Seminar

# SOHINI RAMACHANDRAN

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## *The Causes and Consequences of Human Genomic Variation*

Tuesday, 26 March, 2019, 2:15 p.m.

In the Thunberg Lecture Hall
SCAS, Linneanum, Thunbergsvägen 2, Uppsala
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## ABOUT SOHINI RAMACHANDRAN

Sohini Ramachandran joined the faculty of Brown University in July 2010, after spending three years as a Junior Fellow at the Harvard Society of Fellows and as a Postdoctoral Fellow in Professor John Wakeley's group at the Department of Organismic and Evolutionary Biology at Harvard University. She completed her PhD in 2007 with Professor Marcus Feldman at Stanford University's Department of Biological Sciences. Her research has been funded by the National Science Foundation, US National Institutes of Health, the Pew Charitable Trusts, and the Alfred P. Sloan Foundation.

The research in the Ramachandran lab addresses problems in population genetics and evolutionary theory, via inference from and analysis of present-day human genomes. Ramachandran's research covers a range of questions such as: what loci are under strong adaptive selection in the human genome? (Sugden et al. 2018, *Nature Communications*, "Localization of Adaptive Variants in Human Genomes Using Averaged One-dependence Estimation); are there genetic pathways we can identify that underlie common diseases such as diabetes? (Nakka et al. 2016, *Genetics*, "Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases"); and, are patterns of variation in human genomes similar to those of cultural traits like language? (Creanza et al. 2015, *PNAS*, "A Comparison of Worldwide Phonemic and Genetic Variation in Human Populations").

At SCAS, Ramachandran will pursue two new research directions: 1) integrating ancient DNA and modern genomes into the inference of human population history (via collaboration with the Evolutionary Biology Centre), and 2) developing a novel statistical framework for multi-ethnic disease mapping studies.

## ABSTRACT

The human genome is 3 billion base pairs long, and a random pair of humans only differ at one one-thousandth of those base pairs. Despite this small number of differences, collections of genomic data contain detailed information about the history of our species over the last 100,000 years, regarding natural selection, population size changes, and human migration. I'll offer a tour through my work and that of others on the processes that have generated observed present-day genetic variation, with a focus on the strong signature that population histories have left on human genomes. I'll then move into the "consequences" of human genetic variation, by offering examples of how data-driven research in genomics can overturn long-held views on fundamental genetic processes.