# GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

## THURSDAY OCTOBER 21
## 12:00PM PST
## LIVE @ LEICHTAG & ON ZOOM!

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PASSWORD: GENOME

PRESENTED BY: IGM Institute for Genomic Medicine | UC San Diego Bioinformatics & Systems Biology

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## "HIGH FIDELITY SEQUENCING: NEW METHODS AND INSIGHTS INTO SOMATIC AND CANCER EVOLUTION"


Cancer is the result of a process of somatic evolution that might take decades and it is not clearly understood. A main challenge to study this process is that a large part of it occurs in tissue that appears histologically normal. While mutations in cancer can be easily identified by standard next generation sequencing, mutant clones within normal tissue are extremely difficult to detect because they are small and their mutations get diluted in bulk genomic DNA. To overcome this problem my lab uses high fidelity sequencing methods that decrease the error rate of standard sequencing and enable to detect very low frequency mutations. In this talk I will present two methods developed by our group: CRISPR-DS and PolyG-DS. I will explain how we use CRISPR-DS to characterize cancer driver mutations in normal tissue and how we use PolyG-DS to detect clonal expansions and trace cancer evolution without knowledge of driver mutations. I will also discuss how our findings of prevalent age-related TP53 mutations are leading to a better understanding of somatic evolution and the implications of these findings for early cancer detection.



Organization Committee: J. Gleeson, J. Sebat
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