NIH-FDA IIG

National Institutes of Health // Food and Drug Administration // Immunology Interest Group

NEWSLETTER

NOVEMBER 2024

PUBLICATIONS

IRF8 defines the epigenetic landscape in postnatal microglia, thereby directing their transcriptome programs

Saeki K, Pan R, Lee E, Kurotaki D, Ozato K
Nat Immunol. 2024 Oct;25(10):1928-1942.
PMID: 39313544 doi: 10.1038/s41590-024-01962-2

We demonstrated that IRF8 sets the enhancer landscape of postnatal microglia along with Sall1 and PU.1, reaching a maximum after day 14.

Host-microbe interaction paradigms in acute and recurrent vulvovaginal candidiasis

MacAlpine J and Lionakis MS
Cell Host Microbe. 2024 Oct 9;32(10):1654-1667.
PMID: 39389030. doi: 10.1016/j.chom.2024.08.018

This review summarizes the host and fungal factors that contribute to susceptibility to acute and recurrent vulvovaginal candidiasis. It synthesizes key findings that outline how antifungal immune mechanisms in the vagina are distinct from other mucosal barrier sites and highlight key, unanswered questions in the field.

Focus on fungi

Iliev ID, Brown GD, Bacher P, Gaffen SL, Heitman J, Klein BS, Lionakis MS
Cell. 2024 Sep 19;187(19):5121-5127.
PMID: 39303681. doi: 10.1016/j.cell.2024.08.016

This Commentary highlights the importance of fungal pathogens and the need for concerted research efforts to enhance understanding of fungal virulence, antifungal immunity, novel drug targets, antifungal resistance, and the mycobiota to improve human health.

Loss of HIV candidate vaccine efficacy in male macaques by mucosal nanoparticle immunization rescued by V2-specific response

Rahman MA, Bissa M, Scinto H, Howe SE, Sarkis S, Ma ZM, Gutowska A, Jiang X, Luo CC, Schifanella L, Moles R, Silva de Castro I, Basu S, N'guessan KF, Williams LD, Becerra-Flores M, Doster MN, Hoang T, Choo-Wosoba H, Woode E, Sui Y, Tomaras GD, Paquin-Proulx D, Rao M, Talton JD, Kong XP, Zolla-Pazner S, Cardozo T, Franchini G, Berzofsky JA
Nat Commun. 2024 Oct 22;15(1):9102.
PMID: 39438480 doi: 10.1038/s41467-024-53359-2.

It describes how orally delivered nanoparticles containing pentamers of the V2 loop of SIV envelope can improve protective immunity in several parameters as well as protection against low dose rectal challenge, but empty nanoparticles can actually abrogate protection by increasing local inflammation and activated CD4 T cells as potential target cells for the virus to infect. The presence of the V2 loop overcomes this adverse effect and emphasizes the role of anti-V2 immunity in protection against SIV.

A proteomic atlas of glypican3 interacting partners: Identification of alphafetoprotein and other extracellular proteins as potential immunotherapy targets in liver cancer

Zhang Y, Lin S, Xiao Z, Ho M
Proteoglycan Res. 2024, 2:e70004.
doi: 10.1002/pgr2.70004

This study presents a large-scale proteomic analysis of glypican-3 (GPC3) interactions in liver cancer, identifying 153 associated proteins through co-immunoprecipitation and mass spectrometry. The study identifies alpha-fetoprotein (AFP) as a GPC3 binding partner in cancer cells, enhancing understanding of GPC3's role in cancer biology and offering a new approach for immunotherapy development. Both GPC3 and AFP are oncofetal antigens in liver cancer.

Cancer therapy with antibodies

Paul S, Konig MF, Pardoll DM, Bettegowda C, Papadopoulos N, Wright KM, Gabelli SB, Ho M, van Elsas A, Zhou S
Nature Reviews Cancer 2024, 24:399-426.
PMID: 38740967. doi: 10.1038/s41568-024-00690-x

This review discusses the evolution of targeted cancer therapies, particularly focusing on current and emerging immunotherapeutic targets in cancer as well as therapeutic antibodies and their various mechanisms of action, including antibody-drug conjugates, immune checkpoint inhibition, bispecific antibodies, radioimmunotherapy and immunotoxins. It highlights advancements in antibody technology that enhance target specificity and therapeutic efficacy while minimizing damage to normal cells, along with ongoing basic and clinical research to further improve these treatments.

rhIL-7-hyFc, a long-acting interleukin-7, improves efficacy of CAR-T cell therapy in solid tumors

Li D, Liang T, Hutchins LE, Wolfarth AA, Ferrando-Martinez S, Lee BH, Ho M
J Immunother Cancer. 2024,12(7):e008989.
PMID: 39043602. doi: 10.1136/jitc-2024-008989

This study explores a combination therapy using engineered long-acting interleukin-7 (NT-I7) with CAR-T cells targeting three emerging tumor antigens (glypican-2, glypican-3, and mesothelin) to enhance treatment efficacy against solid tumors including neuroblastoma, liver cancer, ovarian cancer and pancreatic cancer in mice. Results show that NT-I7 significantly improves T-cell expansion and reduces exhaustion markers, leading to tumor regression, suggesting a promising approach for treating solid tumors in patients.

CAR-T cells based on a TCR mimic nanobody targeting HPV16 E6 exhibit antitumor activity against cervical cancer through NFAT and NF-B signaling

Duan Z, Li D, Li N, Lin S, Ren H, Hong J, Hinrichs CS, Ho M
Molecular Therapy: Oncology. 2024,
PMID:39524212 doi: 10.1016/ j.omton.2024.200892

This study investigates T cell receptor mimic (TCRm) nanobodies targeting HPV E6, specifically focusing on the isolation of the F5 camel VHH nanobody by phage display technology. The findings demonstrate that CAR-T cells based on the F5 VHH effectively target and kill HPV-16+ cervical cancer cells, inhibiting tumor growth in xenograft models, thereby presenting a promising strategy for treating HPV-related malignancies.

Thymic inborn errors of immunity

Pala F, Notarangelo LD, Lionakis MS
J Allergy Clin Immunol. 2024 Oct 18:S0091-6749(24)01066-2.
PMID: 39428079. doi: 10.1016/j.jaci.2024.10.009

This Pillars commentary highlights the groundbreaking article by the Gaffen lab "Th17 cells and IL-17 receptor signaling are essential for mucosal host defense against oral candidiasis" that uncovered the critical role of IL-17 signaling in mucosal antifungal immunity.

DNA methylation drives hematopoietic stem cell aging phenotypes after proliferative stress

Yanai H, McNeely T, Ayyar S, Leone M, Zong L, Park B, Beerman I
Geroscience. 2024 Oct 11.
PMID: 39390312. doi: 10.1007/s11357-024-01360-4.

We present evidence that HSC divisional history is imprinted in the DNA methylome and resolve an outstanding conflict in the field regarding DNA damage accumulation in aged HSCs by demonstrating DNA damage in HSC is repaired with low levels of proliferative stress but accumulates following extensive cycling.

IL-17: A Critical Cytokine for Defense against Oral Candidiasis

Dias LS and Lionakis MS.
J Immunol (2024) 213 (8): 1049–1051.
PMID: 39374468. doi: 10.4049/jimmunol.2400510

This Pillars commentary highlights the groundbreaking article by the Gaffen lab "Th17 cells and IL-17 receptor signaling are essential for mucosal host defense against oral candidiasis" that uncovered the critical role of IL-17 signaling in mucosal antifungal immunity.

Whole genome sequencing of CRISPR/Cas9-engineered NF-B reporter mice for validation and variant discovery

Mahesh G, Martin EW, Aqdas M, Oh KS, Sung MH
Sci Data. 2024 Nov 13;11(1):1225.
PMID: 39537647. doi: 10.1038/s41597-024-04064-8.

With decreasing costs of high-throughput sequencing, it is becoming feasible to consider a large-scale validation of a new strain after a targeted genetic perturbation. Here we describe a dataset of whole-genome sequences and the variant analysis results from our four novel reporter mouse strains.

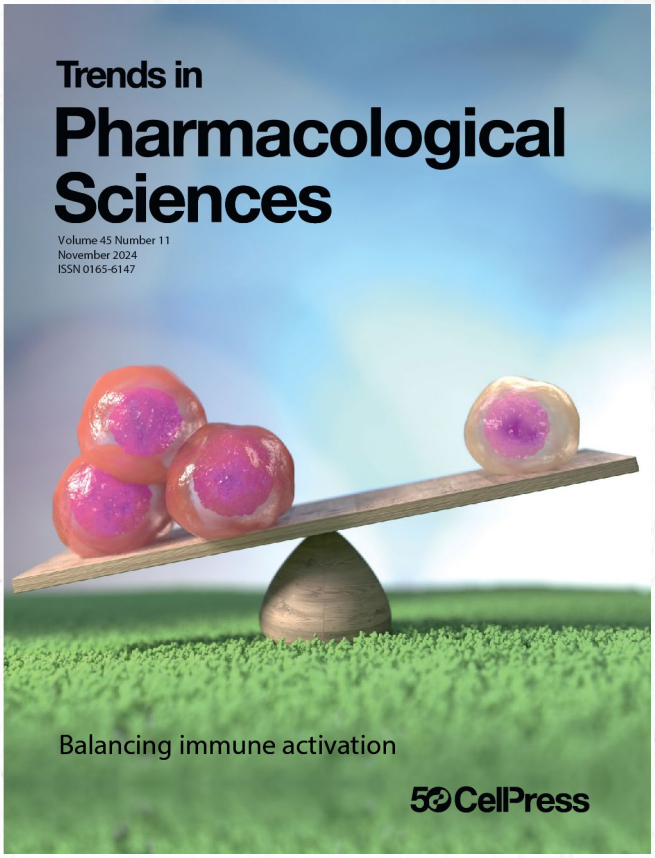
Continued>>

Balancing immune activation with Itk

Kaul Z and Schwartzberg PL
Trends Pharmacol Sci. 2024 Oct 1:S0165-6147(24)00203-7.
PMID: 39358175. doi: 10.1016/j.tips.2024.09.005.

Development of protective immune responses relies on a balance between proinflammatory CD4 T helper (Th) cell populations such as Th17 cells and regulatory CD4 T cells (Tregs) which is regulated by interleukin-2-inducible T cell kinase (Itk) that keeps immune activation in check.

On the cover: Development of protective immune responses relies on a balance between proinflammatory CD4 T helper (Th) cell populations such as Th17 cells and regulatory CD4 T cells (Tregs) that keep immune activation in check. In this issue, Kaul and Schwartzberg discuss the role of interleukin-2–inducible T cell kinase (Itk), which controls the activation of phospholipase C gamma, Ca2+ influx and the activity of the NFAT transcription factor, in regulating the balance between Th17 and Tregs. They also explore the potential of inhibiting Itk as a therapeutic strategy for autoimmune diseases. Dark pink/orange cells are Th17 cells with greater Itk activity and Ca2+ flux. Light pink cell represents a Treg cell with decreased Itk activity and Ca2+ flux. Cover art designed by Alexander Stewart, NIAID using Maxon Cinema4D Software.



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2025 RETREAT

NIH/FDA
Immunology Interest Group
Annual Retreat

University of the District of Columbia
Washington, DC, United States

February 3-4, 2025

All NIH and FDA immunologists are invited to join this annual event held ***February 3-4, 2025*** at the ***University of the District of Columbia Van Ness Campus*** (conveniently located on the Red Metro line). Editors from scientific journals are invited to attend alongside Principal Investigators, Staff Scientists, and trainees across institutes and centers. The IIG workshop is a vital part of the immunology community that provides an organized forum allowing immunologists from distinct intramural institutes to meet, share scientific expertise, and establish collaborations. The annual workshop helps maintain a strong sense of identity within the NIH and FDA immunology community. We hope to have everyone in the NIH and FDA communities participate!

This year will include a special session devoted to the contributions of Dr. Howard Young to the IIG, the NIH, and the broader scientific community.

The 2025 gurus will be **Dr. Shannon Turley** from Genentech and **Dr. Christoph Benoist** from Harvard.

Submit your abstract now! The deadline for abstract submission is ***December 15, 2024***.

Submissions are accepted on a first come, first served basis. Space is limited so do not wait to submit your abstract.

Monetary awards will be given to the best trainee presentations!

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Niki Maria Moutsopoulos, DDS, PhD elected to the National Academy of Medicine

Dr. Moutsopoulos's laboratory has contributed to the understanding of both homeostatic and pathogenic inflammation in the oral cavity, informing interventions for both rare and common forms of aggressive forms of periodontal disease.

Kaitlyn Sadtler, PhD named to the 2024 TIME100NEXT list

Dr. Sadtler is an Earl Stadtman Tenure-Track Investigator and Chief of the Section for Immunoengineering in NIBIB.

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Immunology Interest Group

SPOTLIGHT

Dr. Neeltje van Doremalen is joining Rocky Mountain Laboratories, NIAID as tenure-track investigator in January 2025.

Tell us about your science.

I have just been selected as a tenure-track investigator at the Laboratory of Virology, at Rocky Mountain Laboratories, and will be starting in January 2025. My work focuses on advancing our understanding of mucosal immune responses to respiratory virus infections, identifying correlates of protection in the upper and lower respiratory tract, and designing vaccines to elicit these protective immune parameters. My goal is to achieve durable and broad immune responses within the respiratory tract. While much of my research has relied on virus challenge animal models, I am expanding to include studies with human samples, such as tonsil organoids.

Neeltje van Doremalen, PhD

Currently, we focus on SARS-CoV-2 and H5N1, but with access to the state-of-the-art BSL4 facility at Rocky Mountain Labs, I plan to extend this work to BSL4 agents as well. One of my favorite projects investigates the nasal-associated lymphoid tissue (NALT) in mice, which functions similarly to tonsils in humans. Following mucosal vaccination, we observe a striking reorganization of the tissue architecture, largely driven by an expansion of B cells. I am excited to apply spatial transcriptomics and live imaging to dissect the precise mechanisms underlying these changes and to determine how they vary across viruses and vaccine platforms.

What event(s) lead to your career in science and interest in immunology?

My passion for biology began at a very young age, inspired by my father, who is a beekeeper and teacher. He would teach me all about insects as we explored our backyard together. This curiosity led me to study laboratory sciences in the Netherlands. During my studies, a single lecture on virology by Frank van Kuppeveld, now at Utrecht University, captured my attention. I pursued a nine-month internship with him, which became the foundation for my scientific journey.

From there, I completed a PhD on influenza virus receptor binding at Imperial College London and what was then the Health Protection Agency, under the guidance of Wendy Barclay, Maria Zambon, and Catherine Thompson. Having three exceptional female supervisors, each a powerhouse in the influenza field, inspired me to pursue a career as a principal investigator.

The pandemic further shaped my career path. While conducting preclinical studies on the Oxford-AstraZeneca COVID-19 vaccine in nonhuman primates, we found that although the vaccine fully protected the lower respiratory tract, it did not reduce virus shedding from the nose. This key finding sparked my interest in understanding the interplay between mucosal and systemic immunology, ultimately guiding me toward my current research focus.

Continued>>

How has a mentor or colleague substantially influenced your career trajectory?
Many of the mentors I've mentioned have had a significant impact on my career, and Vincent Munster, a PI at the Laboratory of Virology, has also been an important influence. Over the past 12 years, we've worked closely together, and he has encouraged me to think beyond immediate details and consider the bigger picture. He also supported me in developing my own research plan, even when it diverged from his primary interests. His guidance and honest feedback have been extremely valuable in helping me grow as a scientist and work toward my career goals.

In what area(s) do you expect significant research/medical advances in the next 5-10 years?
Advances in technologies such as single-cell RNA sequencing, high-dimensional flow cytometry, and spatial profiling are opening new opportunities for in-depth research on human samples. For instance, a recent study provided a detailed analysis of immune cells in adenoid tonsil tissue collected using a flocked swab. These approaches have a lot of potential to deepen our understanding of mucosal immunology and guide the development of improved mucosal vaccines.

What do you value most about the NIH-FDA Immunology community?
Improving our understanding of the interplay between immunology and virology is essential for advancing our knowledge of infectious diseases in humans. While many researchers focus on one field or the other, I am drawn to the intersection of both disciplines. The NIH-FDA Immunology community has been incredibly supportive in helping me pursue my immunology goals, and I'm excited about the upcoming retreat in February.

How do you spend your free time?
Living in the heart of the Rocky Mountains, I enjoy spending my time exploring the outdoors with my dogs, husband, family, and friends.

Continued>>

Bench-to-Bedside in Action

Translating immunology to transform clinical care

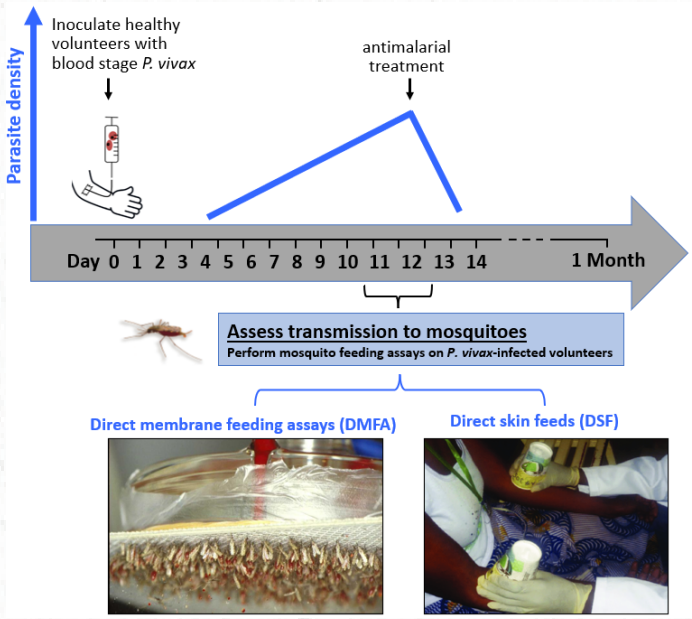
Harnessing fundamental knowledge to advance our understanding of disease and develop novel treatment strategies is a major mission of the NIH. Each month we highlight interesting clinical trials taking place at the NIH Clinical Center that are doing just that.

Induced Blood-Stage Malaria in Healthy Malaria-Naive Adults to Assess the Safety and Infectivity of *Plasmodium Vivax* Challege Agent and Evaluate Transmission in Mosquito Feeding Assays.
PI: Joel A. Goldberg, M.D. – National Insitute of Allergy and Infectious Diseases (NIAID)

Background: *Plasmodium vivax* is the second most common cause of malaria, occurring over a vast geographic area causing approximately 14.5 million global cases per year. Although less virulent than *P. falciparum*, *P. vivax* is also associated with severe disease and infected persons are at risk of significant morbidity and even death. The Laboratory of Malaria Immunology and Vaccinology, NIAID has pioneered clinical development paths for transmission-blocking vaccines (TBVs). TBVs target the parasite's sexual stages inside the vector mosquito, and have shown promise to reduce transmission of *P. falciparum* in field studies. LMIV is now developing TBVs against *P. vivax* to support control and elimination efforts.

The approach taken: To assess the efficacy of new *P. vivax* TBVs, a Controlled Human Malaria Infection (CHMI) model using inoculation of blood-stage *P. vivax* parasites is being established at the NIH Clinical Center. *P. vivax* CHMI (PvCHMI) using blood-stage parasites allows *P. vivax* studies in healthy volunteers without the risk of relapse due to dormant liver stage forms called hypnozoites.

Study Design:



PvCHMI can also be used to study transmission to mosquitoes (called PvCHMI-trans). After blood-stage parasites are inoculated into study volunteers, parasites multiply. At a sufficient density, transmission to mosquitoes can be assessed by feeding mosquitoes on blood samples (direct membrane feeding assay (DMFA)) or directly on skin (direct skin feeding (DSF) assay). For DMFA, mosquitoes feed on blood samples through a membrane in a feeding apparatus. DSF recapitulates natural human-to-mosquito transmission as well as the mechanisms by which vaccine antibodies kill parasites inside mosquitoes. All study volunteers are cured with standard doses of antimalarial medication. The trial is actively recruiting. (ClinicalTrials.gov NCT06607003)

What we hope to learn: The PvCHMI-trans model provides a unique opportunity to test the efficacy of TBVs in healthy volunteers in a rapid, cost-effective fashion. The model will also accelerate our understanding of malaria immunology and support clinical development of other interventions against *P. vivax* malaria.

Continued>>

Multi-omics feature selection for AI applications in small sample size studies

Richard H. Scheuermann, PhD

Scientific Director, National Library of Medicine, National Institutes of Health

With the availability of high-throughput multi-omics technologies, the immunology research community has started to take a systems level approach to understand the functioning of the immune system in health and disease [Villani 2018, Davis 2020]. By combining transcriptomics analysis (bulk and single cell) with epigenomics methods, the regulatory networks that drive transcriptional responses to perturbation of the immune system can be elucidated. Exploring the chemokine and cytokine landscapes using targeted and untargeted proteomics techniques can reveal the long-range interactions of dispersed components of the immune system. And microbiome analysis is starting to reveal how biological ecosystems living in and on our bodies help to orchestrate immune responses.

One important application of systems immunology is to predict the efficacy of vaccines [Rappuoli 2024, Sugrue 2024]. In addition to monitoring the emerging immune response following vaccination, the application of multi-omics analysis to samples collected at baseline, prior to vaccination, can help identify mechanistic biomarkers that predispose to the development of an effective vaccine response [Tsang 2015, Aevermann 2021].

However, two main challenges limit the potential of systems immunology approaches. First, while high-throughput multi-omics assays can generate systems level datasets, their costs can limit the size of the studies being performed. And thus, many systems immunology studies suffer from the "curse of dimensionality" in which the number of variables measured greatly exceeds the number of samples evaluated ($p >> n$) [Mirza 2019]. One of the implications of this limitation is that false positive associations in statistical tests due to stochastic noise will be numerous and can be difficult to distinguish from true positive correlations.

Second, different omics platforms assess different numbers of analytes, from hundreds of proteins using mass spectrometry, to tens of thousands of transcripts using RNA sequencing, to millions of CpG methylation sites from bisulfate sequencing analysis. This can make it challenging to perform an integrative analysis that allows for unbiased representation of variables from different omics platforms.

Canonical correlation analysis (CCA) has emerged as an interesting approach that can simultaneously accomplish dimensionality reduction and multi-omics data integration for predictive modeling [Wróbel 2024]. As with principal component analysis (PCA), CCA achieves dimensionality reduction by generating latent components corresponding to linear combinations of the original input variables. However, rather than selecting latent components that maximize variance within a dataset, as in PCA, CCA selects latent components that maximize correlation between datasets produced with the same set of samples, achieving both dataset integration and dimensionality reduction. Since the sources of experimental noise are likely different between omics platforms, selecting input variables that correlate across datasets will tend to select true positive biological features rather than false positive noisy features for latent component generation, by borrowing information across omics modalities.

Continued>>

The background shows immune receptors (e.g., antibodies) mined for disease-specific patterns by machine learning. Illustration image: Rahmad Akbar and Lonneke Scheffer, UiO. (https://www.med.uio.no/klinmed/english/research/news-and-events/news/2022/uncover-the-hidden-patterns-of-the-immune-system-with-artificial-intelligence.html)

AI in Immunology

In a recent study exploring vaccine responses to the hepatitis B vaccine, we employed a supervised machine learning version of CCA (Diablo) in which the serum antibody titers were used as one of the datasets to drive correlations to this vaccine response variable (antibody titer) [Singh 2019]. The independent variables measured included flow cytometry, whole blood transcriptomics, plasma and white blood cell proteomics and metabolomics, epigenomics, and gut microbiome resulting in ~700,000 measured features in blood and stool samples collected before and after challenge with three doses of a hepatitis B vaccine in 15 study participants [Shannon 2020]. This three-dose regimen produced a broad range of antibody responses, with anti-HepB titers ranging from 147 – 38,000 mIU/ml. In order to determine if baseline (pre-vaccination) predictors of vaccine responses could be identified from the multi-omics data, Diablo was used to simultaneously construct regression models using the correlated latent components captured by CCA across multi-omics datasets that also correlated with serum antibody titers as the response variable. Predicted antibody titers from each of the omics models correlated reasonably well with actual antibody titers, with Spearman's rho values ranging from 0.6 for the white blood cell lipidomics model to 0.73 for the DNA methylation model (Figure 1 A – D). However, given the small sample size of only 15 participants, it was impossible to set aside data for model testing and so the possibility that noisy false positive input features may have been included in model latent components remained a concern.

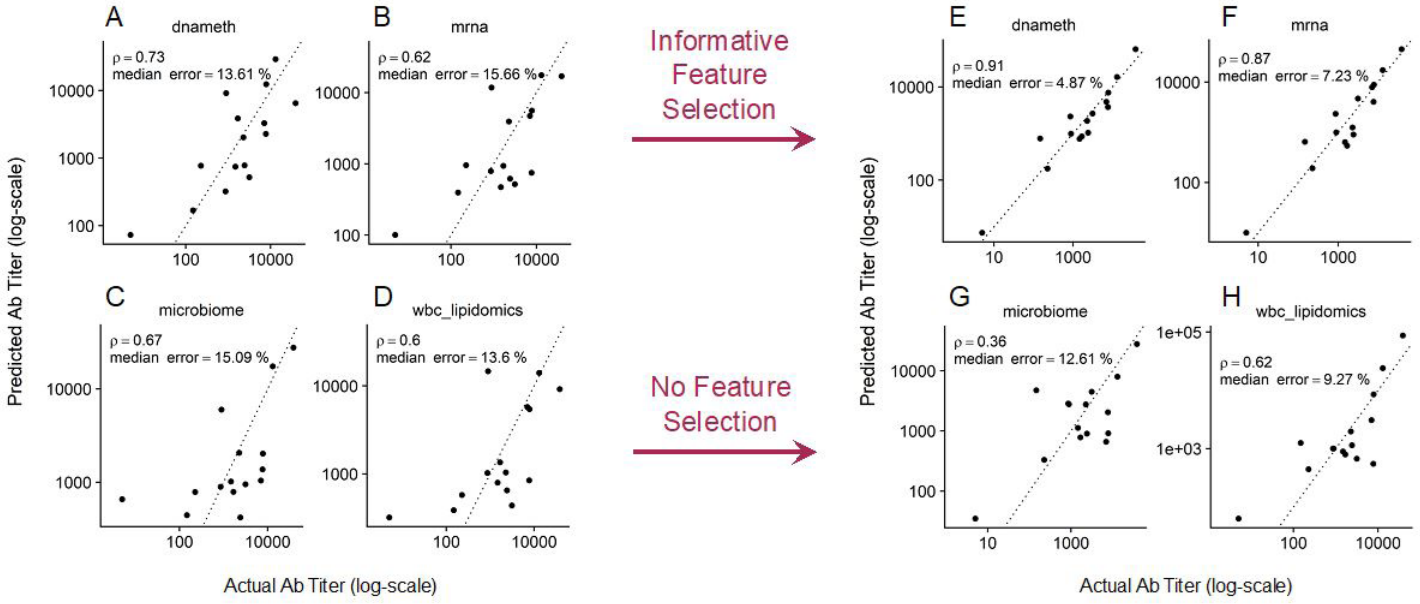


Figure 1 – Effects of informative feature selection on antibody titer prediction. The performance of the individual CCA models in predicting serum antibody titers in comparison with actual antibody titers was quantified using Spearman's rho correlation (A – D). Genes from an mDC module found in the MSigDB database were then used as an approach for informative feature selection for the DNA methylation and bulk RNA sequencing data (E & F), but not the microbiome or white blood cell lipidomics data (G & H). This approach of informative feature selection resulted in a dramatic improvement in antibody titer model prediction, with Spearman's rho correlation increasing from 0.73 (A) to 0.91 (E) for the DNA methylation models and from 0.62 (B) to 0.87 (F) for the bulk transcriptomic models. No improvement was seen in the microbiome (G) and lipidomic (H) models that did not undergo feature selection filtering. Adapted from Aevermann B (2021) Frontiers in Immunology, 12:690470. doi: 10.3389/fimmu.2021.690470. PMID: 34777332. See publication for details.

Continued>>

AI in Immunology

In parallel to the multi-omics assays applied to bulk blood samples, single cell RNA sequencing was also performed on sorted cell subsets isolated from peripheral blood [Aevermann 2021]. Unsupervised clustering of the single cell transcriptional profiles revealed two distinct myeloid dendritic cell (mDC) subsets, and that the ratio of these two mDCs in the baseline pre-vaccination samples seemed to correlate with the initial response to the first vaccination dose. We reasoned that if these mDC subsets were responsible for initial vaccine responsiveness, that focusing the predictive models on features derived from these mDC subsets might produce better results. A list of genes from an mDC module found in the MSigDB database (www.gsea-msigdb.org/gsea/msigdb) was used to filter the bulk transcriptomic and DNA methylation data from the pre-vaccination baseline samples prior to Diablo-based supervised CCA modeling as an additional layer of dimensionality reduction. This approach of informative feature selection resulted in a dramatic improvement in antibody titer model prediction. Importantly, although it was not possible to test the resulting models using set-aside data due to the small sample sizes, experiments showing differential T cell activation by these mDC subsets provided independent validation of the improved model results.

But wait. Those same features used in the improved models were available in the full transcriptomics and methylation gene lists when the original models were built, so why weren't they used to build predictive models with similar high performance. Once again, the curse of dimensionality comes into play. Consider that the latent components are being constructed using linear combinations of variables in two omics datasets. Let's assume that we measured 2000 genes in the bulk transcriptomics data, among which 100 genes were informative, we would have to evaluate 2000 choose 100 combinations, which is approximately 1.1×10^{171} (https://www.hackmath.net/en/calculator/n-choose-k). Assuming the same in the methylation data, the search for the strongest correlation would be among (1.1×10171)2 pairs of latent components, one from each dataset. This number of evaluations is just not possible on any reasonable sized computer in any reasonable amount of time. Therefore, algorithms like CCA use a greedy approach in which they search for an optimal solution starting from a random initialization. While this approach can achieve a local optimum solution, a global optimum is not guaranteed. Thus, any approach that reduces the number of dimensions by informative feature selection will likely result in improved model performance.

In conclusion, canonical correlation analysis has emerged as an effective approach to achieve both multi-omics data integration and dimensionality reduction. Adding additional informative feature selections via some independent orthogonal method, in this case from single cell genomics analysis, can further alleviate the p >> n problem inherent in multi-omics studies with relatively small sample sizes. These strategies, conceptually borrowing information, are enabling the application of advanced artificial intelligence techniques to systems immunology modeling to help us understand the functioning of the immune system in health and disease.

Acknowledgement: Thanks to Yun (Renee) Zhang for helpful suggestions on an early draft of this article.

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AI in Immunology

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Immunology Interest Group
SEMINAR SERIES

Upcoming seminars

December 2024


December 4
Lillian Cohn (Fred Hutch)
Host: Eric Dang


December 11
Florent Ginhoux (Gustave Roussy)
Host: Romina Goldszmid/Joanna Bandola


December 18
Bana Jabri (UChicago)
Host: Brian Kelsall

January 2025


January 8
Dusan Bogunovic (Columbia)
Host: Mihalis Lionakis


January 15
Jakob von Moltke (UW)
Host: Eric Dang


January 22
Andrea Ablasser (EPFL)
Host: Irini Sereti


January 29
Lisa Coussens (OHSU)
Host: Li Yang

February 2025


February 5
Dorothy Schafer (UMass)
Host: Han-Yu Shih


February 12
Eric Meffre (Stanford)
Host: Christian Mayer


February19
Ari Molofsky (UCSF)
Host: Eric Dang


February 26
Luc Van Kaer (Vanderbilt)
Host: Hyun Park

Missed a seminar?

Catch up on prior talks at...

https://www.niaid.nih.gov/research/immunology-seminars

FDA: http://web.microsoftstream.com/channel/5c371a75-2d56-45d3-9f86-7bacc3015066

*Recordings are generally available 1-2 weeks after the presentation.

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