

# RAHMATULLAH ROCHE

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## EDUCATION

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<b>Ph.D. in Computer Science and Application</b> Virginia Tech	August 2021 – Ongoing Blacksburg, Virginia, USA
<b>Master of Science in Computer Science and Software Engineering</b> Auburn University	August 2018 – July 2021 Auburn, Alabama, USA
<b>Bachelor of Science in Computer Science and Engineering</b> Bangladesh University of Engineering and Technology (BUET)	February 2011 – February 2016 Dhaka, Bangladesh

## RESEARCH AND TEACHING EXPERIENCE

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<b>Research Assistant</b> Advisor: Dr. Debswapna Bhattacharya, Department of CS, Virginia Tech <ul style="list-style-type: none"><li>Employing deep learning techniques for predictive modeling</li></ul>	August 2021 – Ongoing Blacksburg, Virginia, USA
<b>Research Assistant</b> Advisor: Dr. Debswapna Bhattacharya, Department of CSSE, Auburn University <ul style="list-style-type: none"><li>Developed methods for protein 3D structure prediction</li><li>Worked on protein 3D structure visualization</li></ul>	August 2018 – July 2021 Auburn, Alabama, USA
<b>Teaching Assistant</b> Department of CSSE, Auburn University <ul style="list-style-type: none"><li>Evaluated projects and assignments</li><li>Conducted question answering sessions and office hours</li></ul>	August 2018 – December 2020 Auburn, Alabama, USA
<b>Lecturer</b> Department of CSE, Eastern University <ul style="list-style-type: none"><li>Taught core courses of computer science</li><li>Supervised and monitored projects</li><li>Prepared report for quality assessment of education provided</li></ul>	September 2016 – July 2018 Dhaka, Bangladesh

## RESEARCH PUBLICATIONS

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- [1] **Rahmatullah Roche**, Sutanu Bhattacharya, Md Hossain Shuvo and Debswapna Bhattacharya. rrQNet: Protein contact map quality estimation by deep evolutionary reconciliation. *PROTEINS: Structure, Function, and Bioinformatics*, 2022.  
doi: <https://doi.org/10.1002/prot.26394>
- [2] Sutanu Bhattacharya, **Rahmatullah Roche** and Debswapna Bhattacharya. DisCover: distance- and orientation-based covariational threading for weakly homologous proteins. *PROTEINS: Structure, Function, and Bioinformatics*, 2021.  
doi: <https://doi.org/10.1002/prot.26254>
- [3] **Rahmatullah Roche**, Sutanu Bhattacharya and Debswapna Bhattacharya. Hybridized distance- and contact-based hierarchical structure modeling for folding soluble and membrane proteins. *PLOS Computational Biology*, 2021.  
doi: <https://doi.org/10.1371/journal.pcbi.1008753>
- [4] Sutanu Bhattacharya, **Rahmatullah Roche**, Md Hossain Shuvo and Debswapna Bhattacharya. Recent Advances in Protein Homology Detection Propelled by Inter-Residue Interaction Map Threading. *Frontiers in Molecular Biosciences*, 2021.  
doi: <https://doi.org/10.3389/fmolb.2021.643752>

[5] Andrew J. McGehee, Sutanu Bhattacharya, **Rahmatullah Roche** and Debswapna Bhattacharya. PolyFold: an interactive visual simulator for distance-based protein folding. *Plos One*, 2020.  
doi: <https://doi.org/10.1371/journal.pone.0243331>

## CONFERENCES AND PRESENTATIONS

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**Rahmatullah Roche**, Sutanu Bhattacharya, and Debswapna Bhattacharya. Folding soluble and membrane proteins via hybridized distance and contact-based hierarchical structure modeling. (Highlight Talk)  
*ACM Bioinformatics Computational Biology*, 2021.

**Rahmatullah Roche** and Debswapna Bhattacharya. Contact-assisted ab-initio protein 3D structure prediction. *Auburn University Graduate Engineering Research Showcase*, 2019.

## AWARDS

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**Best Poster Award for 'PolyFold'** 2020  
ACM Bioinformatics and Computational Biology

## COMMUNITY INVOLVEMENT

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**Volunteered Engineering Day (E-day)** 2019, 2020  
Samuel Ginn College of Engineering Auburn, AL

**Judged Poster Presentation** 2019  
Auburn Research Student Symposium Auburn, AL

## SKILLS

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**Programming Languages:** C, C++, Java, Python, R

**Database:** Oracle, MySQL

**Scripting:** Linux Shell Script, LaTeX, HTML

**Server Side Scripting:** PHP

## RESEARCH PROJECTS

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**Computational Protein Folding** Ongoing  
Working on protein folding problem under the supervision of Dr. Debswapna Bhattacharya, Dept of CS, Virginia Tech. The research focuses on predicting protein residue interactions driven by deep learning, and leveraging the predictions to formulate three dimensional structures of protein through optimization.

**Scheduler** 2015  
Worked on solving scheduling problems under the supervision of Dr. Abu Wasif, Dept of CSE, BUET. Two famous research scheduling problems (Vehicle Routing and Nurse Scheduling Problem) was approximately solved in feasible time, using different approaches: Genetic Algorithm, Local Search and Harmony Search Algorithm, and their hybridization. Developed a software that helps users visualizing and taking decisions in any kind of employee scheduling, and route scheduling problem.