Future Headlines – AI Embeddings Town Halls 2026

****THE GLOBAL SCIENCE HERALD****
****Friday, April 20, 2029****

Thousands of Hidden Drug Targets Discovered, Triggering Global Dash for New Cures

For decades, the dominant strategy in drug discovery has been to identify disease-causing genes and design drugs to target it, which is a paradigm known as precision medicine. While this approach has delivered transformative therapies for some cancers, many types have remained stubbornly resistant. One reason is that real drugs rarely act on just one gene. For example, small molecules typically influence many proteins and pathways simultaneously, producing complex therapeutic and off-target effects known as polypharmacology. By applying AI to generate millions of embeddings from massive, diverse public datasets, scientists have now uncovered a new layer of therapeutic vulnerabilities that exists beyond individual genes. These embeddings capture higher-order biological patterns (e.g., gene networks, cell states, and phenotypes) that naturally incorporate the multi-target behavior of real drugs. Strikingly, the approach rediscovers known therapeutic targets in diseases with established treatments, suggesting that countless additional opportunities remain hidden in the data. Researchers are now racing to explore this newly revealed landscape, where AI can surface the needles in the biological haystacks and translational scientists can turn those discoveries into the next generation of cures.

Compelling Research Question 1:

Can we map the true causal mechanisms of existing therapeutics in disease-matched preclinical models? Most drugs work through complex, multi-target interactions across proteins, pathways, and cell states. To unlock the full potential of embedding-based discovery, we must determine whether we can reconstruct how drugs actually perturb cells and organoids in vivo, identifying the therapeutic's causal biological layers that produce therapeutic effects rather than relying on simplified single-gene models.

Compelling Research Question 2:

Can we identify the true loci of causality for disease in contrast to a healthy system in disease-matched preclinical models? Diseases emerge from interacting genetic, molecular, and cell processes rather than isolated gene defects. A key challenge is

determining whether embedding-based approaches can reveal the correct intervention points within this network identifying where therapeutic perturbation would most effectively reverse disease phenotypes. We also need to understand what the target state is by contrasting the disease model with a healthy system.

Compelling Research Question 3:

What data and modeling frameworks are required to systematically map therapeutic embeddings across biological scales? To realize this vision, we must determine which experimental measurements and computational models are needed to construct embeddings that capture interactions spanning genes, pathways, cell states, and tissues and how to link these embeddings to real-world therapeutic outcomes.

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****Friday, April 20, 2029****

Cancer Care Finally Sees the Whole Patient: AI Breakthrough Unlocks the Hidden Power of Interdisciplinary Narrative Notes

Finally, in 2029, we have reached oncology care 3.0, where the person with cancer is seen holistically. For decades, they were seen as a certain type of cancer and a person with specific comorbidities, but now the whole person, including functional status, mental, social and financial health, social determinants of health and quality of life are being considered with the integration of multimodal data, including labs, vital signs, pathology, and imaging with the rich clinical context found in narrative notes.

This breakthrough was driven by AI that finally learned to 'read' the expertise of the entire team and capture valuable information traditionally lost in narrative notes from interdisciplinary team members, including nurses, social workers, physical therapists, occupational therapists, respiratory therapists, case managers, chaplaincy, and more. For example, it will weigh a note from a physical therapist after a 1-hour long session heavier than a brief note stating "unsteady gait" from a non-specialist. These insights provided by the rich narrative data from interdisciplinary teams help the care team to better identify blind spots in the patient's care, as well as proactively note subtle indications of declining or a decrease in quality of life.

Patients are no longer be forced to act as the primary messenger or 'play telephone' between care teams. This AI provides a complete and portable narrative that follows them throughout their journey, no matter what health system they are in, and is accessible to every member of the care team. By matching this holistic narrative to live research databases, we have collapsed the evidence-to-practice gap from 17 years to near real-time, ensuring that today's bedside care is always powered by tomorrow's discoveries.

Compelling Research Question 1:

How do we help the AI accurately "read" the interdisciplinary team expertise? (e.g., inpatient nurse is with the patient 12 hours in a day and should have higher "observation weight" than a provider who saw the patient for 5 mins during rounds or when a speech pathologist performs a formal swallow study, that should take precedent over a nurse's or doctor's note saying "tolerating liquids")

Compelling Research Question 2:

How do we develop semantic dictionary or map to bridge the gap between diverse clinical observations and language (e.g., a nurse writes "wobbly" and a PT writes "unsteady" and the doctor notes says "patient reported feeling dizzy")?

Compelling Research Question 3:

What do we need to do to allow the patient's narrative to follow them between different health systems and EHRs while maintaining data privacy and institutional security? Or do we look outside those systems and have it live with the patient themselves?

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Continuing with my previous submission about the power behind interdisciplinary team notes.

Compelling Research Question 1:

How do we build an automated safety alert that triggers when there are conflicting notes (e.g., doctor's note says stable and nurse's note hints at declining) or when a high-priority narrative observation hasn't been acknowledged by the primary care team? (e.g., Social Worker note on financial distress)

Compelling Research Question 2:

How do we create an AI that "reads" new research the day it's published and automatically matches it to a patient's current narrative story? How does this new development impact clinician's current workflow and practice?

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LLM is changing every aspect of health care

LLM will facilitate the merging of expertise, data, and domain, simultaneously enabling safety and reliable research environment for patients.

Compelling Research Question 1:

Safety and trustworthiness

Compelling Research Question 2:

LLM embeddings

Compelling Research Question 3:

Interactive analysis enabled by LLMs

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Personalized Cancer treatment Strategy Software has been released

It is universal all hospitals can use it. It also finds the root cause of disease formation.

Compelling Research Question 1:

How to normalize and embed the data to be used for developing this software?

Compelling Research Question 2:

How to develop, select, and train the model?

Compelling Research Question 3:

How to make the software secure?

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Cancer Detection in a Cup

A new cancer detection approach is harnessing artificial intelligence to spot warning signs earlier—and with far more precision. Instead of looking at test results in isolation, the system analyzes a patient's entire medical history, from lifelong health records to genetic risk factors, to build a highly personalized risk profile.

This broader context allows the AI to predict which chemicals and proteins—known as biomarkers—should normally appear in that individual's body. By establishing this personalized baseline, the system can then filter out what's expected and focus on what isn't. Any unusual biomarkers that stand out from the norm are flagged for closer examination.

Some of these anomalies may serve as early indicators of cancer, potentially allowing doctors to detect the disease sooner than traditional methods. By combining big-picture patient data with advanced pattern recognition, researchers hope this technique could transform how cancer is identified and monitored.

Compelling Research Question 1:

How do we bring together high-quality multi-site representative data securely to be able to train artificial intelligence while respecting patient privacy? How do we integrate and harmonize the multimodal data of very different types from different sites?

Compelling Research Question 2:

How can we use artificial intelligence to build a strong baseline biomarker model, i.e., a chemical digital twin to use as a comparator?

Compelling Research Question 3:

How do we use artificial intelligence to accelerate and generalize the identification of cancer-related biomarkers, including a library of well-known biomarkers? Can artificial intelligence work with an alternate paradigm of biomarker analysis?

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HIPAA regulations no longer relevant to biomedical researchers!

Trusted pipelines for embeddings have eliminated the need to publish raw datasets with high risks of protected health information exposure. This has massively expedited the research community's ability to share datasets without fear of risking patient privacy or other legal repercussions.

Compelling Research Question 1:

What are the minimum standards for publishing pipelines used to generate embeddings that are trustworthy enough to enable researchers not to care about seeing the raw input data?

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AI patient advocate combines multimodal data (genomics (tumor, germ line), radiology imaging, pathology imaging) with patient wearable data and comprehensive medical literature to improve outcomes.

A large database of pathology images, radiology images, and genomics allows for the development of useful embeddings for classification/diagnosis of common and rare diseases. This combined with the patient's other medical records allows for suggested diagnoses and follow up testing. In addition, wearable data allows for warnings during follow up care. Doctors have found this proactive advocacy has improved diagnosos and care.

Compelling Research Question 1:

Large accessible databases of radiology, pathology and genomics databases.

Compelling Research Question 2:

Useful embeddings for those databases.

Compelling Research Question 3:

Combination of AI models, recurrent neural networks, LLMs etc into a patient advocate AI.

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The End of Trial-and-Error Oncology: AI Embeddings Predict Effective Colorectal Cancer Treatment in Over 90% of Patients—Paving the Way for Immunotherapy-Era Precision Across Cancers

Why This Is Truly Amazing
AI embedding–based foundation models now predict effective treatment for colorectal cancer with over 90% accuracy, while fewer than 1% of patients fare worse than standard-of-care. By integrating genomics, pathology, imaging, and longitudinal clinical data into a single patient representation, these models overcome the limitations of single biomarkers in a highly heterogeneous disease.
First validated in CRC, this approach has since scaled to all cancers where immunotherapy is standard of care, signaling a shift from trial-and-error treatment toward prediction-driven oncology.

Compelling Research Question 1:

Data / Biostatistics / ML QuestionHow do we build embedding models that are causally informative—not just predictive—across heterogeneous CRC populations and transferable to other immunotherapy-treated cancers?

Compelling Research Question 2:

Clinical Oncology QuestionWhat constitutes "actionable confidence" for embedding-based treatment recommendations in CRC, and how should these thresholds evolve as the approach scales across cancer types?

Compelling Research Question 3:

Implementation, Ethics, and Systems QuestionHow do we ensure embedding-driven oncology improves outcomes equitably as CRC-validated models are deployed across cancers, institutions, and populations?

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Predicting Lung Cancer Early with Data Embedding and AI Saves Lives!

Mining data from Electronic Health Records (EHRs) about demographics, behavioral and Social Determinants of Health (SDoH), phenotype data (Signs and Symptoms) data, biomarkers from laboratory data (structured and reports) imaging, genetics, combining with environmental data (air pollution, Air Quality Index) - develop a well defined embedding to help pattern recognition and develop a prediction model.

Compelling Research Question 1:

1: Population studies to find association and causation between the contributing factors?

Compelling Research Question 2:

Research to delineate best methods to collect and collate quality data to identify the impact factor of each risk factor for disease development?

Compelling Research Question 3:

Develop robust predictive models using data from question 2, representative of diverse populations

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Universal PanCancer Generalized Dynamic Embedding Representation

We are able to select best approach for patient treatment based upon universal embedding(s).

Compelling Research Question 1:

How can we remove bias and noise from embeddings to obtain a universal representation?

Compelling Research Question 2:

How can we match dynamic embeddings to use-case?

Compelling Research Question 3:

How do you extract plausible explainability from embedding representations?

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AI Integrates Genes, Behavior, and Imaging to Redefine Breast Cancer Risk Prediction

In a breakthrough that reshapes how we predict and prevent cancer, researchers have developed an AI-driven, embedding-based model that unifies genetic variation, lifestyle exposures, and medical imaging into a single predictive framework, something long thought impractical due to the fundamentally different nature of these data types. By translating each modality into a shared mathematical representation, the model overcomes decades of fragmentation across epidemiology, genomics, and radiology, enabling patterns to emerge that were previously invisible when analyzed in isolation. Crucially, this approach allows the identification of individuals who fall through the cracks of current risk models, those with elevated but easily overlooked risk profiles that cannot be captured by any single data source alone. By detecting these "hidden high-risk" cases, the model not only improves predictive accuracy but also enables targeted, actionable guidance on modifiable behaviors and screening strategies. Clinically, this means faster, more precise decision-making—where a patient's inherited risk, daily exposures, and imaging features are integrated in real time to guide personalized prevention, rather than reacting to disease after it appears.

Compelling Research Question 1:

Individually, how does each data type predict breast cancer? - use different AI-embeded methods to quantify prediction features

Compelling Research Question 2:

How does integrating multi-modal data transform risk prediction beyond single-modality models?

Compelling Research Question 3:

Can integrated models identify "hidden high-risk" individuals and enable actionable prevention?

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Treatment decisions are made with high accuracy using digital twin representations of human patients.

Compelling Research Question 1:

How to represent a cell with multimodal features and accurate molecular mechanisms?

Compelling Research Question 2:

How to represent cell-cell interactions which have explosive amounts of combinations?

Compelling Research Question 3:

How to derive effective representations from small datasets with limited functional/behavioral labels?

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Break Through in Previously Untreatable Cancer;

Cancer Survivor Rates Double

Compelling Research Question 1:

How do we improve personalization on treatment to enhance patient outcomes?

Compelling Research Question 2:

How do we connect disperse data repositories of varying modalities to advance knowledge and personalized treatment?

Compelling Research Question 3:

How do we improve validation of new models and approaches to quickly take research from the lab to the clinical practice?

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AI Embeddings Allow Patients to be Matched to Appropriate Clinical Trials or Treatments

In the past, the choice of cancer treatment plans was mostly based on 'educated guesses'. Due to the massive amount of data available, and the myriads of relationships between elements of that data, it often is difficult for clinicians to find patterns that could inform their 'guesses'. Embeddings combine information from multiple sources, such as gene sequences, imaging, histopathology, and responses to treatment into a form that allows AI programs to compare this patient with other patients' information to find similarities, and to compare how similar patients responded to various treatment regimens. This comparison helps clinicians to better match new patients to treatments that had worked in the past with patients that had similar characteristics.

Compelling Research Question 1:

How to convert data into appropriate embeddings that might work as characterizations of the patient suitable for comparison?

Compelling Research Question 2:

Comparing different possible embeddings as to their performance in selecting appropriate treatments?

Compelling Research Question 3:

How does one avoid bad advice from the AI comparisons as to what treatments might work best?

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Biomedical research data storage needs plummet, freeing up millions of exabytes for sharing cat pictures!

Disciplines such as genomics, proteomics, and medical imaging have historically generated many exabytes of data to be stored and shared among the research community. Through the power of embeddings, these datasets have been abstracted into numerical values that are many orders of magnitude smaller, driving down the cost of disk storage globally, and leading to an explosion of pet photos taking their place!

Compelling Research Question 1:

What are the unique needs of these different disciplines that will drive the adoption of embeddings?

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20% higher improved outcomes in patients with cancer than in 2026

Using longitudinal multimodal data—including genome, transcriptome, metabolome, microbiome, electronic health records, survey data, and exposome histories spanning nutrition, drugs, and environmental exposures—clinicians can move beyond coarse population-level evidence or isolated biomarkers. Instead, each patient is represented as a point within a shared, high-dimensional multimodal latent space defined by their genomic, clinical, and imaging profiles. In this framework, therapeutic decision-making becomes a form of high-dimensional retrieval: identifying biologically similar patients with known outcomes and selecting treatments that have already demonstrated efficacy within that region of the space.

Compelling Research Question 1:

How can we optimize computational energy consumption so that multimodal embedding models can be built and deployed in a sustainable way?

Compelling Research Question 2:

How can we generate or acquire the massive amounts of longitudinal multimodal data required to build these models?

Compelling Research Question 3:

How effectively can multimodal data integration identify biologically similar patients to guide individualized treatment selection for currently incurable tumors?

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New Language: Overcoming the Limitations of Structured Data

We have a standardized embedding representation of medical languages and the billing codes so there is no more filling out spreadsheets. We are going back to narrative notes which are easier to document and create because we now have the tech such as embedding to harness the nuance. There is a key to open the embedding so that the right people get access to the information. We are also creating a new language that connects research and medical practice. As the paper comes out then the embedding map is updated based on the recent research publication in order to bring practice and evidence gap closer.

Compelling Research Question 1:

How do we create a standardized embedding for billing codes?

Compelling Research Question 2:

How do we create an embedding that will cover different medical languages and bring them together?

Compelling Research Question 3:

How do we use embedding to close the gap between practice and evidence?

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Multimodal integration of clinical, genomic, wearable, and patient experience data cuts cancer mortality by 50%

Embeddings give us the ability to combine data from disparate sources and inform decision making across multidisciplinary teams on a continuous basis.

Compelling Research Question 1:

How do we combine data from many disparate sources to project into a single embedding space that can be updated with continuously streaming data?

Compelling Research Question 2:

How do we ensure that very different patient populations are well served by this model?

Compelling Research Question 3:

How can data from wearables and patient/family/stakeholder experiences combine with more traditional clinical and genomic data?

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****Friday, April 20, 2029****

A Unified Latent Space Across Cell Lines and Patients Enables Predictive, Personalized Cancer Treatment

For decades, cancer research has been constrained by fragmented biological representations: cell lines, patient tumors, and multi-omics datasets each existed in isolated analytical spaces. This made it difficult to translate discoveries from experimental systems into real clinical impact.

This breakthrough demonstrates that a shared latent geometry across biological domains can be learned, allowing embeddings from cell lines, patient data, and multi-omics measurements to align within a unified representation. By replacing unstable adversarial alignment methods with more robust distribution-matching approaches (e.g., optimal transport and kernel-based methods), researchers achieved stable and interpretable cross-domain embeddings.

As a result, models trained on preclinical systems can now generalize to patients, enabling:

Accurate prediction of therapy response and resistance
Integration of heterogeneous datasets (genomics, transcriptomics, proteomics)
Faster translation from discovery to clinical decision-making

This effectively breaks down long-standing data silos and creates a shared computational language for cancer biology, accelerating precision oncology at scale.

Compelling Research Question 1:

Does a shared latent geometry truly exist across biological domains (e.g., cell lines and patients), and under what conditions can it be reliably learned?

Compelling Research Question 2:

What is the most stable and theoretically grounded method for aligning distributions across domains (e.g., replacing GAN-based losses with optimal transport or kernel-based approaches)?

Compelling Research Question 3:

Can integrating multi-omics data into a unified embedding improve downstream prediction (e.g., treatment response), and how do we quantify when cross-domain similarity is meaningful versus spurious?

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NCI's AI Embeddings Receive FDA Approval to Predict Response Across More Than 10 Immuno-Oncology Treatments

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Compelling Research Question 1:

How can embeddings enable secure learning from distributed, siloed cancer data without sacrificing privacy, rigor, or reproducibility?

Compelling Research Question 2:

What incentive structures and data acquisition models will motivate the contribution of high-quality, multimodal cancer data at scale?

Compelling Research Question 3:

How do we build a sustainable ecosystem that aligns data sharing, compute resources, governance, and clinical impact?

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AI Predicts and Prevents Cancer Before It Begins — Disease Declared "Fully Preventable"

A revolutionary AI-powered forecasting system now predicts tumor formation and drug resistance at the individual level, years before cancer develops. By analyzing vast datasets - genetics, lifestyle, and medical history - the system identifies at-risk individuals and triggers ultra-early screening and personalized therapy protocols. For the first time, oncologists are preventing cancer rather than treating it. New AI-designed therapies target diseases before symptoms ever appear, and global cancer mortality rates have plummeted by 80% in just five years.

Compelling Research Question 1:

How can AI models reliably predict individual cancer risk across diverse populations with varying genetic and environmental profiles?

Compelling Research Question 2:

What ethical frameworks should govern pre-symptomatic intervention when AI forecasts disease that may never manifest?

Compelling Research Question 3:

How will AI-generated therapies be validated fast enough to keep pace with evolving resistance patterns?

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Accurate early detection of cancer made possible by AI embeddings

AI embeddings can provide contextual framework to reduce false (positive or negative) results, that is currently the major obstacle in cancer detection

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Compelling Research Question 1:

How can we leverage existing LLM embedding paradigm to translate in to the multidimensional space of cancer diagnostic tests that may involve from simple blood test to images, spectral data, genetic test results

Compelling Research Question 2:

The challenge of finding the right amount training data, how it can be addressed by coming up with generative models

Compelling Research Question 3:

In the cancer treatment space, whether a digital twin model of a given patient can be developed to predict patient-specific treatment variables to balance the effectiveness of the treatment to prevent over or under treatment

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****Friday, April 20, 2029****

"A New Currency for Medicine: How Shared Embeddings Are Replacing Data in Cancer Research"

Three years ago, a little-noticed workshop at the National Cancer Institute proposed an unusual idea: that hospitals might collaborate not by sharing patient data, but by exchanging mathematical representations of disease. Today, that idea is reshaping cancer research worldwide. By allowing institutions to share "embeddings"—compressed, privacy-preserving summaries of biological state—researchers have begun to break long-standing data silos, align insights across genomics, imaging and clinical care, and accelerate discoveries that once took years into months.

Compelling Research Question 1:

Representation: What is the correct embedding?
When does an embedding faithfully capture the true biological state—rather than artifacts of data, model, or modality?

-Identifiability: Are different embeddings equivalent representations of the same biology?
-Sufficiency: Do they contain enough information for prediction and intervention?
-Limits: What is the maximum recoverable signal from each modality?

Goal: Establish embeddings as scientifically valid, measurable representations, not just model features.

Compelling Research Question 2:

Alignment: Do embeddings mean the same thing across systems?
When two embeddings are produced in different contexts, how do we ensure they mean the same biological thing?

-Cross-modal alignment: Integrate genomics, imaging, spatial, clinical data
-Transportability: Predict performance across sites before deployment
-Ontology grounding: Anchor embeddings to biological knowledge
-Agentic alignment: Enable systems to iteratively reconcile differences

Goal: Enable interoperable, federated embedding ecosystems without sharing raw data

Compelling Research Question 3:

Action: Can we reason, intervene, and decide using embeddings?
How do we move from embedding-based prediction to decision-making and intervention?

-Causal structure: Interpret embedding directions as biological effects
-Counterfactuals: Simulate interventions (e.g., drug effects, pathway modulation)
-Combinatorics: Efficiently search vast intervention spaces (quantum/advanced methods)
-Human–AI teaming: Combine machine exploration with human judgment

Goal: Turn embeddings into decision engines for therapy, trials, and strategy.

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****Friday, April 20, 2029****

The 'Zero-Day' Adaptive Treatment: Harmonized Patient Embeddings Preempt Cancer Resistance Before Tumors Physically Change

The problem was never data. We already have too much data from different sources that cannot be integrated. Daily imaging data is in one place, genomics in another, clinical notes somewhere else entirely. Embeddings can provide a shared space where CBCT scans and a liquid biopsy result from different institutions can be interpreted consistently. What does that practically change? We stop chasing the tumor. There is a real signal, weeks early, that something is shifting, before any radiologist would flag it. Whether that lead time is actually enough to matter to patients, we do not yet fully know. That is partly why this needs to happen.

Compelling Research Question 1:

How do we fuse imaging trajectories (dense, daily) with other data types, EMR text, genomic or pathologic signals (sparse, ~weekly), without the imaging data simply overwhelming the biology? The causal structure has to be preserved somehow, still figuring out what that architecture looks like.

Compelling Research Question 2:

Can multiple embedding pipelines truly harmonize across modalities and institutions? It has to solve many issues like PHI, the vectors actually mean the same thing across scanner types, note styles, and protocols. Federated learning only works if the inputs are genuinely comparable.

Compelling Research Question 3:

When the model flags a shift toward resistance and nothing is visible on the scan yet, how do we get a clinician to act on that? A confidence score will not be enough. It may need to look like a 3D projection. Here is where this tumor is expected to grow under each dosing scenario. However, it has to be biologically grounded, not just visually convincing. That gap between "the model is probably right" and "I will change the treatment plan today" is, honestly, the part I am least sure how to close.

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Cancer researchers can finally follow tumors through time: AI now builds longitudinal datasets across hospitals that reveal how genotype drives phenotype

Intra-system heterogeneity creates a particularly informative setting for genotype-to-phenotype mapping, because related clones can differ in molecular state and behavior while still sharing much of their broader biological and environmental background. But that opportunity can only be realized if we can follow such divergence over time and in context. We therefore need more longitudinal datasets, and longer ones, because without them we cannot learn how genetics works in context. The biggest barrier to understanding cancer has not been a lack of molecular data, but a lack of structured longitudinal context. Hospitals and laboratories generate enormous amounts of imaging, pathology, sequencing, and clinical data, yet most of it remains trapped in disconnected snapshots. That has made it difficult to learn how tumor genomes and transcriptomes shape behavior over time, across therapies, and under changing environments. Embeddings changed this by giving agentic systems a way to navigate heterogeneous institutional data, identify related records, and propose biologically meaningful links across events, specimens, and modalities. Combined with an event-based ontology, this turned fragmented local data into reusable longitudinal datasets at a scale that manual curation could never achieve. The result is a new generation of cancer resources that make expensive molecular assays more interpretable, uncover context-specific genotype-to-phenotype relationships, and accelerate more precise, adaptive care.

Compelling Research Question 1:

Can we use embeddings to define what a good longitudinal structure looks like so that agentic systems can discover and assemble connected longitudinal cancer data without losing the event context, specimen provenance, and temporal structure needed for scientific interpretation?

Compelling Research Question 2:

What representations of metadata, context, and record relationships are needed so that embeddings support true longitudinal harmonization rather than superficial similarity driven by local workflows, coding differences, or confounding artifacts?

Compelling Research Question 3:

How can an event-based target ontology for cancer data be combined with embeddings and human-in-the-loop validation to scale the creation of longitudinal

datasets across institutions, so that cheap repeated phenotypic observations and sparse, expensive molecular assays can be analyzed together to learn how genotype gives rise to phenotype?

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GENEVA, SWITZERLAND – October 27, 2029 – In an announcement that will fundamentally rewrite the future of human health, leading medical institutions worldwide today confirmed that breakthroughs stemming directly from the "AI Embeddings for Cancer Research" workshop of 2026 have transformed cancer from a life-threatening diagnosis into a largely treatable, often curable, condition for millions globally. What was once a devastating lottery of treatments is now a science of predictive precision.

Compelling Research Question 1:

How can we develop and evaluate novel embedding architectures and training methodologies that more accurately and robustly capture the extremely nuanced, context-dependent, and often ambiguous semantic meaning inherent in diverse clinical free-text (including negation, temporality, comorbidities, and specific medical jargon), thereby significantly outperforming general-purpose language models in clinical tasks?

Compelling Research Question 2:

What are the optimal strategies for integrating and fusing clinical text embeddings with other critical patient data modalities (e.g., medical images, lab results, genomic data) into a unified, high-fidelity patient representation that unlocks comprehensive, cross-modal insights for diagnosis, prognosis, and personalized treatment planning?

Compelling Research Question 3:

How can we develop novel methods to enhance the interpretability, explainability, and bias mitigation of clinical embeddings and their downstream applications, ensuring clinicians can understand why certain connections or predictions are made, while simultaneously identifying and mitigating inherent biases (e.g., demographic, institutional, data acquisition) to build trust and promote equitable healthcare outcomes?

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Novel Surveillance System Detects Cancer Trends in Real Time, Enabling Health Systems to Intervene Months Earlier

By 2029, a quiet revolution in cancer surveillance has reshaped how health systems detect and respond to disease: a novel AI system powered by embeddings now continuously integrates fragmented data—from oncology notes and pathology reports to imaging summaries and population-level signals—into a unified semantic space, enabling real-time detection of emerging cancer trends that previously took months or years to surface through registry-based methods. Unlike traditional approaches constrained by rigid coding and siloed datasets, embeddings capture nuanced clinical meaning across unstructured and heterogeneous data, effectively unlocking interoperability across systems that were never designed to communicate. This has transformed surveillance from retrospective reporting to proactive intervention—health systems can now identify rising incidence patterns, treatment-related toxicities, and care gaps early enough to act, triggering targeted screening, resource allocation, and clinical alerts within weeks. The result is measurable: earlier diagnoses, faster clinical decision-making, and reduced emergency presentations, as clinicians and public health leaders gain continuous, system-wide awareness of cancer dynamics, fundamentally shifting the paradigm from delayed insight to real-time, life-saving action.

Compelling Research Question 1:

How do we learn clinically valid, temporally aware embeddings that detect true signals—not noise—early enough to matter?

Compelling Research Question 2:

How do we create a shared embedding space across siloed, heterogeneous, and multi-level data sources without requiring full data centralization?

Compelling Research Question 3:

How do we translate embedding-detected signals into actionable, trusted interventions within clinical and public health workflows?

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Enabling clinical insight -- Bringing the power of the cloud to your fingertips

One of the major problems in today's society is that datasets and embeddings are in completely different formats, requiring users to perform the same conversion using their local resources. Instead, if we can standardize data, and provide open-source tools to make this conversion only happen once, embeddings could be accessed faster in a reproducible manner, bringing us closer to the possibility of enabling clinical insight. By using formats such as DICOM and leveraging cloud-based platforms in an open-source manner, we can allow users to quickly access these embeddings, allowing them to train their own models for downstream tasks (think histology classification of tumors, cancer staging prediction) or search for similar patients.

Compelling Research Question 1:

How can we make embeddings open-source and easily accessible for widespread use?

Compelling Research Question 2:

How can we use DICOM and the power of the cloud to enable efficient storage, querying, and viewing of these embeddings?

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Commonalities and differences in all major cancers found. Early prediction with cancer versus benign possible with confidence.

Embeddings helped us detect patterns that are too complex to see reliably one feature at a time. They brought samples with similar biology closer together and separated samples with different biology, making both shared cancer signals and cancer-specific differences easier to recognize. That improved our ability to distinguish malignant from benign cases earlier and with greater confidence as a function of gender, age, race, cancer type and progression.

Compelling Research Question 1:

What is the structure of cancer similarity itself: what is truly shared across major cancers, what is lineage-specific, and what changes with progression?

Compelling Research Question 2:

Under what biological and demographic conditions can cancer be distinguished from benign states early, and where does confidence break down?

Compelling Research Question 3:

How do we turn a statistical separation into a clinically actionable and fair decision framework?

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For advanced cancer care, the physician-AI interaction platform provides real-time diagnostic, treatment-options with patients's clinical information toward to true individualized medicine.

Integrated clinical notes, pathology image and report, radiology imaging and reports, and lab results using embedding and share the features across institutions and globally.

Compelling Research Question 1:

Data sharing across different institutions

Compelling Research Question 2:

Data Security with privacy preserving.

Compelling Research Question 3:

multimodality data integration which capturing macroscopic and microscopic and molecular profiling information.

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New app identifies and prevents metastasis before it happens

A new app helps oncologists and radiologists identify possible instances of metastasis in patients before it happens. Using provided information, the app estimates the risk that a particular tumor may be metastatic. The app then considers how potential treatments may affect this probability. The app has two modalities: if patient-specific information is limited (for example, only tumor images),

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Compelling Research Question 1:

Is it possible to predict and prevent a patient from developing metasisis if their caregiver had access to all possible omics information that is conceivably available for that patients in addition to imaging .

Compelling Research Question 2:

Out of all population-level datasets currently available from electronic health record systems (including imaging, labs, co-morbidities) , which datasets and features are the strongest early stage predictors of subsequent metastasis for different cancer types/ICD codes? Different types of cancers have require different datasets to distinguish datasets.

Different types of "omes" are measured. Combining research datasets and clinical practice detests. Challenge: Can have non-overlapping datasets

Compelling Research Question 3:

How do we define "similarity" of cancer patients? In terms of symptoms (ICD codes), imaging, sequencing, etc? How do these similarity definitions map to metastasis? (i.e. do “similar” patients by each of these metrics have similar rates of metastasis?)

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By unifying records from hospitals across the world we have been able to conduct a multi-site international clinical trial for predicting survivability in a very rare cancer.

Individual institutions cannot gather large enough cohorts to carry out this kind of study. By securely sharing data via embeddings we are able to pool and harmonize data and create a common model to predict most effective treatment pathway. By sharing embedidngs rather than the original text and images we are able to overcome privicy concerns.

Compelling Research Question 1:

How do we ensure that the embedding represents the underlying, important relationships in the data and not irrelevent correlations? Do graphs or structured otologies offer a more structured way of doing this?

Compelling Research Question 2:

Can we be 100% sure that embeddings can not be used to recover PHI?

Compelling Research Question 3:

Can we support federated learning/training in a secure way, in essence sharing models, embeddings, and workflows for model training and inferring in a secure manner?

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AI embedding uncovers hidden cancer signatures

This is easily accessible, utilizes publicly available data, including genomics , wearable data. Patients can have access too trusted resource and early access to care

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Compelling Research Question 1:

na

Compelling Research Question 2:

na

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AI Builds Synthetic Cohorts, Opening New Frontiers in Rare Cancer Research

In the world of rare cancers, progress has long been constrained by a simple but devastating reality: there are too few patients, and their data are scattered across disconnected systems. Traditional methods, reliant on large, well-labeled datasets, have struggled to extract meaningful insights from such sparse and siloed information. Now, embedding-based AI is changing that. By transforming heterogeneous clinical records, imaging, and molecular data into a shared representation space, embeddings can link patterns across institutions without requiring direct data pooling—effectively unlocking signals that were previously hidden behind institutional and technical barriers. This has enabled the creation of synthetic cohorts that mirror real patient populations, accelerating hypothesis generation, improving early detection strategies, and potentially shortening the time from discovery to clinical decision. For patients with rare cancers, where every missed signal matters, this shift could mean faster diagnoses, more personalized treatments, and, ultimately, better outcomes.

Compelling Research Question 1:

How can we learn reliable embeddings from extremely sparse and heterogeneous rare cancer data?

Compelling Research Question 2:

When is a synthetic cohort valid enough, and who decides?

Compelling Research Question 3:

Can embeddings faithfully encode the rarest signal, or do they systematically smooth it away?

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New study shows average life expectancy of cancer patients extended by 10 years using personalized cancer assistant

AI embeddings solved the core problem: they created a shared representation of complex, multimodal data, making the full patient computable for the first time. Cancer care becomes a continuously improving, learning ecosystem—not a series of disconnected decisions.

Compelling Research Question 1:

How to stabilize embeddings temporally

Compelling Research Question 2:

How to interpret embeddings

Compelling Research Question 3:

How to use embeddings to establish causal impact of treatment/prevention

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Cancer patient diagnosed in minutes with prognosis and therapeutic suggestions

Embeddings are a low dimensional way to capture commonalities between data points (patients) in high dimensional space. A cancer subtype space created using embeddings from multiple patients can help place a "new" patient into the appropriate subtype by finding nearest neighbors or other patients who have similar characteristics.

Compelling Research Question 1:

What are the minimal features necessary to compute such embeddings ?

Compelling Research Question 2:

Are embeddings privacy preserving?

Compelling Research Question 3:

Can federated learning be harnessed to share embeddings between clinical sites?

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AI embedding saves ten million lives per year detecting "Stage 0" cancer: A Genomic-Imaging-Social (GIS) AI strategy that predicts cancer before it starts in the body. Three years from now, an AI-enabled cancer early detection system could transform care by identifying patients at risk for cancer “Stage 0” before conventional clinical presentation, using a unified model that integrates whole-body imaging, pathology, genomics, blood-based circulating markers, physician interviews, survey responses, family history, germline and ancestry-informed features, diet, environmental exposures, and other real-world care data. Rather than treating each modality in isolation, the system places each patient in a multidimensional neighborhood of similar patients and summarizes what happened to those neighbors, allowing clinicians to compare likely outcomes under different surveillance and therapy strategies in real time, including during tumor board discussions. As the data resource grows, the system becomes increasingly tailored to each patient, delivering personalized care informed by “the many,” but only by those most relevant to that individual’s biology, history, and lived context. This framework could also help determine which data types matter most for prediction, how missing data can be inferred across modalities, and how models aligned to biological and clinical knowledge rules can make reliable predictions even when some patient information is incomplete.

The amazing aspect would be the predictiveness ahead of time for not only early detection but a risk index that helps find similar people in the embedding space and extrapolating future trajectories from similar patient's outcomes and life histories.

Compelling Research Question 1:

Can we use embeddings to identify similar patients not just based on the disease itself but other aspects of the patient like history, images, social, zip-codes, ancestry, diet, physician notes, medical history. How should patients be represented in a multidimensional similarity space so that their “neighbors” are both biologically

meaningful and clinically useful for guiding surveillance and treatment decisions? What level of evidence, interpretability, and knowledge alignment will be required for clinicians to trust and act on AI predictions for asymptomatic patients flagged as being at high risk for early cancer?

Compelling Research Question 2:

How much missing data can be filled in across modalities? If only have a limited amount of data available, can it be extrapolated to other key aspects of disease or outcome?

Compelling Research Question 3:

Can we prevent the activity from happening and the likelihood of getting it? And can we tease out the driving factors in the data leading to that prediction? Which combinations of data modalities are most informative for predicting cancer risk before overt disease is clinically detectable, and how much performance is lost when certain data streams are missing?

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Searchable AI Embedded Engine to uncovers hidden cancer signatures to improve health

searchable by anyone integrates publicly available information including genomics, wearables. its could be an adhoc chat bot, for patients can access and get trusted information,

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Compelling Research Question 1:

didn't get this far with the team

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Embedding-Powered "Universal Cancer Response Map" Cuts Treatment Trial-and-Error in Half, Boosts Survival Across Multiple Tumor Types

In a breakthrough that reshapes everyday oncology, researchers unveiled a "universal response embedding" that places each patient into a shared, interpretable map of cancer biology and treatment sensitivity. Unlike earlier AI systems that depended on a single data type, a single institution, or narrowly curated cohorts, this approach learned geometry that aligns real-world clinical outcomes with molecular and imaging signals across hospitals, sequencing platforms, and privacy boundaries. The result is a tool clinicians can use during tumor board: within hours, it forecasts which therapies are most likely to work for a specific patient and which are unlikely to help, dramatically reducing the time spent on ineffective regimens. The biggest shift is not just accuracy, but portability: the embedding lets sites contribute knowledge without shipping raw patient data, turning what used to be siloed, restricted datasets into a federated, continuously improving model that directly changes treatment decisions.

Compelling Research Question 1:

****What is the minimal, clinically realistic set of modalities that still yields a stable, generalizable embedding that separates responders from non-responders?****

This includes handling missing modalities and ensuring performance when future patients have only routine clinical data, pathology, and imaging rather than full multi-omics.

Compelling Research Question 2:

****How do we build embeddings that are *causal enough* to guide treatment choice, not just correlate with outcomes, especially under confounding and shifting standards of care?****

If a model is trained on biased treatment patterns, it may learn historical practice rather than true biology. We need methods that distinguish "patients did well" from "patients were given better options" and that remain valid as new drugs emerge.

Compelling Research Question 3:

****How can we train and validate across institutions under privacy and consent constraints (including the small consent fraction) while proving clinical safety, fairness, and calibration?****

This is about federated learning, privacy-preserving evaluation, and rigorous multi-site prospective validation so the embedding works for underrepresented groups and does not degrade outside the originating data environment.

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"Closing the Treatment Gap: Repurposed Drugs and CRISPR Deliver Therapies for the Untreated Majority"

Drug target identification and prioritization: Molecular, genetic, and phenotypic embeddings enable similarity-based inference across genes and pathways. Latent structure in embedding space when used with a second model highlights previously unrecognized disease drivers (backpropagation of features, attention maps, feature importance) and be used to rank drug targets.

Drug repurposing at scale: By embedding drugs (chemical structure, mechanism of action, transcriptomic response) alongside diseases (genomics, clinical phenotypes), proximity in vector space becomes a quantitative signal for therapeutic match. This enables systematic repurposing—identifying approved or shelved compounds with high likelihood of efficacy in new indications.

Predictive modeling of efficacy and toxicity: Multimodal embeddings integrate omics, imaging, and clinical data to predict drug response and adverse effects earlier. This improves the selection of drugs for treatment.

Patient stratification and trial design: Embedding-derived patient representations cluster individuals by molecular and phenotypic similarity, enabling better cohort selection for clinical trials in rare diseases. This increases statistical power and reduces trial size.

Data interoperability and federated learning: Embeddings provide a common representation layer across institutions and data types, allowing models to learn from distributed datasets without direct data sharing. This is particularly impactful for rare diseases where single-center cohorts are underpowered.

Integration with gene editing (e.g., CRISPR): Embedding models can prioritize editable targets, predict off-target effects, and map gene–phenotype relationships, accelerating the design of gene-based interventions alongside small-molecule strategies.

Compelling Research Question 1:

Can multimodal biomedical embeddings prospectively predict clinically effective drug–disease matches that outperform standard target-based discovery approaches in randomized or real-world settings?

Compelling Research Question 2:

How accurately can embedding-derived patient representations stratify responders vs. non-responders, and does this materially improve clinical trial efficiency and success rates?

Compelling Research Question 3:

To what extent do embedding models generalize across institutions and datasets (including federated environments), and what biases or failure modes emerge when applied to rare diseases or underrepresented populations?

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Hotspot of Cold Cases in Cancer Solved: New AI Method Gives Kids with Melanoma Hope

AI embedding models were used to combine patient health record, environment and clinical information that shed new light on the previously-unknown causes of pediatric melanoma cases in the US. Where other efforts have failed to make sense of these complicated datasets, this groundbreaking approach finds the connections between biological and environmental factors that unexpectedly combine to cause skin cancer in some children.

Compelling Research Question 1:

How can we effectively combine multimodal data sources to capture complicated associations that lead to clinically-important outcomes?

Compelling Research Question 2:

Is patient privacy better protected when using embeddings of their information instead of whole files?

Compelling Research Question 3:

Are we able to disentangle and explain the contributions of the input data sources to the embedding vectors?

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Efficient Multimodal Embeddings: Enabling Generalizable and Adaptable AI for Cancer Research

Time was short to come up with a lead paragraph :(

Compelling Research Question 1:

How to design pipelines for training of embeddings for multiple modalities while still anchoring them together even if they are not matching in size and type

Compelling Research Question 2:

How we can interpret the efficacy of the embeddings so that we can rely on them and trust them?

Compelling Research Question 3:

How would it be possible to utilize the embeddings to prevent any side effect during adaption of the models to new data (e.g. populations, patient cohort, demographic groups)?

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New AI models of patients, exposures, and tumors transform early detection of cancer and the monitoring of progress during treatment

New AI models of patients are being generated by integrating information about individual patient's presentation, genetics, and environmental exposures. These digital twins of patients and tumors that make possible in silico experiments to select therapies. These new models have made possible close monitoring of patients based on data from wearables.

Compelling Research Question 1:

How do we create embeddings of patients that capture not only their genetics, but also their environmental exposures, and other factors that would make possible better earlier detection? How would a dramatic increase in early detection make possible better outcomes at a population level.

Compelling Research Question 2:

How do we use patient and/or tumor embeddings to optimize therapy selection, especially as new therapies (CRISPR, etc.) come on line? Including changes in therapy over time?

Compelling Research Question 3:

How do we use patient or tumor embeddings to monitor change during a patient's cancer journey? Is it possible to bring novel technology, e.g. wearables, to monitor response to therapy, metastasis, and other key elements?

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****Friday, April 20, 2029****

Virtual Twin AI Predicts Early-Onset Cancer Risk Years in Advance, Enabling Precision Screening for High-Risk Populations

Recent advancements in collaborative modeling have enabled the completion of the human "ontome" - a dynamic representation of the human organism that arises from an individual's genes and their pre and post-natal environment. The key innovation was developing methods for embedding troves of human clinical data within these models to enable the representation of individuals and disease states. This combination permits the discovery of biomarkers that signal the earliest stages of uncontrolled cell proliferation. This in turn enables the use of dynamic virtual twins receiving telemetry from their live counterparts to signal the earliest signs of cancer.

(Not sure what my breakout group number was, but maybe you can reverse engineer it. - Pietro Michelucci)

Compelling Research Question 1:

How do we crowdsource multi-scale, multi-system in-silico collaborative modeling to researchers with existing models to produce a complete model of human physiology?

Compelling Research Question 2:

How can clinical data be represented and embedded within a dynamic model of human physiology to ensure its fidelity to the human organism and to monitor an individual's health in real time?

Compelling Research Question 3:

What domain knowledge could be embedded within a transformer model to contribute to the development of a virtual human and use it for autonomous exploratory research?

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****Friday, April 20, 2029****

AI Cracks Cancer's Code: Causal, Interpretable Models Predict and Explain Tumor Evolution Before It Happens

In a breakthrough that redefines both cancer research and clinical care, scientists have developed AI systems that can not only predict how tumors will evolve over time but also identify the underlying biological mechanisms driving those changes. By learning stable, causally grounded embeddings from longitudinal, multimodal patient data, these models transform cancer from a reactive diagnosis into a predictable—and explainable—process. Clinicians can now see not just what will happen, but why, enabling earlier, more targeted interventions and marking a decisive shift from pattern recognition to true biological understanding.

Compelling Research Question 1:

How do we learn embeddings that encode causal mechanisms, not just correlations?

Compelling Research Question 2:

How can we design consistent, dynamic embedding spaces that model cancer as a stable, time-evolving trajectory?

Compelling Research Question 3:

How can we enable mechanism interpretability and clinical actionability in high-dimensional embeddings without sacrificing performance?

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AI is your personal healthcare navigator

AI-based tools are helping cancer patients navigate the healthcare delivery system to schedule meetings with their oncologists, fill prescriptions, report drug adverse effects, and communicate current health status with the clinical team members in real-time. Embeddings using the data from clinical and healthcare delivery databases unlocked the information needed to understand the patient's current clinical needs, understand the correct sequence and timing of future clinical visits, communicate current health status, automatically fill prescriptions, and coordinate care among clinical team members to optimize the health of cancer patients.

Compelling Research Question 1:

How to unlock the information in healthcare and clinical databases to predict the care trajectory of a cancer patient?

Compelling Research Question 2:

How to collect, collate, and communicate current health status to the relevant clinical team members?

Compelling Research Question 3:

How to transform the large streams of health and biological data into actionable, real-time clinical alerts to the clinical team taking care of the patient?

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Clinical Trials Go Virtual: Patient Avatars Unlock Faster, More Inclusive Therapies

A paradigm shift from enrollment to simulation: Virtual trials using patient avatars replace slow, exclusionary recruitment with scalable in silico cohorts that faithfully model patients' race and socioeconomic status, disease trajectories and treatment response. The results from these trials will be generalizable across populations.

Embeddings unify fragmented biomedical data: Multimodal embeddings integrate genomics, imaging, EHRs, and longitudinal outcomes into a shared representation, enabling each “avatar” to capture the full biological and clinical complexity of an individual.

Unlocking siloed and restricted datasets: Embedding frameworks enable federated learning across institutions, allowing models to learn from distributed, privacy-protected datasets without moving raw data. This overcomes longstanding barriers in rare disease and multi-site clinical trials.

Direct patient impact and inclusivity: Patients who are historically underrepresented in clinical trials due to their ethnicity, socioeconomic status, geography, comorbidities, or rarity of disease generate biases in clinical trial outcomes. They can now be effectively included through high-fidelity avatars, leading to greater success from phase II to phase III trial outcomes.

Compelling Research Question 1:

Clinical validity and regulatory acceptance of virtual clinical trials. Can patient-avatar–based virtual trials prospectively predict real-world efficacy and safety with sufficient fidelity to support regulatory decisions, partially or fully replacing traditional trial arms?

Compelling Research Question 2:

How good is the representation of subjects in avatar clinical trials ? How accurately do embedding-derived avatars capture biological and social diversity. How accurately do embedding-derived avatars capture biological and social diversity, and do they reduce—or inadvertently amplify—biases for underrepresented populations? Does using avatars reduce, or perhaps inadvertently amplify biases for underrepresented populations?

Compelling Research Question 3:

Model robustness and generalizability. Can we leverage digital twins to generate avatars for clinical trials ? How well do avatar models trained on federated, heterogeneous datasets generalize across institutions. What are critical input data for generating robust avatars ?

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****Friday, April 20, 2029****

AI Embeddings Unlock Global Cancer Data, Cutting Drug Development Time in Half and Enabling Real-Time Precision Treatment

In a breakthrough that is reshaping oncology, researchers have leveraged AI embeddings to unify previously fragmented and siloed cancer datasets across hospitals, clinical trials, and real-world evidence sources. For decades, critical patient data remained locked in incompatible formats, limiting its use for research and treatment decisions.

By embedding clinical, genomic, and real-world patient data into a shared, interoperable representation, scientists can now identify patterns across millions of patients in real time, something that was previously impossible. This has dramatically accelerated drug discovery, enabled more accurate patient stratification, and allowed clinicians to match patients with optimal therapies faster than ever before.

The result: reduced time to develop treatments, more personalized care, and improved survival outcomes for patients worldwide.

Compelling Research Question 1:

How can we create standardized, trustworthy embeddings across heterogeneous clinical and genomic datasets while preserving provenance, privacy, and regulatory compliance?

Compelling Research Question 2:

How do we ensure that embeddings are interpretable and verifiable, so clinicians and regulators can trust the insights derived from them?

Compelling Research Question 3:

How can we enable secure, cross-institutional collaboration using embeddings without requiring raw data sharing, especially across healthcare systems and borders?