DR. JAEOH SHIN

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SUMMARY

- As a theoretical/ computational physicist, I have over a decade of research experience in solving complex biological problems using physics concepts and computational/ statistical methods in multidisciplinary environments.
- I have great strength in theory and computational methods, as shown in a strong publication record (25 peer-reviewed papers).

SKILLS

- Programming language: C (15 years), Fortran (2 years), Python (2 years), C++ (1 year)
- Brownian dynamics, Molecular dynamics, Monte-Carlo simulations, High-Performance Computing (HPC), Agent-based models
- Computational Package: GROMACS, LAMMPS, Mathematica, Octave (Matlab)
- Major Machine learning algorithms (regression, deep-learning, etc)
- Online courses: Python for Data Science and Machine learning Boot camp (Udemy), Machine learning with Python (IBM), Biostatistics Tutorial full course for Beginner to Experts

EDUCATION

- PhD, Physics, POSTECH (Pohang University of Science and Technology), South Korea, 2013, Thesis title: "Barrier crossing Problems in Biopolymer dynamics"
- BS, Physics, Korea University, Seoul, South Korea, 2006

WORK EXPERIENCE

Career Break San Bruno, CA, USA

Professional Development

- Developing computational skills: Python, Machine Learning, R, Git

Synlico Inc.

Scientist - Computational Biology

Burlingame, CA, USA June 2022 to Nov. 2022

Dec. 2022 to Present

- As one of the first employees of a biotech start-up company, I have worked on modelling the immune synapse- the junction between T cell and cancer cell using physics concepts. I have used an agent-based modelling approach to understand the fascinating structure formation at the synapse.

Department of Chemistry, Rice University

Postdoc Research Associate

Houston, TX, USA May 2017 to April 2022

- Led several projects on how proteins can efficiently find target sites on DNA using the theory of stochastic processes and Monte
 Carlo simulations. The research aimed to capture the essential features of complex processes using relatively simple physics
 models.
- Revealed that a fundamental property of transition time symmetry can be broken in non-equilibrium systems. Proposed experimentally testable predictions that can measure the deviation from equilibrium.

Max Planck Institute for the Physics of Complex Systems

Dresden, Germany

Guest Scientist

Mar. 2015 to April 2017

- As a lead theoretician, I successfully explained the mechanism of RNA polymerase elongation along with nucleosomal DNA
 using the concepts of random walks on a lattice. This work was done in collaboration with a single molecule experimental
 group, and the result has been published in prestigious journal PNAS.
- Worked on polymer dynamics in active fluids, and proposed the polymer separation methods based on its elastic properties by using Langevin dynamics simulations.

University of Potsdam Potsdam, Germany

Postdoc Researcher

Mar. 2013 to Mar. 2015

- Led several polymer dynamics projects those are relevant to biological systems, including DNA looping in crowded environments by using Langevin dynamics simulations
- Proposed cheap and efficient virus detection method based on physics principle.

MENTORING AND TEACHING EXPERIENCE

- 2015 2022 Mentored 5 Graduate students and 2 undergraduates (with them, I published five research papers)
- 2006 2007 Graduate Teaching Assistant for General Physics

PUBLICATIONS

25 publications (17 first-authored) in peer-reviewed scientific journals (total citations: >570)

Google scholar profile

Selected top 4 publications:

- 1. J. Shin, A. M. Berezhkovskii, and A. B. Kolomeisky, Biased random walk in crowded environment: Breaking uphill/downhill symmetry of transition times, J. Phys. Chem. Lett. 11, 4530 (2020).
- 2. V. Fitz, J. Shin*, C. Ehrlich, L. Farnung, P. Cramer, V. Zaburdaev, and S. W. Grill, Nucleosomal arrangement affects single molecule transcription dynamics, Proc. Natl. Acad. Sci. U.S.A. 113, 12733 (2016). (*Lead theoretician)

- 3. J. Shin, A. G. Cherstvy, and R. Metzler, Polymer looping with macromolecular crowding: effects of volume fraction and crowder size, Soft Matt. 11, 472 (2015).
- 4. J. Shin, A. G. Cherstvy, and R. Metzler, Sensing viruses by mechanical tension of DNA in responsive hydrogels, Phys. Rev. X 4, 021002 (2014).

Full publications:

- 1. C. Felipe, J. Shin, and A. B. Kolomeisky, How Pioneer Transcription Factors Search for Target Sites on Nucleosomal DNA, J. Phys. Chem. B. 126, 4061 (2022).
- 2. K. Klett, A. G. Cherstvy, J. Shin, I. Sokolov, and R. Metzler, Non-Gaussian, transiently anomalous and ergodic self-diffusion of flexible dumbbells in crowded two-dimensional environments: Coupled translational and rotational motions, Phys. Rev. E (2021).
- 3. J. Clopés, J. Shin, M. Jahnel, S. W. Grill, V. Zaburdaev, Thermal fluctuations assist mechanical signal propagation in coiled-coil proteins, Phys. Rev. E 104, 054403 (2021).
- 4. J. Shin, A. M. Berezhkovskii, and A. B. Kolomeisky, Crowding breaks the forward/backward symmetry of transition times in biased random walks, 154, 204104 (2021).
- 5. C. Felipe, J. Shin, and A. B. Kolomeisky, DNA Looping and DNA Conformational Fluctuations Can Accelerate Protein Target Search, J. Phys. Chem. B. 125, 1727 (2021).
- 6. J. Shin and A. B. Kolomeisky, Asymmetry of forward/backward transition times as a non-equilibrium measure of complexity of microscopic mechanisms, J. Chem. Phys. 153, 124103 (2020).
- 7. C. Felipe, J. Shin, J. Loginova, and A. B. Kolomeisky, The effect of obstacles in multi-site protein target search with DNA looping, J. Chem. Phys. 152, 025101 (2020).
- 8. J. Shin and A. B. Kolomeisky, Target search on DNA by interacting molecules: First-passage approach, J. Chem. Phys. 151, 125101 (2019).
- 9. J. Shin and A. B. Kolomeisky, Facilitation of DNA loop formation by protein-DNA non-specific interactions, Soft Matt., 15, 5255 (2019).
- 10. J. Shin and A. B. Kolomeisky, Molecular search with conformational change: one-dimensional discrete-state stochastic model, J. Chem. Phys. 149, 174104 (2018).
- 11. W. Huang, Y. T. Lin, D. Frömberg, J. Shin, F. Jülicher, and V. Zaburdaev, Exactly solvable dynamics of forced polymer loops, New. J. Phys. 20, 113005 (2018).
- 12. J. Shin and A. B. Kolomeisky, Surface-assisted dynamic search processes, J. Phys. Chem. B 122, 2243 (2018).
- 13. J. Shin, A. G. Chersty, W. K. Kim, and V. Zaburdaev, Elasticity-based polymer sorting in active fluids: A Brownian dynamics study, Phys. Chem. Chem. Phys. 19, 18338 (2017).
- 14. J. Shin, A. G. Cherstvy, and R. Metzler, Self-subdiffusion in solutions of star-shaped crowders: non-monotonic effects of interparticle interactions, New J. Phys. 17, 113028 (2015).
- 15. J. Shin, A. G. Cherstvy, W. K. Kim, and R. Metzler, Facilitation of polymer looping and giant polymer diffusivity in crowded solutions of active particles, New J. Phys. 17, 113008 (2015).
- 16. J. Shin, O.-C. Lee, and W. Sung, How a short double-stranded DNA bends, J. Chem. Phys. 142, 155101 (2015).
- 17. J. Shin, A. G. Cherstvy, and R. Metzler, Polymer looping is controlled by macromolecular crowding, spatial confinement, and chain stiffness, ACS Macro Lett. 4, 202 (2015).
- 18. J. Shin, A. G. Cherstvy, and R. Metzler, Mixing and segregation of ring polymers: spatial confinement and molecular crowding effects, New J. Phys. 16, 053047 (2014). Cited 50+ times
- 19. T. Ikonen, J. Shin, W. Sung, and T. Ala-Nissila, Polymer translocation under time-dependent driving forces: resonant activation induced by attractive polymer-pore interactions, J. Chem. Phys. 136, 205104 (2012).
- 20. J. Shin and W. Sung, Effects of static and temporally fluctuating tension on semiflexible polymer looping, J. Chem. Phys. 136, 045101, (2012).
- 21. J. Shin, T. Ikonen, M. D. Khandkar, T. Ala-Nissila, and W. Sung, Polymer escape from a metastable Kramers potential: Path integral hyperdynamics, J. Chem. Phys. 133, 184902 (2010).

TALKS

I gave 36+ invited seminar talks/ academic conference talks in various institutes/ conferences, including

- (via Zoom) Protein search for target sites: A first-passage time approach, Symposium for the Biological Physics Session of the Korean Physical Society, Feb. 2021
- (via Zoom) How can transition time symmetry be broken? APCTP Workshop on Stochasticity and Fluctuations in Small Systems, Nov. 2020
- (via Zoom) Understanding cellular processes from the molecular point of view, Korea Institute for the Advanced Study (KIAS), Seoul, July, 2020
- Understanding cellular processes from the molecular point of view, APCTP, Pohang, Korea, Nov. 2019
- Facilitated Diffusion: How to exceed the Smolochowski rate?, Helmholtzzentrum, Berlin, June 2018

PEER REVIEW

- I have reviewed over 17 manuscripts in International scientific journals, including Phys. Rev. Lett., Phys. Rev. E., J. Chem. Phys., J. Biol. Phys., Phys. Chem. Chem. Phys. (PCCP).