# How to Build the Virtual Cell with Artificial Intelligence: Priorities and Opportunities

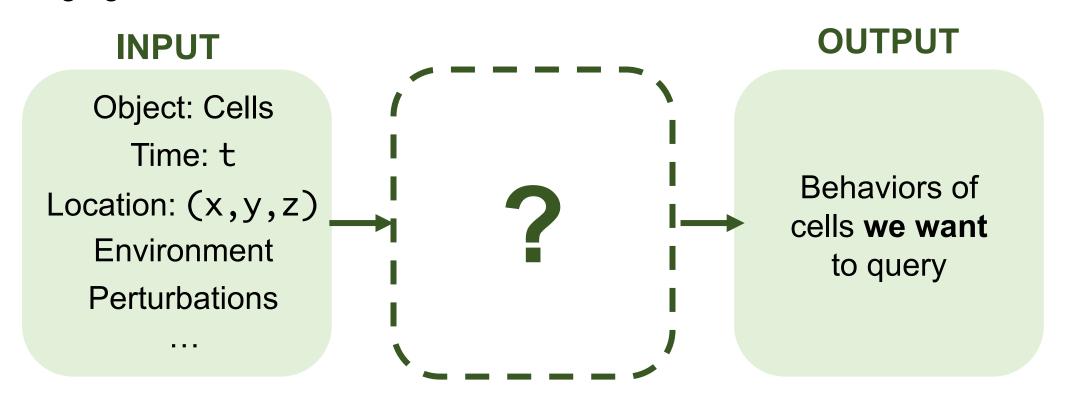
Cell 187, December 12, 2024

Literature Report 12212859 Sijie Li June 4<sup>th</sup>, 2025



#### Definition

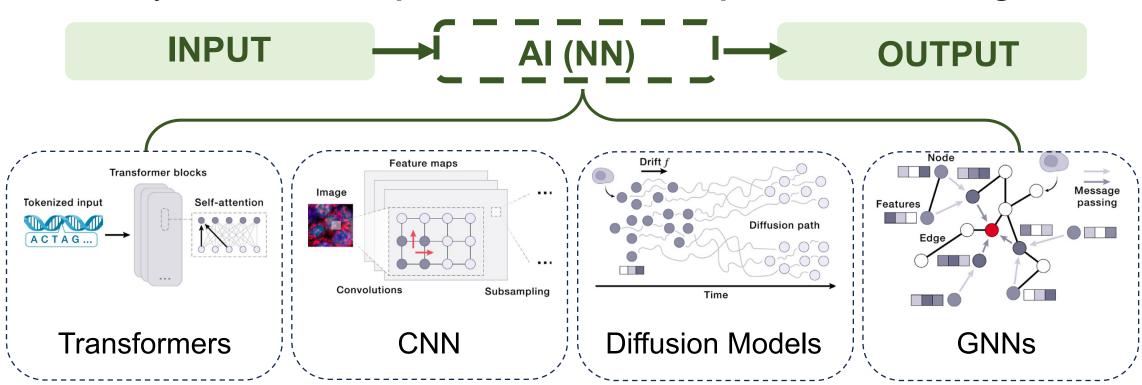
"simulator of cells and cellular systems under varying conditions and changing contexts"





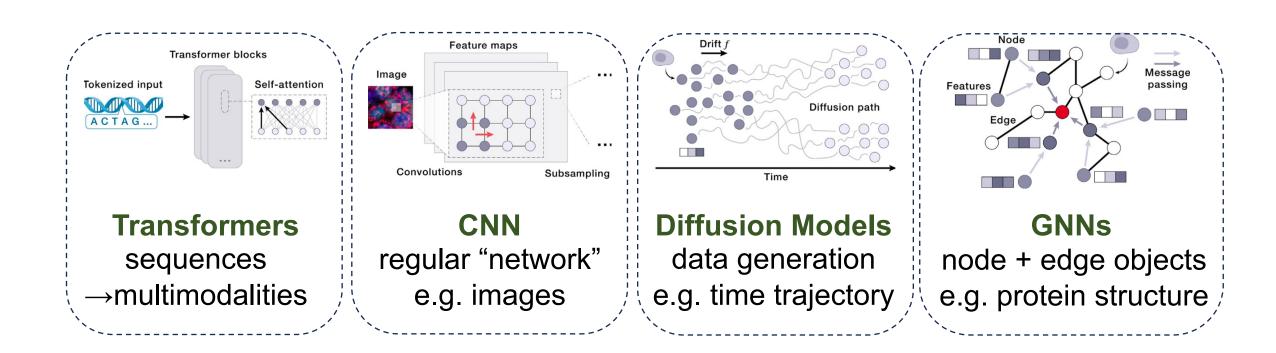
#### Definition

the ability of machines to perform tasks that require human intelligence



Artificial Intelligence (AI) → Machine Learning (ML) → Deep Learning (DL) → Neural Networks (NN)









**Transformers** 

CNN Diffusion Models

	<b>Primary coding</b>	Nueral network	Latent Space
Raw Data	<del></del>	Primary Embedding ———	Embedding

Simple Mapping

Linear projection or table lookup

e.g. self-attention token embedding

contextual embedding

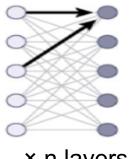
Gene A, B, C, D, E [5.2, 0.0, 1.8, 3.3, 7.1]

**Gene Expression** 

Gene A  $(5.2) \rightarrow [0.4, 1.1, -0.2]$ Gene B  $(0.0) \rightarrow [0.0, 0.0, 0.0]$ 

Gene C  $(1.8) \rightarrow [0.3, 0.2, 0.1]$ Gene D  $(3.3) \rightarrow [0.6, 0.7, -0.1]$ 

Gene E  $(7.1) \rightarrow [1.0, 1.2, 0.4]$ 



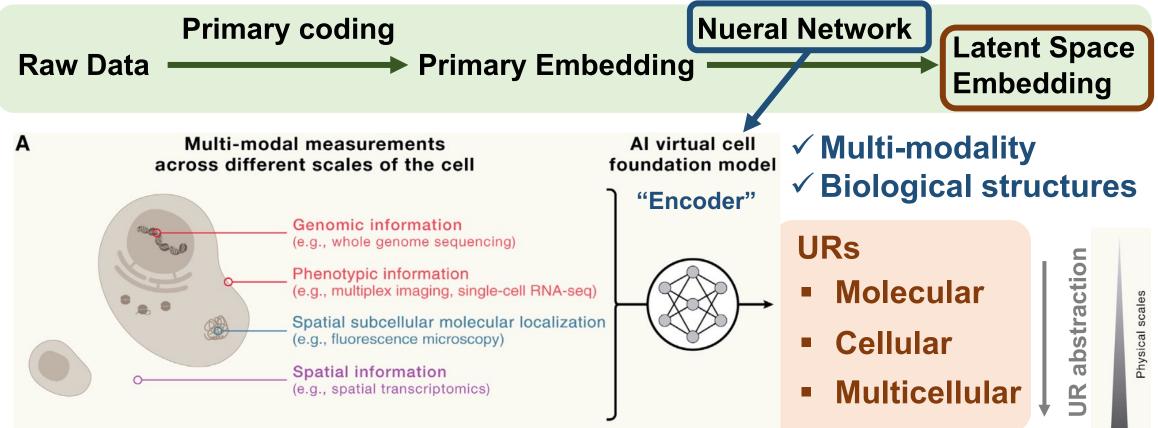
× n layers

- [[0.48, 0.90, 0.03],[0.10, 0.05, 0.12],[0.30, 0.35, 0.25],
- [0.52, 0.60, 0.10],
- [0.95, 1.00, 0.60]]

mean pooling [0.47, 0.58, 0.22]

- **Embedding**: a representation for computation
- numerical (2) preserve structure (3) enable further manipulation





Universal Representations (URs)

"embeddings produced by a multi-modal AIVC foundation model"



Raw Data AIVC Foundation Model UR Neural Network Cells Behavior

#### Manipulator virtual instruments e.g., chemical or genetic pertubation Unperturbed Perturbed cell UR cell UR e.g., changes in phenotype Cell UR Decoder virtual instruments

scale

for the cellular

ġ,

#### Virtual Instruments (VIs)

**Neural networks** that take URs as input and produce a desired output

```
pre UR

[0.47, 0.58, 0.22]

Manipulator VI
e.g. drug administration

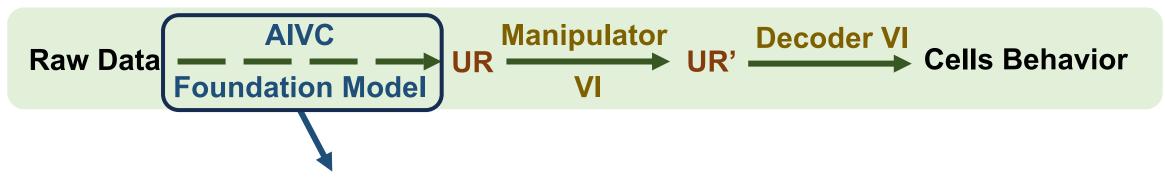
pro UR

[0.97, 0.04, 0.23]

Dcoder VI

Human

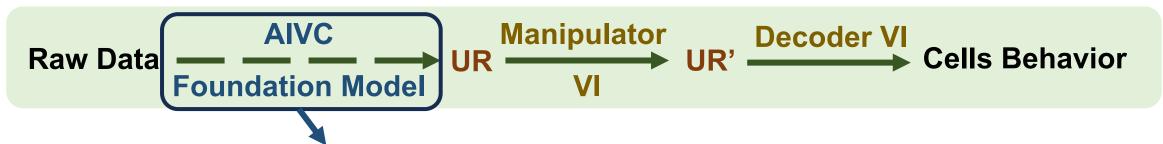
Gene A, B, C, D, E
[4.9, 30.0, 1.7, 17.8, 0.7]
```



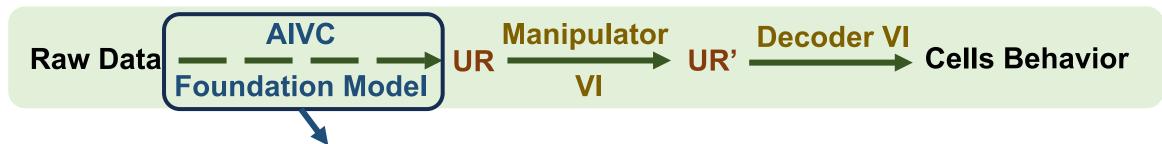
- > Tool Building: Architectures for multi-modal biological data
  - "Interconnection of many large models to capture everything in UR" ---- Charlotte Bunne
  - Self-consistent across scale, modality, and context
  - LACK! DNA ≠ texts, medical images ≠ images



- > Tool Building: Architectures for multi-modal biological data
- Data Collection
  - Multi-modal, multi-scale, multi-dimension (t, x), multi-species
  - Information amount: short read 14 pb > 1,000 × dataset used to train ChatGPT Redundant?
  - Perturbation: large combinatorial space; in vivo? → organoid...



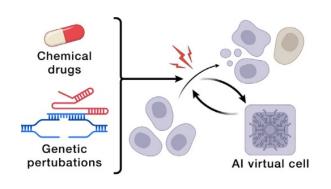
- > Tool Building: Architectures for multi-modal biological data
- Data Collection
- > Model Evaluation
  - Generalizability
  - Discovering new biology, †understanding



- > Tool Building: Architectures for multi-modal biological data
- Data Collection
- Model Evaluation
- > Interpretability VS Utility
  - Modular structure enable pinpointing
  - Project result to interpretable space (decoder VI)



- > Tool Building: Architectures for multi-modal biological data
- Data Collection
- Model Evaluation
- > Interpretability VS Utility
- > Community: non-expert interface, for collaboration!
- > Humanity Consideration: diversity, privacy, ethics...



> Predict Response

Cell state 1
e.g. expression
profile
Engineering
Cell state 2
(Response)
Drug delivery

> Unlock Biological Laws

Cold tumor Hot tumor

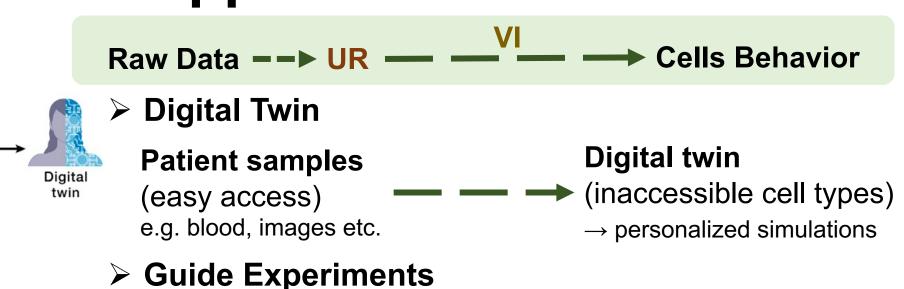
Tumor heterogeneity and microenvironment transcriptomics cell

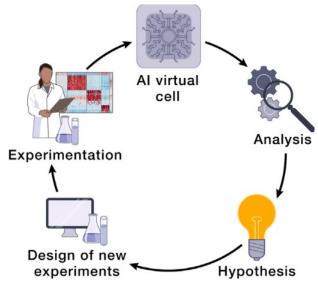
Tumor spatial **omics +**Microenvironment **conditions** 

Laws of tumor→ Heterogeneity insightsPan-cancer markers

Optimization

<sup>&</sup>quot;Machine Learning is the formalism through which we understand high dimensional data."





Al virtual

cell

Tissue sample

Plasma

RBCs/

**WBCs** 

**Cellular system state** 

Gene A, B, C, D, E [5.2, 0.0, 1.8, 3.3, 7.1]

#### intervention

Result with confidence

Gene A, B, C, D, E [4.9, 30.0, 1.7, 17.8, 0.7]

Possibility = 0.0001

**New Biology** or **Model Optimization** 

- Generate hypothesis
- Identify valuable data to collect

# AIVC: Priorities and Opportunities For us!

Charlotte Bunne, 1,2,3,4,50 Yusuf Roohani, 1,3,5,50 Yanay Rosen, 1,3,50 Ankit Gupta, 3,6 Xikun Zhang, 1,3,7 Marcel Roed, 1,3 Theo Alexandrov. 8,9 Mohammed AlQuraishi. 9 Patricia Brennan. 3 Daniel B. Burkhardt. 11 Andrea Califano. 10,12,13 Jonah Cool, Abby F. Dernburg, 14 Kirsty Ewing, Emily B. Fox, 1,15,16 Matthias Haury, 17 Amy E. Herr, 16,18 Eric Horvitz, 19 Patrick D. Hsu, 5,18,20 Viren Jain, 21 Gregory R. Johnson, 22 Thomas Kalil, 23 David R. Kelley, 24 Shana O. Kelley, 25,26 Anna Kreshuk,<sup>27</sup> Tim Mitchison,<sup>28</sup> Stephani Otte,<sup>17</sup> Jay Shendure,<sup>29,30,31,32</sup> Nicholas J. Sofroniew,<sup>33</sup> Fabian Theis,<sup>34,35,36</sup> Christina V. Theodoris, 37,38 Srigokul Upadhyayula, 14,16,39 Marc Valer, 3 Bo Wang, 40,41 Eric Xing, 42,43 Serena Yeung-Levy, 1,44 Marinka Zitnik, 45,46,47 Theofanis Karaletsos, 3,\* Aviv Regev, 2,\* Emma Lundberg, 3,6,7,48,\* Jure Leskovec, 1,3,\* and Stephen R. Quake 3,7,49,\*

- 42-author 50-institute blueprint
- A roadmap for a once-vague dream
- Require interdisciplinary collaboration
- BOLD! Doable?
- Together, I believe YES!

- <sup>1</sup>Department of Computer Science, Stanford University, Stanford, CA, USA
- <sup>2</sup>Genentech, South San Francisco, CA, USA
- <sup>3</sup>Chan Zuckerberg Initiative, Redwood City, CA, USA
- <sup>4</sup>School of Computer and Communication Sciences and School of Life Sciences, EPFL, Lausanne, Switzerland <sup>5</sup>Arc Institute, Palo Alto, CA, USA
- <sup>6</sup>Department of Protein Science, Science for Life Laboratory, KTH Royal Institute of Technology, Stockholm, Sweden
- <sup>7</sup>Department of Bioengineering, Stanford University, Stanford, CA, USA
- <sup>8</sup>Department of Pharmacology, University of California, San Diego, San Diego, CA, USA <sup>9</sup>Department of Bioengineering, University of California, San Diego, San Diego, CA, USA
- <sup>10</sup>Department of Systems Biology, Columbia University, New York, NY, USA
- <sup>11</sup>Cellarity, Somerville, MA, USA
- <sup>12</sup>Vagelos College of Physicians and Surgeons, Columbia University Irving Medical Center, New York, NY, USA
- <sup>13</sup>Chan Zuckerberg Biohub, New York, NY, USA
- <sup>14</sup>Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, CA, USA
- <sup>15</sup>Department of Statistics, Stanford University, Stanford, CA, USA
- <sup>16</sup>Chan Zuckerberg Biohub, San Francisco, CA, USA
- <sup>17</sup>Chan Zuckerberg Institute for Advanced Biological Imaging, Redwood City, CA, USA
- <sup>18</sup>Department of Bioengineering, University of California, Berkeley, Berkeley, CA, USA
- <sup>19</sup>Microsoft Research, Redmond, WA, USA
- <sup>20</sup>Center for Computational Biology, University of California, Berkeley, Berkeley, CA, USA
- <sup>21</sup>Google Research, Mountain View, CA, USA
- <sup>22</sup>NewLimit, San Francisco, CA, USA
- <sup>23</sup>Schmidt Futures, New York, NY, USA
- <sup>24</sup>Calico Life Sciences LLC, San Francisco, CA, USA
- <sup>25</sup>Chan Zuckerberg Biohub, Chicago, IL, USA
- <sup>26</sup>Northwestern University, Evanston, IL, USA
- <sup>27</sup>Cell Biology and Biophysics Unit, European Molecular Biology Laboratory, Heidelberg, Germany
- <sup>28</sup>Department of Systems Biology, Harvard Medical School, Boston, MA, USA
- <sup>29</sup>Department of Genome Sciences, University of Washington, Seattle, WA, USA
- 30Brotman Batv Institute for Precision Medicine, Seattle, WA, USA
- 31Seattle Hub for Synthetic Biology, Seattle, WA, USA
- 32Howard Hughes Medical Institute, Seattle, WA, USA
- 33EvolutionaryScale, PBC, New York, NY, USA
- <sup>34</sup>Institute of Computational Biology, Helmholtz Center Munich, Munich, Germany
- <sup>35</sup>School of Computing, Information and Technology, Technical University of Munich, Munich, Germany
- <sup>36</sup>TUM School of Life Sciences Weihenstephan, Technical University of Munich, Munich, Germany
- <sup>37</sup>Gladstone Institute of Cardiovascular Disease, Gladstone Institute of Data Science and Biotechnology, San Francisco, CA, USA
- 38 Department of Pediatrics, University of California, San Francisco, San Francisco, CA, USA
- <sup>39</sup>Molecular Biophysics and Integrated Bioimaging Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA
- <sup>40</sup>Department of Computer Science, University of Toronto, Toronto, ON, Canada
- <sup>41</sup>Vector Institute, Toronto, ON, Canada
- <sup>42</sup>Carnegie Mellon University, School of Computer Science, Pittsburgh, PA, USA
- <sup>43</sup>Mohamed Bin Zayed University of Artificial Intelligence, Abu Dhabi, United Arab Emirates
- <sup>44</sup>Department of Biomedical Data Science, Stanford University, Stanford, CA, USA
- <sup>45</sup>Department of Biomedical Informatics, Harvard Medical School, Boston, MA, USA
- <sup>46</sup>Kempner Institute for the Study of Natural and Artificial Intelligence, Harvard University, Cambridge, MA, USA
- <sup>47</sup>Broad Institute of MIT and Harvard, Cambridge, MA, USA
- <sup>48</sup>Department of Pathology, Stanford University, Stanford, CA, USA
- <sup>49</sup>Department of Applied Physics, Stanford University, Stanford, CA, USA
- 50These authors contributed equally

#### References

Bunne, C., Roohani, Y., Rosen, Y., Gupta, A., Zhang, X., Roed, M., Alexandrov, T., AlQuraishi, M., Brennan, P., Burkhardt, D. B., Califano, A., Cool, J., Dernburg, A. F., Ewing, K., Fox, E. B., Haury, M., Herr, A. E., Horvitz, E., Hsu, P. D., ... Quake, S. R. (2024). How to build the virtual cell with artificial intelligence: Priorities and opportunities. *Cell*, *187*(25), 7045–7063.

https://doi.org/10.1016/j.cell.2024.11.015

Topol, E. (2025, March 18). Steve Quake and Charlotte Bunne: The Holy Grail of Biology. *Ground Truths*. https://erictopol.substack.com/p/the-holy-grail-of-biology