

Sairam Behera

✉ sbehera@cse.unl.edu 🐦 @srbehera11
🌐 <http://cse.unl.edu/~sbehera/>
🌐 <https://www.linkedin.com/in/srbehera/>



Research Interests

Graph Theory, Algorithm Optimization, Bioinformatics, NGS data analysis

Education

- | | |
|---------------------|---|
| Aug 2012 – | Ph.D. Computer Science, University of Nebraska-Lincoln, NE
Thesis title: <i>Error correction of long reads and improving transcriptome assembly.</i> |
| Aug 2009 – Dec 2011 | M.S. Computer Science, University of Texas at Dallas, TX
Thesis title: <i>Algorithm and simulation for optimal delivery of volumetric modulated arc therapy (VMAT).</i> |
| Aug 2001 – May 2005 | B.Tech. (Hons) Computer Science, National Institute of Technology, Rourkela, India.
<i>First Class Honors.</i> |

Employment History

- | | |
|---------------------|---|
| Aug 2016 – | Graduate Research Assistant at Moriyama Lab, School of Biological Sciences, University of Nebraska-Lincoln. |
| Aug 2012 – May 2016 | Graduate Teaching Assistant at Department of Computer Science and Engineering, University of Nebraska-Lincoln. |
| Mar 2012 – Aug 2012 | Software Developer at Tech Mahindra, USA. |
| May 2010 – Aug 2011 | Graduate Research Assistant at Department of Computer Science and Engineering, University of Texas at Dallas. |
| May 2005 – Jun 2009 | Software Developer at Cognizant Technology Solutions, India. |

Research Publications

Journal Articles

- 1 Behera, S., Lai, X., Liang, Z., Lu, Y., Deogun, J. S., & Schnable, J. C. (2017). Stag-cns: an order-aware conserved noncoding sequences discovery tool for arbitrary numbers of species. *Molecular Plant*, 10(7), 990–999.
doi:<https://doi.org/10.1016/j.molp.2017.05.010>

Conference Proceedings

- 1 Behera, S., Gayen, S., Deogun, J. S., & Vinodchandran, N. V. (2018). Kmerestimate: a streaming algorithm for estimating k-mer counts with optimal space usage. In *Proceedings of the 2018 acm international conference on bioinformatics, computational biology, and health informatics* (pp. 438–447). BCB '18. Washington, DC, USA. doi:10.1145/3233547.3233587

- 2 Behera, S., Li, X., Schnable, J., & Deogun, J. S. (2017, November). Dice: discovery of conserved noncoding sequences efficiently. In *2017 ieee international conference on bioinformatics and biomedicine (bibt)* (pp. 79–82). doi:10.1109/BIBI.2017.8217628
- 3 Behera, S., Voshall, A., Deogun, J. S., & Moriyama, E. N. (2017, November). Performance comparison and an ensemble approach of transcriptome assembly. In *2017 ieee international conference on bioinformatics and biomedicine (bibt)* (Vol. 00, pp. 2226–2228). doi:10.1109/BIBI.2017.8218005
- 4 Pavlovikj, N., Begcy, K., Behera, S., Campbell, M., Walia, H., & Deogun, J. S. (2016, December). Analysis of transcriptome assembly pipelines for wheat. In *2016 ieee international conference on bioinformatics and biomedicine (bibt)* (pp. 137–140). doi:10.1109/BIBI.2016.7822507
- 5 Pavlovikj, N., Begcy, K., Behera, S., Campbell, M., Walia, H., & Deogun, J. S. (2014a, May). A comparison of a campus cluster and open science grid platforms for protein-guided assembly using pegasus workflow management system. In *2014 ieee international parallel distributed processing symposium workshops* (pp. 546–555).
- 6 Pavlovikj, N., Begcy, K., Behera, S., Campbell, M., Walia, H., & Deogun, J. S. (2014b). Comparing and optimizing transcriptome assembly pipeline for diploid wheat. In *Proceedings of the 5th acm conference on bioinformatics, computational biology, and health informatics* (pp. 603–604). BCB '14. Newport Beach, California: ACM. doi:10.1145/2649387.2662450
- 7 Pavlovikj, N., Begcy, K., Behera, S., Campbell, M., Walia, H., & Deogun, J. S. (2014c). Evaluating distributed platforms for protein-guided scientific workflow. In *Proceedings of the 2014 annual conference on extreme science and engineering discovery environment* (38:1–38:8). XSEDE '14. Atlanta, GA, USA: ACM. doi:10.1145/2616498.2616551
- 8 Pavlovikj, N., Begcy, K., Behera, S., Campbell, M., Walia, H., & Singh Deogun, J. (2014, March). Evaluating assembly pipeline for transcriptomes. In *Proceedings of the 6th international conference on bioinformatics and computational biology, bicob 2014*.
- 9 Behera, S., Daescu, O., & Papiez, L. (2011, November). Optimal delivery of volumetric modulated arc therapy (vmat) for moving target. In *2011 ieee international conference on bioinformatics and biomedicine workshops (bibt)* (pp. 297–304). doi:10.1109/BIBI.2011.6112390

Skills

Languages	Strong reading, writing and speaking competencies for English, Hindi, Odia.
Coding	C, C + +, Java, Python, R, \LaTeX
Databases	MySQL, Oracle
Web Dev	HTML, CSS, JavaScript

Miscellaneous Experience

Awards and Achievements

- 2010 **Merit Award**, Dean's Excellence Scholarship for Graduate Students, University of Texas at Dallas.
- 2015 **Department Prize for Outstanding Teaching Assistant**, Department of Computer Science and Engineering, University Nebraska-Lincoln.

References

Available on request.