

## Ayan Chatterjee

<b>Short Bio</b>	I am currently a fourth-year Ph.D. student at the Network Science Institute (NetSI) of Northeastern University, Boston. My research interests primarily lie in the field of graph machine learning, with a specific focus on areas such as link prediction, graph embeddings, and the application of network science in the context of biological networks. Prior to my time at NetSI, I gained valuable experience while working at NVIDIA Graphics, where I contributed to the development of various GPU architectures, including Turing, Ampere, and Hopper. These advancements in GPU technology have played a significant role in fueling the ongoing revolution in artificial intelligence.
<b>Contact Information</b>	177 Huntington Ave. Boston, MA 02115 E-mail: chatterjee.ay@northeastern.edu Mobile: (617) 840-8467
<b>Education</b>	<b>Northeastern University</b> (2019 - Present) Ph.D. Student, Network Science Institute Advisor: Prof. Tina Eliassi-Rad Research Interests: Graph Machine Learning, Link Prediction, Interpretability, XAI, and Network Science.
<b>Publications</b>	<p><b>Ayan Chatterjee</b>, Robin Walters, Giulia Menichetti, Tina Eliassi-Rad. 2023. Disentangling Node Attributes from Graph Topology for Improved Generalizability in Link Prediction. Under review to NeurIPS 2023. Pre-print: <a href="https://arxiv.org/abs/2307.08877">https://arxiv.org/abs/2307.08877</a>.</p> <p><b>Ayan Chatterjee</b>, Robin Walters, Zohair Shafi, Omair Shafi Ahmed, Michael Sebek, Deisy Gysi, Rose Yu, Tina Eliassi-Rad, Albert-László Barabási, Giulia Menichetti. 2021. Improving the generalizability of protein-ligand binding predictions with AI-Bind. Nat Commun 14, 1989 (2023). <a href="https://doi.org/10.1038/s41467-023-37572-z">https://doi.org/10.1038/s41467-023-37572-z</a>.</p> <p>Zohair Shafi, <b>Ayan Chatterjee</b>, Tina Eliassi-Rad. 2023. Explaining Node Embeddings. Submitted to Applied Network Science.</p> <p><b>Ayan Chatterjee</b>, Qingtao Cao, Amirhossein Sajadi, Babak Ravandi. Deterministic random walk model in NetLogo and the identification of asymmetric saturation time in random graph. Appl Netw Sci 8, 33 (2023). <a href="https://doi.org/10.1007/s41109-023-00559-2">https://doi.org/10.1007/s41109-023-00559-2</a>.</p> <p>Tünde Pacza, Mayara L. Martins, Maha Rockaya, Katalin Müller, <b>Ayan Chatterjee</b>, Albert-László Barabási &amp; József Baranyi. MilkyBase, a database of human milk composition as a function of maternal-, infant- and measurement conditions. Sci Data 9, 557 (2022). <a href="https://doi.org/10.1038/s41597-022-01663-1">https://doi.org/10.1038/s41597-022-01663-1</a>.</p> <p><b>Google Scholar:</b> <a href="#">here</a>.</p>

<b>Book Chapter</b>	<b>Ayan Chatterjee</b> , Debayan Das, Amitava Mukherjee, Mrinal Kanti Naskar, Design of structural controllability for complex network architecture, in the book ‘Advanced Methods for Complex Network Analysis, IGI Global Publishers, 2016. <a href="https://doi.org/10.4018/978-1-4666-9964-9.ch004">https://doi.org/10.4018/978-1-4666-9964-9.ch004</a> .		
<b>Invited Talks</b>	2022	Identifying interactions between novel protein targets and ligands: AI-Bind and AI-assisted molecular docking. Khoury College of Computer Sciences, Northeastern University, Boston. <a href="#">[Slides]</a>	
	2022	Channing Methods Meeting on identifying interactions between novel protein targets and ligands: AI-Bind and AI-assisted molecular docking . Harvard T.H. Chan School of Public Health, Harvard University, Boston. <a href="#">[Slides]</a>	
<b>Work Experience</b>	<b>Alexion AstraZeneca Rare Disease - Summer Intern</b> May 2023 - Aug 2023 Inductive link prediction on protein-protein interaction network for rare-disease centric target identification.		
	<b>NVIDIA - Computer Architect</b> Aug 2017 - Aug 2019 Designing GPU architecture for AI acceleration and ray tracing.		
<b>Reviewer</b>	Journal of Machine Learning Research Workshop on Graph Learning Benchmarks Learning on Graphs Conference Transactions on Knowledge Discovery from Data		