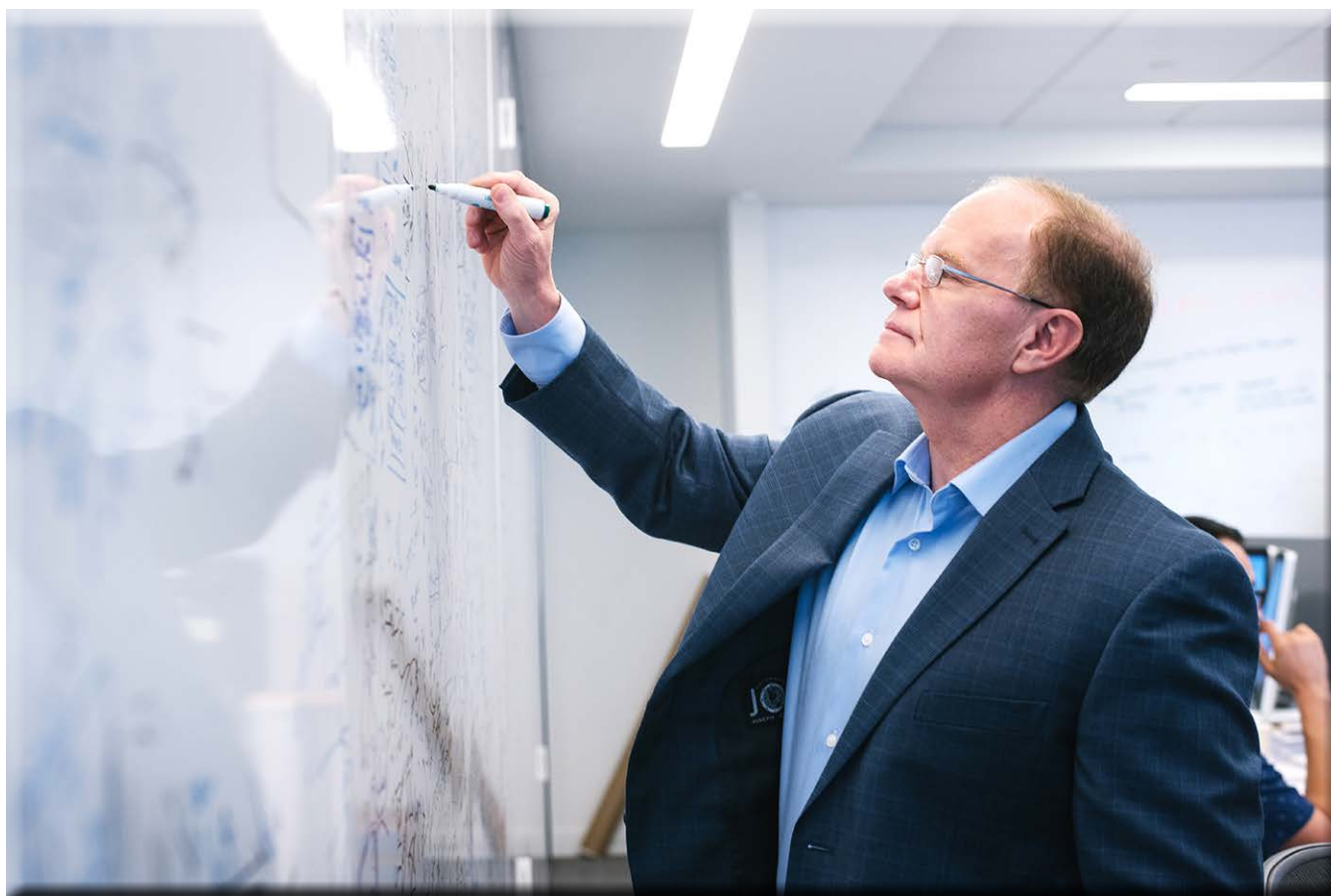


Tom Chittenden's AI Breakthrough in Cardiovascular Disease

by Kathy Kendrick, FSPE



Thomas Chittenden, PhD, DPhil, PStat, Chief Data Science Officer at WuXi NextCODE, is a Senior Fellow within ISPE and also serves as ISPE's Chief Statistical Sciences Advisor.

Telicom is extremely proud to share the remarkable news of a recent breakthrough in cardiovascular disease research made by Thousander Thomas “Tom” Chittenden, PhD, DPhil, and his team. As the Chief Data Science Officer of the WuXi NextCODE's Advanced AI Research Laboratory, Tom and his team, in cooperation with a group of Yale researchers led by Michael Simons, MD, have recently published the results of two of their studies: one in the *Journal of Experimental Medicine (JEM)* and the other in *Nature Metabolism*. An article titled, “Biologically-Validated A.I. Yields Breakthrough in Cardiovascular Disease,” which describes these two recent papers, can be read on

the *Genetic Engineering & Biotechnology News (GEN)* website.¹

About these remarkable findings, the *JEM* press release shared the following:

“It is a real milestone to be able to draw out and validate a causal biological network using such an efficient and replicable AI approach,” said Dr. Simons, Professor of Medicine and Cell Biology at Yale and senior author on the paper. “We have become quite good at making observations that correlate a genotype and a phenotype, but tracing the biology that lies between has always been elusive

because it is so complex. The promise of AI is that it is powerful enough to bring together all the biology and genetic data we now have to unravel this complexity, and Tom's group is leading the way in showing how this can be done."²

To further explain this breakthrough research, Tom Chittenden was also quoted in the press release as follows:

"Today we are providing a first concrete look at what we call phenotype projection: an efficient AI-driven approach that can predict complex phenotypes by teasing out the causal molecular underpinnings of disease," said Dr. Chittenden, Ph.D., DPhil, co-senior author. "By furthering our collective understanding of biology, such approaches hold the potential to be truly transformative. It means that we can understand virtually any disease in much greater detail using cost-effective experimental designs, a fundamental capability for creating precision medicine. The result is a range of validated potential points for developing therapeutic interventions; validated markers for designing smaller clinical trials with a greater chance of success; and a wealth of information for identifying patients likely to respond to approved compounds."³

Tom shared with *Telicom* that his team's work, which provides a new molecular understanding of aortic aneurysm, is currently in press at *Cell Stem Cell*, a leading cell journal. As Tom explained, "We have developed novel quantum and neuromorphic machine learning/AI strategies that allow integration and analysis of various aspects of single-cell, high-dimensional, genome-wide molecular time course data." The latest manuscript by Tom and his team, which describes the very first quantum machine learning (qML) method for the classification of actual human cancer data, can be read at Arxiv.org.⁴

To further share this remarkable breakthrough with the world, Tom presented a keynote address at the BioData World Congress in Basel, Switzerland, in December 2019. The webpage for BioData World Congress 2019 reports, "In 2019, Dr. Chittenden was named among the top 100 A.I. Leaders in Drug Discovery and Advanced Healthcare by Deep Knowledge Analytics. Dr. Chittenden holds a PhD in Molecular Cell Biology and Biotechnology from Virginia Tech and a DPhil in Computational Statistics from the University of Oxford."⁵ Tom's presentation for BioData World Congress 2019, which was titled, "Unconventional Machine Learning of Genome-wide Human Cancer Data," is summarized by him as follows:

We evaluated several unconventional machine learning (ML) strategies on actual human tumor data and showed for the first time the efficacy of multiple annealing-based ML algorithms for classification of high-dimensional, multi-omics human cancer data from the Cancer Genome Atlas. To assess algorithm performance, we compared these classifiers to a variety of standard ML methods, and results indicate the feasibility of using annealing-based ML to provide comparable classification of human cancer types and associated molecular subtypes and superior performance with smaller training datasets. Our results provide compelling empirical evidence for the potential future application of unconventional computing architectures in the biomedical sciences.⁶

Tom has also recently been interviewed by *GEN* for an upcoming article on AI in the life sciences; and, in December, he was invited to present a National Data Science Strategy/Vision to the National Institutes of Health. While it is obvious that Thousander Tom Chittenden is very busy working on this exciting research and sharing the discoveries with the world, *Telicom* is humbled that he has also agreed to author a technical

article, further explaining this exciting research, for a future *Telicom* issue.

On behalf of all of ISPE, *Telicom* extends hearty congratulations to you, Tom Chittenden, on the outstanding discoveries and breakthroughs you

have made in cardiovascular disease research.

Your findings are truly a benefit to mankind.

We at ISPE are excited about your research and sincerely wish you many more successes in your future work.

NOTES

1. “Biologically-Validated A.I. Yields Breakthrough in Cardiovascular Disease,” *Genetic Engineering & Biotechnology News* 39, no. 10 (October 1, 2019), <https://www.genengnews.com/sponsored/biologically-validated-a-i-yields-breakthrough-in-cardiovascular-disease/?fbclid=IwAR1XXlhbCCBUhsjvcky5oVHnCbAjOugPX3SZsJQixIs8foVHbuN7o1ok8z4>.

2. “Yale and WuXi NextCODE Use AI to Predict Phenotypes *In Vivo*,” *Journal of Experimental Medicine*, https://wxnc-7c45.kxcdn.com/wp-content/uploads/2019/06/YaleAndWXNCvalidateAIinVivo_13June2019-1.pdf.

3. Ibid.

4. Richard Y. Li, Sharvari Gujja, Sweta R. Bajaj, Omar E. Gamel, Nicholas Cilfone, Jeffrey R. Gulcher, Daniel A. Lidar, and Thomas W. Chittenden, “Unconventional Machine Learning of Genome-Wide Human Cancer Data,” Cornell University, arXiv, <https://arxiv.org/abs/1909.06206>.

5. “Tom Chittenden: Chief Data Science Officer, WuXi NextCODE,” BioData World Congress 2019, <https://www.terrapinn.com/conference/biodata/speaker-tom-CHITTENDEN.stm>.

6. Ibid. Ω

“I do not fear computers.
I fear the lack of them.”

—Isaac Asimov