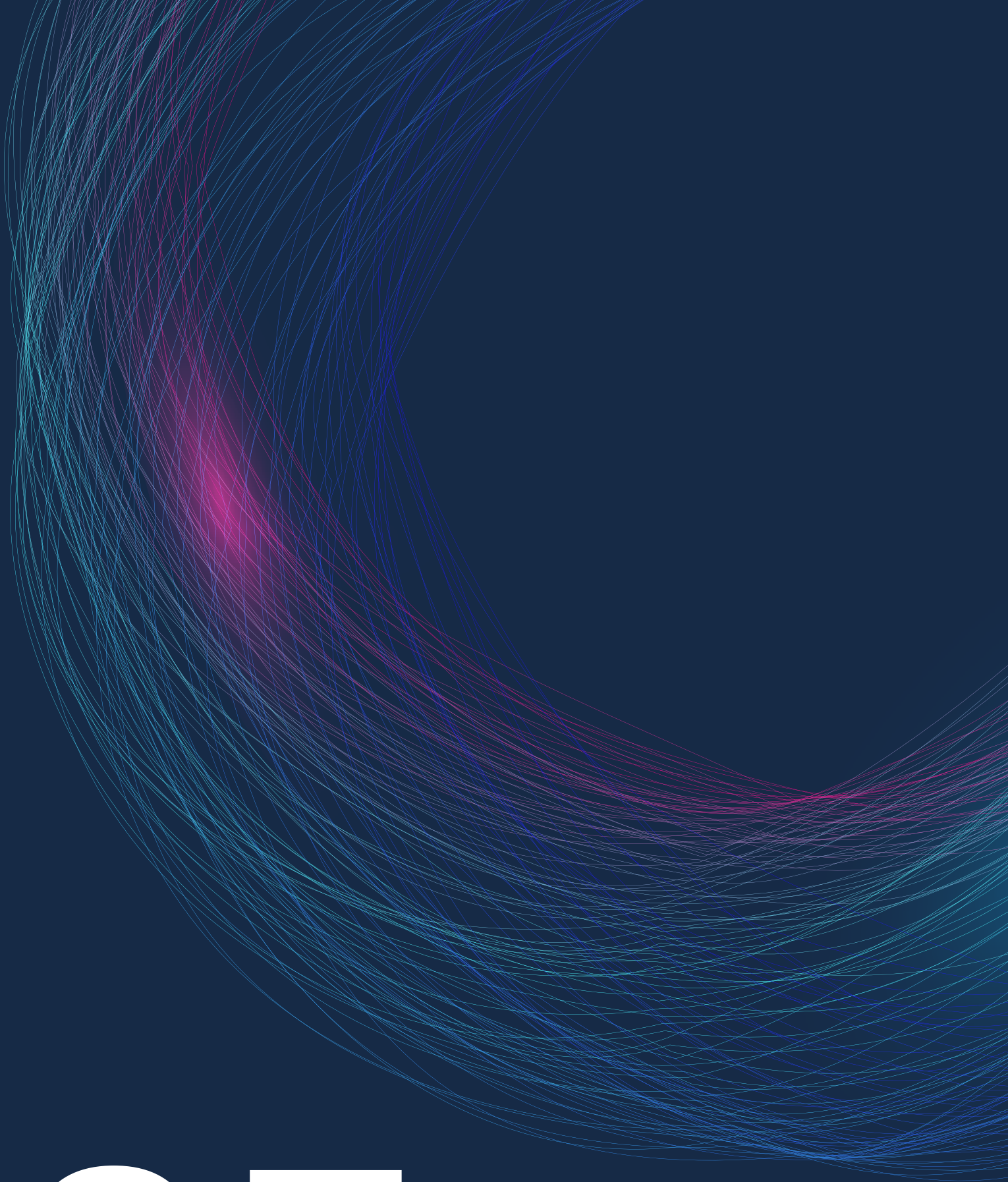
Doctoral Theses

Maria Nikoghosyan

Maria Nikoghosyan defended her PhD thesis at Leipzig University entitled Portrayal of Genomic Variation Landscapes of Armenians and Armenian Grapevines: Genetic Diversity and History of Still Understudied Populations, supervised by Dr. Arsen Arakelyan and Dr. Hans Binder.

Siras Hakobyan

Siras Hakobyan defended her PhD thesis at Leipzig University entitled Topology-Aware Pathway Analysis of Omics Data, supervised by Dr. Arsen Arakelyan and Dr. Hans Binder.



05

BIOINFORMATICS CORE FACILITY

BIOINFORMATICS CORE FACILITY

ABI has provided bioinformatics services to academic and industry partners since its early years, supporting data-driven research across genomics and multi-omics. In 2025, these activities were formalized and consolidated into a dedicated organizational unit, the Bioinformatics Core Facility, establishing a structured framework for service delivery, project coordination, and external engagement.

The Bioinformatics Core Facility supports research projects involving large-scale and complex biological datasets, spanning the full analytical workflow from primary data processing to advanced integrative analysis and biological interpretation. The growing volume and complexity of high-throughput sequencing and multi-modal data have increased demand for analytical approaches that combine computational rigor with biological domain expertise. Accordingly, the facility supports projects in cancer genomics, microbiome research, biomarker discovery, and single-cell and spatial transcriptomics.

Core Facility activities include routine and advanced bioinformatics analyses, integrative multi-omics modeling, custom workflow and pipeline development, and public data mining, depending on project needs. The facility also provides consultation on experimental design and contributes to the development of custom computational methods and software tools. In 2025, the establishment and operation of the Bioinformatics Core Facility were partially supported by the SASTIC initiative.

BIOTECH CLIENTS AND ACADEMIC PARTNERS

Agenus

Transcriptomic profiling of metastatic solid tumors under immunotherapy

ABI has collaborated with Agenus since 2022 on projects investigating resistance mechanisms in metastatic solid cancers, including colorectal and ovarian cancer, in the context of immunotherapy clinical trials such as BOT/BAL. The analysis, led by Dr. Hans Binder and his team, focuses on tumor heterogeneity and molecular determinants of response in patients who show limited benefit from immunotherapy. ABI analyzes integrated clinical multi-omics datasets, including bulk, single-cell, and spatial transcriptomics. The work includes data processing and quality control, integrative modeling, definition of molecular subtypes of metastatic disease, and identification of genomic features associated with therapy response, supporting stratification of colorectal cancer liver metastases and interpretation of response patterns observed in immunotherapy trials.

Vivan Therapeutics

Machine learning-based cancer biomarker discovery for precision medicine

ABI has continued its collaboration with Vivan Therapeutics, initiated in 2022, supporting development of the TuMatch® platform for precision oncology. The analysis, coordinated by Dr. Nicolas Borisoff, integrates computational modeling with patient-specific tumor models in Drosophila to enable high-throughput drug screening and personalized treatment selection. ABI provides bioinformatics and data science support, including analysis of complex mutational profiles and development of machine-learning classifiers for biomarker discovery and treatment stratification. These classifiers are used to improve predictive performance and support selection of candidate therapeutic combinations based on tumor-specific genomic features.

École Polytechnique Fédérale de Lausanne

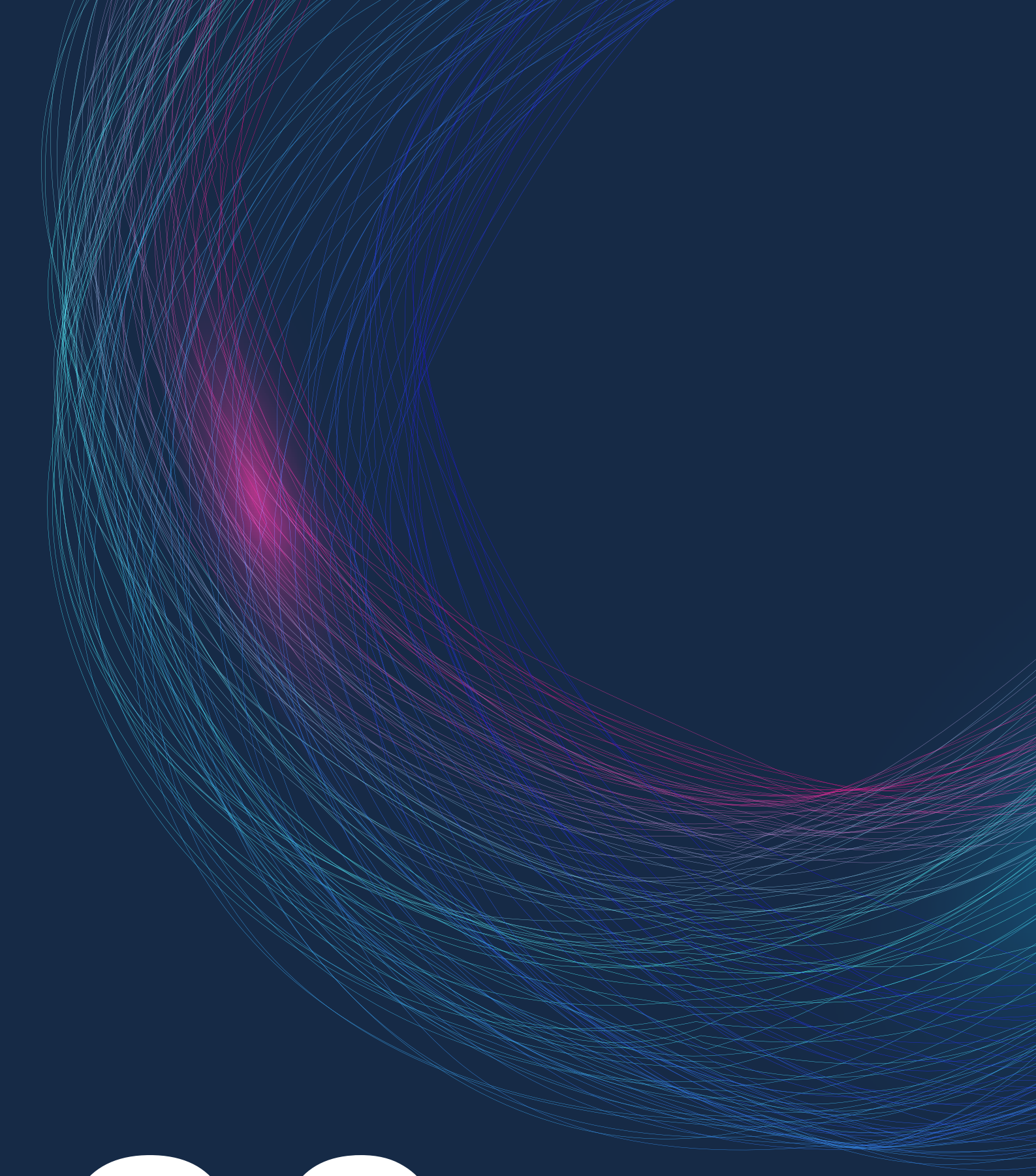
Host defense mechanisms in chronic lung infection

In 2025, ABI supported a project at EPFL investigating host defense responses in chronic lung infections caused by Pseudomonas aeruginosa. The single-cell transcriptomic analysis, led by Arpine Grigoryan, focused on cellular and molecular mechanisms underlying persistent bacterial infection. ABI carried out data preprocessing, quality control, cell-type annotation, and downstream interpretation, enabling characterization of host immune and epithelial responses and integration of transcriptomic findings with experimental observations.

California Institute of Technology

Single-nucleus transcriptomic analysis in a mouse model of Parkinson's disease

ABI collaborated with Caltech in 2025 on a study examining olfactory alterations in a mouse model of Parkinson's disease using single-nucleus RNA sequencing. The analysis, led by Tatevik Jalatyan, focused on transcriptomic characterization of neural cell populations associated with neurodegenerative pathology. ABI performed quality control, preprocessing, cell-type annotation, differential expression analysis, and gene-set enrichment using structured and reproducible analytical workflows to support interpretation of single-nucleus transcriptomic data and downstream mechanistic studies.



06 EVENTS, TRAININGS, AND OUTREACH

INTERNATIONAL CONFERENCES AND TRAININGS

PARTICIPATION IN FEMS MICRO 2025, MILAN

In July 2025, four members of the ABI Nersisyan Lab participated in the FEMS MICRO 2025 Congress in Milan, presenting recent research in microbiome science and bioinformatics.

- Lusine Adunts presented a flash talk and poster on tsantsR, an R package for constructing and analyzing bacterial co-abundance networks, demonstrated using oral microbiome data from periodontitis studies.
- Davit Hakobyan presented a poster on machine learning-based identification of bacterial signatures associated with smoking and disease in the oral microbiome.
- Nelli Vardazaryan presented a meta-analysis of the honeybee gut microbiome, incorporating Armenian datasets and revealing microbial adaptation mechanisms to pesticide exposure. The participation of Nelli was supported by the Gulbenkian Foundation.
- Razmik Sargsyan presented results from applying novel sequencing and statistical approaches to study bacterial responses to antibiotics in Staphylococcus aureus strains isolated from Armenian clinics.

RESEARCH VISIT TO THE KAROLINSKA INSTITUTE

From October 5 to 10, 2025, Razmik Sargsyan conducted a research visit to the Karolinska Institute (KI), working in the laboratory of Dr. Juan Du as part of the ongoing collaboration between ABI and KI. The visit focused on gaining hands-on experience in cultivation and analysis of anaerobic microorganisms, which are central to the project Temporal Dynamics of Microbiome Communities.

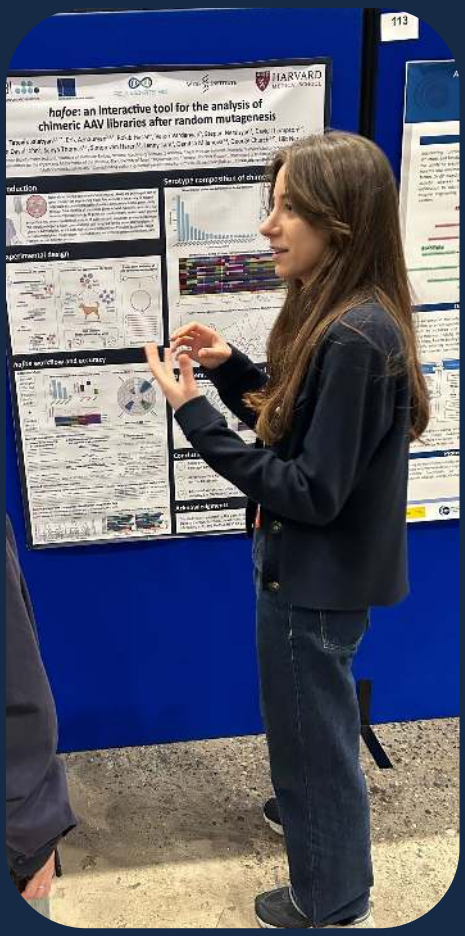
INTERNATIONAL CONFERENCES AND TRAININGS

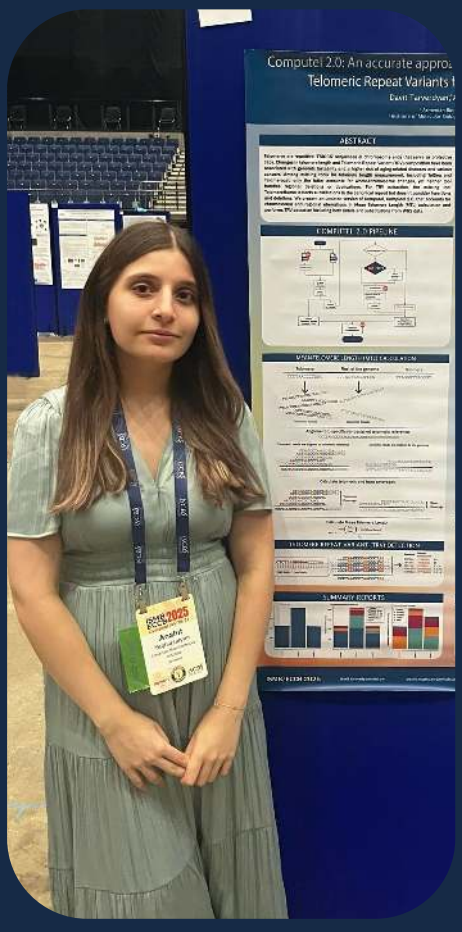
PARTICIPATION IN ISMB/ECCB 2025, LIVERPOOL

In July 2025, members of the ABI Nersisyan Lab presented their work at the ISMB/ECCB 2025 Conference in Liverpool, the leading international forum for bioinformatics and computational biology.

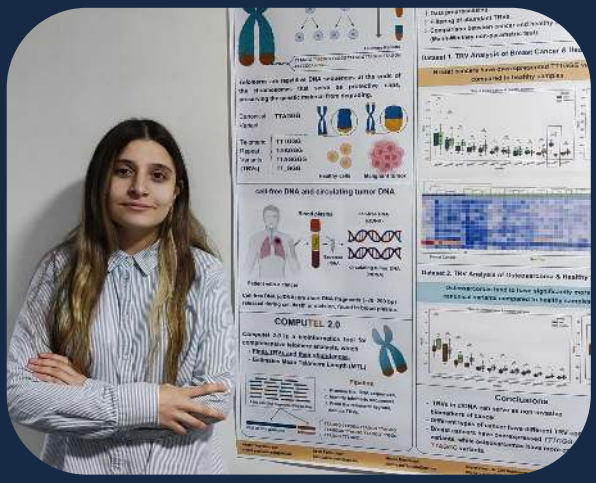
- Tatevik Jalatyan presented her recent paper on hafoe, a computational tool for the analysis of chimeric AAV viral vectors used in gene therapy.
- Davit Tarverdyan and Anahit Yeghiazaryan introduced a new version of Computel, a tool for estimating telomere length and telomeric repeat variation from whole-genome sequencing data.
- Mher Kurghinyan presented a bioinformatics approach for estimating gene expression from cancer cell-free DNA sequencing datasets.

Participation of Anahit Yeghiazaryan and Mher Kurghinyan was supported by the H. Hovnanian Family Foundation Fellowship.



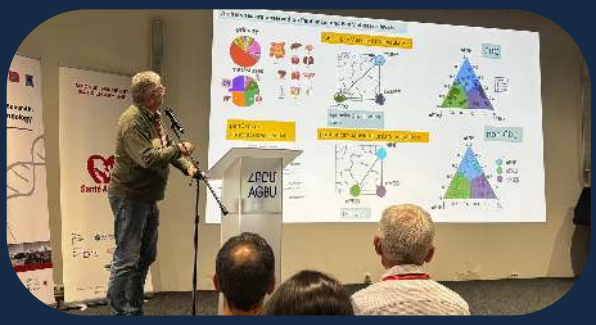


LOCAL CONFERENCES & SCIENTIFIC EVENTS



ANAHIT YEGHIAZARYAN IN AUA COMPETITION

Anahit Yeghiazaryan participated in the AUA CSE Research Showcase Competition, presenting a poster entitled “Telomeres in cfDNA as Non-Invasive Biomarkers of Cancer.” Her project focuses on identifying telomere-associated cancer biomarkers in cell-free DNA through the development of bioinformatics tools for comprehensive telomere analysis and comparative studies of healthy and cancer-derived genomic datasets.



INTERNATIONAL IMMUNO-ONCOLOGY SUMMIT

ABI researchers participated in the International Immuno-Oncology Summit, held in Yerevan on October 16–18, 2025, organized by Santé Arménie in collaboration with INSERM, the Armenian Association of Clinical Pathologists and Cytologists, and IMB.

- Melina Tamazyan presented her research on heterogeneity of response to immuno- and chemotherapy in solid tumors, as revealed by single-cell and spatial transcriptomics.
- Dr. Hans Binder delivered a presentation on ongoing work on transcriptomic profiling of immunotherapy response in microsatellite-stable metastatic colorectal cancer, highlighting computational approaches in precision oncology.
- Dr. Arsen Arakelyan presented recent advances in bioinformatics-driven analysis of cancer and inflammatory diseases.

OUTREACH

VISITS FROM SHIRAKATSY LYCEUM AND AYB SCHOOL STUDENTS

As part of professional orientation initiatives, ABI welcomed students from Shirakatsy Lyceum and AYB School for introductory visits to the field of bioinformatics. Led by Dr. Lilit Nersisyan and Davit Hakobyan, the sessions introduced students to modern genomics research, ABI's ongoing projects, and the daily work of computational biologists.
During the visits, participants explored how biological and microbial data are analyzed using programming tools such as R and discussed how bioinformatics supports discoveries in life sciences. These outreach activities aimed to inspire interest in science, technology, and data-driven research careers among pre-university students.

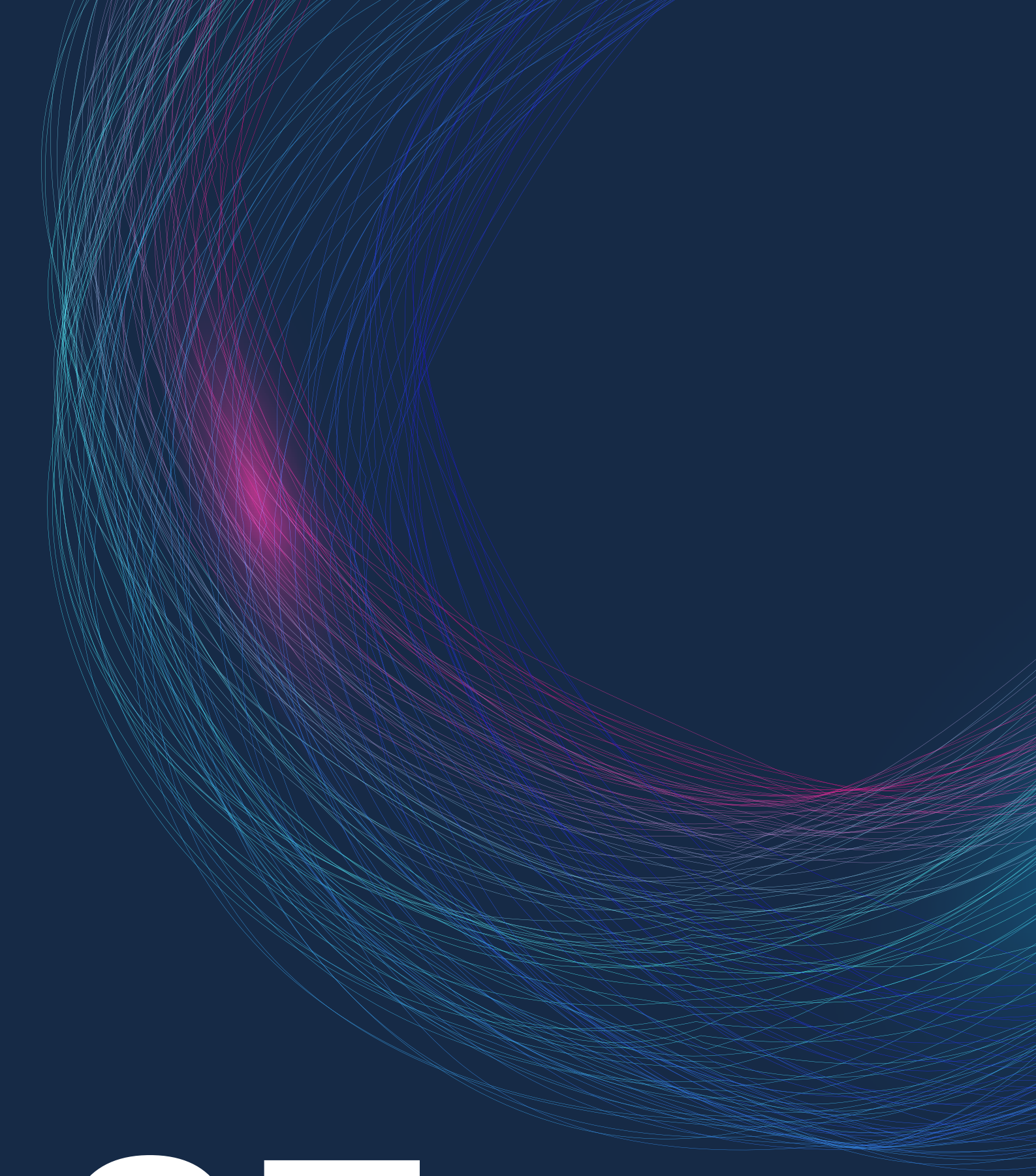
SEASON OF CHANGE AT ADOBE ARMENIA

As part of Adobe's Season of Change initiative, ABI was invited to present its work at the Adobe Armenia office. The visit included an overview of ABI's research and training activities, informational materials, and discussion with Adobe employees. The event followed ABI's receipt of support from the Adobe Employee Community Fund and strengthened engagement with the local technology community.

MEDIA PRESENCE

ABI founder and director Dr. Lilit Nersisyan appeared on the **Re:Arrange podcast**, discussing bioinformatics, genetics, and the role of science in Armenia. Topics covered included insights gained from decoding the human genome, the impact of bacteria on human health, the role of bioinformatics in biological research, and the realities of conducting scientific research in Armenia.

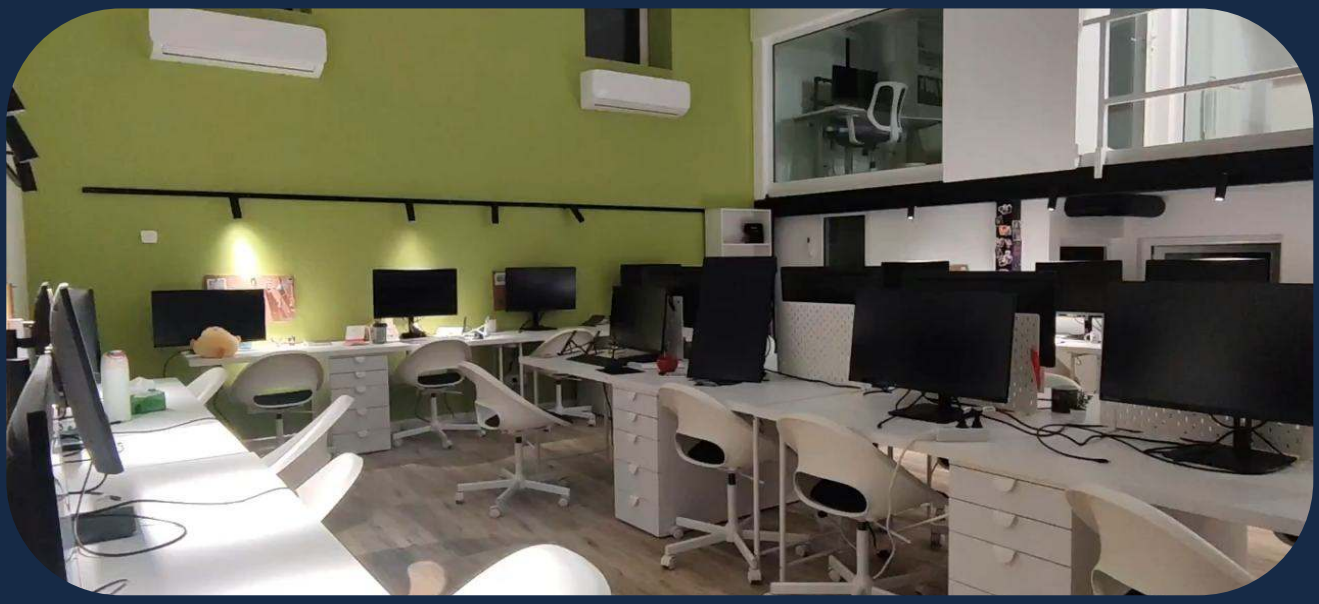
In the EVN Report article **"The Climate Is Changing: How Are Armenian Winemakers Adapting?"**, Dr. Hans Binder highlighted Armenia's mountainous landscape as a key asset for climate adaptation and emphasized the importance of close collaboration between scientists and winemakers in developing evidence-based strategies for resilient viticulture.



07

ABI'S NEW RESEARCH AND TRAINING CENTER

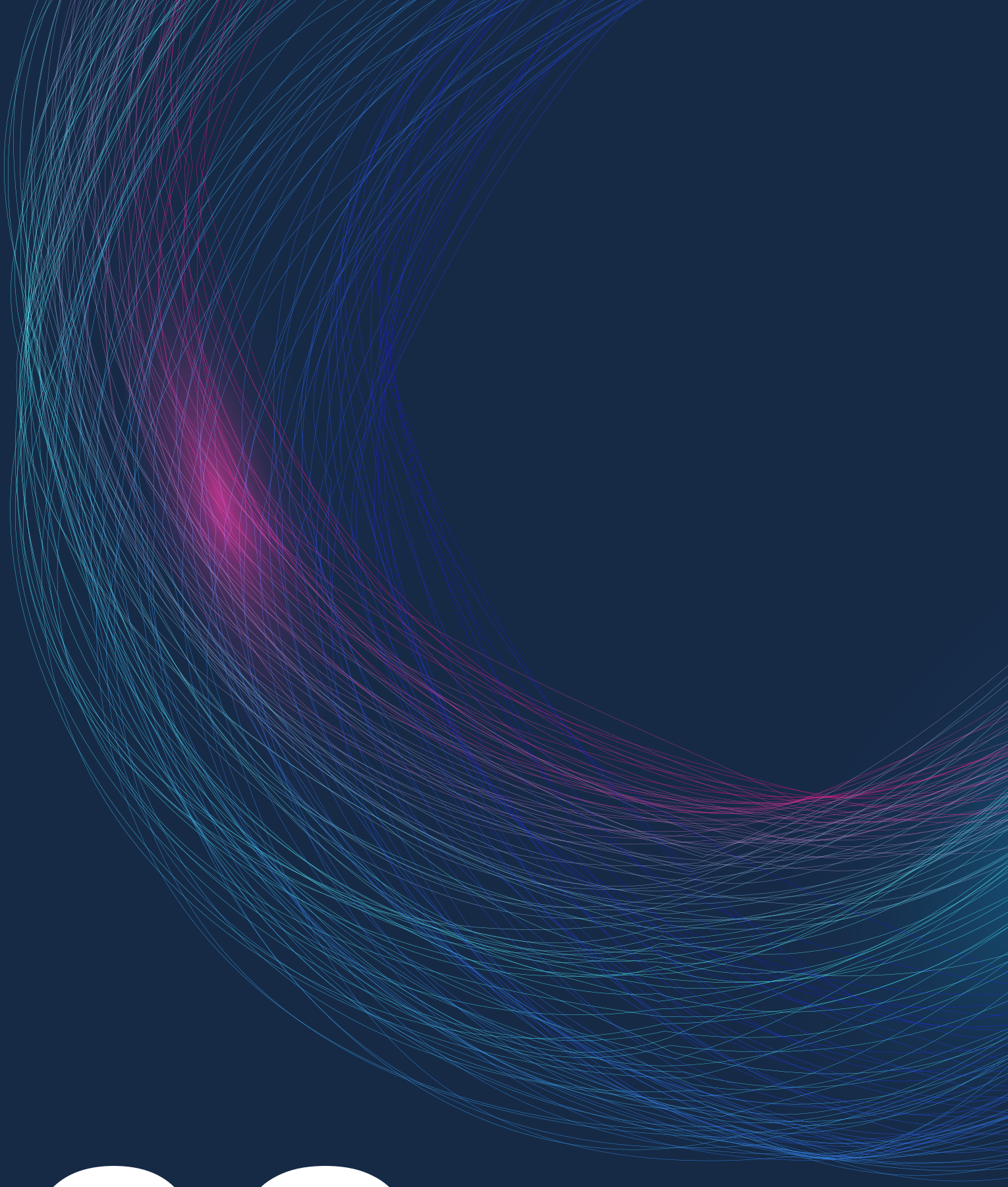
ABI'S NEW RESEARCH AND TRAINING CENTER: A NEW HOME FOR ABI



The renovation of ABI's new space was completed in 2025, transforming a previously unused area at the Institute of Molecular Biology (IMB) into ABI's first dedicated office and training facility. The two-floor center comprises nine rooms, including open workspaces, meeting and seminar rooms, and shared areas designed to support discussion and informal interaction. The layout was intentionally designed to accommodate daily research activity, hands-on training, mentoring, and collaborative work, reflecting ABI's emphasis on openness, teamwork, and leadership development.

Establishing a permanent physical base has enabled ABI to consolidate activities that were previously distributed across temporary locations and online platforms. The new environment supports closer interaction among researchers, trainees, and collaborators, and allows training programs and research projects to be conducted within a shared, purpose-built setting. Co-location within IMB further enables direct integration with shared wet-lab and computational infrastructure, facilitating coordinated and efficient scientific workflows.

The renovation was made possible through a combination of external support and ABI's own investment. The project was partially supported by a $40,000 contribution from the H. Hovnanian Family Foundation, with remaining costs covered by ABI through infrastructure-focused support grants, donations, and reinvestment of funds generated via service-based activities.



08 PEOPLE

OPERATIONS

Lilit Nersisyan, PhD, Director, Founder
Karine Shahgaldyan, HR Administrative Assistant
Tatevik Grigoryan, Former Operations and Development Manager
Anahit Simonyan, Accountant
Antranik Wartanian, Systems Administrator
Siras Hakobyan, PhD, Bioinformatics Engineer
KeyStone Law, Legal Expert
Ruzan Adyan, Graphic Designer
Garik Vanyan, Former Graphic Designer
Mariam Hovsepyan, Former Legal Expert
Tigran Petrosyan, Volunteer, Software Engineer

BOARD OF TRUSTEES

Hans Binder, PhD rer. nat. habil., Chairman, University of Leipzig, Germany
Arsen Arakelyan, PhD, Institute of Molecular Biology, NAS, Armenia
Aram Adourian, PhD, Flagship Pioneering, USA

ADVISORS

Jonathan Schug, PhD, University of Pennsylvania, USA
Rafi Baghdjian, Center for Scientific Innovation and Education Foundation, Armenia
Hripsime Hovakimyan Kuzevska, Primi Digital, USA
Eduard Avetisyan, PhD, European Molecular Biology Laboratory, Germany
Peter Stadler, PhD rer. nat. habil., University of Leipzig, Germany
Ogsen Gabrielyan, PhD, Boehringer Ingelheim, Germany
Hovhannes Harutyunyan, Financial Planning and Analysis Manager at Pliant, Germany

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Melina Tamazyan
Arpine Grigoryan
Luiza Stepanyan
Tomas Konecny
Nate Zadirako
Nane Pivazyan
Lusine Gevorgyan
Hasmik Zaqaryan (intern)
Emma Hovhannisyan (alumna)
Sveta Mnatsakanyan (alumna)
Maria Arakelyan (alumna)

RESEARCH STAFF: LILIT NERSISYAN LAB

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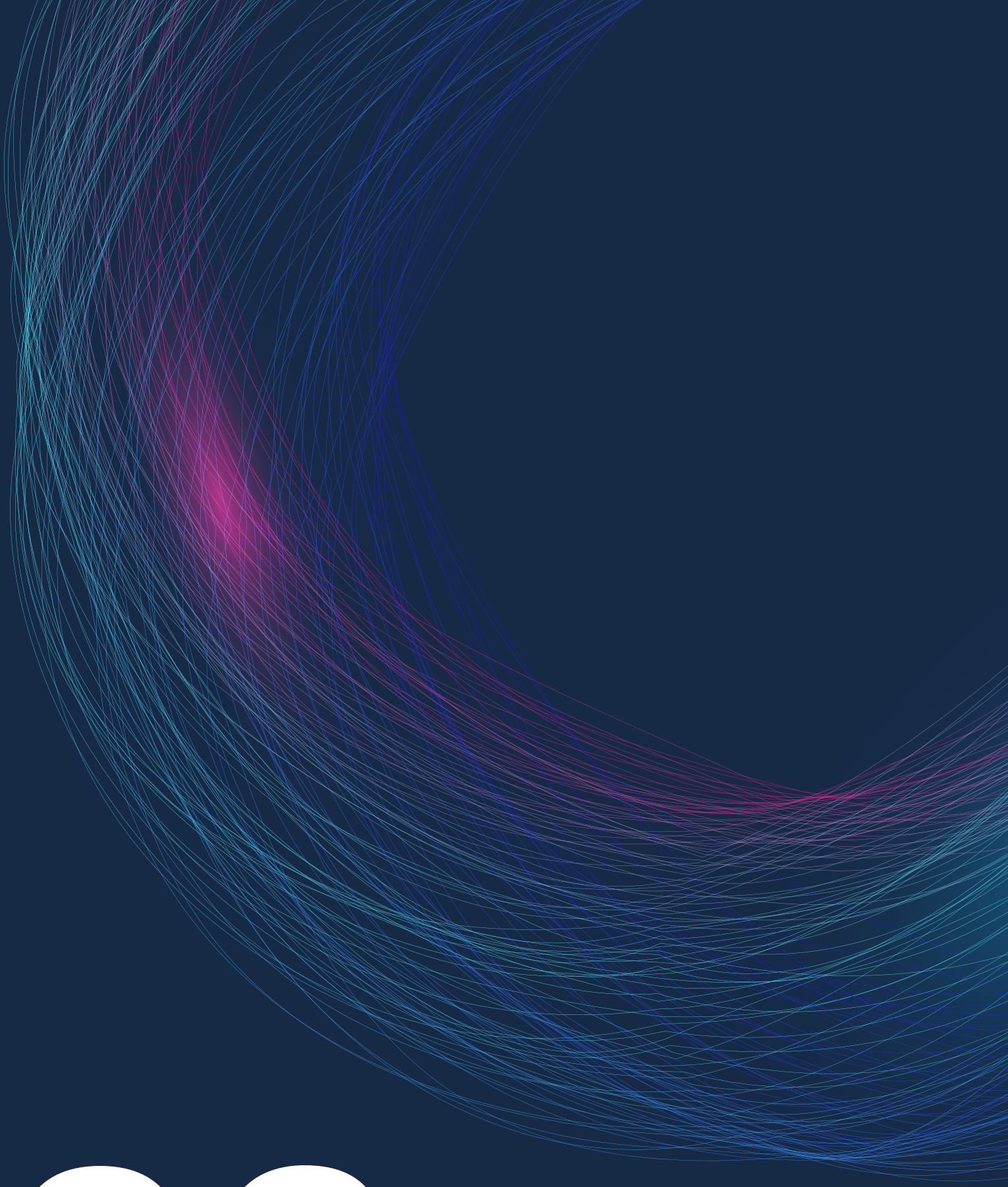
Tatevik Jalatyan
Mher Kurghinyan
Rozi Mkrtchyan
Lusine Adunts
Razmik Sargsyan
Davit Hakobyan
Davit Tarverdyan
Anahit Yeghiazaryan
Mariam Yayloyan

RESEARCH STAFF: VIVAN THERAPEUTICS LAB

Nikolay Borisov, PhD
Lilya Hovhannisyan



09

PARTNERS AND FUNDING

PARTNERS AND COLLABORATORS IN 2025

ACADEMIC LABS

UNIVERSITÄT LEIPZIG

Penn
University of Pennsylvania

Karolinska Institutet

Utrecht University

Sanford Burnham Prebys

Institute of Molecular Biology
National Academy of Sciences of Armenia

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Caltech

WYSS INSTITUTE

EPFL

BIOTECH COMPANIES

agenus

VIVAN THERAPEUTICS

DONATIONS AND GRANTS

H. HOVNANIAN FAMILY FOUNDATION

ARPA

Adobe

SASTIC
Strategic Armenian Science & Technology Investment Community

BostonGene

DeepOrigin

CALOUSTE GULBENKIAN FOUNDATION

MATCHED DONATIONS THROUGH BENEVITY

Adobe

AMD

SYNOPSYS®

Spotify®

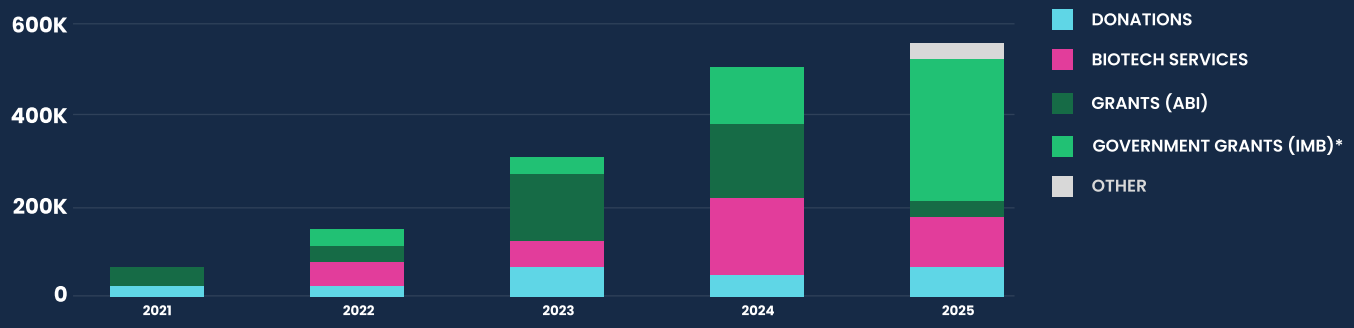
NVIDIA

NETFLIX

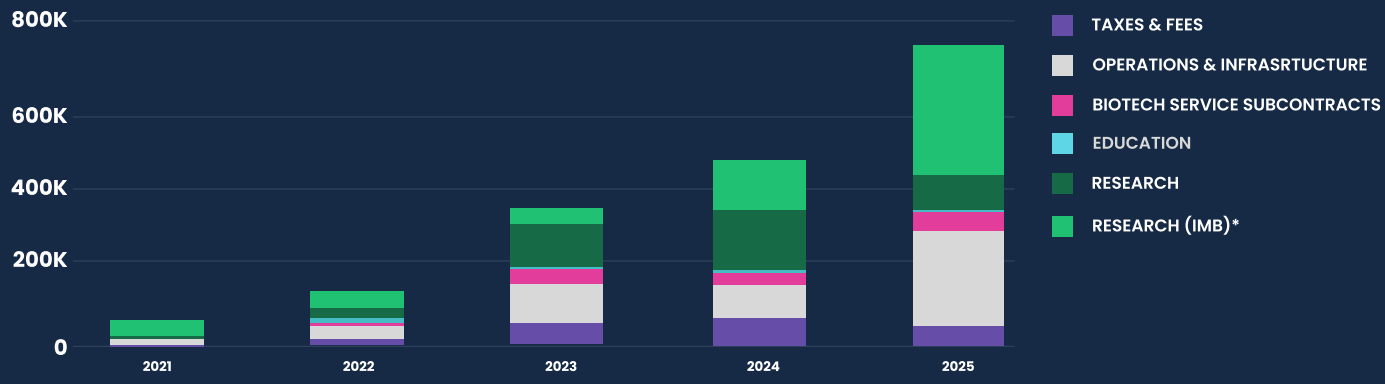
Agilent Technologies

BUDGET

INCOME (USD)



EXPENSES (USD)



** Research partially funded through government grants formally awarded to IMB and implemented via shared research infrastructure by ABI researchers. One grant originated at ABI under FAST Foundation support and was later transitioned to the ADVANCE program of the Higher Education and Science Committee of Armenia.*

In-Kind Contributions

Our expanding budget supports the growth of our team and broadens the scope of ABI's research, training, and service activities. As a private organization, we actively diversify our funding streams to ensure the long-term sustainability of our mission. Our work is supported through a combination of research and general support grants, industry partnerships, and donations from individual supporters, some of which are matched through corporate giving programs.

In addition to direct financial support, ABI benefits substantially from in-kind contributions provided by individuals who voluntarily contribute expertise in research, training, mentoring, and technical support. These contributions, while not reflected in financial statements, are essential to the Institute's operations, particularly during its formative and expansion phases.

In 2025, expenditures were primarily directed toward research activities and training initiatives. Notably, several training efforts, including the OMICSS-25 summer school, were made possible in large part through voluntary contributions of time and expertise by ABI team members and the broader local and international research community. A significant portion of expenses also supported core operational needs, including administrative functions, system management of ABI's compute infrastructure, and the renovation of the new research and training center.

Looking ahead, ABI is committed to maintaining and strengthening this model through strategic fundraising, expanded industry collaborations, and continued engagement with international funding agencies to support sustainable growth.

ABI

DONATE

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