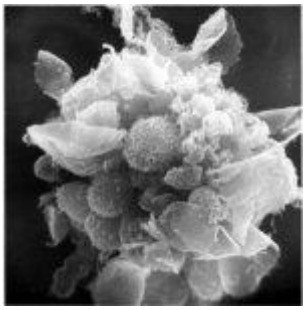
# Novel model provides quantitative explanation of CD4+ T Cells pathway in vivo



Vaccine regimens are often administered in prime-boost combinations. This approach is aimed at eliciting antigen-specific B and T-cell responses against a pathogen. However, experimental measures are limited, as they only characterize only a few features of proliferation and dissemination of T cells. Furthermore, the lymph node is not an isolated site but part of a complex immunological network, therefore challenging to study in vitro. The present study published in PLoS One, was designed to utilize a combination approach incorporating both systems immunology and mathematical modelling to provide a complete quantitative explanation of CD4+ T cells pathways in vivo following nasal immunization. Using stochastic simulations, they team of researchers observe the typical T cell dynamics pathways during the initial phase of the adaptive immune response after the first encounter with an antigen. This is a successful model that provides insight into the proliferation and dissemination of the antigen-specific CD4+ T cells following vaccination.

The model demonstrates proliferation is based on branching process theory, for the dissemination network of antigen-specific CD4+ T cells. Furthermore, this model allows an approximation of the different cell frequencies in different nodes of the body’s dissemination network linked to a time function (hours after immunization). Specifically the study

demonstrates proliferation during 72 to 96 hour period is slower than during the early phase of 42 to 57 hours after immunization. In addition, the model demonstrates T cell migration from draining lymph nodes to the blood occurs between 72 to 96 hours post immunization and the model parameters show, the spleen represents the largest storage of CD4+ T cells. This is a novel model which can be applied to better understand immune responses following immunization and highly relevant in the prediction of immunogenicity following vaccination.

Boianelli, A. et al. 2015. A Stochastic Model for CD4+ T Cell Proliferation and Dissemination Network in Primary Immune Response. *PLOS*.