

Postdoctoral opportunity at Wisconsin

preliminary applications **due 20 Feb** 2021 for June 2021 start

The GEOPop Grand Challenge

A key challenge of biology is to map interactions between genomes (G) and their environments (E) to predict fitness correlates of an organism (O) and ultimately forecast population-level (Pop) ecological and evolutionary dynamics; this is the GEOPop grand challenge. Recent advances in computational modeling and high-throughput quantitative phenotyping have set the stage to address this challenge; machine-learning can now establish sequence-to-function models for individual genes [1], biophysical modeling can integrate multiple gene functions in different environments to predict growth and correlates of fitness [2], and genome-wide rates of spontaneous mutation can reveal evolutionary potential [3]. To pursue the GEOPop challenge for viruses, a team at the University of Wisconsin-Madison is forming around a core of computational and experimental investigators: Philip Romero (biochemistry), Nathaniel Sharp (genetics), and John Yin (systems biology of viruses).

We seek candidates for a postdoctoral traineeship to join the GEOPop team. The strongest applicants will possess experience and publications in two or more of the following areas: machine learning of biomolecular structure/function, mathematical modeling of biophysical processes; high-throughput molecular or virus phenotyping, deep mutational scanning, protein engineering, molecular virology; or evolutionary genetics, population genetics.

This postdoctoral trainee has potential to be supported through opportunities at the University of Wisconsin-Madison; applicants must be U.S. citizens or hold permanent resident status. To apply, submit a CV, cover letter, and contact info for three references to john.yin@wisc.edu by 20 Feb 2021 for full consideration. Women, minorities, and others who are underrepresented in science, technology, engineering, and mathematics, are especially encouraged to apply.

1. Song H, Bremer BJ, Hinds EC, Raskutti G, Romero PA: **Inferring protein sequence-function relationships with large-scale positive-unlabeled learning**. *Cell Systems* 2021, 12(1):92-101. e108.
2. Yin J, Redovich J: **Kinetic Modeling of Virus Growth in Cells**. *Microbiology and Molecular Biology Reviews* 2018, 82(2).
3. Sharp NP, Sandell L, James CG, Otto SP: **The genome-wide rate and spectrum of spontaneous mutations differ between haploid and diploid yeast**. *Proceedings of the National Academy of Sciences* 2018, **115**(22):E5046-E5055.