Curriculum Vitae

Yen-Lin Chen, Ph.D.

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https://scholar.google.com/citations?user=tNrpPbcAAAAJ&hl=en#

Education

| 12/2020 | Ph.D. in Applied Physics, Cornell University |
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| 06/2018 | M.S. in Engineering Physics, Cornell University |
| 01/2014 | B.S. with Honors in Physics, National Taiwan University |

Professional Experiences

Seismic Therapeutic, Cambridge, MA

Machine Learning Scientist and Project Lead

- Develop noise2noise image processing pipeline for denoising cryoEM images and achieve higher resolution and throughput.
- Conceptualize and implement novel representations of protein complexes with SOTA B-cell and T-cell epitope prediction performances.
- Apply and develop geometric machine learning algorithms to model biomolecular structures for drug discovery applications.
- Design structure-informed sequences using graph neural networks and evolutionary models for desired molecular properties with high hit rate.
- Lead drug creation and discovery programs by outlining screening tree, timeline, tasks, presentations and working with CROs.

ReviveMed Technologies, Cambridge, MA

Senior Computational Biologist

- Provided ReviveMed's platform reviews and support CEO in fundraising, shareholders', and board meetings with approved tech dev direction.
- Ideated and streamline statistical testing of graphs with GNN and identify driving cells in tumor micro env under immunotherapy responses.
- Developed novel Meta-Learning pipelines to tackle few-sample cases and derive biomarkers for in-vivo experimental validations.
- Designed and oversee diverse projects that suit personal interests, create values and are applicable/scalable to the fast-moving field.

Computational Biologist

- Developed algorithms for biological network optimization, integrated multiomics data, inference, and delivered successful therapeutic targets.
- Integrated graph representation learning and Bayesian causal models on knowledge graphs to assess robustness of targets.
- Constructed computational pipeline to infer single-cell biological processes from bulk patient data with a provisional patent.

02/2022 -

08/2021 - 02/2022

01/2021 - 08/2021

Graduate Researcher

- Integrated experiments (sm-FRET and X-ray scattering), all-atom MD simulations and computations (Genetic Algorithms and ML/DL) to study the dynamics of functional RNA domains with interactions with ions, ligands, proteins, and RNA binding partners.
- Designed a large-scale optimization algorithm in Julia and discovered high-resolution electron density of biomolecules in vitro.
- Initiated and led 5 multidisciplinary collaborations and delivered 7 first-authored peer-reviewed publications in PNAS, Science Advances and more.

Honors and Awards

08/2015 - 12/2020

Cornell University, Ithaca, NY

| 2015 | Cornell Fellowship |
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| 2017, 18, 20 | Cornell Graduate Travel Grant |
| 2021 | William Nicholas Findley Award |

National Taiwan University, Taipei, Taiwan

| 2009, 10, 11 | Presidential Awards |
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| 2013 | Dean's List |

Invited Talks

- <u>Chen, YL.</u>, Decoding Hidden Structural Information in Solution Wide-Angle X-ray Scattering (WAXS): from Ensemble Modeling to Machine Learning. 71st Annual Meeting of the American Crystallographic Association, Aug 2021, Online
- 2. <u>Chen, YL.</u>, Twisting the Helix: Salt Dependence of Conformations of RNA Duplexes. *Cornell High Energy Synchrotron Sources: Science Highlight*. Dec 2019. Ithaca, NY, USA

Conference Presentations

- <u>Chen, YL.</u>, He, W., Kirmizialtin, S. and Pollack, L. Decoding Hidden Structural Information in Solution Wide-Angle X-ray Scattering (WAXS): from Ensemble Modeling to Machine Learning, *Acta Crystallographica A-Foundation and Advances* 2021, 77, A126
- 2. He, W., <u>Chen, YL.</u>, Pollack, L. and Kirmizialtin, S. Visualization of biomolecular structures by WAXS and MD, *Acta Crystallographica A-Foundation and Advances* 2021, 77, A124
- <u>Chen, YL.</u>, He, W., Kirmizialtin, S. and Pollack, L. Breaking the Boundary between Solution X-ray Scattering and Molecular Dynamics Simulations of Structured Nucleic Acids. *Biophysical Journal* 2021; 120, 3 315A
- 4. Pabit, S.A., <u>Chen, YL.</u>, Usher, G.A., Cook, E.C., Pollack, L., and Showalter, S.A. Evidence that primary microRNA bends in the presence of DGCR8, *Biophysical Journal* 2020; 118, 3, S.1., 222A
- 5. <u>Chen, YL</u>., and Pollack, L. Convolutional Neural Networks Bridge Between Molecular Models and Solution X-ray Scattering Experiments. *Biophysical Journal* 2020; 118, 3, S.1, 301A
- 6. <u>Chen, YL.</u> and Pollack, L. Quantitative Analysis of Salt-induced RNA Duplex Variations by Wide-Angle X-ray Scattering. *Biophysical Journal* 2020; 118, 3, S.1, 68A

- 7. <u>Chen, YL</u>., Lee, T., Elber, R. and Pollack, L. Understanding an RNA Helix-junction-Helix Construct by SAXS Refinement of MD Models. *Biophysical Journal* 2018; 114, 3, S.1, 433A
- 8. <u>Chen, YL</u>., Pabit, S.A., Katz, A.M. and Pollack, L. Using WAXS to Study RNA Conformations. *Biophysical Journal* 2017; 112, 3, S.1, 580A

Peer-Reviewed Journal Publications

- 1. <u>Chen, YL.*</u>, He, W.*, Kirmizialtin, S. and Pollack, L. RNA triplex structures revealed by WAXSdriven MD simulations**. *Cell Reports Physical Sciences*, 2022, 3, 7
- 2. He, W.*, <u>Chen, YL</u>.*, Pollack, L. and Kirmizaltin, S. The structural plasticity of nucleic acid duplexes revealed by WAXS and MD. *Science Advances*, 2021, 7, 17
- Torabi, S.*, <u>Chen, YL</u>.*, Zhang, K.*, Wang, J., DeGregorio, S., Vaidya, A. Su, Z., Pabit, S.A., Chiu, W. Pollack, L., and Steitz, J. Structural analyses of an RNA stability element interacting with poly(A). *Proceedings of the National Academy of Sciences of the United States of America* 2021, 118, 14
- Pabit, S.A.*, <u>Chen, YL.*</u>, Usher, E.T., Cook, E.C., Pollack, L. and Showalter, S.A. Elucidating the Role of Microprocessor Protein DGCR8 in Bending RNA Structures, *Biophysical Journal* 2020 Dec 15; 119, 12, 2524-2536
- 5. <u>Chen, YL.</u> and Pollack, L. Machine learning deciphers structural features of RNA duplexes measured with solution X-ray scattering, *International Union of Crystallographic Journal* 2020, 7, 5, 870-880
- 6. <u>Chen, YL</u>. and Pollack, L. Salt Dependence of A-Form RNA Duplexes: Structures and Implications. *Journal of Physical Chemistry B* 2019, 123, 46, 9773-9785
- 7. <u>Chen, YL</u>., Lee, T., Elber, R. and Pollack, L. Conformations of an RNA Helix-Junction-Helix Construct Revealed by SAXS Refinement of MD Simulations. *Biophysical Journal* 2019;116(1):19-30
- 8. <u>Chen, YL</u>.*, Sutton, J.L.* and Pollack, L. How the Conformations of an Internal Junction Contribute to Fold an RNA Domain. *Journal of Physical Chemistry B* 2018;122(49):11363-11372

* Contributed Equally

Preprint

- 1. <u>Chen, YL.</u> and Pollack, L. In Vitro Electron Density Refinement from Solution X-ray Scattering in the Wide-Angle Regime, *arXiv e-prints* 2020, arXiv:2012.13370
- 2. <u>Chen, YL.</u> Bridging Theories and Experiments: Modeling Solution X-Ray Scattering of Small RNA Molecules. *Ph.D. Thesis, Cornell University* 2020

Provisional Patent Application

- <u>Chen, YL.</u>, et. al. Engineered Fc Polypeptides and Uses There of, (U.S. Provisional Patent Application No. 63/380842). Filed Sept 2022 by Seismic Therapeutic.
- <u>Chen, YL</u>, Biological Mechanism Identification System, (U.S. Provisional Patent Application No. 63/181473). Filed Jul 2021 by ReviveMed Technologies.