

Keck School of Medicine of USC

Department of Population and  
Public Health Sciences

## Division of Biostatistics Seminar



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USC Division of Biostatistics**

### **“Analysis of Single Cell T-Cell Receptor Sequencing”**

**Thursday, January 12, 2023**

**12:00pm to 1:00pm**

**In-person: SSB Room 114**

**Zoom:** <https://usc.zoom.us/j/93886997766?pwd=S2crakJ0OWJLWEt6S0g1ZytnTXVXQT09>

Meeting ID: 938 8699 7766

Passcode: 886908

T-cell receptors (TCRs) are hypervariable protein complexes that recognize foreign antigens and play an important role in immune response. Modern sequencing technology allows for the full characterization of these complexes at single-cell resolution, providing an unprecedented view of the immune repertoire. This new technology illuminates the process of immune response and has the potential to serve as a broadly applicable diagnostic tool. However, single-cell TCR sequencing data is often ambiguous, making it difficult to differentiate between cells with distinct clonotypes. Many modern analyses have focused solely on cells with complete information, discarding ambiguous cells and thereby losing data. We propose an expectation maximization (E-M) algorithm for clonotype assignment, which leverages data from ambiguous cells to provide superior repertoire characterization.