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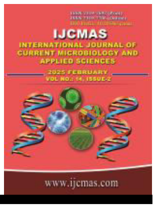

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Detection of Initial Donozology Stage Using Virtual Cell with AI

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ABSTRACT

Cells amaze us by showing remarkable resilience to some serious disturbances, while being surprisingly sensitive to minor changes. Creating a digital twin of a cell, a virtual copy of it, will allow different treatments to be tested on a computer before they are used. This will be particularly revolutionary for the treatment of early-stage pre-clinical diseases. Doctors will be able to simulate how different combinations of drugs that might affect a particular pre-clinical disease might affect, potentially avoiding harmful side effects and finding the most effective treatment faster. Detecting early-stage pre-clinical diseases at the molecular level using virtual cells with artificial intelligence is a hot international interdisciplinary research project. This mammoth project requires collaboration across disciplines, industries and countries. Creating virtual cells requires unprecedented collaboration between biologists, computer scientists, mathematicians and many other specialists. The process starts at the molecular level, creating detailed artificial intelligence models of the interactions of DNA, RNA and proteins. These will then be integrated into larger models that show how entire cells function, and eventually scaled up to show how cells work together in tissues and organs. Medical data is collected to identify specific prenosologies at the molecular level. Molecular microdiagnostics are developed and implemented to collect medical data on prenosologies. Solutions are found to neutralize prenosologies using synthesized virtual cells with artificial intelligence. The functionality of synthesized virtual cells with artificial intelligence is formed on the basis of medical data. Medical information is quite specific. Its main feature is the heterogeneity of data, which can be represented as both quantitative (numeric continuous or discrete) and qualitative (categorical ordinal and nominal) variables. Another feature is the long shelf life of medical data. It is also worth noting that the task of storing medical data is complicated by several aspects: the legal significance of the information, its large volume, heterogeneity and complex structure. Health Level 7 (HL7) — the standard for the exchange, management and integration of electronic medical information works with seven levels of open system interaction (OSI). The organization of the medical data storage system begins with the approval of the concept of creating synthesized virtual cells and their modeling, which is decisive in the choice of software and hardware. The creation of synthesized virtual cells will allow identifying diseases at the earliest stage, collecting the necessary data on the state of organs and the body as a whole, making smart analysis, conducting intelligent microdiagnostics and carrying out molecular and genetic healing.

Keywords

Prenosology, virtual cell, artificial intelligence, molecular microdiagnostics

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Introduction

At the intersection of bioimaging and proteomics are fundamental aspects of human cell biology. It is necessary to determine how human proteins are distributed in time and space, and how variations and biases in localization may contribute to cell type specificity and disease. Compartmentalization of biological processes is a fundamental principle of eukaryotic cells, allowing several processes to occur in parallel. Compartments are specialized for a particular cellular function and contain the molecules necessary for its execution. Defects in compartment organization or protein mislocalization underlie many forms of human disease. Despite a large number of studies, fundamental questions about the spatial organization of many proteins and biological processes remain unanswered. Using computational image analysis, variations in spatiotemporal patterns of protein expression at the level of individual cells are studied in relation to the cell cycle or other deterministic factors.

Researchers are creating artificially intelligent virtual cells (AIVC) to replicate the behavior of real human cells and their components (Theofanis Karaletsos *et al.,* 2024). This innovative concept is transforming biomedical research, personalized medicine, drug discovery, and cell engineering (Elizaveta Perepelitsa, 2024). Creating AIVC artificially intelligent virtual cells for early-stage pre-clinical research requires a multi-scale approach.

Starting at the molecular level, the system will use AI techniques such as transformers and neural networks to learn representations of DNA, RNA, and proteins from sequence data. These molecular representations will then be integrated into cellular-scale models incorporating data from various experimental techniques such as RNA sequencing and microscopy (Wenpin Hou and Zhicheng Ji, 2024). Finally, they will be combined into tissue-scale models using spatial data about how cells interact. The AI will be trained directly on the experimental data. The AIVC project is supported by various institutions, including the Chan Zuckerberg Initiative, Stanford University, Genentech, Microsoft Research, Google Research, and others (Bunne et al., 2024; Laura Thomson, 2024; By The Physics arXiv Blog, 2024).

For the AIVC project to be successful, it must develop models for different cell species and types. Accurately predict cell behavior. Support cost-effective computer experiments. This ambitious project requires massive data sets, global collaboration, and open sharing of results. AIVC will enable artificial intelligence to analyze data and unlock biological secrets without relying on assumptions. It can help scientists test ideas digitally, speeding up research and reducing the need for live experiments. A virtual cell could help study cancer, predict the effects of viruses, and provide personalized medicine by simulating treatments on digital patient models.

Cancer biologists could use these virtual cells to better understand how certain genetic mutations turn healthy cells into cancerous ones. Developmental biologists could track how cells change as organisms grow, potentially discovering new ways to treat birth defects or age-related diseases. Microbiologists could model viral infections to predict not only how viruses affect individual cells, but also how they might affect entire organs or systems.

The technical and technological challenges are enormous. Beyond simply managing vast amounts of data, scientists need to ensure that these virtual cells accurately reflect the incredible complexity of living systems. The authors stress that this must be an open scientific endeavor, with all models and results freely available to the entire scientific community. This approach ensures that researchers around the world can contribute to and benefit from the project. With today's rapidly expanding capabilities of artificial intelligence and our vast and growing data sets, the time has come for science to come together and begin working to revolutionize the way we understand and model biology. This revolution could fundamentally change the way we study life itself, offering new ways to understand disease, develop treatments, and unlock the mysteries of human biology.

Identification of pre-clinical diseases at the molecular level

Molecular preclinical identification is the process of identifying and analyzing molecular mechanisms associated with diseases that may arise as a result of genetic, epigenetic, or environmental factors. Preclinical identification, in this context, can be understood as the study of predisposition to diseases, their molecular markers, and the mechanisms that contribute to their development (Smagulov *et al.,* 2016; Evgeniy Bryndin *et al.,* 2020). Below we list the main aspects of molecular preclinical identification.

1. Genetic predisposition. Genome analysis using sequencing methods can identify mutations or polymorphisms associated with various diseases. For example, certain gene variants may be associated with an increased risk of developing cardiovascular disease, diabetes, or cancer.
2. Epigenetic changes. Epigenetic modifications, such as DNA methylation and histone modifications, can affect gene expression and contribute to the development of diseases. Studying these changes helps to understand how environmental factors can influence predisposition to diseases.
3. Molecular markers. Identification of specific molecular markers (e.g. biomarkers) can help in early diagnosis and prognosis of the course of diseases. These markers may include changes in the expression level of certain genes, the presence of specific proteins and metabolites.
4. Technological approaches. The use of high-throughput technologies such as microarray analysis, next-generation sequencing (NGS) and proteomics allows us to simultaneously study many molecules and identify associations between them and diseases.
5. Personalized medicine. The introduction of molecular analysis results into clinical practice allows us to develop individualized approaches to the prevention, diagnosis and treatment of diseases, taking into account the patient's molecular profile.

Identification of pre-nosology at the molecular level is an important direction in medicine, which opens up new possibilities for diagnostics and treatment of diseases.

This allows for a better understanding of the mechanisms of their development and the use of more effective and targeted therapeutic strategies and molecular diagnostics.

Molecular and spectral microdiagnostics

Molecular diagnostics is a field of medicine that uses molecular methods to detect diseases, determine their causes, and monitor the condition of patients. This approach is based on the analysis of molecules such as DNA, RNA, and proteins, which allows for more accurate and rapid diagnosis of diseases compared to traditional methods.

Molecular diagnostic methods

PCR (polymerase chain reaction) is one of the most common methods that allows amplification (increase the amount) of specific DNA fragments, making them more accessible for analysis.

Sequencing is a method that allows you to determine the sequence of nucleotides in DNA or RNA, which can be used to identify mutations or infections.

Genetic testing allows you to identify hereditary diseases, predisposition to diseases, etc.

Fluorescent in situ hybridization (FISH) is used to visualize and identify chromosomal abnormalities.

Diagnostics of infectious diseases allows you to quickly and accurately identify pathogens such as viruses, bacteria and fungi.

Oncological diagnostics are used to identify genetic changes in tumors, which can help in choosing targeted therapy.

Genetic diagnostics allows us to identify mutations associated with hereditary diseases.

Personalized molecular diagnostics helps in choosing the most effective treatment methods based on the patient's genetic characteristics.

Advantages of molecular microdiagnostics

High sensitivity and specificity. Possibility of early diagnosis of diseases. Quick results. Possibility of monitoring disease progression and response to treatment (Karen Aughton *et al.,* 2024; Bryndin and Putmakov, 2020).

Molecular diagnostics continues to evolve, and new technologies such as CRISPR and nanotechnology promise further breakthroughs in this field.

Spectral microdiagnostics

Spectral microdiagnostics of the body is based on the analysis of light spectra reflected or absorbed by tissues and cells of the body (Bryndin and Putmakov, 2020). This approach can be used to diagnose various diseases, monitor health and assess the effectiveness of treatment.

The method is based on the principle that each tissue and cell have unique spectral characteristics that depend on their structure and composition. Using various spectroscopic methods (for example, infrared spectroscopy, fluorescence spectroscopy and others), you can obtain information about the condition of tissues, identify pathological changes and even determine the level of some biomarkers.

The advantages of spectral microdiagnostics include:

1.Most methods do not require invasive procedures and can be performed on the surface of the skin or mucous membranes.
2.Obtaining analysis results can take only a few minutes.
3.Spectroscopy allows detecting changes in the early stages of the disease.

Further research and validation of methods on large patient samples, as well as the development of standards and protocols for clinical practice are necessary for the widespread use of spectral microdiagnostics.

Synthesized cells with artificial intelligence

Synthetic cells with artificial intelligence combine biology and technology to create cells with improved or new functions controlled by artificial intelligence algorithms. This field of science and technology is at the intersection of bioengineering, synthetic biology, and computer technology. Synthetic biology is concerned with the creation of new life forms or the modification of existing ones based on engineering and biology. Synthetic cells can be designed to perform specific functions, such as the production of drugs or other useful substances (Matteo Valentini *et al.,* 2024; Amara Angelica, 2024; Daly *et al.,* 2024; Ronit Freeman *et al.,* 2025).

Synthesis of brain cells

Brain cell engineering involves researching and developing methods to create brain cells in the laboratory. This includes approaches such as:

1. Stem cells. Researchers use stem cells, which have the potential to differentiate into a variety of cell types, including neurons and glia. This can be achieved by inducing stem cells to differentiate into neuronal cells using specific growth factors and culture conditions.
2. Brain organoids. These are small, three-dimensional structures that mimic aspects of the brain. They are created from stem cells and can help study brain development, neurodegenerative diseases, and drug testing.
3. Genetic techniques. Using gene editing techniques such as CRISPR-Cas9 to modify genes responsible for neuronal development and function.
4. Tissue engineering. Creating artificial tissues that can support neuronal growth and function to study neural networks and interactions.

These techniques open up new frontiers in neuroscience and may help treat diseases such as Alzheimer's, Parkinson's, and other neurodegenerative disorders. However, this area is still actively researched, and many aspects of brain cell synthesis require further study and understanding.

Artificial Intelligence

Artificial intelligence (AI) is used to optimize the design and creation of synthetic cells. Machine learning algorithms analyze data on cellular processes and predict how changes in genes or metabolic pathways affect cell function. Synthesized cells with AI can be used in medicine (for example, to create cells that can recognize and destroy cancer cells), ecology (for example, to clean up polluted water bodies), and manufacturing (for example, for the biosynthesis of materials).

Overall, synthetic cells with artificial intelligence represent a promising area of research that could lead to significant breakthroughs in various fields of science and technology.

Virtual organic cells with artificial intelligence

Virtual organic cells with artificial intelligence combine technologies from biology, computer science, and artificial intelligence. Although the technology is largely experimental at the moment, it could have many interesting applications and implications.

1. Virtual cells mimic the behavior of living cells. Such cells can be used to study cell biology, interactions between cells in organs and the body, and responses to external influences. Virtual cells can be created using simulations based on mathematical and physical models. Virtual cells can help model diseases and test new drugs without the need for living organisms.
2. Artificial intelligence is integrated into virtual cells to automate and optimize their behavior. Machine learning algorithms analyze data obtained from simulations to

predict how cells will respond to different conditions. This can help in the development of new drugs or in understanding disease mechanisms.

3. Synthetic biology research aims to create artificial cells or modify existing ones so that they perform specific functions. For example, creating artificial cells to produce useful substances. Or to simulate the interaction of cells with the environment to study the impact of climate change or pollution.
4. With the development of technologies such as bioinformatics, computational biology and synthetic biology, the idea of virtual cells with artificial intelligence may gain more attention and application in scientific research and industry.

Medical data for modeling intercellular interactions

Modeling cell-cell interactions requires a large and diverse set of medical data. Here are the key types of data that can be used in this area:

Genomic data: Information about DNA sequences, including gene variants, regulatory elements, and mutations. This data helps us understand how genetic factors influence cell function and interactions.

Transcriptomic data: Data about gene (RNA) expression in different cells and tissues. Each human cell contains 20,000 different genes. This data can help us determine which genes are active in which cells and how their expression changes in response to different conditions or diseases.

Proteomic data: Information about proteins, including their expression levels, modifications, and interactions. Each human cell contains about 42 million protein molecules. The Human Protein Atlas determines the subcellular location of all human proteins. Cell proteomes can provide information about cell function and interactions.

Metabolomic data: Data about metabolites, small molecules that participate in metabolic processes. This data helps us understand metabolic interactions between cells and their role in disease.

Cell signaling data: Information about the signaling pathways that control cell behavior. This may include data on signaling molecules, receptors, second messengers, and signaling cascades. 6.6. Clinical data. Patient data, including information on diseases, treatments, drug responses, and outcomes. This data can be used to create models that reflect the real-world health of patients and their cellular interactions.

Images and visualization: Microscopic images obtained using various techniques (e.g., fluorescence microscopy) can be used to analyze cell morphology and observe their interactions in real time.

Cell line data: Information about different cell lines, their characteristics, types, and behavior in culture. This data is useful for modeling and comparing the behavior of different cells.

Cell dynamics models: Models based on existing data that describe the interactions between cells, including mathematical and computer simulations.

Micromedia data: Information about the cellular environment, including the composition of the extracellular matrix, the presence of other cells and molecules that influence intercellular interactions.

By collecting and analyzing this data, researchers can create more accurate models of cell-cell interactions, which could lead to a better understanding of biological processes and the development of new treatments for disease.

Modeling body cells with virtual cells using artificial intelligence

Modeling the functional interactions of body cells using virtual cells and artificial intelligence (AI) is a rapidly developing field that has great potential in biomedical research and therapy (Theodoris, 2023; Le, 2023; Loconte *et al.,* 2023; Rosen *et al.,* 2023; Dalla-Torre *et al.,* 2023; Saar *et al.,* 2024; Lipman *et al.,* 2024; Chen *et al.*, 2024; Abramson *et al.*, 2024; Cesnik *et al.,* 2024; Cui *et al.,* 2024; Kraus *et al.,* 2024; Chen and Zou, 2024; Krishna *et al.,* 2024; Nguyen *et al.* 2024; Nguyen *et al.,* 2024; Roohani *et al.,* 2024; Nikitich *et al.,* 2024; Zimian Wang *et al.,* 2024). Some of the main areas in this field are:

Virtual cells: Researchers are developing virtual cell models that can mimic the behavior of real cells. These models take into account biochemical processes, signaling mechanisms, and interactions between cells and the environment. Virtual cells can be used to study various cellular functions and disease pathogenesis.

Artificial intelligence: Machine learning is used to analyze large amounts of data obtained from cellular studies. AI algorithms can identify patterns in cellular interactions, predict cell responses to drugs, and optimize conditions for cell therapy.

Systems biology: By combining virtual cells and artificial intelligence, scientists can model complex biological systems at the organ and whole-body level. This allows for a better understanding of how cells interact in health and disease, as well as the development of new approaches to therapy.

Predicting drug effects: Modeling cell interactions using AI-powered virtual cells helps predict how different drugs will affect cells, speeding up the drug discovery process and reducing the risk of negative side effects.

Personalized Medicine: Using AI-powered virtual cells leads to the creation of individualized patient models, allowing treatment to be better tailored to the specific characteristics of the body.

Education and Simulations: Virtual cells can be used to educate students and researchers by providing real-time simulations of cellular processes and interactions.

Despite significant advances, the field still faces many challenges, including the need for more accurate models, integration of data from different sources, and ensuring reproducibility of results. Ongoing research and development by the international AIVC project promises to expand our understanding of cell biology and improve approaches to disease treatment (Celaj *et al.,* 2023).

Creating an AIVC is not an easy task. It must, at a minimum, meet three key requirements: - Universality: the model must be able to represent cells of different species and types.

- **Accuracy:** the model must accurately predict the behavior of the cell and understand all the processes that occur in it.
- **Experimental flexibility:** the model must allow experiments to be carried out on the computer to test hypotheses and control data collection.

The successful implementation of the project will require the combined efforts of scientists from all over the world working in a variety of fields: genetics, proteomics, medical imaging and many others. It is also important that all the data and models obtained are available to the scientific community without any restrictions.

The AIVC project makes it possible to study cells in detail using powerful computer models. And this opens up completely new prospects for the development of biology and medicine.

An important component in creating a virtual cell will be the BioUML platform developed by scientists. It serves as a tool for building models of complex biological systems. It is planned to obtain virtual cells by 2026 (Elina Stoyanova *et al.,* 2024; Pavel Ivlev, 2024). With the help of the BioUML platform, models of programmed cell death and blood pressure regulation have already been created.

The time of virtual cells, virtual cell biology and medicine has come, and their potential is limitless. Rapid international creation and research of virtual cells requires powerful, ultra-fast, compact supercomputers. Nvidia has introduced the Jetson Orin Nano Super Developer Kit, a powerful, hand-sized AI supercomputer. This kit delivers 70% more performance, achieving 67 INT8 TOPS, and boosts memory bandwidth by 50% to 102GB/s, making it ideal for creating AI chatbots, visual agents, and robots. Existing Jetson Orin Nano users can unlock enhanced performance via a simple software update.

Designed for edge AI applications, the kit includes an Nvidia Ampere GPU, a 6-core Arm CPU, and support for up to four cameras, enabling on-device AI tasks without relying on remote data centers. Nvidia complements the hardware with robust software tools like Isaac for robotics, Metropolis for vision AI, and Holoscan for sensors, alongside resources from the Jetson AI Lab.

Developers can speed up projects using tools like Omniverse Replicator and TAO Toolkit. The thriving Jetson community and ecosystem offer additional support, including hardware add-ons and design services. The new ‘Super’ mode is now available through the JetPack SDK, enabling all Jetson Orin Nano and NX users to maximize their device’s potential.

The international network of Nvidia supercomputers Kit based on blockchain technology will be an effective tool for detecting diseases at the earliest stage, collecting necessary data on the condition of organs and the body as a whole, making smart analysis, helping to conduct intelligent microdiagnostics and carrying out molecular and genetic healing.

Research in the fields of immunology, infectious and viral diseases, mental health and near-death states have accumulated important big data for medicine and science in general.

Research on the functioning of the immune system, including the mechanisms of recognition and destruction of pathogens, the study of autoimmune diseases and allergies, as well as the practice of immunotherapy such as vaccines and monoclonal antibodies to combat infections and tumors have accumulated a large amount of data on an international scale.

Research on the prevalence of infections such as HIV, tuberculosis and hepatitis, the problem of bacterial resistance to antibiotics, which requires the development of molecular-level treatments using organic virtual cells with artificial intelligence.

Studying the structure, life cycles of viruses and big data on viruses such as influenza, hepatitis and coronaviruses, as well as investigating the mechanisms by which viruses cause diseases and how the body responds to them, will help in the development of virtual cells with artificial intelligence.

Understanding how mental disorders affect physical health and the immune response, as well as studying the physiological and psychological changes that occur in the body before death are important tasks in medicine. Synergy between immunology, infectious diseases and mental diseases will lead to a deeper understanding of human diseases at an early stage and the development of effective treatment and prevention strategies.

Identifying disease patterns using artificial intelligence based on big data from immunological, infectious, viral, psychosomatic and antemortem studies will reveal the common mechanism of diseases at an early stage at the molecular level (Fei-Fei Li, 2023; Evgeny Bryndin, 2024; MIT scientists *et al.,* 2024; MIT scientists *et al.,* 2024; Evgeny Bryndin 2024; Fei-Fei Li, 2025; Evgeny Bryndin, 2025). The external environment has a significant impact on the health of the body's cells. This impact can be manifested through various factors, such as physical, chemical, biological and social conditions. Key aspects of how the external environment affects cells:

Physical factors

- Temperature. Temperature changes can affect cell metabolism. High temperatures can lead to protein denaturation and damage to cellular structures, while low temperatures can slow down metabolism.
- Oxygen levels. Oxygen is critical for cellular respiration. Its deficiency (hypoxia) can lead to anaerobic metabolism, which is less efficient and can cause the accumulation of toxic products.
- Mechanical pressure and force. Physical impacts, such as pressure or stretching, can affect cell function, such as muscle and connective tissue cells.

Chemical factors

- Toxins and pollutants. Chemicals such as heavy metals or pesticides can damage cells by causing oxidative stress, inflammation or even DNA mutations.
- Nutrients. The availability of nutrients (glucose, amino acids, vitamins and minerals) affects the metabolism of cells and their ability to grow and reproduce.

Biological factors

- Infections. Viruses, bacteria and other pathogens can directly affect cells, causing their damage or death. The body's immune response to infection can also affect the state of cells.
- Microbiota. Microorganisms that inhabit the human body (for example, intestinal flora) can affect the metabolism and immune response of cells.
- External factors can cause epigenetic changes that affect the expression of genes in cells, which can lead to long-term changes in their function and condition.
- The body's cells are in constant interaction with the environment, and this interaction can significantly affect their condition, health and functionality.
- The body's cells adapt to the external environment through mechanisms that ensure their survival and functioning in changing conditions.

Intelligent systems with human-like spatial intelligence that explores the physical world as we do will add important capabilities to the AI toolbox that detects the impact of the environment on the health of human cells (Evgeny Bryndin 2024; Fei-Fei Li, 2025; Evgeny Bryndin, 2025; Greg Schuette *et al.,* 2025).

Author Contributions

Evgeniy Bryndin: Investigation, formal analysis, writing—original draft.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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