Scientific Publications of Methods and Results

CytoReason

Science is the backbone of our methodologies and applications, and it must stand the test of scientific scrutiny. To date we have 16 research papers published in top quality peer-reviewed scientific journals, including four in 2018 alone – 3 of which were published in journals from the Nature group.

Method	**Found In Translation: a machine learning model for mouse-to-human inference.** *Nature Methods, November 2018 »*	Groundbreaking model translates the results of new mouse experiments into the equivalent human condition, outperforming traditional methods of extrapolation by up to 50%.
Application	**Immune-centric network of cytokines and cells in disease context identified by computational mining of PubMed.** *Nature Biotechnology, June 2018 »*	Immune-Focused AI Model Creates the Largest Library of Inter-Cellular Communications - Uses It to Predict 335 Novel Cell-Cytokine Interactions.
Application	**Cell-centred meta-analysis reveals baseline predictors of anti-TNFα non-response in biopsy and blood of patients with IBD.** *GUT, 2018 »*	Application of our deconvolution and machine learning methods to predict biomarkers of non-responders prior anti-TNFα treatment.
Method	**Alignment of Single-cell trajectories to compare cellular expression dynamics.** *Nature methods, 2018 »*	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.** *Science Immunology, 2017 »*	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.** *Nature Immunology, 2017 »*	Application of our system wide knowledgebase of immune inter-cellular interactions to identify putative novel inter cellular regulation from proteomic profiles of immune cells.
Application	**Defective signaling in the JAK-STAT pathway tracks with chronic inflammation and cardiovascular risk in aging humans.** *Cell Systems, 2016 »*	Integrated analysis of multi-modal immune data over three years of aging adults, detecting novel predictor of atherosclerosis burden.

Method	**A single-cell transcriptomic map of the human and mouse pancreas reveals inter-and intra-cell population structure.** *Cell Systems, 2016 »*	A new method of gene expression deconvolution methodology used to infer cell specific expression profiles from heterogeneous biopsy data using single cell profiles.
Application	**Tofacitinib for polyarteritis nodosa: a tailored therapy.** *Annals of the Rheumatic Diseases, 2016 »*	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.** *Nature Medicine, 2016 »*	A new method of high dimensional cellular immune profiling coupled with novel algorithm for increased signal to noise detection.
Method	**Systems immunology reveals markers of susceptibility to West-Nile Virus infection.** *Clinical and Vaccine Immunology, 2015 »*	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.** *Immunity, 2015 »*	Application of our gene expression deconvolution techniques to estimate cell type proportions where flow data was missing, validating the observed cell differences post-vaccination.
Method	**Reconstructing the genomic content of microbiome taxa through shotgun metagenomic deconvolution.** *Computational Biology, 2013 »*	A new method for increased resolution of meta-genomic data
Method	**Sensitivity analysis for inference with partially identifiable covariance matrices.** *Computational Statistics, 2013 »*	A new method for an ultra-high dimensional single cell cytometry measurement by estimation from overlapping marker panels.
Method	**Extracting cell-type-specific gene expression differences from complex tissues.** *Nature Methods, 2010 »*	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.** *Pacific Symposium on Biocomputing, 2009 »*	A novel method for generating an immune inter-cellular interactions from the literature using text-mining.