Nicolae Sapoval

POSTDOCTORAL RESEARCHER · DEPARTMENT OF COMPUTER SCIENCE

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Education

Rice University *Houston, TX*

PHD COMPUTER SCIENCE *08/27/2019 - 05/02/2024*

- Advisor: Dr. Todd J. Treangen
- Thesis: *Interrogating microbial populations: from large-scale data to algorithms to field-deployed software.*

University of Chicago *Chicago, IL*

BS MATHEMATICS, BS COMPUTER SCIENCE *09/14/2014 - 06/12/2018*

- Undergraduate research advisor: Dr. Monisha Ghosh

Professional Experience

2024-pres.	**Postdoctoral Researcher**, Dept. of Computer Science, Rice University
2019-2020	**Graduate Teaching Assistant**, Dept. of Computer Science, Rice University
2018-2019	**Software Consultant**, TruQua Enterprises LLC, Chicago, IL
2018-2019	**Undergraduate Research Assistant**, Dept. of Biological Sciences, University of Chicago
2016-2018	**Undergraduate Research Assistant**, Dept. of Computer Science, University of Chicago
2015-2018	**Undergraduate Teaching Assistant**, Dept. of Computer Science, University of Chicago

Publications

ARTICLES AND PREPRINTS   778 citations, h-index: 9

Sapoval, N., Liu, Y., Curry, K., Kille, B., Huang, W., Kokroko, N., Nute, M.G., Tyshaieva, A., Dilthey, A.T., Molloy, E. and Treangen, T.J., 2024. Lightweight taxonomic profiling of long-read sequenced metagenomes with Lemur and Magnet. bioRxiv, pp.2024-06. [DOI:10.1101/2024.06.01.596961]

Liu, Y., **Sapoval, N.**, Gallego-García, P., Tomás, L., Posada, D., Treangen, T.J. and Stadler, L.B., 2024. "Crykey: rapid identification of SARS-CoV-2 cryptic mutations in wastewater". *Nature Communications*, 2024. [DOI:10.1038/s41467-024-48334-w, medRxiv:10.1101/2023.06.16.23291524]. 1 citation

Sapoval, N., Tanevski, M., Treangen, T.J. "KombOver: Efficient k-core and K-truss based characterization of perturbations within the human gut microbiome." In *Pacific Symposium on Biocomputing* 2024, pp. 506-520. 2023.

Sapoval, N., Liu, Y., Lou, E., Hopkins, L., Ensor, K.B., Schneider, R., Stadler, L.B., Treangen, T.J. "Enabling Early and Accurate Detection of Recently Emerged SARS-CoV-2 Variants of Concern in Wastewater". *Nature Communications*, 2023. [DOI:10.1038/s41467-023-38184-3, medRxiv:10.1101/2021.09.08.21263279]. 22 citations

Wang, M.X., Lou, E.G., **Sapoval, N.**, Kim, E., Kalvapalle, P., Kille, B., Elworth, R.L., Liu, Y., Fu, Y., Stadler, L.B. and Treangen, T.J., 2023. "Olivar: fully automated and variant aware primer design for multiplex tiled amplicon sequencing of pathogen genomes." bioRxiv, pp.2023-02. 1 citation

Sapoval, N.[*], Aghazadeh, A.[*], Antunes, D.A., Balaji, A., Baraniuk,R., Barberan, CJ, Dannenfelser, R., Dun, C., Edrisi, M., Elworth, R.A.L., Kille, B., Kyrillidis, A., Nakhleh, L., Nute, M.G., Wolfe, C.R., Yan, Z., Yao, V., Treangen, T.J. "Current progress and open challenges for applying deep learning across the biosciences". *Nature Communications*, 13(1), 2022. [DOI:10.1038/s41467-022-29268-7]. 163 citations

Balaji, A., **Sapoval, N.**, Seto, C., Elworth, R.A.L., Nute, M. G., Savidge, T., Segarra, S., Treangen, T.J. "KOMB: K-core based De Novo Characterization of Copy Number Variation in Microbiomes". *Computational and Structural Biotechnology Journal* (2022). [DOI:10.1016/j.csbj.2022.06.019, bioRxiv:10.1101/2020.05.21.109587v2]. 6 citations

Lou, E., **Sapoval, N.**, McCall, C., *et al.*, "Direct Comparison of RT-ddPCR and Targeted Amplicon Sequencing for SARS-CoV-2 Mutation Monitoring in Wastewater". *Sci. Tot. Env.* 833 (2022): 155059. [DOI:10.1016/j.scitotenv.2022.155059].   35 citations

Gallego-García, P., Varela, N., Estévez-Gómez, N., De Chiara, L., Fernández-Silva, I., Valverde, D., **Sapoval, N.**, Treangen, T.J., Regueiro, B., Cabrera-Alvargonzález, J.J. and del Campo, V. "Limited genomic reconstruction of SARS-CoV-2 transmission history within local epidemiological clusters". *Virus Evolution* (2022): veac008.   [DOI:10.1093/ve/veac008, medRxiv:10.1101/2021.08.08.21261673].   9 citations

Kirby, A.E., Welsh, R.M., Marsh, Z.A., *et al.*, 2022. "Notes from the Field: Early Evidence of the SARS-CoV-2 B.1.1. 529 (Omicron) Variant in Community Wastewater—United States, November–December 2021". *Morbidity and Mortality Weekly Report*, 71(3), p.103. [DOI:10.15585/mmwr.mm7103a5].   70 citations

Sapoval, N., de Mesquita, P.J.B., Liu, Y., Wang, R., Liu, T.R., Garza, J., Williams, T., Cadiz, C., Tan, G.S., Van Bakel, H., Elworth, R.A.L., EMIT Investigators, Milton, D.K., Treangen, T.J. "Intrahost-diversity of influenza A virus in upper and lower respiratory tract derived samples from a college community". 2021. [medRxiv:10.1101/2021.10.27.21265424]

Adenaiye, O.O., Lai, J., de Mesquita, P.J.B., Hong, F.H., Youssefi, S., German, J.R., Tai, S.H.S., Albert, B.J., Schanz, M., Weston, S., Hang, J., Fung, C., Chung, H. K., Coleman K. K., **Sapoval, N.**, Treangen, T.J., Maljkovic Berry, I., Mullins, K., Frieman, M., Ma, T., Milton, D. K. "Infectious SARS-CoV-2 in Exhaled Aerosols and Efficacy of Masks During Early Mild Infection". *Clinical Infectious Diseases* (2021). [DOI:10.1093/cid/ciab797, medRxiv:10.1101/2021.08.13.21261989]   128 citations

McDonald, J.T., Enguita, F.J., Taylor, D., Griffin, R.J., Priebe, W., Emmett, M.R., McGrath, M., Sajadi, M., Harris, A.D., Clement, J. and Dybas, J.M., Aykin-Burns, N., Guarnieri, J.W., Singh, L.N., et al. "Role of miR-2392 in driving SARS-CoV-2 infection". 2021. *Cell Reports* (2021): 109839. [DOI:10.1016/j.celrep.2021.109839, bioRxiv:10.1101/2021.04.23.441024].   63 citations

Kille, B., Liu, Y., **Sapoval, N.**, Nute, M., Rauchwerger, L., Amato, N., Treangen, T. "Accelerating SARS-CoV-2 low frequency variant calling on ultra deep sequencing datasets". 20th IEEE International Workshop on High Performance Comput. Bio. (HiCOMB'21). [arXiv:2105.03062].   6 citations

Mc Cartney, A.M., Mahmoud, M., Jochum, M., Agustinho, D.P., Zorman, B., Al Khleifat, A., Dabbaghie, F., Kesharwani, R.K., Smolka, M., Dawood, M. and Albin, D. et al. "An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates". *F1000Research* 10, no. 246 (2021): 246. [DOI:10.12688/f1000research.51477.1]   6 citations

Sapoval, N., Mahmoud, M., Jochum, M., Liu, Y., Elworth, R. A. L., Wang, Q., Albin, D., Ogilvie, H., Lee, M., Villapol, S., Hernandez, K., Maljkovic Berry, I., Foox, J., Beheshti, A., Ternus, K., Aagaard, K., Posada, D., Mason, C., Sedlazeck, F., Treangen, T. "SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission". *Genome Res.* 31, no. 4 (2021): 635-644. [DOI:10.1101/gr.268961.120]   55 citations

da Silveira, Willian A., Hossein Fazelinia, Sara Brin Rosenthal, Evagelia C. Laiakis, Man S. Kim, Cem Meydan, Yared Kidane et al. "Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact". *Cell* 183, no. 5 (2020): 1185-1201. [DOI:10.1016/j.cell.2020.11.002]   203 citations

Awards, Fellowships, & Grants

2022-2023	**Andrew Ladd Memorial Excellence in Computer Science Graduate Fellowship**, Ken Kennedy Institute
2022	**Pan-Structural Variation Hackathon: Third Prize**, Baylor College of Medicine
2021	**Pan-Structural Variation Hackathon in the Cloud: First Prize**, Baylor College of Medicine
2019	**Undergraduate Student Travel Award**, Biophysical Society
	Undergraduate Poster Competition Award, Biophysical Society
2018	**Numbers Game Challenge Winner**, Optiver
2014	**Bronze Medal**, International Mathematical Olympiad
	Silver Medal, Balkan Mathematical Olympiad
2013	**Honorable Mention**, International Mathematical Olympiad
	Bronze Medal, Balkan Mathematical Olympiad

2012   **Bronze Medal**, International Mathematical Olympiad

Presentations

* presenting author

INVITED TALKS

October 2023. *Enabling Early and Accurate Detection of Recently Emerged SARS-CoV-2 Variants of Concern in Wastewater*. Invited talk: RAD Genomics Workshop, Rice University, Houston, TX.

March 2021. *SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission*. Invited talk: Center for Translational Data Science (CTDS) Symposium, University of Chicago, Chicago, IL.

CONTRIBUTED PRESENTATIONS

Sapoval, N.*, Tanevski, M., Treangen, T. J. KombOver: Efficient k-core and K-truss based characterization of perturbations within the human gut microbiome. Oral presentation: AI in Health Conference 2023, Ken Kennedy Institute, Houston, TX. 2023.

Sapoval, N.*, Liu, Y., Lou, E. G., Hopkins, L., Ensor, K. B., Schneider, R., Stadler, L. B., Treangen, T. J. Enabling Early and Accurate Detection of Recently Emerged SARS-CoV-2 Variants of Concern in Wastewater. Poster: ASM Microbe 2023, Houston, TX. 2022.

Sapoval, N.*, Liu, Y., Lou, E. G., Hopkins, L., Ensor, K. B., Schneider, R., Stadler, L. B., Treangen, T. J. Enabling Earlier Detection of Recently Emerged SARS-CoV-2 Variants of Concern in Wastewater. Oral presentation: ASM NGS Conference, Baltimore, MD. 2022.

Sapoval, N.*, OliVar: Variant-aware, push-button primer and probe design for SARS-CoV-2. ASM NGS Conference, Virtual. 2020.

Sapoval, N.*, Liu, Y., Elworth, R. A. L., Michael, N., Sedlazeck, F., Treangen, T. Mining SARS-CoV-2 interhost and intrahost genomic variation. Oral presentation: Ken Kennedy Institute Data Science Conference, Houston, TX. 2020.

Sapoval, N.*, Haddadian, E., Tang, W.-J. A new open structure of the insulin degrading enzyme provides insights into the conformational transition of the molecule. Poster: Biophysical Society Annual Meeting, Baltimore, MD. 2019.

Ghosh, M.*, **Sapoval, N.**, Mahmud S. K. Coexistence of Wi-Fi and WAVE in the DSRC spectrum: impact on WAVE latency and throughput. Oral presentation: WCX'18: SAE World Congress Exp., Detroit, MI. 2018.

Sapoval, N.*, Ghosh, M. Coexistence of Wi-Fi and WAVE in the DSRC spectrum. Poster: University of Chicago Undergraduate Research Symposium, Chicago, IL. 2017.

Teaching Experience

July 2023	**Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS)**, Teaching Assistant	*Woods Hole, MA*
Spring 2023	**Algorithmic Thinking**, Course Assistant, Co-instructor	*Rice University, Houston, TX*
Fall 2020	**Reasoning about Algorithms**, Teaching Assistant	*Rice University, Houston, TX*
Fall 2019	**Reasoning about Algorithms**, Teaching Assistant	*Rice University, Houston, TX*
Winter 2018	**C Programming**, Teaching Assistant	*University of Chicago, Chicago, IL*
Winter 2017	**Honors Intro to Computer Science II**, Teaching Assistant	*University of Chicago, Chicago, IL*
Winter 2016	**Honors Intro to Computer Science II**, Teaching Assistant	*University of Chicago, Chicago, IL*

Mentoring

2023	**Marko Tanevski**, Genome Sleuths REU: KombOver	*Houston, TX*
2022-2023	**Maggie Simmons**, Undergraduate Research Project: Transmission analysis toolkit	*Houston, TX*
2022	**Youth Science Workshop**, Mentor	*Houston, TX*
2022	**Genome Sleuths REU**, Co-director	*Houston, TX*
2021	**HackRice**, Mentor	*Houston, TX*
2021	**Summer STEM Institute**, Research mentor	*Virtual*
2020	**Mary Brady**, Undergraduate Research Project: Transmission analysis toolkit, Rice University	*Houston, TX*
2020	**Hung Nguyen, Audrey Deigaard**, Genome Sleuths REU	*Houston, TX*
2020	**Abdelrahman Abouzeid**, Undergraduate Research Project: Feline infectious peritonitis diagnostics	*Houston, TX*

Outreach & Professional Development

SERVICE AND OUTREACH

2023	**HackRice**, Judge	*Houston, TX*
2022-now	**Computer Science Graduate Student Association**, Vice President	*Houston, TX*
2021-2022	**Computer Science Graduate Student Association**, President	*Houston, TX*
2020	**Rice Undergraduate Research Symposium**, Volunteer Judge	*Houston, TX*
2019-2020	**Computer Science Graduate Student Association**, Social chair	*Houston, TX*

DEVELOPMENT

Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS), 2023, participated as a teaching assistant in an advanced course on computational techniques for microbiome analysis. Assisted attendees in an active learning environment focused on the hands on analyses.

Pan-Structural Variation Hackathon, 2022, attended a four-day research hackathon hosted by Baylor College of Medicine as a part of NCBI Hackathons initiative. Worked on a tool for comparison of taxonomic composition of sequence databases.

Pan-Structural Variation Hackathon, 2021, attended a four-day research hackathon hosted by Baylor College of Medicine as a part of NCBI Hackathons initiative. Worked on a database of low frequency variants for SARS-CoV-2.

Hands-on SARS-CoV-2 Genome Analysis Workshop, co-lead a session on reference guided-assembly and low frequency variant calling for SARS-CoV-2. Assisted attendees with practical session and presented workflows in an interactive setting.

Pan-Structural Variation Hackathon, 2020, attended a four-day research hackathon hosted by Baylor College of Medicine as a part of NCBI Hackathons initiative. Worked on copy number variation and structural variation linking problems in human genomics.

Ken Kennedy Institute Machine Learning Bootcamp, attended a two-day workshop on machine learning with focus towards reinforcement learning and applications in data science.

The Workshop on ns-3 (WNS3), attended a hands-on workshop on network simulations as a part of undergraduate research training experience.