Curriculum Vitae

Matthew Cserhati

Detail-oriented, experienced bioinformatics programmer

Personal Information

- Citizenship: born US citizen
- Email: csmatyi@protonmail.com
- Telephone: 531-301-1167
- Github account: www.github.com/csmatyi
- LinkedIn profile: https://www.linkedin.com/in/matthew-cserhati-17090234

Journal Editor Experience

- Volunteer editor for PLOS One for three years; completed 27 editorial assignments.
- Reviewed 5 papers for Springer Nature, Journal of Biogeography, and BMC Genomics.

Education

- Biology, M.Sc. (Eotvos Lorand University, 2003)
- Ph.D., Bioinformatics (University of Szeged, 2011)
- B.Sc., Software Developer (University of Szeged, 2010)

Computer skills, main programming languages

- Linux and Windows operating systems
- PYTHON (certified at Python Institute, PCAP-31-03; PCET Entry-level Python tester)
- Javascript (JSA Certified Associate JavaScript Programmer)
- HTML/CSS (certified WDE Entry-level Web developer)
- R (edX Statistical analysis in R professional certificate)
- MySQL, SQLite, PERL, C/C++, PHP, JAVA, MATLAB

Past and Present Research Experience

Concordia University Irvine: Irvine, CA, associate professor, Aug 2023–May 2025

- Taught courses: Programming Fundamentals, Operating Systems, Server-side Development/Databases, Introduction to Bioinformatics, Object-oriented Programming, and Programming Languages.
- Participation in two academic showcase competitions; won first prize in Tier 1 in 2025 on subject of calculating expected value of k-mer sequences in DNA sequences.
- Assembly and annotation of sand cat whole genome sequence to discover hair-follicle growth-related genes.

Abbvie: Irvine, CA, bioinformatics programmer III, June 2022–July 2023

- Shiny app development for integrated querying of data from The Cancer Genome Atlas including comparison and visualization of gene/protein expression, survival plot analysis, and mutation analysis.
- Data analysis and visualization of results for various research projects.
- Development of statistical framework to evaluate drug genotoxicity via micronucleus test.

Fulgent Genetics, Temple City, CA, bioinformatics programmer I, Aug 2020–Jan 2022

- Development and testing of data processing pipelines for demultiplexing and variant calling.
- Updating of several bioinformatics databases, such as ClinVar, HGMD, and Alamut.
- Inclusivity and exclusivity analysis for primer design for a pathogen panel, including 25 virus and bacterial pathogens, including SARS-CoV-2.
- Development of kraken2 analysis for the metagenomics analysis of patient samples.
- Lead on a project for non-invasive prenatal testing (NIPT), to estimate fetal fraction (FF) in cell-free DNA to discover diagnostic markers for genetic birth defects using a selection of around 300 SNPs from across the human genome, selected from the gnomAD database.

University of Nebraska Medical Center, Omaha, NE, bioinformatics programmer, Oct 2013–Jan 2018

- Development of the NNTC-DCC database, a browsable, integrated website for storing experimental and clinical data on neuroAIDS patients (Java, JavaScript, hibernate, MySQL).
- Next Generation sequencing data generation and storage. Sequencing reads were generated (both single and paired end) for Truseq, Nextera and Agilent reads (CASAVA, bcl2fastq).
- Analysis of RNA-seq data using Tuxedo, STAR and RSEM pipelines.
- Post-analysis of differentially expressed genes using IPA software.
- De novo genome assembly of ten NCLDV strains, using CLC Genomics Workbench GUI tool.
- Assembly of whole genome sequences of Neanderthal and Denisovan, comparison with human and chimpanzee genomes based on enhanced and developed version of the WGKS algorithm (published in BMC Genomics, 2018).

Publications (selection)

Textbook: Object-Oriented Programming, Theory and Practice, Innovative Ink Publishing, 2025.

Cserhati, M., Turóczy, Z., Zombori, Z., Cserzo, M., Dudits, D., Pongor, S., Györgyey, J. Prediction of new abiotic stress genes in Arabidopsis thaliana and Oryza sativa according to enumeration-based statistical analysis. *Mol Genet Genomics* **285**(5):375-91, 2011. PubMed PMID: 21437642.

Brueggeman, A.J., Gangadharaiah, D.S., **Cserhati, M.**, Diaz-Cano, D.C., Weeks, D.P., Ladunga, I. Activation of the Carbon Concentrating Mechanism by CO2 Deprivation Coincides With Massive Transcriptional Restructuring in *Chlamydomonas reinhardtii*. *Plant Cell* **24**(5):1860–75, 2012.

Cserhati, M., Pandey, S., Beaudoin J.J., Baccaglini, L., Guda, C., Fox, H.S. The National NeuroAIDS Tissue Consortium (NNTC) Database: an integrated database for HIV-related studies. *Database* (Oxford) 2015:bav074.

Cserhati, M., Mooter, M.E., Fan, M., Wicks, B., Xiao, P., Pauley, M., Guda, C. Motif comparison between human, Neandertals and Denisova. *BMC Genomics* **19**(1):472, 2018 | doi:10.1186/s12864-018-4710-1, 2018 | doi: 10.1186/s12864-018-4710-1.

Das, D., Wang, X., Chiu, Y-C., Bouamar, H., Sharkey, F., Lopera J.E., Lai, Z., Weintraub, S.T., Han, X., Zou, Y., Chen, H.H., Torrez, C.R., Gu, X., **Cserhati, M.**, Michalek, J.E., Halff, G.A., Chen, Y., Zheng, S., Cigarroa, F.G., and Sun, L-Z. Integrative multi-omics characterization of hepatocellular carcinoma in Hispanic patients. *Journal of the National Cancer Institute*, 2024 | doi: 10.1093/jnci/djae207