

Scientific Publications of Methods and Results



method	A clinically meaningful metric of immune age derived from high-dimensional longitudinal monitoring <i>Nature Medicine, March 2019.</i>	➤ The first ever method to reliably quantify a person's "immune age" providing a much more reliable predictor for the status of your immune system potentially leading to fundamental changes in drug & vaccine development and medical practice.	2019
method	Found In Translation: a machine learning model for mouse-to-human inference. <i>Nature Methods, November 2018.</i>	➤ Groundbreaking model translates the results of new mouse experiments into the equivalent human condition, outperforming traditional methods of extrapolation by up to 50%. Leveraging existing mouse and human gene expression data, the new approach demonstrates ability to uncover novel disease-related genes, providing new disease understanding and new targets for drug discovery.	
application	Identification of the involvement of adipocytes in nivolumab (anti-PD1) response in ipilimumab (anti-CTLA4) resistant melanoma patients using a machine learning model of the immune system. <i>American Association for Cancer Research Special AI Conference, October 2018</i>	➤ Identification of new cellular players in the tumor microenvironment that could impact the treatment process for patients who have failed to respond to ipilimumab (anti-CTLA4) immunotherapy	
application	Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed. <i>Nature Biotechnology, June 2018.</i>	➤ Immune-Focused AI Model Creates the Largest Library of Inter-Cellular Communications - Uses It to Predict 335 Novel Cell-Cytokine Interactions.	2018
application	Cell-centred meta-analysis reveals baseline predictors of anti-TNFα non-response in biopsy and blood of patients with IBD. <i>GUT, 2018</i>	➤ Application of our deconvolution and machine learning methods to predict biomarkers of non-responders prior anti-TNF α treatment.	
method	Alignment of Single-cell trajectories to compare cellular expression dynamics. <i>Nature methods, 2018</i>	➤ A new method for comparing expression dynamics within and between single-cell trajectories.	
application	Multi-cohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology, 2017</i>	➤ Application of our cross-trial data integration used to identify novel gene biomarkers that are predictive of Influenza vaccination responders.	
application	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology, 2017</i>	➤ Application of our system-wide knowledgebase of immune inter-cellular interactions to identify putative novel inter-cellular regulation from proteomic profiles of immune cells.	2017
application	Defective signaling in the JAK-STAT pathway tracks with chronic inflammation and cardiovascular risk in aging humans. <i>Cell Systems, 2016</i>	➤ Integrated analysis of multi-modal immune data over three years of aging adults, detecting novel predictor of atherosclerosis burden.	2016

Scientific Publications of Methods and Results (continued)



method	A single-cell transcriptomic map of the human and mouse pancreas reveals inter-and intra-cell population structure. <i>Cell Systems, 2016</i>	➤	A new method of gene expression deconvolution methodology used to infer cell specific expression profiles from heterogeneous biopsy data using single cell profiles.	2016
application	Tofacitinib for polyarteritis nodosa: a tailored therapy. <i>Annals of the Rheumatic Diseases, 2016</i>	➤	Repositioning case study of tofacitinib for vasculitis with potential for companion diagnostic based on JAK-STAT baseline and response levels.	
method	Activation of the reward system boosts immunity. <i>Nature Medicine, 2016</i>	➤	A new method of high dimensional cellular immune profiling coupled with novel algorithm for increased signal to noise detection.	2015
method	Systems immunology reveals markers of susceptibility to West-Nile Virus infection. <i>Clinical and Vaccine Immunology, 2015</i>	➤	A new method for identifying cell type specific gene expression differences, undetectable otherwise, via flow cytometry and NanoString data integration.	
application	Systems analysis of immunity to Influenza vaccination across multiple years and in diverse populations reveals shared molecular signatures. <i>Immunity, 2015</i>	➤	Application of our gene expression deconvolution techniques to estimate cell type proportions where flow data was missing, validating the observed cell differences post-vaccination.	2013
method	Reconstructing the genomic content of microbiome taxa through shotgun metagenomic deconvolution. <i>Computational Biology, 2013</i>	➤	A new method for increased resolution of meta-genomic data	
method	Sensitivity analysis for inference with partially identifiable covariance matrices. <i>Computational Statistics, 2013</i>	➤	A new method for an ultra-high dimensional single cell cytometry measurement by estimation from overlapping marker panels.	2010
method	Extracting cell-type-specific gene expression differences from complex tissues <i>Nature Methods, 2010</i>	➤	A new method for estimating cell-type specific expression differences from whole blood. Applied to identify a signature of graft rejection in specific cell-type, undetectable otherwise.	
method	Towards a cytokine-cell interaction knowledgebase of the adaptive immune system. <i>Pacific Symposium on Biocomputing, 2009</i>	➤	A novel method for generating an immune inter-cellular interactions from the literature using text-mining.	2009