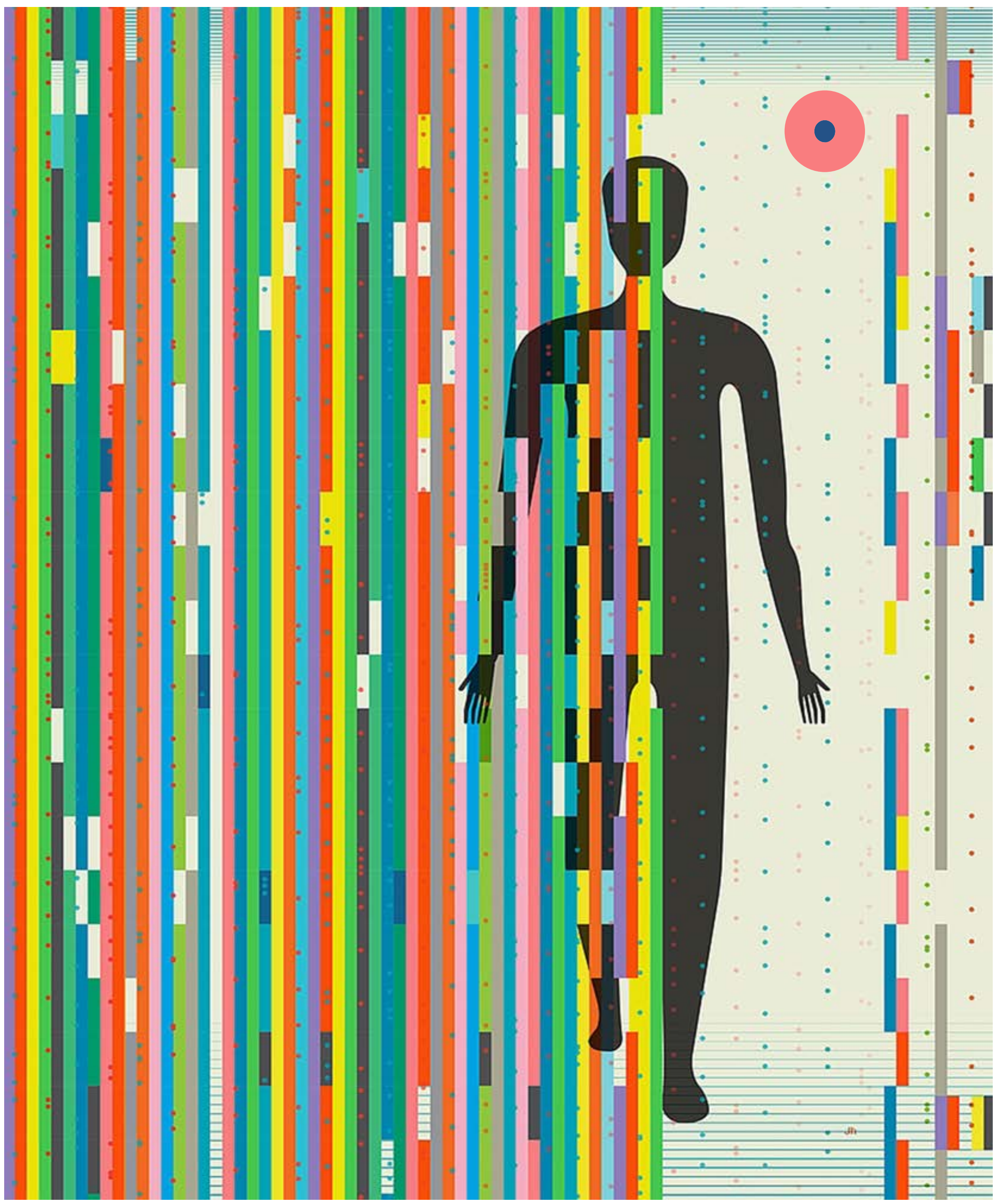
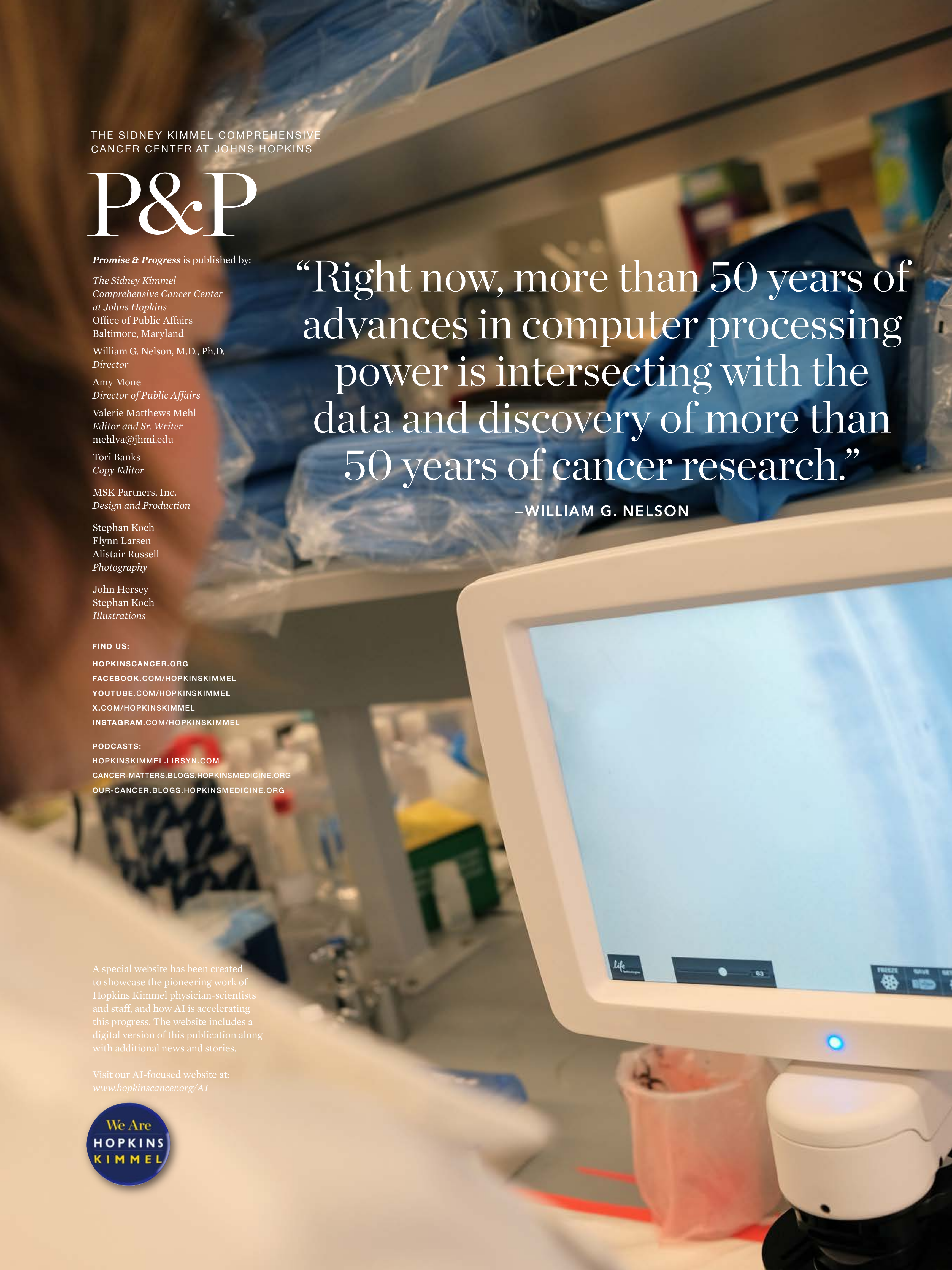
PROMISE & PROGRESS

THE SIDNEY KIMMEL COMPREHENSIVE CANCER CENTER AT JOHNS HOPKINS



AI UNLOCKED

SEE CANCER SOONER. TREAT IT SMARTER. CURE IT FASTER.



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P&P

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"Right now, more than 50 years of advances in computer processing power is intersecting with the data and discovery of more than 50 years of cancer research."

—WILLIAM G. NELSON

A special website has been created to showcase the pioneering work of Hopkins Kimmel physician-scientists and staff, and how AI is accelerating this progress. The website includes a digital version of this publication along with additional news and stories.

Visit our AI-focused website at:
www.hopkinscancer.org/AI

We Are HOPKINS KIMMEL

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This new model quickly identifies the cells targeted by immunotherapy to help experts distinguish patients who will respond to immunotherapy from those who will not.

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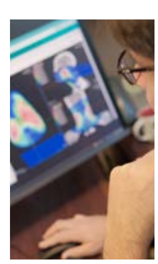
Managing and interpreting the billions of data points generated by genetic sequencing and other cancer research was a barrier to cancer discovery, but today, it is part of the solution.



Oncospace

A data-mining system that learns from every patient's prior experience to improve treatment for the next.

Artificial intelligence may be powered by computers, but at the Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, cancer research is anything but artificial. It is the realization of the ultimate collaboration—the collective wisdom of thousands of clinicians and scientists around the world, brought together through AI to solve the cancer puzzle and improve cancer medicine. By securely harnessing and learning from vast amounts of data, AI is helping us understand this complex disease in ways never before possible. AI is accelerating progress, making early detection more precise, treatments more individualized, and the hope for the eradication of cancer more real than ever before. The promise is a future where cures are not the exception, but rather the expectation.

FROM THE DIRECTOR

Harnessing the Power and Setting the Vision for AI-Assisted Cancer Medicine

ADVANCES IN INFORMATION science and technology have created an astonishing capacity to gather, transfer, store and analyze large and diverse collections of data — measured in sizes exceeding the imagination. For cancer, these data include genetic information, imaging, laboratory results, pathology, patient-reported symptoms, patient histories, and physical examination findings.

Computing itself — the basic principles of how computers process information — hasn't really changed since the invention of the computer. What has changed dramatically is the power, speed, and scale of modern computers. They can process vastly more data, at much higher speeds, and do it in parallel, shared platforms. This provides us the opportunity to analyze these enormous datasets in ways that were impossible just a decade ago.

Right now, more than 50 years of advances in computer processing power is intersecting with the data and discovery of more than 50 years of cancer research. The result, which we call artificial intelligence, or AI, has given rise to a learning health care system that incorporates innovation in real time to glean insights into cancer and its treatments, assess their impact seamlessly, and transform cancer medicine.

At the Johns Hopkins Kimmel Cancer Center, we are implementing AI with guardrails in place so that it improves research and patient care by augmenting and supporting — not replacing —our cancer experts. AI will help us decipher the complexities of cancer and advance and guide new therapies faster, safer, cheaper, and with far fewer resources.

Still, the ability to do this is not enough. We believe it is as important to do it correctly, realizing the promise of AI within a framework that respects the rights and dignity of patients, always incorporates physician judgement, delivers optimal care, avoids undue risks and burdens, and fosters better outcomes for all.

In this issue, you will read about progress already being made and our vision for the future. Through our collaborations with the Cancer AI Alliance, of which our Cancer Center is a founding member, our Convergence Institute, Johns Hopkins inHealth, the Johns Hopkins Data Science and AI Institute, the Institute for Data-Intensive Engineering and Science, and more, we are positioned to make revolutionary advances against cancer.

If today we have surpassed what could be accomplished only a decade ago, just imagine the promise the next decade holds.

William G. Nelson, M.D., Ph.D.
The Marion I Knott Professor and Director
The Sidney Kimmel Comprehensive Cancer Center
at Johns Hopkins

Q&A | VASAN YEGNASUBRAMANIAN

The Time Is Now

AS DIRECTOR OF INHEALTH PRECISION MEDICINE, **VASAN YEGNASUBRAMANIAN**, M.D., PH.D., IS LEADING THE JOHNS HOPKINS STRATEGIC INITIATIVE TO REALIZE THE FULL POWER OF AI AND DATA SCIENCE TO CREATE THE INTELLIGENT, INNOVATIVE HEALTH SYSTEM OF THE FUTURE.

Q | Why is AI important in cancer research and treatment?

A | Artificial intelligence (AI) is poised to fundamentally transform health care. It's not just about adding a new tool, it's about rethinking how we deliver medicine. Data is a valuable asset, but it's only powerful when we can position it properly to enable innovation. AI helps us deliver on that innovation. It holds the promise to enable predictive, real-time and consistent care, and opens the door to innovations we couldn't even imagine before. Think about early cancer detection, individualized treatments, and accelerated drug discovery. AI gives us the potential to change everything, but we must do it responsibly and ethically.

Q | You mentioned four main priorities needed to prepare the data to use in AI innovation. Can you walk us through them?

A | It's often said that data is the new oil. Just like oil, it's incredibly valuable, but not in its raw form. To extract the value from data, we must invest in making it ready for innovation, just as the oil industry has invested in extracting value from crude oil mined from the ground.

Priority 1 is data ingestion: figuring out where the high-value data assets live and pulling them from their source systems, like medical records or imaging databases. Data sitting in a medical record helps us deliver clinical care, but it doesn't help us innovate. We have to extract it first.

Priority 2 is annotation and curation: structuring, cleaning, and organizing the data so it can be used. Most of it isn't ready for computing and research in its original form. This process is like refining oil, turning raw material into fuel and other byproducts for innovation.

Priority 3 is building advanced computing and analytic platforms. The oil industry has developed expansive distribution channels and pipelines for refined oil and byproducts to reach the industries that utilize them. For data, we would aim to do the opposite. Rather than copying and distributing massive data sets to researchers, which is risky and inefficient, we will develop computing platforms that can bring researchers and their tools to the data, where it securely resides. This is critical for both privacy and performance. In a way, this is like having the distribution channels and pipelines for refined oil and byproducts to reach the industries they can serve.

Priority 4 is responsible stewardship: We can't allow unbridled access to sensitive data. There is a lot of power here, and we must build in governance and ethical and equitable frameworks to ensure that our innovation doesn't cause harm. At Johns Hopkins, we established an AI and Data Trust Council to help oversee this.

Q | How else are you addressing concerns around privacy and public trust?

A | We take security very seriously. Security is most vulnerable when data is decentralized, sitting on individual computers. A bad actor or hacker only needs to breach one machine. That's why we're shifting to centralized, monitored systems where access is logged, and unusual activity can be flagged immediately. Our IT@JH team and the office of the chief information security officer help us develop secure computing environments and establish ways to identify and prevent potential breaches and generate an immediate response if a breach occurs. Our goal is to innovate with the data while ensuring that we maintain patient privacy and data security.



Q | What does it mean to be a steward of public trust in this context?

A | Much of the data we use was collected for clinical care. Now, we're repurposing it for secondary research. We have legal frameworks for that, but more importantly, we have an ethical obligation to show that what we are doing is truly for society's benefit. The public must be a partner in this. That means being transparent, thoughtful and inclusive. We make progress by building trust.

Q | What can science enable with this approach?

A | This is where it gets really exciting. With interdisciplinary collaboration spanning medicine, data science and engineering, we're not just making tweaks, we are transforming health care. Here's how:

We're shifting from reactive to preventive, predictive care. AI tools can help detect disease earlier, allowing us to act before symptoms become an illness. We can also develop models to forecast an individual's disease course or response to a given therapy, and develop a treatment plan accordingly.

We're turning ad hoc care into real-time care. AI agents can use monitoring systems and wearable and smart device data 24/7, flag issues, and alert care teams in real time.

We're reducing unwanted variation. Whether it's differences in access, knowledge gaps, or errors, AI helps ensure that best practices are consistently applied.

We're accelerating innovation. AI can detect patterns in imaging that the human eye cannot. It can screen billions of virtual drug compounds, design new ones from scratch, and drastically reduce development timelines — and this is only the beginning.

Q | How do these innovations help individual patients?

A | What we're building is designed for both scale and personalization. The data sets we use are broad and deep, but the discoveries we make feed directly back into individualized care. That's the essence of an intelligent, innovative health system — data from many helps the one. It's a full-circle model in which innovation informs better care.

Q | What about concerns that AI might lead to overdiagnosis or overtreatment?

A | That's a real concern, especially with early detection. Just because we can find something early doesn't always mean we should treat it. AI can help us pair early detection with risk stratification — figuring out whether what we found is likely to become dangerous. For example, in prostate cancer, we're developing biomarkers to distinguish aggressive from indolent cases, so patients get the right level of care. We will look to develop similar strategies for every cancer type.

Q | How is this getting back into the health care delivery system?

A | We're developing tools like Patient Insight — a dashboard that helps doctors see a patient's journey in context of thousands of others. Another project, the Health General Reasoner, is a backend tool to embed AI into clinical workflows. We are piloting a collaboration with Microsoft of a tool developed in-house at Johns Hopkins that helps identify patients at risk for blood clots — a common risk of hospitalization — and suggests preventive treatment in real time.

Q | Do you have plans to expand what we're doing with AI beyond the Kimmel Cancer Center?

A | No single institution has all the data or expertise. That's why we're part of a national initiative called the Cancer AI Alliance (CAIA) with four other top cancer centers. We're working to build a federated learning platform where each center keeps its data secure, but shares its models. AI tools travel to the data, not the other way around. This preserves security and privacy while enabling broad collaboration. If we succeed, it could serve as a model for every cancer hospital in the country to join CAIA in this collaborative effort.

Q | Is Johns Hopkins helping to lead the way?

A | Yes, in many ways we are, but we're not doing this alone. We're working across institutions, with industry, and with our communities. The technology is powerful, but it's the people and partnerships that will make it truly impactful. The future is incredibly promising. We're exploring how AI can accelerate drug development, personalize treatments, and help us understand cancer in ways we couldn't before. But we're also focused on making sure the technology is inclusive, equitable, and trusted. If we do it right, AI will raise the standard for everyone. That's our mission.

BILL NELSON/VASAN PODCAST

INHEALTH: WWW.HOPKINSMEDICINE.ORG/INHEALTH

Web Exclusive

Transforming Cancer Drug Discovery

Drug discovery is among the most complex and costly types of cancer research. Now, however, with an assist from AI technologies, Kimmel Cancer Center researchers are reimagining cancer drug research and development, launching a new model that will make it faster, more precise, and less expensive to bring new cancer medicines to patients.

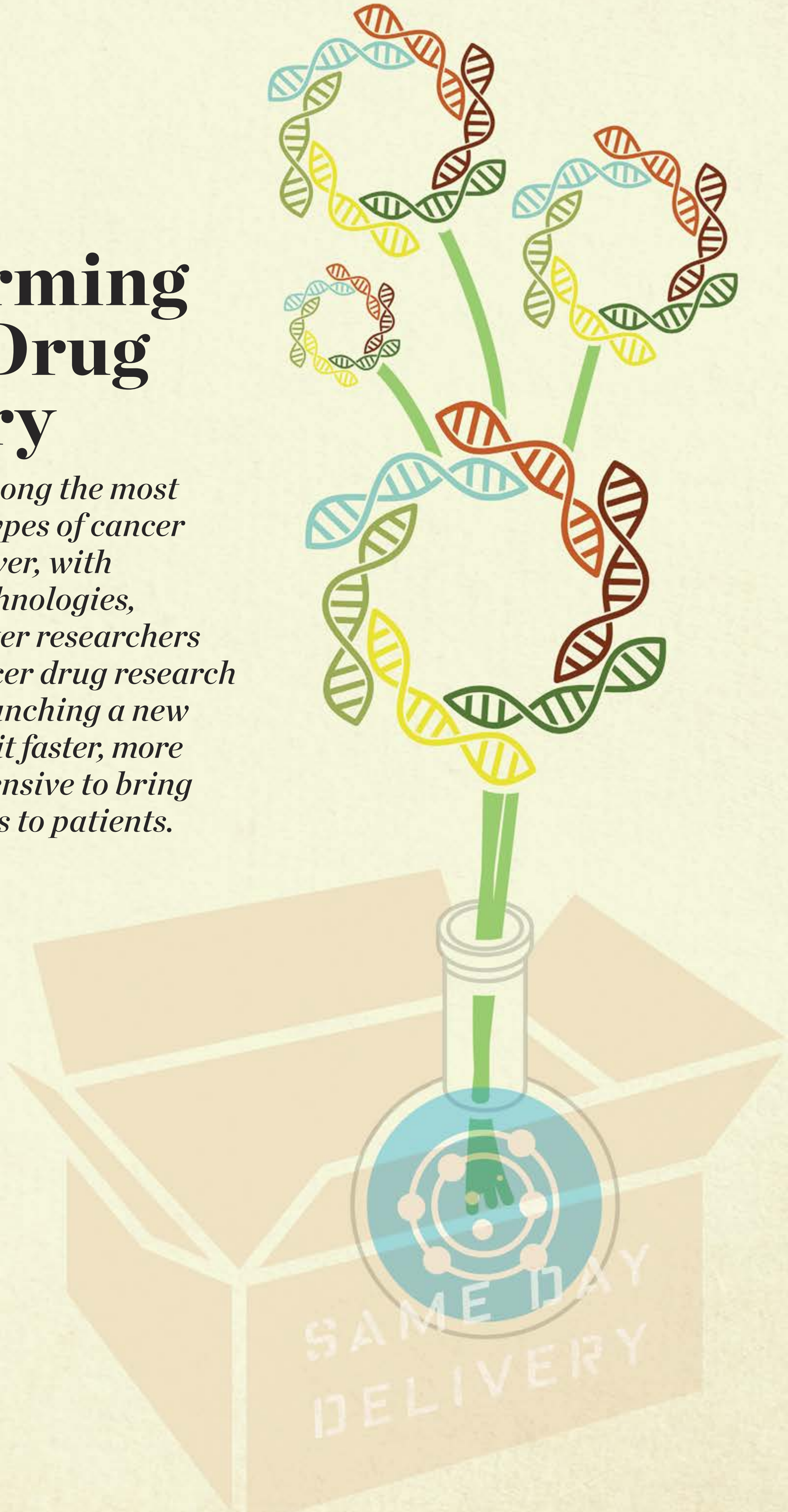
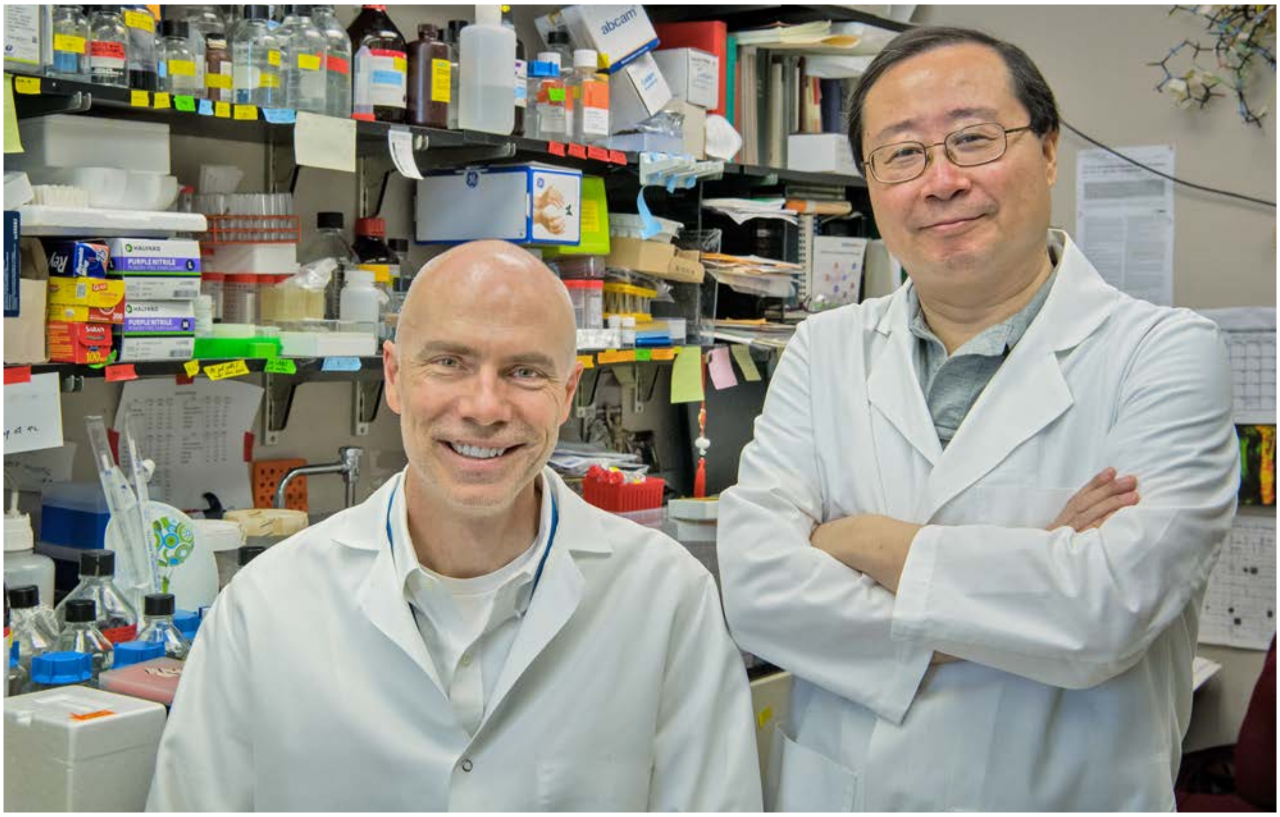


ILLUSTRATION: ©STEPHAN KOCH

JAMES BERGER (LEFT) WITH **JUN LIU**



"TRADITIONALLY, finding a new cancer drug could take more than a decade and cost more than a billion dollars," says **James Berger**, Ph.D., the Michael and Ann Hankin and Partners of Brown Advisory Professor in Scientific Innovation and Co-Director of the Cancer Chemical and Structural Biology Program. "With AI, we see the potential to substantially compress both the time and cost of the process."

FROM BROAD SHOTS TO PRECISION TARGETS

Fifty years ago, cancer therapy was largely trial and error. Chemists tested chemicals that killed cells, hoping they destroyed cancer faster than healthy tissue. It was a blunt tool, and side effects, from hair loss, nausea and fatigue, and suppression of immune cells were harsh for patients.

Today, precision medicine is the goal. We have new therapeutics in the arsenal, including immunotherapies and gene-targeted medicines. Scientists increasingly know more about how cancers are driven by genetic mutations and molecular pathways, and new drugs aim to hit those targets with surgical accuracy or employ immune cells to destroy cancer cells. The progress has been revolutionary, but finding the right patient-drug match remains a challenge.

This is where AI could excel, Dr. Berger explains. By analyzing mountains of genetic data, AI is poised to help researchers identify which patients are most likely to benefit from a particular therapy. Our researchers may soon be able to design clinical trials that better match specific drugs to specific patients. The result, he says, should be faster approvals, lower costs, and treatments that reach patients sooner.

At the Kimmel Cancer Center, this represents a chance to bring its long history of excellence in drug discovery into a new era.

SMARTER, FASTER, CHEAPER

AI is already helping Dr. Berger and colleagues make inroads into nearly every type of therapy, from small molecules and peptides to RNA-based medicines and biologics.

Dr. Berger's expertise is in small molecules, cancer medicines created from tiny chemical compounds that can easily enter cells and interfere with proteins and protein pathways that fuel cancer growth. He collaborates with scientists working in the other areas of drug development. **Jun Liu**, Ph.D., who co-directs the Cancer Chemical and Structural Biology Program with him collaborates on

"TRADITIONALLY, FINDING A NEW CANCER DRUG COULD TAKE MORE THAN A DECADE AND COST MORE THAN A BILLION DOLLARS. WITH AI, WE SEE THE POTENTIAL TO SUBSTANTIALLY COMPRESS BOTH THE TIME AND COST OF THE PROCESS."

small-molecule drugs but is also using AI to help develop peptide drugs, therapeutics made from the building blocks of proteins that work by mimicking or directing drugs to cancer cells and also by stimulating immune responses. **Jeff Coller**, Ph.D., Bloomberg Distinguished Professor of RNA Biology and Therapeutics, is exploring how AI can accelerate the development of RNA-based medicines, genetic messengers that edit the instruction manual and change how cells make proteins to silence genes that support cancer growth, replace missing instructions, and train the immune system to respond to cancer cells. Biomedical engineers **Jamie Spangler**, Ph.D., and **Jeffrey Gray**, Ph.D., are focused on biologics – in particular, antibody therapies – which are made from living cells or lab-made versions of natural proteins and which typically work on the outside of cancer cells to make them visible to the immune system, block growth, or deliver anticancer drugs directly to cancer cells.

SPANGLER

AI is helping these scientists predict and analyze protein structures, search vast chemical libraries, and even design new drug candidates with extraordinary speed and accuracy.

In the past, scientists might have biochemically screened tens of millions of compounds in hopes of stumbling on one that worked. AI changes the approach. By predicting the natural 3D shapes proteins take and how they interact with other molecules, researchers can now design a handful of promising drug candidates on a computer and move them straight into laboratory testing. Pathologists **Laura Wood**, M.D., Ph.D., and **Ralph Hruban**, M.D., are already doing this kind of work in pancreatic cancer.

WOOD

HRUBAN

The promise is not only in creating new drugs but also in improving old ones. By using AI to identify why cancers develop resistance, existing therapies can be re-engineered to work better and longer.

Despite the power of these tools, Dr. Berger emphasizes that involvement and oversight of scientists and clinicians remain essential to drug discovery.

> **"AI can propose molecules, but it can't yet account for every nuance of efficacy, safety and biology. We still need experienced researchers across a range of life science and clinical disciplines to keep us on track."**

"AI can propose molecules, but it can't yet account for every nuance of efficacy, safety and biology," he says. "We still need experienced researchers across a range of life science and clinical disciplines to keep us on track."

A NEW VISION

Johns Hopkins already has world-class basic scientists and clinical researchers working together. With AI, Dr. Berger sees a key opportunity to enhance this expertise. His vision includes AI experts who specialize in drug design as members of the School of Medicine's research team. In the exploding field of AI, these new collaborators—which include specialists in computer-guided chemistry and biology, protein and nucleic acid engineers, and antibody designers—are in short supply and high demand, but Dr. Berger believes they are essential to making real progress.

Ultimately, it will save money and lives, but on the front end, adding these experts and the technology required to do the work requires a multimillion dollar investment, ranging from $10 million to $25 million to build the infrastructure and recruit senior experts.

"We have the scientists who know the targets inside and out. Sometimes they've spent decades studying them," says Dr. Berger. "What we need now are the AI researchers and the tools to match that expertise.

> **"Academic research thrives on fresh ideas and the freedom to take risks. Instead of thousands of blind shots, AI gives us more targeted shots on goal and the chance to succeed faster for patients."**

Working together, he believes they can make drug discovery faster, smarter, and more patient focused. From designing antibodies in weeks instead of years, to reimagining small molecules for hard-to-treat cancers, AI is poised to accelerate progress against cancer in ways once thought impossible.

The vision is ambitious but achievable. In the next five to 10 years—perhaps sooner—Dr. Berger believes small groups of Kimmel Cancer Center scientists could design a new cancer drug with just a handful of people, using off-the-shelf computational tools. The time and cost savings could be staggering. What once took a dozen years and over a billion dollars could shrink to 3-4 years and many millions less, he says.

"Academic research thrives on fresh ideas and the freedom to take risks," Dr. Berger says. "Instead of thousands of blind shots, AI gives us more targeted shots on goal and the chance to succeed faster for patients."

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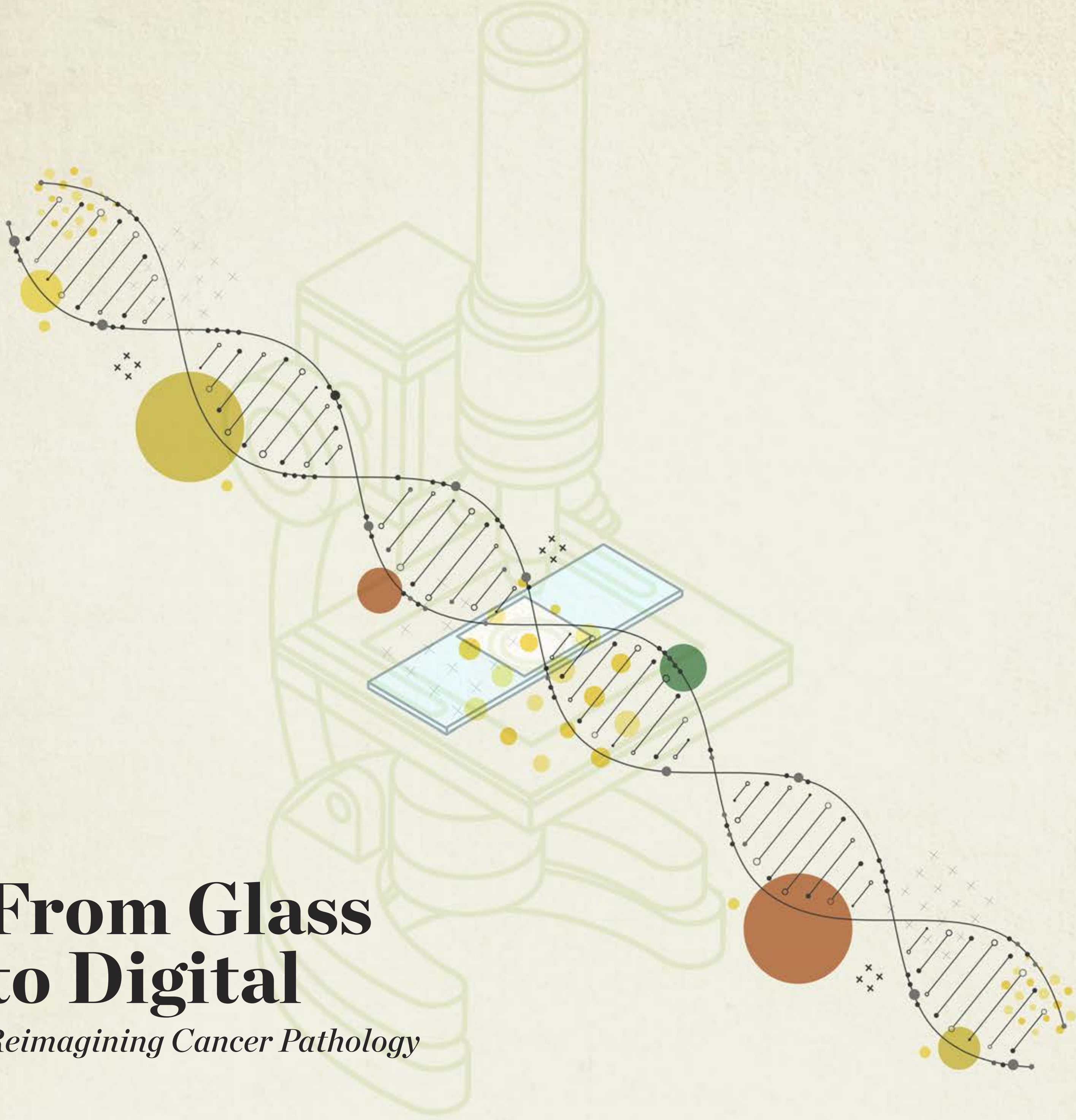


ILLUSTRATION: ©STEPHAN KOCH

From Glass to Digital

Reimagining Cancer Pathology

"EVERY YEAR, WE GENERATE CLOSE TO A MILLION SLIDES AT HOPKINS. EACH ONE CONTAINS GIGABYTES OF INFORMATION. TOGETHER, THEY REPRESENT AN IMMENSE ARCHIVE OF KNOWLEDGE, BUT THEY ARE STORED IN DRAWERS AND WARE-HOUSES, ACCESSIBLE ONLY BY PULLING THE GLASS AND PUTTING IT UNDER A MICROSCOPE."

DE MARZO

FOR MORE THAN a century, pathologists have relied on a microscope and a glass slide to diagnose cancer. At the Kimmel Cancer Center, this powerful tool has guided care for generations of patients. Now, however, with the help of digitization and artificial intelligence (AI), the familiar glass slide is being transformed into a digital treasure trove, one that promises faster, more precise diagnoses, better training for future pathologists and new opportunities for discovery.

"Every year, we generate close to a million slides at Hopkins," says **Angelo De Marzo**, M.D., Ph.D., associate director of cancer research pathology. "Each one contains gigabytes of information. Together, they represent an immense archive of knowledge, but they are stored in drawers and warehouses, accessible only by pulling the glass and putting it under a microscope."

A VIRTUAL MICROSCOPE

A robust effort to scan these slides and digitize them so they can be easily accessed and viewed on a computer screen opens up a world of possibility.

The idea of scanning pathology slides into a "virtual microscope" has been envisioned for decades, but now, the technology has caught up with our imagination.

At the Kimmel Cancer Center, **Alex Baras,** M.D., Ph.D., director of digital pathology and precision medicine informatics, is helping bring it to fruition, developing plans to ramp up from scanning tens of thousands of slides to hundreds of thousands of slides each year, and eventually scaling up to 1 million annually in five years. Together with **Lisa Rooper**, M.D., director of the Division of Surgical Pathology, and other colleagues across surgical pathology, Dr. Baras is building momentum to digitize the enormous Johns Hopkins pathology archive.

BARAS

Although the task is an onerous one, the benefits are immediate and, ultimately, immensely more efficient. Pathologists would no longer need to request slides from an off-site warehouse. Instead, these digitized slides could be pulled up on a computer instantly, and experts could confer with one another from as close as the office next door to the far reaches of the globe. Slides from other hospitals, which often must be returned after a short time, could now be preserved indefinitely. Samples stored at Johns Hopkins dating back to the 1918 influenza pandemic could now be digitized and studied, Dr. De Marzo says.

ROOPER

For patients with cancer, that means greater efficiency and better care. If a cancer recurs years after an initial diagnosis, doctors can compare the new biopsy with the original digital record in seconds, a process that often required shipping fragile slides across the country. For research, this provides a gold mine of samples that can be analyzed and incorporated into research data to enhance cancer discovery.

AI AT THE MICROSCOPE'S SIDE

Scanning slides is the key first step to employing AI in cancer pathology, but it is only the beginning. Once digitized, pathologists can begin to use AI tools to assist in cancer detection, precision diagnosis, and treatment guidance. In breast cancer, for example, Dr. De Marzo says AI can help quantify key biomarkers that reveal what is fueling the cancer, such as estrogen and HER2 receptor levels, more consistently and quickly than humans alone, helping ensure patients quickly receive the targeted therapies that will combat the cancer.

When reviewing slides for the presence of prostate cancer, Dr. De Marzo says he often examines 50 slides for a single patient. In one day, he may review these for 10 different patients. It requires a highly trained eye to find cancer, precisely grade the cancer and — just as importantly — correctly assess when no cancer is present.

LOTAN

Experts like Dr. De Marzo are in short supply and high demand, often sought out by hospitals around the world to review cancer pathology slides. His colleague and prostate cancer expert **Tamara Lotan**, M.D., the Rose-Lee and Keith Reinhard Professor of Urologic Pathology, is leading efforts employing novel AI systems that can screen trays of biopsy slides and highlight areas most likely to contain cancer, so the pathologist can immediately zero in on concerning areas. Dr. Lotan's team has found that these algorithms can also accurately grade the cancers and predict outcomes.

"Instead of spending 20 minutes per tray, AI could cut that to just a few minutes," says Dr. De Marzo. "It frees us to take on more cases and to collaborate and spend more time on the most challenging cases."




He is quick to point out that AI tools will be used to augment and amplify, not replace, the pathologist's judgment. He says studies at Johns Hopkins and elsewhere found that AI can match the accuracy of top pathologists, while also lifting the quality of diagnoses across the board. Considering the significant shortage of highly qualified pathologists, AI can help expand the capabilities of top pathologists like Drs. De Marzo, Lotan and Rooper, and help ensure all patients have access to this level of review.

3D and Molecular Prediction

In addition, researchers are now taking pathology from the two-dimensional images on a slide into the realm of 3D. Johns Hopkins faculty members — including **Laura Wood**, M.D., Ph.D., **Ralph Hruban**, M.D., **Denis Wirtz**, Ph.D., **Ashley Kieman**, Ph.D., and others — are exploring how AI and new imaging technologies can reconstruct tissue in 3D, offering a more complete picture of diseases such as pancreatic cancer.

Meanwhile, the Cancer Center's co-associate director of precision oncology, Vasan Yegnasubramanian, M.D., Ph.D., who is the director of inHealth Precision Medicine at Johns Hopkins, along with Dr. Baras and computational collaborators, are working rapidly to marry digital pathology with genomics and big data. The goal broadens the reach of pathology beyond diagnostics to forecast molecular changes, and predict treatment response — including a response to immunotherapy — all based on the subtle features contained in the standard H&E pathology slide.

"Imagine guiding therapy without having to order additional expensive tests. We see that as part of the promise of AI," says Dr. De Marzo.

Training the Next Generation

These advances are changing pathology now, but it is the next generations of pathologists who will uncover the full promise of this new landscape.

Traditionally, residents learn and sharpen their diagnostic skills by spending hours at a multiheaded microscope under the mentorship of a senior faculty member. As a school of medicine faculty member who trains the next generation of pathologists, Dr. De Marzo, along with departmental leadership and several up-and-coming young pathology faculty members with a passion for teaching, are working to ensure that young pathologists learn to master the fundamentals, with AI serving as a tool, not a crutch.

"With the right design, AI could actually enhance training," he says. "Imagine asking the system to show you 20 examples of a rare cancer, all verified by experts. That kind of resource could accelerate learning in ways we've never had before."

Challenges and Opportunities

Still, the path ahead isn't without obstacles. Storing millions of digital slides requires immense amounts of space. Implementing AI tools clinically will also demand FDA approvals, careful validation, and new safeguards for privacy. Training programs will need to adapt to ensure young pathologists still learn core skills. The investment needed to realize these goals, particularly in light of the current economic pressures on academic medicine, is challenging.

"In the short term, it costs more," Dr. De Marzo acknowledges, "but over time, it will save money, improve efficiency, and make us better."

Johns Hopkins leadership is committed to meeting the challenge, and has already begun addressing these issues.

"Johns Hopkins' unique strength lies in its ecosystem. With collaborations across medicine, engineering, and computer science, and the launch of a $400 million AI Institute, the pieces are in place to connect digital pathology with genomics, large language models, and big data analysis," says Dr. De Marzo.

Looking Ahead

Within five years, Dr. De Marzo predicts, most Johns Hopkins diagnostic slides will be scanned prospectively, and AI tools will be embedded into daily practice, improving speed, accuracy, and patient outcomes.

Dr. De Marzo says the promise of AI in pathology reflects a long-held Johns Hopkins tradition, in which mentors — such as Johns Hopkins cancer pioneer Dr. **Donald Coffey** and leaders such as Kimmel Cancer Center Director **William Nelson** and school of medicine Dean T**ed DeWeese** — foster a culture in which collegiality thrives and bold ideas take root.

"This place has always respected every discipline — mathematicians, engineers, biologists, clinicians, all of them," he says. "That culture of respect is what lets us solve problems together. Now, AI is becoming part of that story."

"MODERN COMPUTING HAS BEEN TAKEN OVER BY AI. THE KEY IS DATA. GOOGLE AND OTHERS CAN BUILD POWERFUL ALGORITHMS, BUT THEY DON'T GENERATE THE DATA THAT SCIENCE NEEDS. THAT IS WHERE UNIVERSITIES, AND PLACES LIKE HOPKINS, CAN LEAD."

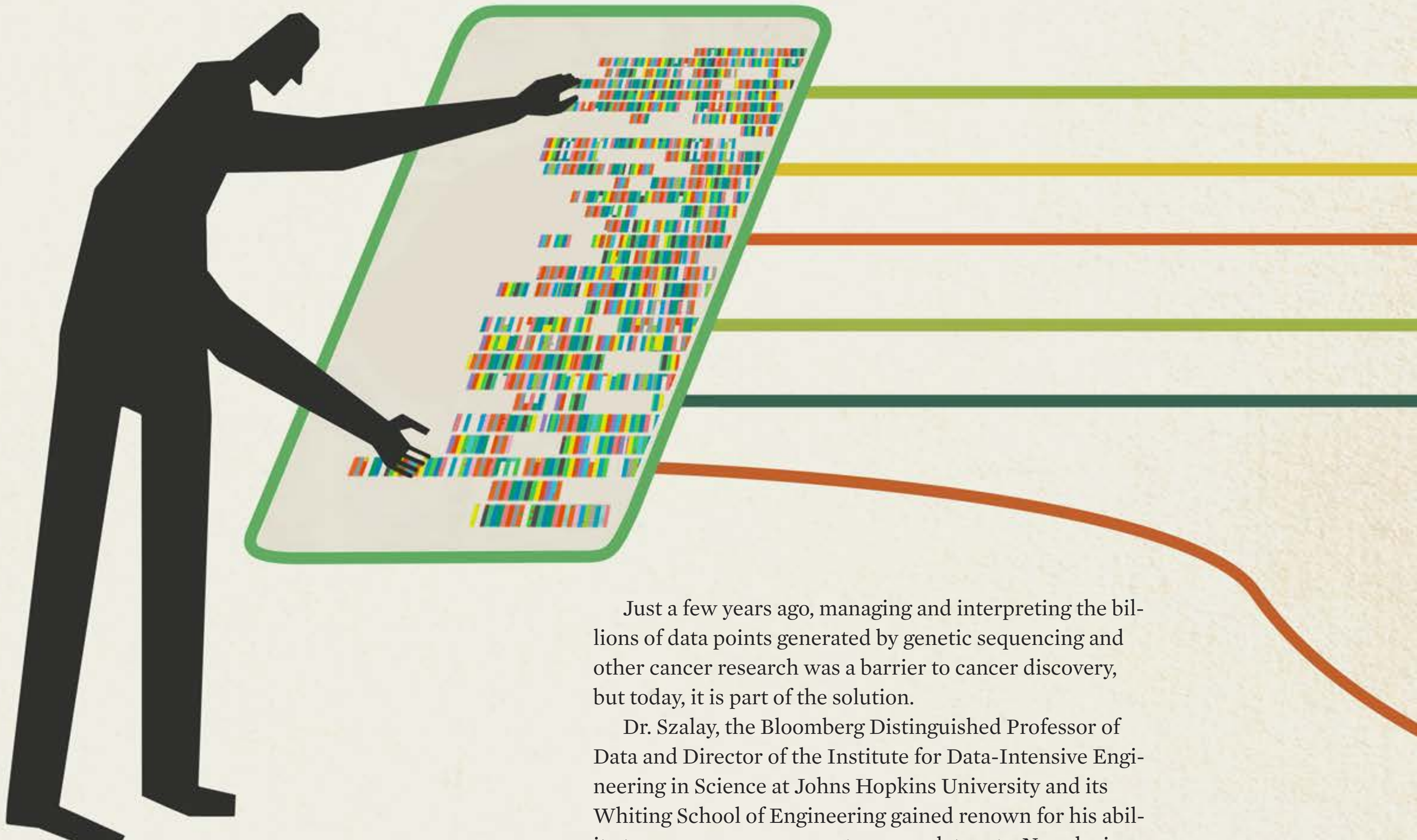


ILLUSTRATION: ©STEPHAN KOCH

Data Driven

Using AI to Solve the Complexities of Cancer

WHEN IT COMES TO harnessing artificial intelligence (AI) for cancer breakthroughs, Johns Hopkins researchers **Alex Szalay**, Ph.D., and **Janis Taube**, M.D., M.Sc., believe the future begins with data. Lots of it.

In fact, Dr. Szalay points out that one of the greatest challenges is not too much data, but too little. While efforts are underway to securely digitize pathology slides, images, and other patient information, AI tools are advancing even faster. Their potential is limited only by the amount of data available to explore—data that can help uncover new answers to complex questions about cancer.

Just a few years ago, managing and interpreting the billions of data points generated by genetic sequencing and other cancer research was a barrier to cancer discovery, but today, it is part of the solution.

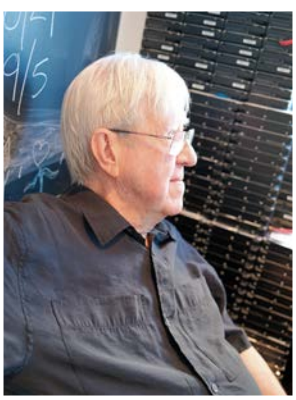
Dr. Szalay, the Bloomberg Distinguished Professor of Data and Director of the Institute for Data-Intensive Engineering in Science at Johns Hopkins University and its Whiting School of Engineering gained renown for his ability to manage enormous astronomy data sets. Now, he is turning that expertise toward cancer.

ASTRONOMY TO MICROSCOPY

The Johns Hopkins astrophysicist worked with Janis Taube, M.D., to build the AstroPath platform from his Sloan Digital Sky Survey, a 3D digital map of the universe. The science that allowed his sky survey to "stitch" together billions of telescopic images of celestial objects—each expressing distinct light signatures—to quantify the statistical properties and spatial arrangement of stars and galaxies in the Universe, allowed them to create a similar detailed view of how and where tumor cells interact with surrounding cells, particularly immune cells.

Just as the Sloan survey mapped the cosmos on an astronomical scale, Dr. Taube, director of dermatopathology and co-director of the Bloomberg~Kimmel Institute's Tumor Microenvironment Program and the Mark Foundation Center for Advanced Genomics and Imaging, says AstroPath mapped tumor cells on a microscopic scale.

JANIS TAUBE IS WORKING TO DEVELOP A NEW MULTISPECTRAL TISSUE IMAGING PLATFORM TERMED 'ASTROPATH' TO FURTHER BIOMARKER DEVELOPMENT.



USING AI, **CHARLES LU** IS WORKING WITH DRS. TAUBE AND SZALAY TO BUILD HIGHLY DETAILED IMAGES OF THE BOUNDARY BETWEEN TUMOR CELLS AND SURROUNDING NORMAL TISSUE.

Now, working together at the intersection of physics, computer science, pathology, and cancer immunotherapy, they are accelerating the way discoveries move from lab to clinic by creating massive, high-quality cancer data sets—the essential building blocks for AI.

"Modern computing has been taken over by AI," says Dr. Szalay. "The key is data. Google and others can build powerful algorithms, but they don't generate the data that science needs. That is where universities, and places like Hopkins, can lead."

GEOGRAPHY OF TUMORS

Drs. Taube and Szalay began their AstroPath work with a project to map the geography of tumor and immune cells. Dr. Taube recalls how labor-intensive it was, drawing tumor boundaries by hand on slides and annotating each image. Today, AI is doing that work in minutes, with greater precision, she says.

"These are supervised tools," says Dr. Taube. "We still oversee the process, but AI allows us to generate data sets much faster and with far more detail than we could by hand."

The result is a new generation of "AI-ready" data—digitized slides enriched with spatial maps showing where all the cells that influence cancer are located and how they interact. These maps are proving vital in the search for predictive biomarkers of immunotherapy response.

"We are using AI to build the data sets that can be queried by deep learning algorithms to aid in the depth and speed of cancer research," says Dr. Taube

The tool is transforming how oncologists deliver cancer immunotherapy, revealing what geographic interactions are transpiring and what interactions are responsible for inhibiting immune cells from killing cancer cells.

"Across all solid tumor types, only about 30% of patients currently benefit from immunotherapies, but by combining spatial mapping with genomic and molecular data, we believe they begin to uncover why so more patients can be helped," she says.

INVESTING IN THE FUTURE

Building these data sets is not cheap. Staining and analyzing a single specimen can cost around $1,000. But Drs. Taube and Szalay see this as a small investment compared to the $150,000 price tag of some cancer drugs.

"If we can identify the right patients for the right drugs, the cost savings, and most importantly, the patient benefit, are enormous," says Dr. Taube. "This is how we reduce side effects, avoid financial harm, and expand the number of patients who respond."

"If we can identify the right patients for the right drugs, the cost savings, and most importantly, the patient benefit, are enormous," This is how we reduce side effects, avoid financial harm, and expand the number of patients who respond."

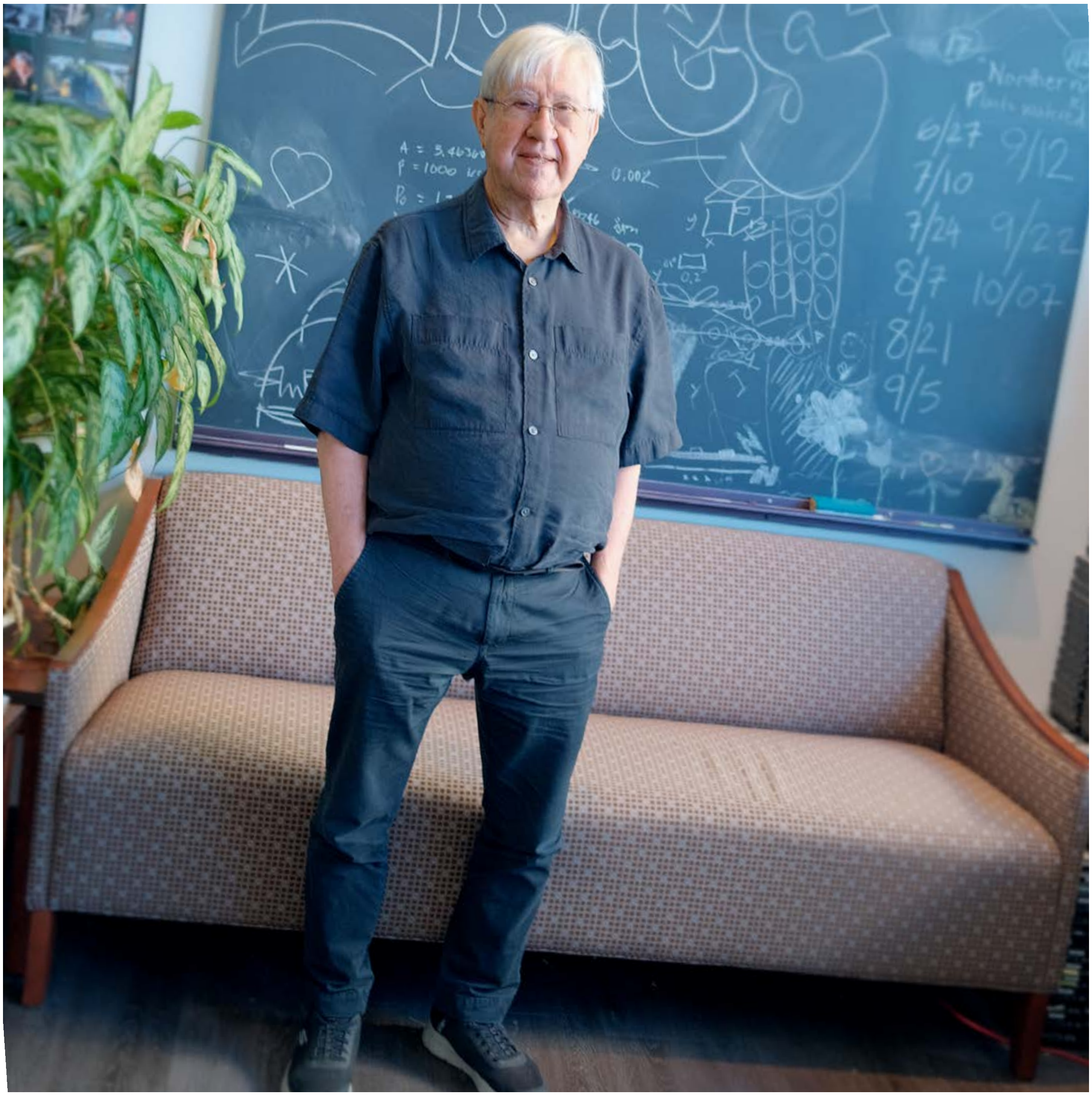
Dr. Szalay adds that Johns Hopkins is well positioned to lead. Decades of expertise in handling "big data" from astronomy and other sciences, he says, now meets a medical school brimming with students, like **Charles Lu**, equally comfortable in AI and medicine. Charles is working with Drs. Taube and Szalay, using AI to build highly detailed images of the boundary between tumor cells and surrounding normal tissue, as well as the molecular markers that the tumor and immune cells display at this interface.

"It's exciting to see in Charles the next generation of researchers," he says. "They are as much at home in AI techniques as in biology, and they are bringing fresh energy and ideas."

"We are sitting on a treasure trove, and we want to move quickly so we can identify more causes of cancer, discover new treatments, and save lives."

–ALEX SZALAY

ALEX SZALAY GAINED RENOWN FOR HIS ABILITY TO MANAGE ENORMOUS ASTRONOMY DATA SETS. NOW, HE IS TURNING THAT EXPERTISE TOWARD CANCER.



A SPATIAL REVOLUTION

Dr. Taube calls this moment a "spatial revolution." Her team is applying AI to Cancer Genome Atlas melanoma slides—data already de-identified and publicly available—to create AstroPath maps that link melanoma cell geography to genomic profiles. She plans to create similar maps with Johns Hopkins' own cancer data sets.

To manage this responsibly, Drs. Taube, Szalay and team developed "AstroID," a de-identification system that allows researchers to securely track patients across multiple visits, biopsies, and scans without compromising privacy.

"This is not a technical problem," says Dr. Szalay. "We know how to do this safely. What's needed is the intellectual energy, an attention to the ethical framework, and the support to scale it."

A TREASURE TROVE

For both Drs. Szalay and Taube, the urgency is clear. They believe that with sufficient funding, they could take their proof-of-concept studies to large-scale production within a year.

"This is the tip of the iceberg," says Dr. Szalay. "By letting AI take over routine tasks, just as we now trust it to guide our cars, we can hand it the microscopes too, freeing scientists to focus on discovery. These smarter, faster experiments will lead to the next generation of drugs and clinical trials."

At institutions around the world, scientists are grappling with these issues to figure out how best to use AI to harness big data and accelerate discovery.

"At Johns Hopkins, we are probably one step ahead. Astronomy, fluid dynamics, ocean circulation models, you name it, Hopkins scientists have decades of experience and are incredibly competitive. Now, that expertise—combined with the strength of the School of Engineering and collaborations across medicine—is being turned toward cancer," says Dr. Szalay. "We are sitting on a treasure trove, and we want to move quickly so we can identify more causes of cancer, discover new treatments, and save lives."

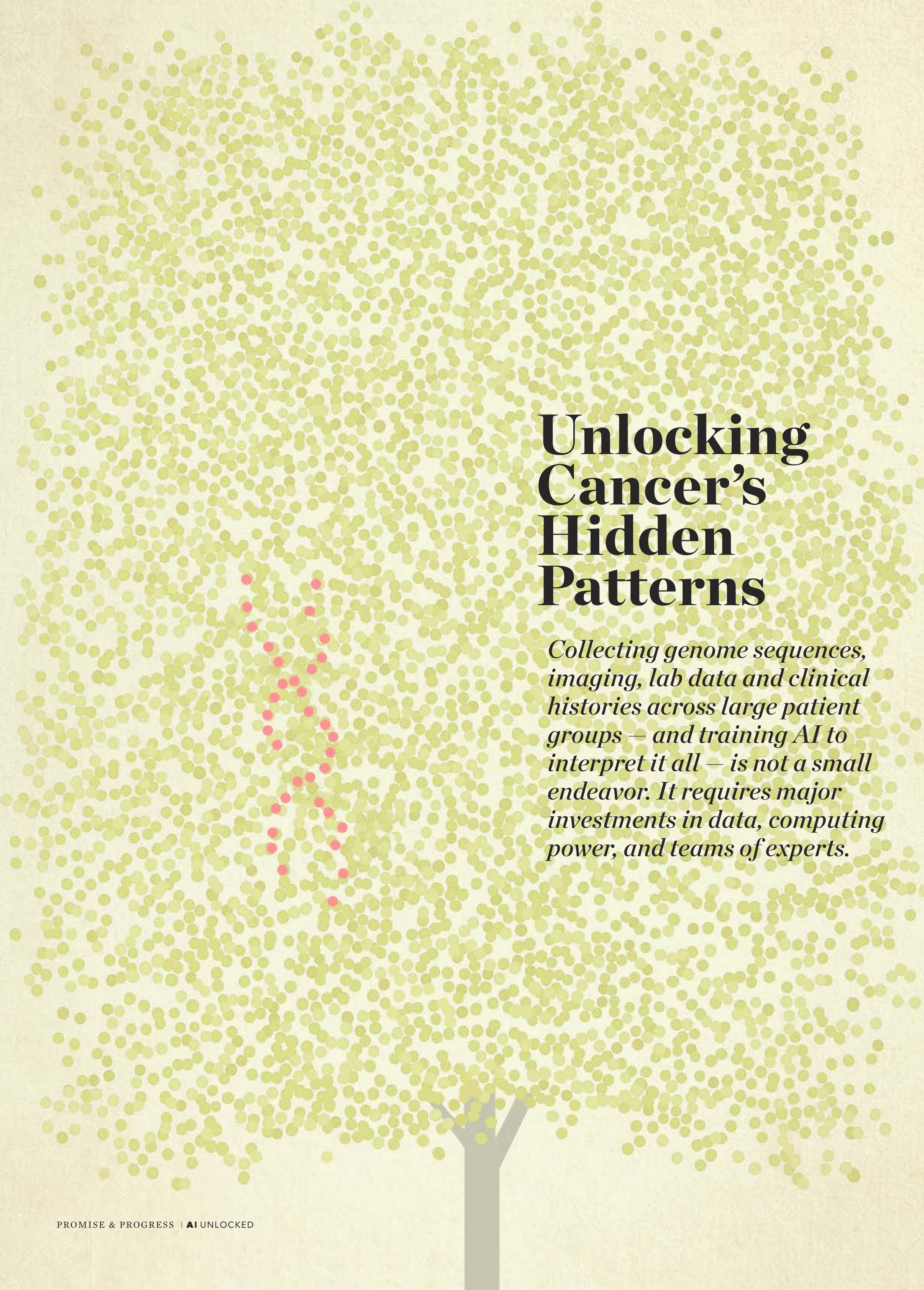


ILLUSTRATION: ©STEPHAN KOCH

Unlocking Cancer's Hidden Patterns

Collecting genome sequences, imaging, lab data and clinical histories across large patient groups — and training AI to interpret it all — is not a small endeavor. It requires major investments in data, computing power, and teams of experts.

To **Alexis Battle**, Ph.D., artificial intelligence is not the medicine of tomorrow, but a powerful tool already at work today, beginning to help doctors and researchers decode hidden clues about cancer and other diseases that would be impossible for any human to detect alone.

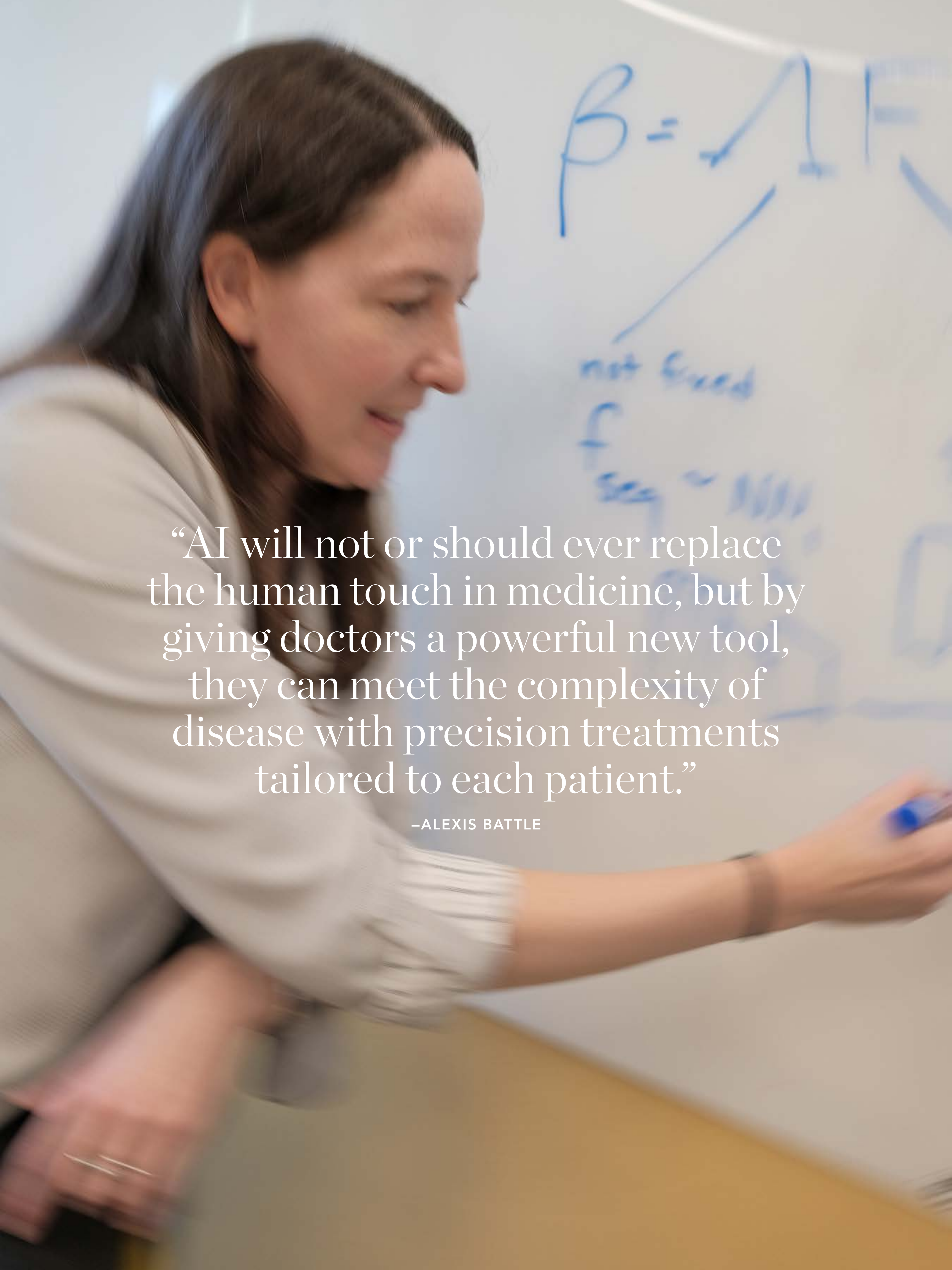
"Every patient's disease is a moving target," says Dr. Battle, professor of biomedical engineering and computer science, director of the Malone Center for Engineering in Healthcare, and director for research strategy and partnerships at the Data Science and AI Institute at the Whiting School of Engineering. "It changes over time — from diagnosis to treatment to remission or sometimes recurrence. Add in imaging, lab tests, genomics and clinical notes, each coming from different parts of the body over time, and it becomes clear that the sheer volume and complexity of this data makes it impossible for any single person to see all of the patterns and piece it all together. This is where AI can help."

AI, she explains, is not just recent AI tools in the press — AI is more broadly the performance by computers of tasks that are traditionally associated with human intelligence, and that includes everything from complex reasoning, use of human language, visual recognition tasks, artistic and creative activities, planning and learning from experience.

BRINGING EXPERTS TOGETHER

Dr. Battle is an expert in machine learning, a type of AI that teaches computer systems to automatically identify complex patterns from data. She has devoted her career to building and training AI models that can see through the convoluted sea of data to create order from chaos. With training in computer science and experience at Google, she turned her expertise toward human genetics and genomics to inform health, including cancer.

"I really wanted to be doing something with the technical knowledge that I had built in machine learning that I felt could contribute to human health," she says.



“AI will not or should ever replace the human touch in medicine, but by giving doctors a powerful new tool, they can meet the complexity of disease with precision treatments tailored to each patient.”

–ALEXIS BATTLE

Applying machine learning, her lab is focused on a better understanding of how genes interact with each other and how individuals' genetic differences influence health and disease. These insights are already informing the understanding of heart disease, rare childhood disorders, autism, and cancer.

What sets Johns Hopkins apart, she says, is the broad expertise and how people from seemingly different worlds — engineering, computer science, applied math, biology, public health and medicine — come together. Many Malone Center faculty straddle engineering and medicine, creating a shared desire to solve real problems in health. This collegial environment, Dr. Battle believes, is unique.

"I came from industry, but I've been at Johns Hopkins for more than a decade," she says, "It's a place where people from across so many disciplines so readily sit down together to work through problems. This collegiality is combined with a scientific environment of very high standards and rigor. We innovate as an institution."

FINE-TUNING AI FOR CANCER CARE

One recent project illustrates what's possible with this kind of interdisciplinary collaboration. Working with the faculty at the Malone Center and the Kimmel Cancer Center, Dr. Battle joined **Mathias Unberath**, Ph.D., to help fine-tune a large language model — a type of AI program that learns patterns of words, sentences, and meaning from massive amounts of text — using structured electronic health record data. The model was trained to follow patient trajectories, learning how a diagnosis at one point in time might predict future outcomes, including treatments, side effects, or complications.

This work, initiated through the Cancer AI Alliance (CAIA), preserved patient privacy through what is known as a federated system. Put simply, this means that Johns Hopkins data can inform cancer research without ever leaving the institution. The Kimmel Cancer Center and Whiting School of Engineering are founding members of CAIA, which is under the leadership of **Vasan Yegnasubramanian**, M.D., Ph.D., and Dr. Battle.

"It shows the potential of tailoring large AI models specifically for cancer patients," Dr. Battle explains. "This particular project, pulled together under an aggressive timeline, was a deeply collaborative effort, one that drew in faculty, students, research IT, and the Data Science and AI Institute's research software engineering team."

FROM RARE VARIANTS TO COMMON DISEASES

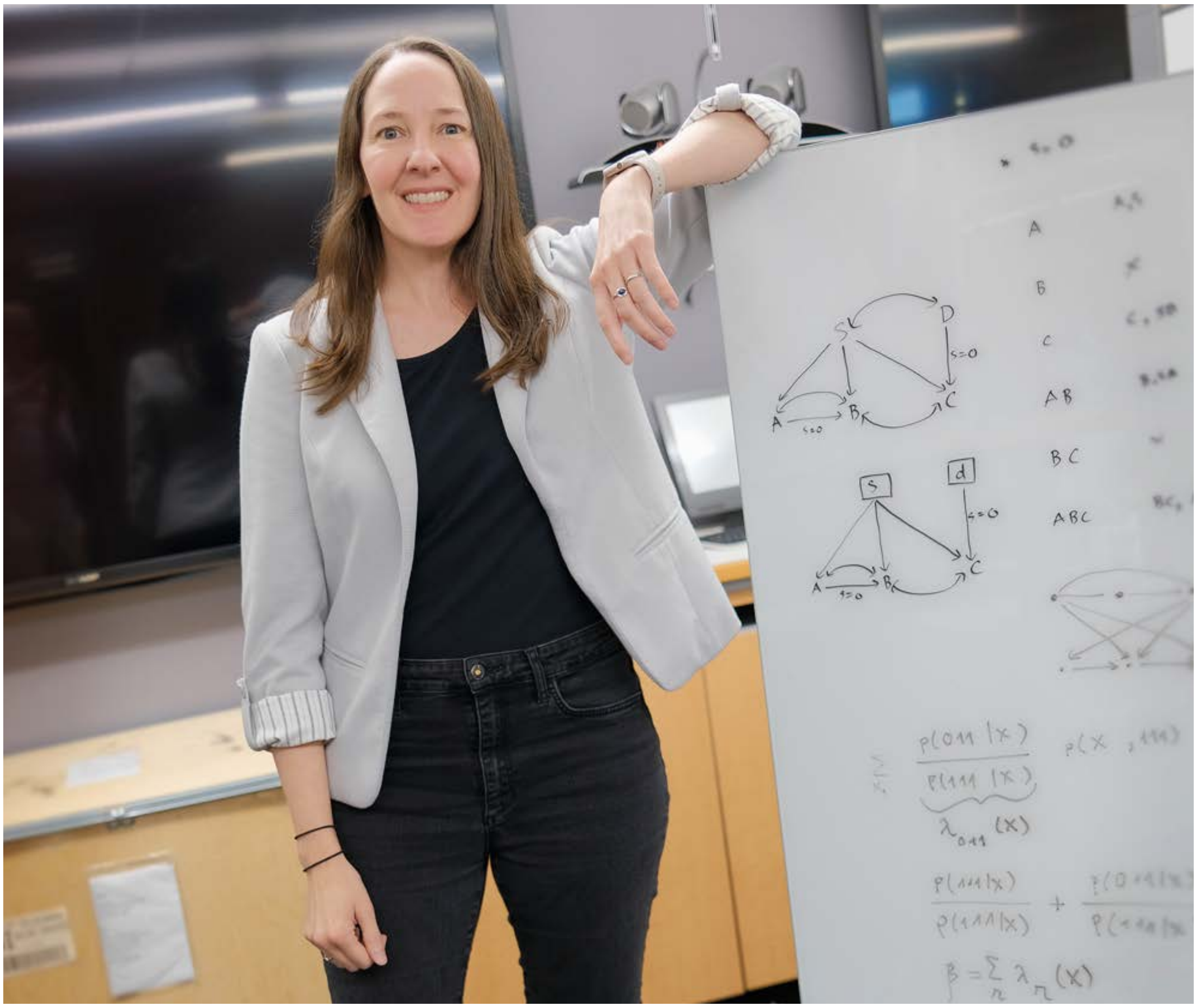
Much of Dr. Battle's research centers on variations in the human genome. While some genetic variants are common, many are rare — sometimes observed in a single individual. However, by using AI, these seemingly rare variants can be found and deciphered among large populations of people. Her lab builds machine learning and AI models to understand the effects of those unique changes.

Our DNA is spelled out in a four-letter code — A, T, C, and G, each representing a different chemical. A gene variant is a change in that code. Sometimes it's just one letter switched for another, like a typo in a word. Other times, a letter might be missing, an extra one added in or even a stretch of the code is repeated. This four-letter alphabet carries the instructions that cells need to build proteins and keep people's bodies working. The sequence makes every individual unique, but it also forecasts health differences and disease processes. For example, she explains, a rare change of a letter in the ATCG genetic code could flip a nearby gene on at the wrong time, making a person susceptible to a disease or even revealing a disease-protective mechanism.

"It is different from person to person, and we don't know most of the mechanisms," she says. "These genetic changes interact with different environments too. For example, a change could make one person more susceptible to cigarette smoke exposure, while making others more resistant to the exposure."

This type of research has immense impact on understanding and treating human diseases, including cancer, and some of these rare genetic mechanisms may point directly to therapeutics. However, these variant patterns and

"EVERY PATIENT'S DISEASE IS A MOVING TARGET. IT CHANGES OVER TIME – FROM DIAGNOSIS TO TREATMENT TO REMISSION OR SOMETIMES RECURRENCE. ADD IN IMAGING, LAB TESTS, GENOMICS AND CLINICAL NOTES, EACH COMING FROM DIFFERENT PARTS OF THE BODY OVER TIME, AND IT BECOMES CLEAR THAT THE SHEER VOLUME AND COMPLEXITY OF THIS DATA MAKES IT IMPOSSIBLE FOR ANY SINGLE PERSON TO SEE ALL OF THE PATTERNS AND PIECE IT ALL TOGETHER. THIS IS WHERE AI CAN HELP."



the potential for drugs to intercept the harm they might cause — or protection from disease they might confer — would be much more difficult to identify without the aid of artificial intelligence.

"Although these differences can help answer why some people exposed to risks stay healthy while others develop disease, they also shed light on why only some cancers respond to treatment and why others are resistant," says Dr. Battle. "Exploring this space so fully and quickly was a challenge 15 years ago, but now, we finally have the tools to make progress."

AN INVESTMENT IN PATIENTS

The scale of this work is enormous. Collecting genome sequences, imaging, lab data and clinical histories across large patient groups — and training AI to interpret it all — is not a small endeavor. It requires major investments in data, computing power, and teams of experts.

Dr. Battle is candid. She acknowledges that funding major new initiatives is a challenge, but she believes an investment now could be transformative with a payoff of stronger science and, most importantly, better care for patients.

THE RIGHT PLACE

For Dr. Battle, Johns Hopkins is the right place to lead this revolution. The breadth of expertise, the culture of collaboration, and bold institutional investments in data science and AI have created fertile ground.

"We're already using AI in some parts of cancer care detection and treatment," she says. "New efforts will allow us to move from slower, incremental steps to a new speed and energy. The potential is enormous."

> **"We're already using AI in some parts of cancer care detection and treatment. New efforts will allow us to move from slower, incremental steps to a new speed and energy. The potential is enormous."**

Her message is one of both realism and hope. She does not believe AI will or should ever replace the human touch in medicine, but by giving doctors a powerful new tool, they can meet the complexity of disease with precision treatments tailored to each patient.

PATIENT PRIVACY AND SAFEGUARDS

Securing the Future of AI in Cancer Medicine

Artificial intelligence is reshaping cancer research and treatment at an astonishing pace— so swiftly, in fact, that some experts compare it to the early days of the internet. At Johns Hopkins, leaders are determined that this progress will always be matched with equal care in protecting the sensitive patient and research data that fuel discoveries.

"CYBERSECURITY is a team sport," says **Janet Rathod**, vice president and chief information security officer at Johns Hopkins. With more than two decades of experience leading security efforts in government and industry, Ms. Rathod is guiding Johns Hopkins through a new era in which data is the engine of innovation but also has the potential to be the target of new threats.

As the Kimmel Cancer Center employs the tools of AI to advance cancer discovery and medicine, its experts are looking to Ms. Rathod and her team of technical experts for guidance.

INNOVATION MEETS SECURITY

Kimmel Cancer Center investigators are using AI to read pathology slides, map genomes, interpret imaging scans, and study blood tests, known as liquid biopsy, with unprecedented speed and accuracy. These tools hold the promise of earlier detection, more precise treatments, and faster development of new therapies.

"However, key to using AI to aid in these advances is the certainty that we have gained and will protect the trust our patients and families place in our institution when they share their most personal information," Ms. Rathod says.

Preserving that trust begins with rigorous safeguards. Johns Hopkins uses what is called a defense-in-depth strategy — multiple overlapping layers of protection so no single point of failure can put information at risk, Ms. Rathod explains. Technical controls, such as advanced firewalls, intrusion prevention systems, network detection tools, and log collection act like security cameras and motion sensors, quietly watching for anything unusual and alerting experts if something doesn't look right. Regarding AI specifically, Ms. Rathod's team conducts a thorough security assessment of AI vendors and products. Over the past few years, the cybersecurity team advanced their AI skills by learning how to build large language models. This enabled them to understand the technology from the ground up, so they can better recognize how to secure it.

GOVERNANCE AND ETHICS

The practice of medicine is already highly regulated, and has many guardrails in place that prioritize the safety of patients. Government regulations, such as HIPAA, provide strong safeguards for privacy. Building on this, Johns Hopkins has created new councils and committees to guide how AI is used.

The Data Trust Council and its subcouncils are setting standards for research data, privacy, security, and stewardship. A newly established IT Policy Committee oversees IT policies and guidelines for AI, while a privacy subcouncil, co-chaired by Ms. Rathod, works hand in hand with Johns Hopkins attorneys to protect our patients and their medical data. These subcouncils build in checks and balances, policies, and legal oversight to ensure AI at Johns Hopkins is developed and deployed responsibly, protecting patients and upholding the institution's ethical standards.

RATHOD

Johns Hopkins leadership recognizes that AI systems have the potential to bring about significant benefits when properly vetted and used within a framework that balances privacy, security, ethical, legal and social considerations with a focus on ensuring safe deployment.

"AI is another tool of science, and we are treating it with the same seriousness and responsibility as we make sure it is safely and securely deployed," Ms. Rathod says.

COLLABORATION WITHOUT COMPROMISE

Advancing cancer research and treatment requires collaboration. The Kimmel Cancer Center is a founding member of the Cancer AI Alliance, a partnership with other leading cancer centers. Instead of sending data back and forth, the alliance uses federated models, systems that let each institution keep its data secure while still contributing to collaborative research. This is an example of how AI allows scientists from different cancer centers to work together without sacrificing the security or privacy of their patient data.

For Rathod, the most reassuring measure of success is that innovation has not slowed.

"We have not compromised on speed or discovery," she says. "By building strong security from the ground up, we've created an environment where scientists can move quickly and safely."

BUILDING TRUST FOR TOMORROW

Patients and donors alike often ask how their information is being protected. For Ms. Rathod and team, the answer is clear: Security and privacy are not afterthoughts, they are built into the foundation of its AI efforts. That reassurance is vital in an age when headlines about hacked data or manipulated information can easily erode confidence.

"The science is moving fast, but so are we," Ms. Rathod says. "With strong governance and ethical guardrails, we are ensuring that AI lives up to its promise to bring faster cures, earlier detection, and more personalized care while also keeping patient trust at the center of everything we do."

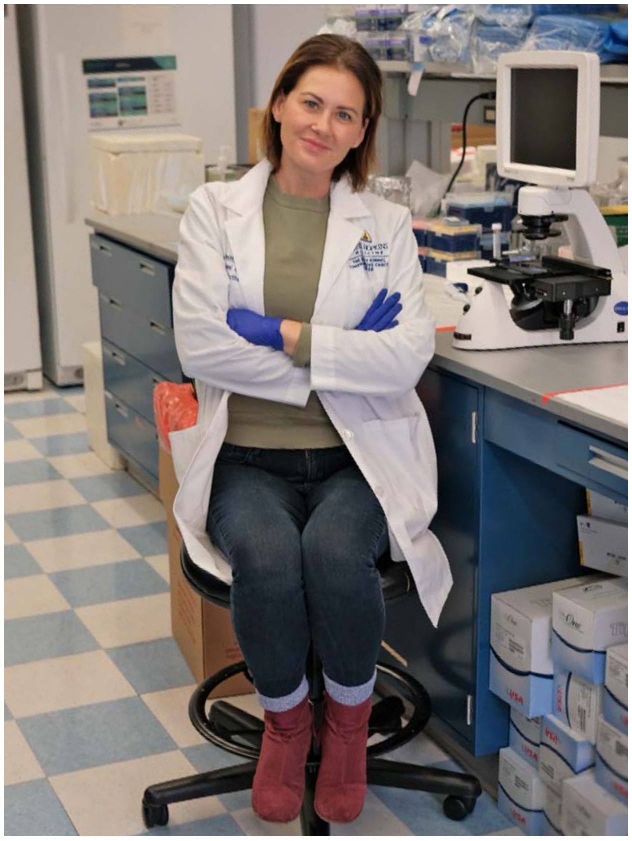
Web Exclusive

ILLUSTRATION: STEPHAN KOCH

AI in Action

MANAscore Tool Moves Closer to Clinic

“OUR MODEL ALLOWS US TO SKIP A TIME-CONSUMING AND EXPENSIVE PROCESS TO IDENTIFY THE CELLS TARGETED BY IMMUNOTHERAPY. IT WILL HELP US LEARN WHAT DISTINGUISHES PATIENTS WHO WILL RESPOND FROM THOSE WHO WILL NOT.”



KELLIE SMITH

ONE OF THE greatest challenges in cancer immunotherapy is finding the rare immune cells, called tumor reactive T cells, whose job it is to recognize and eliminate tumor cells. The immune cells collected from a tumor are specific for other targets the patient may have encountered in the past—viruses like flu, COVID or other pathogens unrelated to the tumor—with very few that are tumor-specific. Yet those rare cells often hold the key to whether immunotherapy will work.

"To identify predictors of response to immunotherapy, we need to be able to study the immune cells that recognize tumors," says Bloomberg~Kimmel Institute for Cancer Immunotherapy researcher **Kellie Smith,** Ph.D., so she and her team developed a powerful new tool, called MANAscore, to identify these critical but elusive tumor reactive immune cells.

The idea grew out of years of time-consuming and costly research that yielded only small glimpses of tumor-specific immune cells. The findings, however limited, were revealed through sophisticated research strategies, but Dr. Smith was determined to find a better approach.

"It was very expensive. It took a really long time, and it used a lot of patient samples, and we were still only able to find these cells in three patients," says Dr. Smith.

Using the tools of AI, Dr. Smith and team were able to sort through immense data sets and condense terabytes of complex data into a model built on just three well-known genes—CD39, CXCL13, and the IL-7 receptor.

MANAscore's genius is in its simplicity. The three-gene panel works better than other models that require 200 genes or more, making MANAscore a practical way to routinely test for tumor reactive immune cells, including on archival tissue samples already collected from patients. Early study results show that the frequency of these three-gene–positive cells correlate strongly with how well patients respond to immune checkpoint inhibitors.

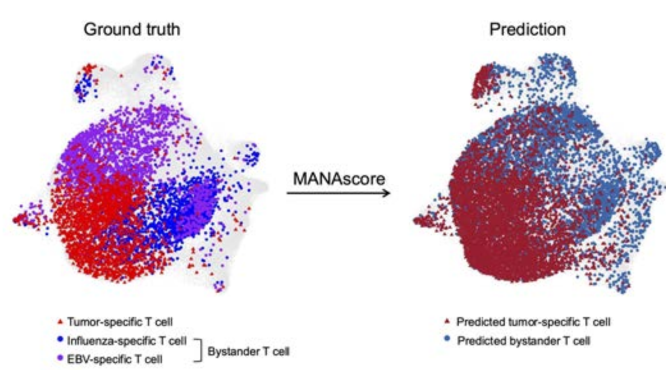
These three key genes help reveal how T cells respond to cancer, marking cells that recognize the tumor but are worn down, yet still targetable by therapy, those that draw in other immune cells to build strong local hubs of immune activity, and those that help T cells survive and remember the cancer for lasting protection. Together, they show which T cells are most engaged and, even in tiny numbers, capable of initiating an immune response.

The team is now validating MANAscore by looking back at pretreatment biopsies from patients whose outcomes are already known and then moving forward to test the model prospectively as new patients begin treatment. They are also using the tool to explore how tumor-reactive T cells interact with their cellular "neighbors," including regulatory T cells that may suppress the immune response. Insights from these studies could point to new treatment strategies.

ZHANG

Dr. Smith says this is where the power of AI shines, making the overwhelmingly complex understandable and clinically useful in record time.

"Our model allows us to skip a time-consuming and expensive process to identify the cells targeted by immunotherapy," she explains. "It will help us learn what distinguishes patients who will respond from those who will not."



MANAscore is still a research tool, but Dr. Smith believes it may be ready for clinical use to guide the treatment of patients within the next two years.

She says, "by applying MANAscore to a single biopsy slide, we may soon be able to quickly predict which patients are most likely to benefit from immunotherapy."

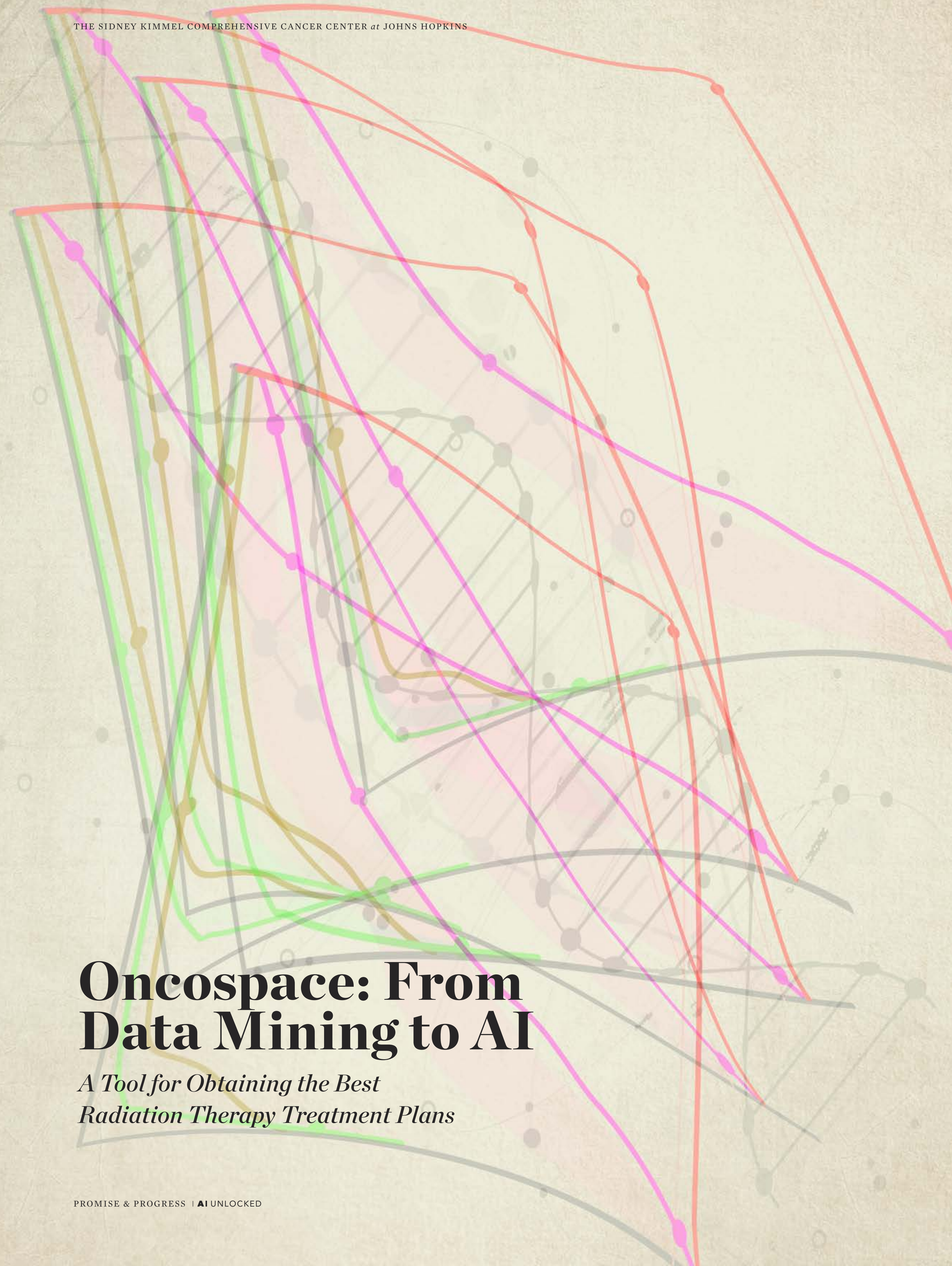
For patients like REBB, who received immunotherapy for her pancreatic cancer, and who lost her daughter Valerie to breast cancer, progress can't come soon enough.

"I am passionate about research and the idea that we can move so much faster using AI is extremely exciting," says REBB, who describes feeling so weak before beginning treatment that she needed a wheelchair for any prolonged distance. She believes her life was saved by Kimmel Cancer Center research and an immunotherapy clinical trial. "Almost immediately I started feeling better. My immune system was destroying the cancer. By April, I was running through the airport, and by December 2022, I was cancer free. Today, I am back to my normal, busy life, doing things I would have never been able to do if not for the immunotherapy I received. I want this for all cancer patients."

Web Exclusive

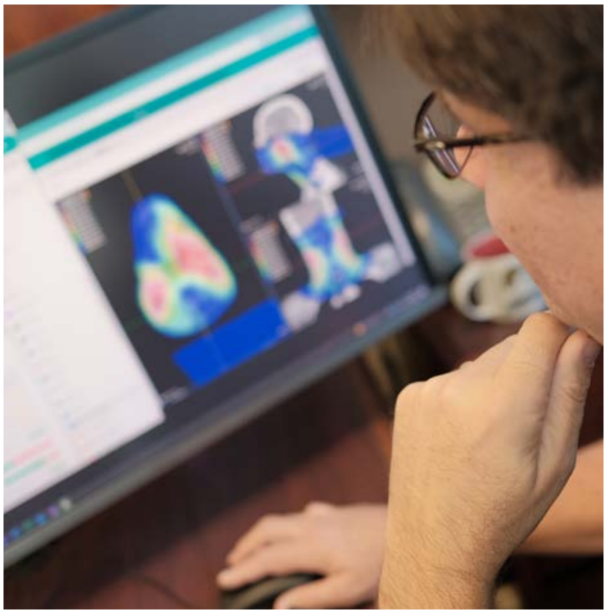
"By applying MANAscore to a single biopsy slide, we may soon be able to quickly predict which patients are most likely to benefit from immunotherapy."

–KELLIE SMITH



Oncospace: From Data Mining to AI

A Tool for Obtaining the Best Radiation Therapy Treatment Plans



ADVANCES IN CANCER medicine don't always come in the form of a new drug or therapy. After years of seeing valuable information collected in cancer care left untapped, radiation oncology physicist, **Todd McNutt**, Ph.D., envisioned a data-mining system that could learn from every patient's prior experience and improve treatment for the next.

The vision began more than a decade ago, when Dr. McNutt partnered with head and neck cancer radiation oncologist **Harry Quon**, M.D., and computer scientists **Russell Taylor**, Ph.D., and **Misha Kazhdan**, Ph.D. Together, they built a system that could mine data from thousands of patients treated with radiation therapy.

By connecting diagnoses, treatments, side effects and outcomes, the tool, called Oncospace, helped guide therapy, evaluating the treatments that worked best for a particular cancer and learning from those that resulted in less-than-favorable outcomes to generate an optimal treatment plan.

Oncospace simultaneously took into account and connected variables including age, underlying health conditions and other treatments patients were receiving to determine how these factors influenced toxicities and response to treatment. As a result, Oncospace sharpened treatment plans, lowered toxicities, and improved quality of life.

Every patient who receives treatment adds to the data, so it is ever improving as new information — and more types of data, such as structured physician notes and imaging — are included.

It was a tool that no other cancer center in the world had, so Dr. McNutt took steps to make it available beyond Johns Hopkins.

Better, Smarter, Faster

In 2019, with support from grants, donors, and Johns Hopkins Technology Ventures, Dr. McNutt, programmer **Michael Bowers**, and colleagues, including **Pranav Laksminarayanan** and **Julie Shade,** and a few outside partners, founded Oncospace, Inc. The current version is boosted by AI to even further improve the quality of radiation therapy treatment plans.

"We built a tool that can predict — for each patient — the best achievable treatment plan before the planning process even begins," says Dr. McNutt. "We think it will raise the level of quality for everyone, so a small practice can use the tool and obtain the same standards and level of quality as an academic research institution like the Kimmel Cancer Center, and that benefits patients everywhere."

A Smarter Way to Plan Care

Drawing on a knowledge base built from the histories of over 5,000 patients and growing, Oncospace gives radiation oncologists and dosimetrists an AI "assistant" — a powerful starting point optimized to balance tumor control with protecting nearby healthy tissue. As Dr. McNutt and colleagues refine their plans, Oncospace is a guide always pointing toward the most optimal plan and also indicating when the plan quality is less than adequate.

"Unlike other commercial systems, which require hospitals to build their own models from scratch, a time-consuming process that often draws on only small patient cohorts, Oncospace offers an advanced, validated model from day one," Dr. McNutt says.

It was designed to raise the level of care anywhere it is used, providing consistency, built-in safety checks, and the ability to compare results.

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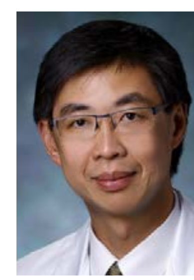


QUON

BOWERS

Global Reach

Oncospace has gone through rigorous studies and has received Food and Drug Administration approval for multiple cancer types, including prostate, gynecological, head and neck, liver, pancreatic, lung and esophageal cancers.

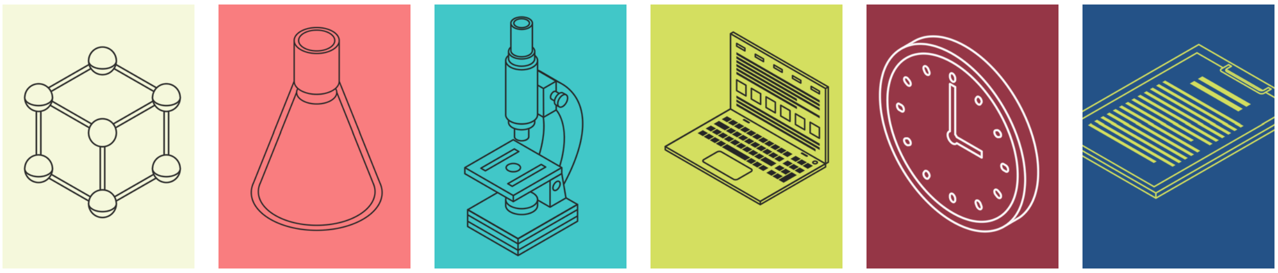
In April 2025, the company was acquired by Sun Nuclear (Mirion Medical), a global leader in radiation oncology quality assurance. With Sun Nuclear's worldwide reach, Oncospace, which was renamed Plan AI, has already expanded from two clinical sites — Johns Hopkins and Montefiore Hospital — to six to eight centers internationally, extending the benefits of the Kimmel Cancer Center-born innovation to patients around the globe.

"WE BUILT A TOOL THAT CAN PREDICT – FOR EACH PATIENT – THE BEST ACHIEVABLE TREATMENT PLAN BEFORE THE PLANNING PROCESS EVEN BEGINS. WE THINK IT WILL RAISE THE LEVEL OF QUALITY FOR EVERYONE."

“Oncospace has sharpened treatment plans, lowered toxicities, and improved quality of life.”

–TODD MCNUTT

News In Brief



Johns Hopkins Joins Cancer AI Alliance

In Brief:

SNAPSHOT: Johns Hopkins joined the new national Cancer AI Alliance (CAIA), aimed at harnessing artificial intelligence for precision cancer care. In collaboration with other top cancer centers, the initiative will develop AI-powered tools to improve individualized cancer detection, interception, and treatment.

HOW IT WILL HELP PATIENTS: By combining AI with vast, diverse data sets — including electronic health records, pathology and medical images, and genetic data — CAIA will help uncover new insights into tumor biology, treatment resistance, and therapeutic targets. This approach aims to create more accurate, timely, and personalized cancer treatment strategies, while ensuring data privacy and security through federated AI learning.

KEY TAKEAWAY: With CAIA's strength in engineering and cancer research, participation in the alliance positions Johns Hopkins at the forefront of a secure, collaborative, and data-driven AI revolution in cancer care, designed to benefit diverse patient populations through smarter, faster and more equitable innovation.

New Method Advances Reliability of AI with Applications in Medical Diagnostics

In Brief:

SNAPSHOT: A new AI method called MIGHT could significantly improve the accuracy and reliability of cancer detection blood tests.

HOW IT WILL HELP PATIENTS: MIGHT and a companion algorithm, called CoMight, can better distinguish cancer signals from those caused by other inflammatory or vascular diseases, reducing false positives and unnecessary procedures. It allows for more precise early detection of cancers, such as breast and pancreatic, by analyzing DNA fragments circulating in the blood. The method's flexibility also opens doors to future diagnostic tools for noncancer diseases, and contributes to safer, more personalized care.

KEY TAKEAWAY: By incorporating uncertainty measurement and training on real-world data, including signals from noncancer illnesses, MIGHT enhances trust and reliability in AI-based diagnostics, setting a new standard for how AI can be responsibly integrated into medical decision-making.

Fast-Fail AI Blood Test Could Steer Patients with Pancreatic Cancer Away from Ineffective Therapies

In Brief:

SNAPSHOT: ARTEMIS-DELFI is a new artificial intelligence-based blood test that can quickly and accurately determine if pancreatic cancer treatments are working.

HOW IT WILL HELP PATIENTS: The test allows our doctors to assess treatment response as early as four weeks after therapy begins and, if needed, switch to more effective treatments sooner.

KEY TAKEAWAY: ARTEMIS-DELFI uses artificial intelligence to analyze DNA fragments in the blood, offering a simpler, faster, and more accurate way to monitor treatment response, paving the way for more individualized cancer care.

AI-Based Liquid Biopsy Shows Promise for Detecting Brain Cancer

In Brief:

SNAPSHOT: Researchers developed a next-generation AI-based liquid biopsy that detects brain cancer by analyzing DNA fragments and immune cell signals in blood samples, successfully identifying tumors in about 75% of cases, far surpassing previous methods.

HOW IT WILL HELP PATIENTS: This innovative test enables earlier and more accurate detection of brain cancer, which is notoriously difficult to diagnose. By recognizing both cancer-related DNA and immune system changes, without relying on brain tissue, it could allow physicians to identify tumors sooner, expand treatment options, and potentially improve survival. Simulations show it could

lead to the detection of nearly 1,700 additional cases annually in patients with symptoms like headaches who would otherwise go undiagnosed.
KEY TAKEAWAY: This AI-powered liquid biopsy leverages the unique biological features of brain cancer and the immune system's response to it, offering a noninvasive, more sensitive, and earlier detection method that may transform how brain tumors are diagnosed and managed.

Computer Model Helps ID Cancer-Fighting Immune Cells Key to Immunotherapy:

In Brief:

SNAPSHOT: MANAscore, a simple three-gene computer model, helps identify tumor-targeting immune cells in patients with lung cancer who are receiving immune checkpoint inhibitor therapy.

HOW IT WILL HELP PATIENTS: By pinpointing which T cells are actively responding to immunotherapy, the model helps scientists and clinicians better understand why some patients benefit from checkpoint inhibitors while others do not. This could lead to more accurate biomarkers, improved therapies for nonresponders and, eventually, a clinical test to guide treatment decisions more effectively.
KEY TAKEAWAY: MANAscore uses AI and just three genes to identify immune cells activated by cancer therapy, making it a faster, more affordable, and more practical tool than previous models and paving the way for personalized immunotherapy across multiple cancer types.

AI Liquid Biopsies Using Cell-Free DNA, Protein Biomarkers, Could Aid Early Detection of Ovarian Cancer

In Brief:

SNAPSHOT: DELFI-Pro, an artificial intelligence-powered blood test that combines DNA fragment analysis with two protein biomarkers (CA-125 and HE4), may improve early detection of ovarian cancer, even in its earliest stages.
HOW IT WILL HELP PATIENTS: This AI-enhanced test detected significantly more early-stage ovarian cancers than current biomarker tests, with minimal false positives. It also successfully distinguished between benign and cancerous ovarian growths, potentially sparing women unnecessary surgeries prompted by inconclusive imaging results. The approach could lead to more accurate, noninvasive, and accessible ovarian cancer screening.
KEY TAKEAWAY: Through integrating AI with cell-free DNA "fragmentomics" and established protein markers, DELFI-Pro demonstrates a powerful and precise method for ovarian cancer detection, offering new hope for earlier diagnosis and improved outcomes in a disease that is often caught too late.

Machine Learning Can Help Predict Patient Response to Cancer Immunotherapy

In Brief:

SNAPSHOT: A deep-learning algorithm called DeepTCR predicted which patients with melanoma would respond to immunotherapy. The AI model identified responders and nonresponders and also revealed underlying biological differences in their immune responses.
HOW IT WILL HELP PATIENTS: DeepTCR helps uncover the immune system's readiness to fight cancer by analyzing T cell receptor (TCR) patterns from tumor biopsies. This insight could guide more precise and individualized immunotherapy decisions, potentially avoiding ineffective treatments for nonresponders and enabling better-targeted therapies. The findings also point to virus-specific T cells — not tumor-specific ones — as key predictors of success, opening new doors for future research and clinical strategies.
KEY TAKEAWAY: DeepTCR brings "explainable AI" into cancer immunotherapy, helping researchers understand and predict treatment responses by decoding the immune system's T cell behavior, an advancement that could transform how immunotherapies are tailored to individual patients.

New Machine-Learning Method May Aid Personalized Cancer Therapy

In Brief:

SNAPSHOT: BigMHC, a deep-learning tool, accurately predicts which cancer-related protein fragments, called neoantigens, can trigger an immune system response. This breakthrough could accelerate the development of individualized immunotherapies and cancer vaccines.
HOW IT WILL HELP PATIENTS: BigMHC dramatically improves scientists' ability to identify which tumor mutations are most likely to provoke a T-cell attack on cancer cells. This has the potential to make individualized immunotherapy more efficient, accurate, and accessible, allowing clinicians to better match treatments to each patient's unique tumor profile, while also aiding in the design of vaccines and therapies tailored to specific immune responses.
KEY TAKEAWAY: BigMHC trains on vast data sets, offering a powerful, AI-driven way to decode tumor "foreignness" and guide precision immunotherapy, as well as marking a significant leap toward making individualized cancer treatments faster, cheaper, and more widely available.

Novel Machine Learning Blood Test Detects Cancers with Genome-Wide Mutations in Single Molecules of Cell-Free DNA

In Brief:

SNAPSHOT: A blood test called GEMINI uses whole-genome sequencing and machine learning to detect early-stage lung and other cancers by analyzing single molecules of tumor-derived DNA in the blood.

HOW IT WILL HELP PATIENTS: GEMINI identified over 90% of lung cancers, including stage 1 and 2 disease, and showed promise in detecting other cancers, such as liver cancer and lymphoma. When combined with an existing test, called DELFI, the detection rate improved even further. It also identified abnormalities in patients years before clinical diagnosis and tracked response to therapy, offering a powerful tool for early detection, diagnosis, and treatment monitoring, especially in high-risk individuals.

KEY TAKEAWAY: GEMINI represents a scalable, cost-efficient approach to noninvasive cancer detection, combining genome-wide mutation analysis with AI to catch cancer early, potentially years before symptoms arise, to transform cancer screening and personalized care.

SpaceMarkers Novel AI Method Identifies Locations, Interactions Among Genes in and Around Tumors

In Brief:

SNAPSHOT: SpaceMarkers is a new computational tool that analyzes spatial transcriptomics data to uncover how cell-to-cell interactions in the tumor microenvironment influence gene expression and drive cancer progression.

HOW IT WILL HELP PATIENTS: SpaceMarkers pinpoints genes activated by interactions between different cell types and can help researchers understand why some cancers progress more rapidly or why certain treatments work for some patients but not others. This insight could guide the development of more targeted therapies and improve the precision of cancer diagnosis and treatment selection, especially for solid tumors like breast and liver cancers.

KEY TAKEAWAY: SpaceMarkers leverages spatial transcriptomics and AI to map molecular changes triggered by cell interactions, offering a powerful new lens to decode the tumor microenvironment and uncover biological mechanisms that influence cancer behavior and treatment response.

Junk DNA No More: Johns Hopkins Investigators Develop Method of Identifying Cancers from Repeat Elements of Genetic Code

In Brief:

SNAPSHOT: ARTEMIS, a machine learning–powered blood test, analyzes repetitive “dark matter” DNA elements to detect cancer, predict its origin, and monitor treatment response, offering a powerful new way to explore previously overlooked regions of the genome.

HOW IT WILL HELP PATIENTS: ARTEMIS enables noninvasive cancer detection by analyzing repeat DNA elements in cell-free DNA, achieving high accuracy across multiple cancer types. When combined with the DELFI fragmentation method, it improves early detection and can distinguish between tumor types and locations. It also shows potential for monitoring treatment response and detecting recurrence, making it a promising tool for both diagnosis and ongoing cancer management.

KEY TAKEAWAY: ARTEMIS uncovers the dark matter of the genome to reveal a new class of cancer biomarkers, demonstrating that repeat DNA sequences — once considered junk — hold vital clues for detecting, classifying, and tracking cancer through a simple blood test.

Small and Overlooked: Amount of Repetitive DNA in Blood Hints at Cancer Early

In Brief:

SNAPSHOT: A-PLUS, a machine learning–based blood test, analyzes repetitive DNA elements — specifically Alu elements, a type of repetitive DNA — to detect cancer accurately and early, offering a new layer of insight beyond traditional genomic markers.

HOW IT WILL HELP PATIENTS: A-PLUS adds Alu DNA profiles to an existing liquid biopsy framework, and improves early detection, identifying 41% of cancer cases missed by current biomarkers, while maintaining 98.9% specificity to avoid false positives. It is cost-effective, reproducible across large samples, and works regardless of cancer type or location, making it a strong candidate for noninvasive, wide-scale cancer screening in asymptomatic individuals.

KEY TAKEAWAY: A-PLUS leverages the overlooked power of repetitive DNA to enhance early cancer detection, proving that even “junk DNA,” like Alu elements, can serve as meaningful, clinically relevant biomarkers when analyzed through AI.

AI Helps Predict Lung Cancer Risk

In Brief:

SNAPSHOT: DeepLR is a deep-learning algorithm that can predict an individual's lung cancer risk more accurately than current clinical guidelines — up to three years in advance — using routine CT scan reports and image features.

HOW IT WILL HELP PATIENTS: DeepLR can help doctors individualize lung cancer screening schedules by identifying which patients are at highest risk and who can safely wait longer between scans. This could reduce unnecessary imaging, radiation exposure, and overdiagnosis, while ensuring earlier treatment for those who truly need it, potentially improving outcomes and lowering health care costs.

KEY TAKEAWAY: DeepLR mimics expert tumor boards by integrating CT imaging patterns over time, providing a powerful and scalable AI tool to guide early lung cancer detection and optimize screening strategies in high-risk patients.

Novel AI Blood Testing Technology Can ID Lung Cancers with High Accuracy

In Brief:

SNAPSHOT: DELFI, an artificial intelligence–based blood test that analyzes DNA fragmentation patterns, detected lung cancer with over 90% accuracy, including in early-stage disease, using a simple, noninvasive liquid biopsy.

HOW IT WILL HELP PATIENTS: DELFI provides a cost-effective and scalable tool to enhance lung cancer screening, particularly for high-risk individuals who avoid CT scans due to cost, radiation, or fear of false positives. It accurately distinguishes between cancerous and noncancerous cases and identifies early-stage cancers, potentially improving survival by enabling timely intervention. It also reduces unnecessary imaging and can be integrated with clinical risk factors and protein biomarkers for even greater precision.

KEY TAKEAWAY: DELFI transforms early lung cancer detection by decoding cell-free DNA "fragmentomes" with AI, offering a promising new avenue for widespread, noninvasive screening that could save lives through earlier diagnosis and treatment.

Artificial Intelligence Blood Test Provides a Reliable Way to Identify Lung Cancer:

In Brief:

SNAPSHOT: Researchers developed and validated a noninvasive blood test using artificial intelligence to detect lung cancer based on DNA fragment patterns. The test, when used to guide follow-up CT scans, could significantly improve early detection in high-risk individuals.

HOW IT WILL HELP PATIENTS: The test could be done easily in a doctor's office, and it has a 99.8% negative predictive value, meaning it can reliably rule out cancer for most patients. If broadly adopted, it could increase screening participation, catch cancers earlier, and potentially prevent up to 14,000 deaths over five years, making lung cancer screening more accessible, scalable, and patient-friendly.

KEY TAKEAWAY: Using AI, the test analyzed disorganized DNA fragments in the blood to offer a low-cost, high-accuracy alternative to conventional screening methods, boosting early detection while reducing the burden of CT scans, especially in underserved populations.

Novel AI Blood Test Detects Liver Cancer

In Brief:

SNAPSHOT: The AI-powered DELFI blood test was extended to liver cancer, and successfully detected more than 80% of these cancers, including early-stage disease, across diverse high-risk populations in the U.S., Europe, and Hong Kong.

HOW IT WILL HELP PATIENTS: Liver cancer screening is currently underutilized and often ineffective. DELFI offers a noninvasive, highly accurate, and accessible screening tool that could dramatically improve early detection for the 400 million people globally at risk for hepatocellular carcinoma. In clinical testing, it detected early-stage liver cancers with 88% sensitivity and 98% specificity, outperforming current blood-based tests and nearly doubling the number of cases detected in high-risk groups.

KEY TAKEAWAY: DELFI's ability to analyze chaotic DNA fragmentation patterns in blood offers a groundbreaking approach to liver cancer screening, showing strong performance across stages and populations and providing a cost-effective method to expand early detection and save lives globally.

Computational Tool Developed to Predict Immunotherapy Outcomes for Patients with Metastatic Breast Cancer

In Brief:

SNAPSHOT: Advanced computational modeling and artificial intelligence were used to simulate clinical trials and identify biomarkers that can predict which patients with metastatic triple-negative breast cancer are most likely to respond to immunotherapy, potentially reducing overtreatment and improving outcomes.

HOW IT WILL HELP PATIENTS: This method may allow clinicians to avoid invasive biopsies and instead use blood-based or imaging-derived biomarkers to guide treatment decisions. By identifying on-treatment biomarkers — particularly changes in tumor size within two weeks — the model could help physicians better individualize care, minimizing toxic side effects for nonresponders while ensuring effective treatment for those likely to benefit.

KEY TAKEAWAY: Virtual clinical trials and AI-powered modeling may offer a new, noninvasive path to precision immunotherapy, enabling early, accurate identification of responders among patients with metastatic triple-negative breast cancer and providing a framework for improving patient selection across other cancer types.

Johns Hopkins Investigators Win Life Sciences Award for AstroPath Cancer Mapping Technology

In Brief:

SNAPSHOT: Astrophysicist **Alexander Szalay,** Ph.D., and pathologist **Janis Taube**, M.D., M.Sc., received the Life Sciences 2021 award at the Falling Walls Science Summit for their development of AstroPath, a groundbreaking platform that uses astronomical data-mapping principles to guide precision immunotherapy through tumor imaging.

HOW IT WILL HELP PATIENTS: AstroPath maps microscopic tumor sections to identify spatial patterns of biomarkers — molecules that indicate how a patient's cancer is likely to behave or respond to treatment. This powerful imaging and data integration tool enables more accurate patient selection for immunotherapy, potentially improving outcomes and minimizing ineffective treatment.

KEY TAKEAWAY: AstroPath merges astronomy and cancer science to bring 3D mapping techniques from cosmic exploration into the tumor microenvironment, offering a revolutionary approach to understanding and treating cancer through precision-guided therapy.

Astronomy Meets Pathology to Identify Predictive Biomarkers for Cancer Immunotherapy

In Brief:

SNAPSHOT: **AstroPath**, a novel AI-powered imaging platform, uses sky-mapping algorithms from astronomy to analyze cancer biopsies. The platform accurately predicts which patients with melanoma are likely to respond to anti-PD-1 immunotherapy based on detailed spatial mapping of multiple immune and tumor markers.

HOW IT WILL HELP PATIENTS: AstroPath allows researchers and clinicians to analyze up to 12 biomarkers simultaneously in a single biopsy, producing a spatial map of the tumor microenvironment at single-cell resolution. This enables highly precise identification of patients most likely to benefit from immunotherapy, avoiding unnecessary toxicity for nonresponders. The approach may also apply to other cancer types, such as lung cancer, and helps usher in next-generation companion diagnostics.

KEY TAKEAWAY: AstroPath combines immunofluorescent imaging with astronomical mapping techniques to transform diagnostic pathology from a one-marker-at-a-time approach to a multiparameter, data-rich platform, bringing powerful precision to cancer immunotherapy and laying the foundation for individualized treatment strategies.

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