Bilgenur Baloglu, PhD

Pasadena, CA | bilgenurb@gmail.com | bbaloglu.github.io | bilgenur-baloglu | 734-578-8142

Skills Summary

Programming Languages R, Python
Tools Pandas, SciPy, NumPy, Scikit-learn, Matplotlib, Seaborn, Jupyter, Bash, Git, Linux Systems, PyTorch

Recent Experience

Sequential Skin *Remote, part time*
LEAD BIOINFORMATICIAN *2021 - Present*

Towards Data Science (TDS) & Asian Scientist & Barcode Bulletin *Remote*
FREELANCE SCIENCE WRITER *2018 - Present*

- Developed a model using PyTorch to predict water temperature on 60 years of oceanographic data (50,000 data points). The article based on this model was featured on TDS with 454k followers.
- Led an article on Great Lakes biomonitoring with >15 collaborators, which got featured on the US EPA official government website.

University of Guelph & Centre for Biodiversity Genomics *Ontario, Canada*
POSTDOCTORAL FELLOW *2018 - 2020*

- Developed (Python, Jupyter) an error correction code for metabarcoding with nanopore sequencing, improving sequence consensus accuracy from 85% to 99.3%.
- Coordinated a $1million project through the US EPA on Great Lakes biodiversity discovery using DNA barcodes.
- Received AllGenetics postdoc award for industrial applications using DNA barcoding and DNA metabarcoding.

National University of Singapore *Singapore*
GRADUATE RESEARCH ASSISTANT *2013 - 2018*

- Co-developed (Python) an error correction code for DNA barcoding with nanopore sequencing, improving accuracy from 85% to 100%.
- Provided consulting to Singapore's National Water Agency (PUB) for insect outbreak surveillance, saving the agency thousands of dollars.
- Decreased the sequencing cost by a 100-fold from $30 to $0.3/specimen using an optimized NGS barcoding workflow.

Education

National University of Singapore *Singapore*
PHD IN BIOLOGICAL SCIENCES *2018*

Istanbul Technical University *Istanbul, Turkey*
BSC IN MOLECULAR BIOLOGY AND GENETICS *2012*

Publications

[1] **Baloglu, B.**, Chen. Z., Elbrecht, V., Braukmann, T., MacDonald, S., Steinke, D. 2021. *A workflow for accurate metabarcoding using Nanopore MinION sequencing*. *Methods Ecol Evol*. 2021; 00:1–11. https://doi.org/10.1111/2041-210X.13561

[2] Shepherd, B. A., Tanjil, M. R. E., Jeong, Y., **Baloglu, B.**, Liao, J., Wang, M. C. 2020. *Ångström- and Nano-scale Pore-Based Nucleic Acid Sequencing of Current and Emergent Pathogens.* MRS Advances. pp. 1-18.

[3] **Baloglu, B.**, Clews E., Meier R., 2018. *NGS barcoding reveals high resistance of a hyperdiverse chironomid (Diptera) swamp fauna against invasion from adjacent freshwater reservoirs.* Frontiers in Zoology, 15(1):31.

[4] Srivathsan, A.*, **Baloglu, B.***, Wang, W., Tan, W.X., Bertrand, D., Ng, A.H.Q., Boey, E.J.H., Koh, J.J.Y., Nagarajan, N. and Meier, R., 2018. *A MinION™-based pipeline for fast and cost-effective DNA barcoding*. Molecular ecology resources, 18(5), 1035-1049. *Equal contribution.

[5] **Baloglu, B.** 2018. *Biological assessment and monitoring of Singapore aquatic environments* (Doctoral dissertation).

[6] Lim, N.K., Tay, Y.C., Srivathsan, A., Tan, J.W., Kwik, J.T., **Baloglu, B.**, Meier, R. and Yeo, D.C., 2016. *Next-generation freshwater bioassessment: eDNA metabarcoding with a conserved metazoan primer reveals species-rich and reservoir-specific communities.* Royal Society Open Science, 3(11), p.160635.

Manuscripts in Preparation

[1] **Baloglu, B.**, Hempel, C., Adamowicz, S., Steinke, D. *A phylogenetic perspective on the distribution of aquatic midges (Chironomide) in sub-arctic ponds as revealed by PacBio Sequel sequencing of COI gene*.

[2] **Baloglu, B.**, MacDonald, S., Braukmann, T., Steinke, D. 2020. *Does size sorting matter? Validation of COI metabarcoding primers for aquatic invertebrates.*

[3] Deiner, K., Marshall, C., Simonin, P., Burlakova, L., Karatayev, A., **Baloglu, B.**, Coggins, B., Daniel, S., Frankiewicz, A., Whitmore, E., Connolly, J., DeWalt, E., Andres, K., Andres. J., Rogalskyj, G., Pilgrim, E., Westergaard, S., Watkins, J., Rudstam, L., Pfrender, M., Lodge, D., *A new reference database for Great Lakes benthic invertebrate diversity based on DNA based identification.*

[4] Marshall, C., Connolly, J., Daniel, S., Whitmore, E., **Baloglu, B.**, Dewalt, E., Simonin, P., Deiner, K., Rudstam, L., Watkins, J. *Barcoding Sheds Light on the Natural History of Various Aquatic Invertebrate Taxa in the Great Lakes.*

Other Products

[1] **Baloglu, B.**, Chen, Z. Python-based bioinformatics algorithm for analyzing metabarcoding data obtained with Nanopore sequencing. Github site

[2] Srivathsan, A.*, **Baloglu, B.***, Wang, W., Tan, W.X., Bertrand, D., Ng, A.H.Q., Boey, E.J.H., Koh, J.J.Y., Nagarajan, N. and Meier, R. Python-based bioinformatics algorithm for analyzing DNA barcoding data obtained with Nanopore sequencing. Github site

Certifications

2020 "Deep Learning with PyTorch: Zero to GANs", Jovian.ml

2020 "Machine learning with Python", Udemy

2020 "Python: Python Programming for Artificial Intelligence and Data Science", Udemy