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Lecture covers joint work with Alex Ioannidis, Euan Ashley, Manuel Rivas, and Jennifer Frankovich

**Title: Enabling Precision Health At Scale For All**

**Abstract:**

The last 20 years have seen an explosion of genetic information and data. New technological advances have made it faster and less expensive to understand the human genomes but most of those resources have focused on northern European communities.

Throughout his workshop, I will elaborate on the major challenge to enabling precision health at a global scale, and the bias between those who enroll in state sponsored genomic research and those suffering from chronic disease. More than 30 million people have been genotyped by direct-to-consumer (DTC) companies and/or sequenced by large biobank efforts, providing a potential mechanism for democratizing access to medical interventions and thus catalyzing improvements in patient outcomes as the cost of data acquisition drops. I will discuss development and deployment of geno::pheno platforms that integrate heterogeneous data sources and apply machine learnings to understand the genetics of rare and common chronic disease conditions.

I will also cover how we use computational tools to probe the potential roles of race, ethnicity and socioeconomic status on disease presentation particularly in the context of the the SARS-CoV-2 pandemic. This includes coverage of work by a multidisciplinary research team at Stanford (<https://covid-omics.org/>) that leveraged a pandemic tracking strategy to sequence viral and host genomes and transcriptomes from nasopharyngeal swab residuals and integrated them with digital phenotypes from electronic health records. This work demonstrated the power of multi-omic pandemic tracking and genomic analyses to reveal distinct epidemiologic, genetic and biological associations for those at the highest risk.

The next phase of this work will leverage clinical-grade biobanking, research and clinical genomics, paired with best-in-class ancestry genome annotation algorithms towards better understanding the genetic architecture of underserved populations and powering the next generation of precision medicine studies. We are particularly interested in understanding post-infectious acute syndromes including those with neuropsychiatric components such as long-covid and associated disorders including Pediatric Acute-onset Neuropsychiatric Syndrome with and without Streptococcus triggers (PANS/PANDAS).

**Readings:**

**Deconvoluting complex correlates of COVID-19 severity with a multi-omic pandemic tracking strategy.**

**Nature Communications volume 13, Article number: 5107 (2022)**

<https://www.nature.com/articles/s41467-022-32397-8>

**Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients.**

<https://www.sciencedirect.com/science/article/pii/S1532046420302926>

**Neural ADMIXTURE for rapid genomic clustering**

<https://www.nature.com/articles/s43588-023-00482-7>

**High Resolution Ancestry Deconvolution for Next Generation Genomic Data**

<https://www.biorxiv.org/content/10.1101/2021.09.19.460980v1>