



# Genome Sciences Seminar

Wednesday, 10.11.17 | 3:30 | Foege Auditorium

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## Dr. Gill Bejerano

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# “One genome to rule them all, one genome to find them”

### Bejerano Lab:

The Bejerano Lab focuses on a fundamental question in Human Genomics: the relationship between geno(me)type and phenotype. We attempt to integrate three major and complementary viewpoints in tackling this question:

In 2013 we started a fruitful journey into the genomic causes of human disease. We have since joined Stanford Hospital's Pediatrics Department, through which we now have access to thousands of patients' genomes, and a flood of many more genomes to come. We are dedicated to help improve the lives of patients and their families, through genomics.

We have been examining human genome function since joining Stanford's Developmental Biology Department in 2007. The streamlined efficiency that is obvious at the organism level, shaped by the forces of natural selection, are not as obvious in the molecular level of genes and gene regulation. A recent flood of functional data is helping us make better sense of the human genome, and helps turn it into insights of development, disease and evolution.

We have been studying human genome evolution since 2003 aided by our deep roots and primary affiliation with Stanford's Computer Science Department. There are now whole genomes for hundreds of vertebrates. Hundreds more are being sequenced. The wealth of information captured in these genomes is as staggering as the wealth of adaptations of the species that carry them. We work to mine this data for meaning, linking animal phenotype to animal genome loci, and back to human patient genomes.

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Refreshments served outside the Auditorium at 3:20pm

Questions? Contact Brian Giebel at [bgiebel@uw.edu](mailto:bgiebel@uw.edu) or visit the Seminar website at <http://www.gs.washington.edu/news/seminars.htm>

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