Workshop on Computational Oncology: Decoding Cancer Dynamics using Omics, Imaging and Machine Learning

In Collaboration With

Param Hansa Centre for Computational Oncology (PHCCO), IISc Bangalore

The Centre for Excellence in Mathematical Biology (CEMB), Sri Sathya Sai Institute of Higher Learning (SSSIHL), in collaboration with the Param Hansa Centre for Computational Oncology (PHCCO), IISc Bangalore, organised a two-day Workshop on Computational Oncology: Decoding Cancer Dynamics using Omics, Imaging and Machine Learning at the Prasanthi Nilayam Campus, SSSIHL, on 28–29 August 2026. The workshop brought together researchers from academia and industry, along with students and early-career professionals, to explore emerging approaches in computational and experimental cancer biology. Key themes included dynamical modelling, AI/ML, omics, imaging, and computational approaches for understanding cancer progression and advancing therapeutic strategies. The programme featured expert lectures, a poster session, and a panel discussion with eminent scientists, providing students across UG, PG, PhD, and Postdoctoral levels with valuable exposure to current research and practical applications in computational oncology.

Introductory Remarks and Setting the Context

Dr. D. K. K. Vamsi, Coordinator of the Centre for Excellence in Mathematical Biology (CEMB), SSSIHL, delivered the introductory remarks and set the context for the programme. He highlighted that the programme was designed to introduce participants to the emerging field of computational oncology and to demonstrate how mathematics, computational modelling, and biological sciences can be integrated to understand complex cancer-related problems.

Dr. Vamsi emphasised the importance of creating opportunities for students and researchers to interact with experts and gain exposure to current research approaches and interdisciplinary methodologies in oncology. The programme aimed to encourage scientific curiosity, promote interdisciplinary learning, and provide a platform for exploring potential research directions at the intersection of mathematical biology and cancer research. His remarks established the academic context and set the stage for the expert talks and discussions that followed.





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Inaugural Address

Prof. N. Srividya, Dean of Sciences, SSSIHL

The inaugural address was delivered by Prof. N. Srividya, Dean of Sciences, SSSIHL. She highlighted the importance and growing relevance of oncology as an interdisciplinary field, emphsising its significance in understanding cancer and addressing the complex challenges associated with cancer research and treatment. She spoke about the need for integrating diverse scientific disciplines, including mathematics, biology, computational science, and data science, to develop a deeper understanding of cancer and improve approaches to its prevention, diagnosis, and management.

Prof. Srividya also emphasised the increasing role of computational and data-driven approaches in modern cancer research, particularly in understanding the complexity and dynamics of tumour progression. She encouraged students to develop an interdisciplinary perspective and remain open to emerging technologies and innovative research methodologies. She highlighted the importance of collaboration between theoretical researchers, experimental scientists, clinicians, and computational experts in translating scientific discoveries into meaningful healthcare solutions.

The address provided an overview of the broader scope of oncology and encouraged students to recognize the diverse opportunities for research, innovation, and meaningful contributions in this field. Her inspiring remarks set the context for the discussions that followed during the programme and emphasised the importance of scientific curiosity, collaboration, continuous learning, and sustained research in addressing complex health challenges and advancing the understanding and treatment of cancer.





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Day 1: August 28, 2026 (Morning Session)

Speaker: Dr. Mohit Kumar Jolly, IISc Bangalore

Dr. Mohit Kumar Jolly's talk addressed the challenge of drug resistance and tumour relapse in cancer treatment. The talk explained that treatment failure can occur not only because drug-resistant cells are already present, but also because treatment itself can induce cancer cells to switch into drug-tolerant states. Phenotypic plasticity and cellular heterogeneity were highlighted as important factors in drug resistance and tumour relapse. Cancer cells can dynamically change their states in response to targeted therapy or immunotherapy, allowing them to evade treatment. To study these transitions, the research examines regulatory networks that control cell-state switching and the trajectories followed by cancer cells. Computational models of regulatory networks are integrated with single-cell high-throughput and multi-omics data and supported by experimental validation. This approach helps explain how different cancers develop escape routes under therapeutic pressure. The talk also demonstrated how an in silico framework can be used to identify rational combinations of therapies that may reduce cancer aggressiveness and resistance. The concept of creating digital twins of cancer progression showed how mathematical modelling can complement laboratory experiments. Overall, the talk demonstrated that understanding the dynamic behaviour of cancer cells can help researchers anticipate therapeutic escape and design more effective strategies to overcome resistance.





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Speaker: Dr. Monika Sharma, Plaksha University

Dr. Monika Sharma's talk explored both the potential and the limitations of artificial intelligence in biomedical research. The talk explained how AI can organise complex biomedical datasets, integrate heterogeneous evidence, improve quantitative measurements, and help researchers prioritise promising hypotheses. These ideas were illustrated through three research areas: population-aware interpretation of BRCA1/2 variants, automated estimation of bone-marrow cellularity from whole-slide pathology images, and multi-omic prioritisation of candidate genes in ALS. The talk demonstrated that AI is particularly useful for exposing representation gaps, producing reproducible tissue measurements, integrating different forms of evidence, and narrowing large experimental search spaces. However, AI predictions cannot automatically be considered clinical or causal evidence. The talk emphasised that AI cannot independently establish definitive variant classifications, autonomous diagnoses, or causal and therapeutic claims. Trustworthy AI therefore depends not simply on a powerful algorithm, but on an evidence architecture involving representative data, orthogonal validation, transparent uncertainty, and clearly defined limits of action. The key message was that AI is most valuable when it identifies the next scientifically defensible step while maintaining a clear distinction between prediction and evidence.





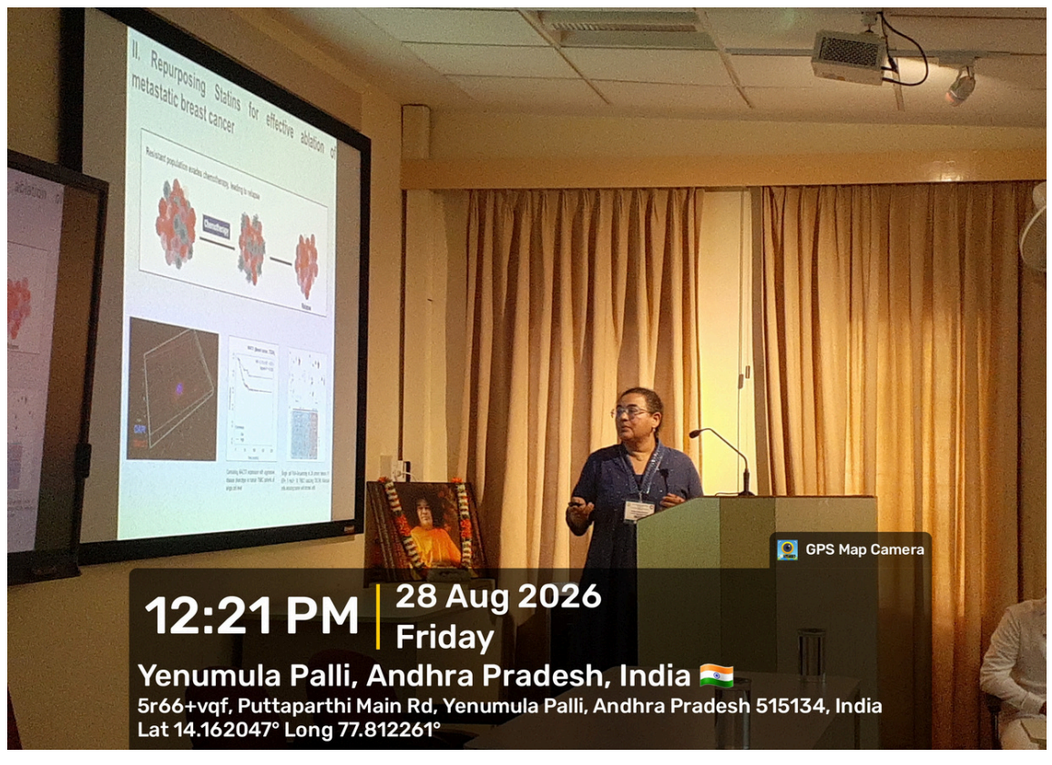
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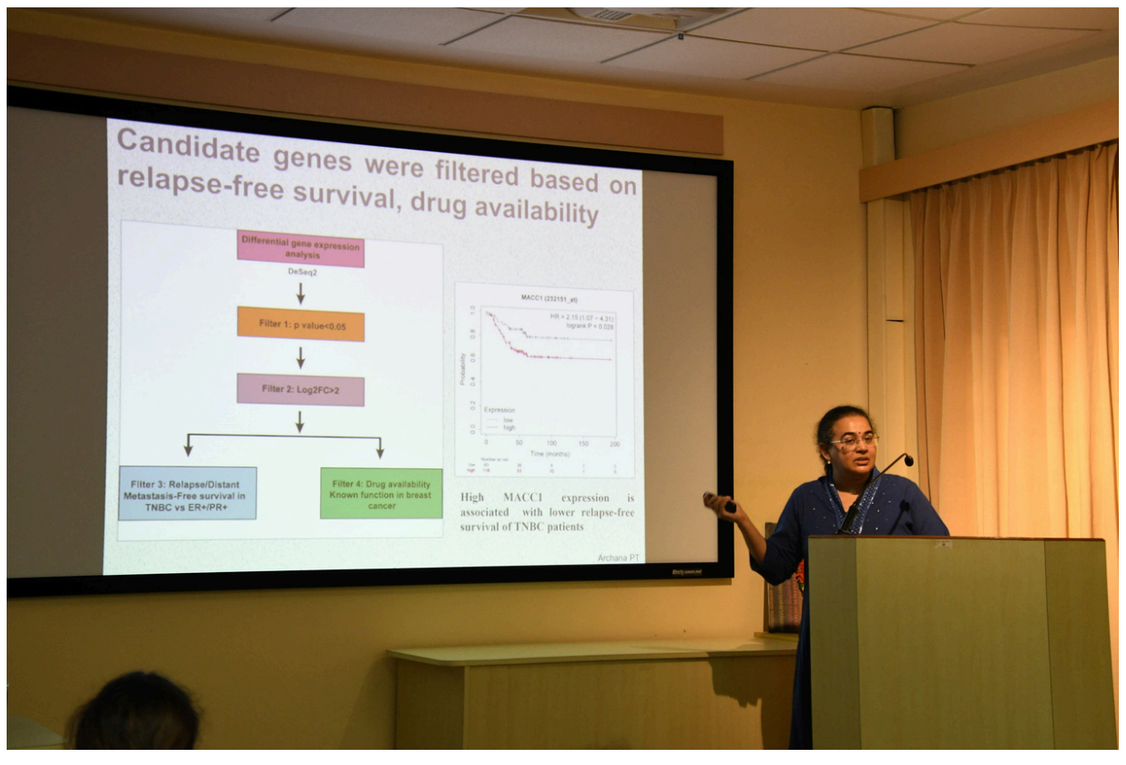
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Speaker: Dr. Radhika Nair, Centre for Human Genomics

Dr. Radhika Nair's talk addressed why metastatic breast cancer remains a major clinical challenge even though substantial progress has been made in detecting and treating primary breast tumours. Once tumour cells move from the breast to distant organs such as the lung through metastasis, the disease becomes considerably more difficult to manage. The talk explained that metastatic progression is a complex process influenced by both intrinsic cues within cancer cells and extrinsic signals from their surrounding environment. These factors affect how tumour cells survive, spread, adapt to new tissues, and contribute to end-stage disease. The research focuses on understanding the molecular mechanisms that drive metastatic breast cancer, with the aim of identifying genes and pathways that may serve as potential drug targets. Laboratory investigations are being used not merely to describe metastatic behaviour, but to uncover mechanisms that reveal actionable vulnerabilities. The talk highlighted the importance of studying metastasis at the molecular level because a deeper understanding of these processes can guide the development of new therapeutic strategies. Overall, the talk showed that metastatic disease results from complex interactions between cancer cells and their environment, and that deciphering these interactions may provide new opportunities to improve treatment for patients with advanced breast cancer.





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Speaker: Prof. Vijayalakshmi Mahadevan, Institute of Bioinformatics and Applied Biotechnology (IBAB)

Prof. Vijayalakshmi Mahadevan's talk examined how loss or mutation of the tumour suppressor p53 can reshape the epigenetic regulation of colorectal cancer and contribute to aggressive tumour progression. The research focuses particularly on enhancer regulation, an area that is less understood than the genetic consequences of p53 loss. Genome-wide profiling of the active enhancer mark H3K27ac shows an overall gain of enhancer activity around promoter and intronic regions in p53-deficient colorectal cancer cells. These enhancers are strongly associated with oncogenes and MYC and E2F target pathways, suggesting an enhancer-mediated mechanism of oncogenic progression. The study also identifies gains in oncogenic super-enhancers mediated by E2F and KLF factors. Increased H3K27ac at the promoters of EZH2 and SuV39H1 indicates additional epigenetic regulation. Validation in colorectal cancer cohorts links super-enhancer-associated genes with the CMS4 subtype and lower survival. The talk also explained that the p53 R273H mutation is associated with a distinct epigenetic signature involving YAP/TAZ signalling. Studies of TGFβ-induced EMT further reveal links between EMT transcription factors, epigenetic regulators, and poor outcomes. Overall, the talk showed that p53 status can shape colorectal cancer progression through mutation-specific epigenetic mechanisms, creating possible opportunities for tailored epigenetic therapy.





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Day 1: August 28, 2026 (Afternoon Session)

Speaker: Dr. Saipradeep V. G., TCS Research

Dr. Saipradeep V. G.'s talk demonstrated how artificial intelligence and computer vision can support precision cancer care in a practical and scalable manner in India. Cancer shows considerable biological heterogeneity, so patients with similar disease can respond very differently to treatment. The talk explained that routine histopathology images can contain information that AI can use to discover prognostic biomarkers and predict patient risk. The presentation also showed how imaging of 2D and 3D organoids can help model treatment response and potentially guide personalised therapy selection. These approaches connect computational pathology with patient-derived tumour models and translate visual information into clinically relevant predictions. The talk also addressed the computational challenges involved, including multi-scale image analysis, tumour heterogeneity, sparse labels, domain generalisation, graph learning, and modelling dynamic biological systems. Rather than being only limitations, these challenges create opportunities for innovation in AI, computer vision, and applied mathematics. The idea of frugal vision AI emphasises solutions that can use practical and routinely available data while remaining affordable and scalable. Overall, the talk demonstrated how computational methods can contribute to risk stratification, treatment-response prediction, and personalised cancer care, particularly in a diverse and large healthcare setting such as India.





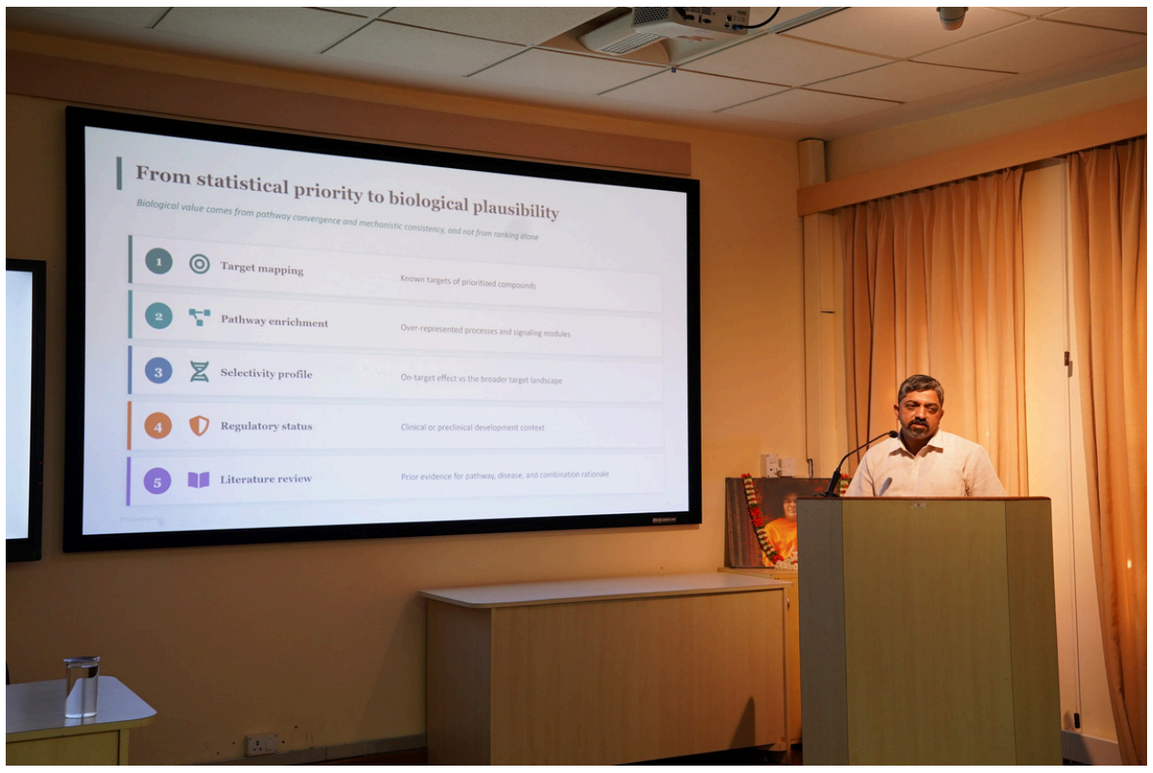
Workshop on Computational Oncology: Decoding Cancer Dynamics using Omics, Imaging and Machine Learning

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Speaker: Dr. Aditya Rao, TCS Research

Dr. Aditya Rao's talk addressed why high-throughput drug-combination screening, despite generating large numbers of candidates, requires careful computational analysis before useful combinations can be identified. The presented framework used a colorectal cancer study as a methodological case study and combined several stages of analysis. The workflow includes data preprocessing, control normalization, missing-value assessment, dose-response organisation, and the use of complementary drug-synergy models. Concordance analysis and rank aggregation allow evidence from different models to be compared and combined, reducing dependence on any single synergy assumption. The framework then connects computational rankings with biological interpretation through kinase-target mapping, pathway enrichment, inhibitor selectivity, regulatory status, and literature-based mechanistic assessment. This layered approach makes it possible to move from screening measurements to biologically interpretable and experimentally testable hypotheses. The emphasis is therefore not simply on ranking drug combinations, but on understanding why particular combinations may be promising and whether they have a plausible biological basis. Because the underlying study was under data embargo, the talk focused on the analytical strategy rather than specific compounds or findings. Overall, the talk demonstrated how computational integration can make large-scale drug-combination screening more reproducible, interpretable, and useful for experimental oncology.





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Panel Discussion Report

Moderator: Dr. Mohit Kumar Jolly
Associate Professor, Department of Bioengineering, Indian Institute of Science (IISc), Bangalore

Panelists/Speakers:

- **Prof. Vijayalakshmi Mahadevan**
- **Dr. Monika Sharma**
- **Dr. Aditya Rao**
- **Dr. Saipradeep V. G.**
- **Mr. Prasanna CVS**

Introduction

A panel discussion was conducted with distinguished scientists and researchers from diverse academic and research backgrounds. The session was moderated by Dr. Mohit Kumar Jolly, Associate Professor in the Department of Bioengineering at the Indian Institute of Science (IISc), Bangalore. The discussion focused on the personal journeys of scientists, career choices, qualities required in candidates, changing academic fields, and the importance of continuing to move forward despite an unconventional career path.

Journey Towards Becoming a Scientist

The first question addressed to the panelists was “How did you reach where you are today as a scientist?” Each speaker shared their individual journey, experiences, challenges, and decisions that shaped their careers. Their stories demonstrated that there is no single fixed pathway to becoming a scientist. Different people may arrive at their current field through different academic backgrounds and experiences. The panelists emphasised that career paths can change with time, and that an individual's interests and opportunities can lead them into areas that they may not have originally planned to pursue.

Qualities Looked for in Candidates

The discussion then moved towards the question of what qualities they would look for if they were in the position of an HR or recruiter. The speakers discussed the importance of qualities beyond academic marks and qualifications. The discussion highlighted the value of a candidate's attitude, willingness to learn, adaptability, curiosity, and ability to work towards solving problems. This part of the discussion showed that having a strong academic background is important, but personal qualities and the ability to learn and adapt also play an important role in building a career.

Changing Fields and Taking an Unconventional Path

Another important topic was whether it is appropriate for a student or professional to change their field of study or career. The panelists explained through their experiences that changing fields is not necessarily wrong. A person may discover a new interest or opportunity after completing a degree in another discipline.

A particularly interesting example was shared by Mr. Prasanna CVS, who spoke about his own academic journey. He completed his B.Tech, later pursued a Master's degree in Physics, and eventually moved into a biology-related PhD. His journey demonstrated that academic paths do not always have to follow a straight line. Moving from one field to another is possible when a person is willing to learn and adapt.

The key message from this discussion was that one should not be overly concerned about having an unconventional academic path. What matters is continuing to learn, gaining the necessary knowledge, and moving forward.

The Role of Elimination in Career Decisions

Dr. Mohit Kumar Jolly also added an interesting perspective by sharing his own experience. He explained how some of his career decisions were influenced by eliminating options that he did not want to pursue. He gave the example of not wanting to pursue the UPSC examination, which eventually contributed to the direction his career took. This provided an important perspective: career decisions are not always made because a person knows exactly what they want from the beginning. Sometimes knowing what one does not want to do can also help in finding the right direction.

Importance of a Good Guide or Mentor

Another major theme that emerged throughout the panel discussion was the importance of having a good guide or mentor. This point was emphasised by almost all the speakers during their individual experiences and career stories. The panelists explained that a person's growth is influenced not only by their own efforts but also by the guidance and mentorship they receive at different stages of their career.

Dr. Aditya Rao and Dr. Saipradeep V. G. particularly shared their experiences from their time at TCS, highlighting how the nature of guidance and mentorship can significantly influence a person's professional development. Their experiences illustrated the difference that a supportive and knowledgeable guide can make in helping someone understand their strengths, overcome difficulties, and make better career decisions. The discussion also highlighted that a good guide can provide direction, encourage independent thinking, and help a student or researcher develop confidence, whereas poor guidance can create confusion or make the journey more difficult. However, the speakers also emphasized that guidance should complement an individual's own effort and responsibility. This idea connected with the experiences shared by the other speakers as well. From the beginning of the discussion, when the panelists described how they reached their present positions, mentorship and guidance appeared as an important part of their journeys.

Therefore, one of the key lessons from the panel was that choosing and learning from the right mentor can have a lasting influence on one's academic and professional journey. At the same time, students should remain proactive, curious, and responsible for their own growth.

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Conclusion

The panel discussion provided valuable insights into the realities of scientific careers and academic journeys. The experiences shared by the speakers showed that there is no single formula for becoming a scientist. Career paths can be diverse, and changing fields can be a part of discovering one's interests and strengths. One of the major takeaways from the discussion was to remain curious, adaptable, willing to learn, and focused on moving forward. The examples shared by the panelists, particularly Mr. Prasanna CVS's transition from engineering to physics and then to a biology-related PhD, demonstrated that an unconventional path can still lead to a successful scientific career. Overall, the discussion encouraged students to look beyond rigid career paths, learn from their experiences, and make thoughtful decisions based on their interests and opportunities.













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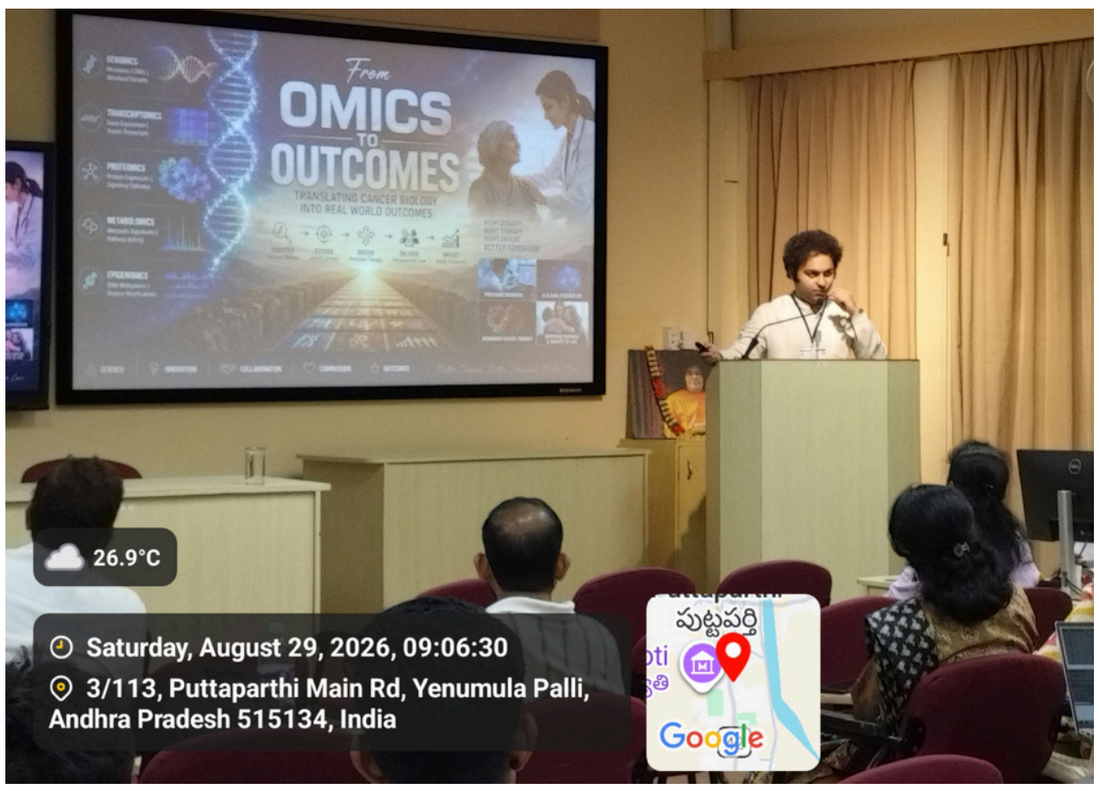
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Day 2: August 29, 2026 (Morning Session)

Speaker: Dr. Nitin Yashas, Manipal Hospital Bangalore

Dr. Nitin Yasha's talk examined how advances in genomics, multi-omics, immunotherapy, and targeted therapy are being translated into real-world cancer treatment. Oncology has increasingly moved beyond conventional cytotoxic therapy toward precision approaches that use information about the molecular characteristics of an individual tumour. The talk explained that biomarkers such as PD-L1 and MSI/dMMR can help guide immunotherapy, while molecular profiling can identify actionable drivers and receptor targets for targeted treatments. The integration of genomic, transcriptomic, proteomic, and imaging information also helps reveal tumour heterogeneity, predict treatment response, and understand acquired resistance. Through clinical examples, the talk demonstrated how advanced laboratory and molecular tests can become part of treatment selection and real-world clinical decision-making. The value of precision oncology lies in translating complex biological information into a specific clinical action for an individual patient. The presentation also highlighted the changing outcomes possible with modern treatments, including cases where patients with Stage 4 cancer who respond to immunotherapy can have survival measured in years. Overall, the talk showed that the journey from omics to outcomes depends on successfully connecting molecular discoveries with practical treatment decisions, with the ultimate aim of improving survival and quality of life.





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Speaker: Dr. Divya Kumar, JSS Medical College

Dr. Divya Kumar's talk addressed the important role of the tumour microenvironment in hepatocellular carcinoma (HCC), the most common form of primary liver cancer. The tumour microenvironment consists of non-cancerous cells and molecular signals surrounding the tumour and can influence tumour progression, inflammation, immune responses, angiogenesis, and resistance to therapy. The research focuses on Apoptosis Antagonizing Transcription Factor (AATF), which had previously been identified as a regulator of angiogenesis in HCC. Selective silencing of AATF within the liver tumour microenvironment significantly suppresses HCC growth. Using an orthotopic mouse model together with transcriptomic and molecular analyses, the study identifies AATF as a central regulator of inflammation, immune responses, angiogenesis, and extracellular-matrix remodelling. The talk also explained the significance of the newly identified AATF–MIR100HG–TGF-β signalling axis, which regulates communication between the tumour microenvironment and cancer cells. This pathway influences tumour proliferation and metabolic reprogramming and provides insight into how the surrounding environment supports cancer progression. Overall, the talk demonstrated that cancer cells cannot be studied in isolation and that molecular interactions within the tumour microenvironment can reveal promising therapeutic targets. AATF therefore emerges as a potential target for developing new treatment strategies for HCC.





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Speaker: Dr. Neha Arya, AIIMS Bhopal

Dr. Neha Arya's talk discussed the role of computational biology, multi-omics, and Artificial Intelligence (AI) in understanding cancer and advancing precision oncology. She highlighted that the molecular and cellular heterogeneity of cancer creates challenges in accurate diagnosis, prognosis, and treatment. Dr. Arya presented her work on understanding the role of stromal populations in breast cancer metastasis using a combination of computational and experimental approaches. She also discussed an integrated computational framework involving miRNA-omics, miRNA-target network analysis, survival analysis, and machine learning. These approaches were applied to identify potential diagnostic biomarkers, prognostic signatures, and therapeutic targets in breast cancer, obesity-associated breast cancer, and glioblastoma. She further emphasised the growing importance of AI and computational biology in biomedical research. Dr. Arya highlighted how students with interdisciplinary knowledge and computational skills can contribute to solving complex biological and healthcare problems in the future. Overall, the talk demonstrated how integrating omics, network biology, machine learning, and experimental validation can generate valuable insights into cancer biology. The session also highlighted the expanding opportunities for students and researchers in AI-driven computational biology and its potential contribution to future advances in precision medicine.





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Speaker: Prof. B. V. Rathish Kumar, IIT Kanpur

Prof. B. V. Rathish Kumar's talk demonstrated how mathematical modelling and deep learning can be combined to study the dynamic behaviour of cancer. Cancer progression is influenced by many interacting processes within the tumour microenvironment, and these changing molecular interactions can be represented using ordinary differential equations (ODEs). A major difficulty in such models is the estimation of unknown parameters from experimental measurements that are often limited and noisy. Traditional methods include least-squares fitting, genetic algorithms, and Bayesian approaches, but the presentation focused on deep-learning-based, systems-informed neural networks. In particular, physics-informed neural networks incorporate the governing ODEs directly into the neural-network training process. This means that the biological model acts as a constraint during optimization rather than relying only on observed measurements. This approach can help estimate unknown parameters and infer the dynamics of biological components that cannot be directly observed experimentally. The use of mechanistic equations can also make the method more robust when data are sparse or noisy. Overall, the talk demonstrated that deep learning does not have to replace mathematical models; instead, it can work together with them to recover hidden biological dynamics and improve our understanding of cancer progression.





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Speaker: Dr. Pankaj Yadav, IIT Jodhpur

Dr. Pankaj Yadav's talk addressed how computational methods are becoming essential for interpreting the increasingly complex data produced by single-cell and spatial omics technologies. These technologies provide detailed information about cellular heterogeneity, but they also create challenges in accurately identifying cell types and recovering missing or unmeasured gene information. The talk introduced three open-source computational frameworks developed to address these challenges. ScInfeR is designed for accurate cell-type annotation across single-cell and spatial omics datasets. SpatialPrompt focuses on scalable spot deconvolution and spatial-domain identification, helping researchers interpret the cellular composition and organisation of spatial measurements. ImputeFISH addresses atlas-scale spatial gene imputation by using compatible single-cell references to recover gene information. These tools address complementary aspects of multi-omics analysis: cell annotation, spatial deconvolution, and gene imputation. Together, they aim to improve the accuracy, scalability, and interpretability of complex omics datasets. The presentation also showed how these computational advances can support downstream applications such as biomarker discovery, disease-mechanism studies, and precision medicine. Overall, the talk demonstrated that better computational tools are crucial for converting large and complex single-cell and spatial datasets into interpretable biological information that can support biomedical research and future clinical applications.





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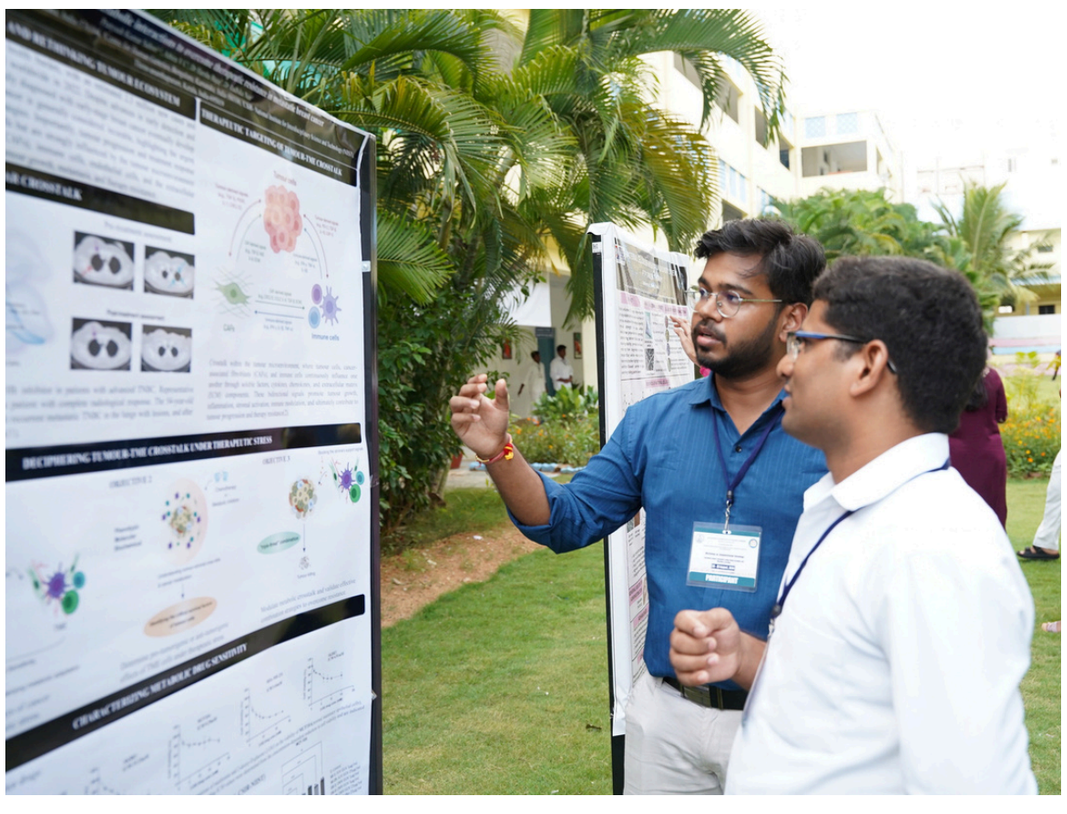
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Feedback from Participants:

- It was quite new to learn and would like to implement it in our work.
- I got some thoughtful insight into some topics and i wish to extend that ideas into my own research area.It was a wonderful experience and nice hospitality too.
- The workshop is good, meticulously planned, good lineup of speakers and research topics and hospitality is great. I love the interaction with the research faculties and especially with the students.
- It was something new and liked the implementation of bioscience with mathematics and computer science.
- It was an excellent workshop, the speakers were brilliant and the topics covered gave us a view of the interesting works going on in the field.
- It is an excellent workshop regarding oncology ,it gave me the view how computational biology is used in the industrial level.
- The workshop was really enjoyable and informative. I had already completed a summer training in Computational Biology, so I was able to relate to many of the concepts discussed. It was a great opportunity to strengthen my understanding of computational oncology and learn how these methods are applied in cancer research. Thank you to the organisers and speakers for conducting such a valuable workshop.
- Attending the Workshop on Computational Oncology Decoding Cancer Dynamics Using Omics, Imaging and Machine Learning was a very valuable and enriching experience for me. As a student, the workshop helped me understand many concepts that I had previously learned only theoretically in my course. The different sessions gave me a clearer picture of how computational approaches, omics, imaging, mathematical modelling, and machine learning are actually being applied to understand cancer and develop better therapeutic strategies. One of the most useful aspects of the workshop was that it helped me clear many of the doubts and unclear concepts that I had from my coursework. Listening directly to researchers and experts made the topics much easier to understand and also helped me connect what I study in my course with real-world research. Another major takeaway for me was the opportunity to interact with eminent scientists, researchers, faculty members, and professionals from different institutions and fields. These interactions gave me a broader perspective on research and helped me understand the different career and research possibilities available in computational biology and oncology. The poster session and panel discussion were also particularly useful because they provided an opportunity to learn from the experiences and ideas of people working in the field. Overall, the workshop was not just an academic learning experience for me, but also an opportunity to gain confidence, broaden my perspective, and understand how my academic knowledge can be connected to current research. I am grateful to the organisers and all the speakers for providing such an informative and interactive platform. The workshop has definitely motivated me to explore computational biology and related research areas more deeply.
- I really liked it the workshop . I got a confidence on my future as a AICB student.
- The workshop was good it taught a lot about oncology that i didn’t know but I think it should have justified its name a lot more and there should be a mention of how AI can be used to help biology but it told more about biology and the use case of ai in it but no mentions of any AI tools we can use or something. but overall it was a good and new experience for me.
- The Oncology Workshop was very informative and useful. I gained a better understanding of oncology, recent developments, and the practical approaches used in patient care. The sessions were well organised, and the speakers explained the topics clearly with relevant clinical examples.
- It's very Nice Workshop , Very helpful for me as a Computational Biology Student.
- As an AICB student, whenever we attended conferences before, they were usually either mathematics-centric or biology-based, which could sometimes feel challenging to relate to our own field. This time, however, the conference felt much more connected to what we study and what we aspire to do. What made it even more special was the way the speakers not only shared their knowledge but also gave us suggestions and insights into where we could fit ourselves within this field. It helped us understand our own course from a much broader perspective and gave us new ideas about the opportunities ahead. More than just gaining knowledge, this conference boosted our confidence and helped us see the relevance and potential of what we are learning. I think that is what a conference is truly meant to do , like not just inform us, but inspire us and help us see where we can go from here. I don’t know about everyone else, but I’m pretty sure the AICB students definitely left the conference with a smile on their faces. Thank you so much for organising such a wonderful and meaningful conference!

Gallery


SRI SATHYA SAI INSTITUTE OF HIGHER LEARNING
Workshop on Computational Oncology: Decoding Cancer Dynamics using Omics, Imaging and Machine Learning
28 – 29 August, 2026


DECIPHERING TUMOUR-TME CROSSTALK UNDER THERAPEUTIC STRESS
CHARACTERIZING METABOLIC DRUG SENSITIVITY


SRI SATHYA SAI INSTITUTE OF HIGHER LEARNING
(Deemed to be University)
In Collaboration with
PARAM HANSA CENTRE FOR COMPUTATIONAL ONCOLOGY (PHCCO), IISC BANGALORE
Workshop on Computational Oncology: Decoding Cancer Dynamics using Omics, Imaging and Machine Learning
28 – 29 August, 2026
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Friday
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A. AI Candidate Prioritization
Top 15 Clinical Benchmarks vs. Top 15 Computationally Prioritized Candidates


Exploring cell intrinsic and extrinsic mechanisms of breast cancer metastasis
Radhika Nair
SSSIHL


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(Deemed to be University)
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