Narges Baniasadi

Academic Staff - Hourly - CSL, Medicine - Stanford Prevention Research Center

Bio

BIO

Dr. Narges Baniasadi is founder and executive director of Emergence program at Stanford. She develops educational and translational programs for improving societal health through entrepreneurship. She is also Adjunct Professor with the Department of Medicine where she teaches impact entrepreneurship in the areas related to Prevention and Health Equity. Narges has led multiple initiatives and businesses in the intersection of Technology and Life Sciences for more than a decade. She founded Bina, a pioneering Bioinformatics company, out of a decade of research at Stanford and UC Berkeley. Bina developed high performance computing platforms and AI solutions for cancer research and genomics analysis. Later, upon acquisition of Bina by Roche, she led the clinical software development and AI research as VP of Informatics at Roche Sequencing until 2018.

ACADEMIC APPOINTMENTS

- Academic Staff - Hourly - CSL, Medicine - Stanford Prevention Research Center

ADMINISTRATIVE APPOINTMENTS

- Founder and Executive Director, Emergence, (2020- present)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Advisory Board, Ethics, Society, and Technology Hub at Stanford (2021 - present)
- Leadership Council, Advisor on Digital Health Innovation, Advisor on Health Equity, Byers Center for Biodesign (2022 - present)
- Global Health Faculty Fellow, Center for Innovation in Global Health (CIGH) (2022 - present)

Teaching

COURSES

2024-25

- Biodesign and Entrepreneurship for Societal Health: BIOE 375, CHPR 275, MED 236 (Win)

2023-24

- Biodesign and Entrepreneurship for Societal Health: BIOE 375 (Win)

2022-23

- Biodesign and Entrepreneurship for Societal Health: BIOE 375, MED 236 (Spr)

Publications

PUBLICATIONS

- **Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis** *NATURE COMMUNICATIONS*

  Sahraeian, S., Mohiyuddin, M., Sebra, R., Tilgner, H., Afshar, P. T., Au, K., Asadi, N., Gerstein, M. B., Wong, W., Snyder, M. P., Schadt, E., Lam, H. Y. K.

  2017; 8: 59

- **MetaSV: an accurate and integrative structural-variant caller for next generation sequencing** *BIOINFORMATICS*

  Mohiyuddin, M., Mu, J. C., Li, J., Asadi, N. B., Gerstein, M. B., Abyzov, A., Wong, W. H., Lam, H. Y.

  2015; 31 (16): 2741-2744

- **VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications** *BIOINFORMATICS*

  Mu, J. C., Mohiyuddin, M., Li, J., Asadi, N. B., Gerstein, M. B., Abyzov, A., Wong, W. H., Lam, H. Y.

  2015; 31 (9): 1469-1471

- **Leveraging long read sequencing from a single individual to provide a comprehensive resource for benchmarking variant calling methods.** *Scientific reports*

  Mu, J. C., Tootoonchi Afshar, P., Mohiyuddin, M., Chen, X., Li, J., Bani Asadi, N., Gerstein, M. B., Wong, W. H., Lam, H. Y.

  2015; 5: 14493-?

- **Leveraging long read sequencing from a single individual to provide a comprehensive resource for benchmarking variant calling methods.** *Scientific reports*

  Mu, J. C., Tootoonchi Afshar, P., Mohiyuddin, M., Chen, X., Li, J., Bani Asadi, N., Gerstein, M. B., Wong, W. H., Lam, H. Y.

  2015; 5: 14493-?

- **Fast and accurate read alignment for resequencing** *BIOINFORMATICS*

  Mu, J. C., Jiang, H., Kiani, A., Mohiyuddin, M., Asadi, N. B., Wong, W. H.

  2012; 28 (18): 2366-2373