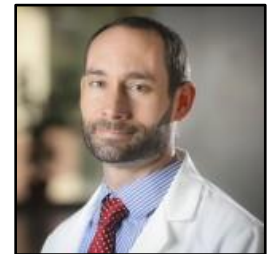




nPOD Webinar:
Immunosequencing: Generating a Potential New Class of Diagnostics

- **DATE:** Tuesday, December 15th, 2015
- **TIME:** 11:00AM (EST) – 12:00PM (EST)
- **WHERE:** WebEx
[Join WebEx meeting](#)
Meeting Number: 736 057 315
Meeting Password: diabetes
Join By Phone: 1-650-479-3208
(Call-in toll number - US/Canada)
Access Code: 736 057 315



- **SPEAKER:** Erik Yusko, PhD, [Adaptive Biotechnologies](#)
Todd Brusko, PhD, [University of Florida](#)
- **ABSTRACT:** The cellular and humoral adaptive immune system generates a remarkable breadth of diversity of antigen receptors by combinatorial shuffling of gene segments in somatic cells. The diversity of possible receptors is large and until recently this diversity precluded the possibility of capturing the antigen receptor repertoires. We have developed a method for unbiased amplification of rearranged T-cell and B-cell receptor variable regions and the use of high throughput sequencing to capture millions of these sequences. We have applied the technology to a variety of clinical problems including hematological malignancies, solid tumor immunology, and the immune response to pathogenic stimulation. The technology is used clinically in Adaptive Biotechnologies' CLIA lab for diagnosis/patient stratification for leukemia and lymphoma, monitoring minimal residual disease, and measuring immune reconstitution after transplant. For application to solid tumors, infiltrating lymphocyte count and clonality are both predictive of response to immunotherapy and prognostic of clinical outcome with standard treatment. Preliminary results from TCRB profiling of various tissues from nPod donors will also be presented.
- **REFERENCES:** PairSEQ: <http://stm.sciencemag.org/content/7/301/301ra131>
Reading Immunological Memory: <http://biorxiv.org/content/early/2015/09/11/026567>
PCR Bias Control: <http://www.ncbi.nlm.nih.gov/pubmed/24157944>