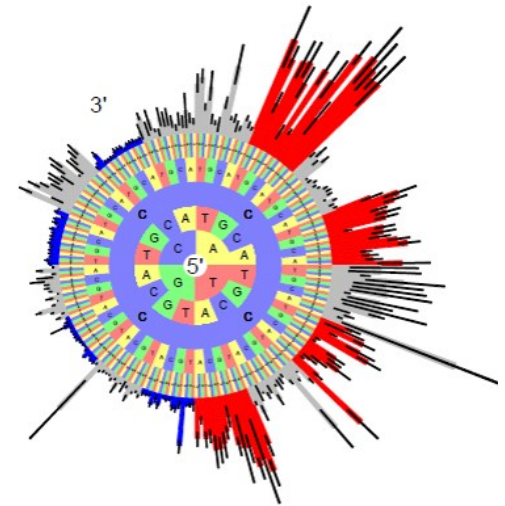# LAUFER CENTER
FOR PHYSICAL AND QUANTITATIVE BIOLOGY

Seminar 2017

ANALYSIS OF B CELL ANTIBODY REPERTOIRES FROM NEXT-GENERATION SEQUENCING IN MULTIPLE SCLEROSIS AND OTHER DISEASES

Multiple sclerosis (MS) is an autoimmune disease characterized, in part, by expanded clones of antigen-experienced B cells that reside in several compartments of the central nervous system (CNS), including the brain and cerebrospinal fluid (CSF). While it is known that B cells in the CSF can exchange with those in peripheral blood, it is not understood whether this immune infiltrate initiates its development in the CNS or in peripheral tissues. We addressed this question through deep sequencing of B cell immunoglobulin repertoires from paired tissue samples from MS patients. Our results demonstrate that the CNS of patients with MS is populated by B cells that gain antigen experience and mature peripherally, in the draining cervical lymph nodes, prior to trafficking across the blood-brain barrier [1]. Analysis of these large-scale data was made possible through the development of several computational tools and methods that we currently make available to the wider scientific community through the Immcantation tool suite (http://immcantation.readthedocs.io) [2].

Full abstract: http://laufercenter.stonybrook.edu/seminar

Steven H. Kleinstein
Associate Professor, Pathology
Yale University
School of Medicine

Friday April 7, 2017

2:30 PM Laufer Center 101

Host: Tom MacCarthy

Refreshments: Hub 110   after seminar

Stony Brook University

For a disability related accommodation, please call 631-632-5400