

## **Leveraging long range phasing to detect mosaicism in blood at ultra-low allelic fractions**

Most genotyping methods lose information about maternal vs. paternal inheritance of alleles, producing only diploid total allele counts at each genomic position. However, the relative parental inheritance of heterozygous sites can be recovered at high accuracy using statistical techniques. This estimation problem -- termed "phasing" -- is a fundamental challenge in human genetics. In this talk, I will first describe recent advances in phasing methodology that enable efficient phase estimation with chromosome-scale accuracy in the 500,000-sample UK Biobank data set. I will further describe how phase information can be harnessed to detect subtle imbalances between maternal and paternal allelic fractions in blood DNA -- the hallmark of mosaic chromosomal alterations -- revealing new insights into the causes and consequences of clonal hematopoiesis.

### **List of relevant papers:**

- [1] <http://dx.doi.org/10.1038/ng.2270>
- [2] <http://dx.doi.org/10.1038/ng.2271>
- [3] <http://dx.doi.org/10.1038/ng.3571>
- [4] <http://dx.doi.org/10.1038/ng.3679>

### **Bio:**

Po-Ru Loh leads a statistical genetics research group at the Brigham and Women's Hospital / Harvard Medical School Center for Data Sciences. His circuitous path to the field began with an undergraduate mathematics education at Caltech followed by a PhD in applied mathematics with Bonnie Berger at MIT. During his graduate studies, he developed an interest in genetics, which he pursued during a postdoc with Alkes Price at Harvard School of Public Health. His recent work on mosaic chromosomal alterations (the topic of this talk) was recently recognized with a Burroughs Wellcome Fund Career Award at the Scientific Interfaces and an American Society of Human Genetics (ASHG) Charles J. Epstein research award.