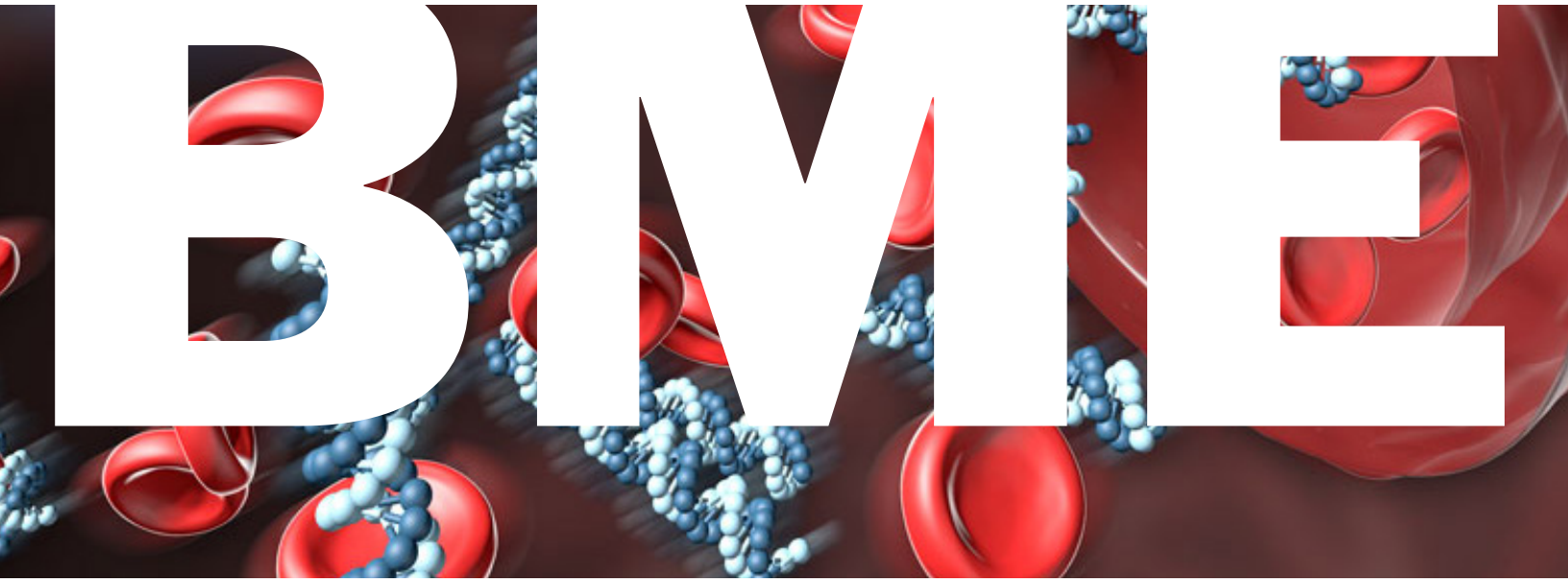
CornellEngineering
Meinig School of Biomedical Engineering



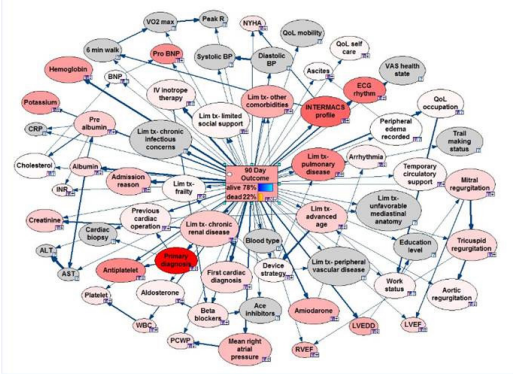
Systems and Synthetic Biology

Systems biology is the integration of experimental and modeling approaches to dissect complex cellular phenomena. Fundamentally, systems biology aims to better quantify and comprehend the highly multivariate and interactive networks of genes, proteins, and metabolites that regulate cellular function. The faculty in Cornell's Meinig School apply new experimental and computational approaches to understand how these gene, signal transduction, and metabolic networks are regulated in healthy tissues and dysregulated, resulting in aberrant cell fates, in pathological settings such as development, cancer and aging. Furthermore, our researchers use modeling efforts to better engineer both novel biomolecules and new combinatorial therapeutic strategies to treat these pathophysiologies. Increasingly, our efforts aim to marry experiment and modeling at the single-cell level so as to elucidate how cell-to-cell variability arises and underlies disease progression and response to therapy. These efforts rely on connections with Cornell's Single Cell Working Group, NIH-funded Physical Sciences Oncology Center, and Stem Cell Program, as well as in collaborations with clinical and research scientists at Weill Cornell Medicine, including the Englander Institute for Precision Medicine.

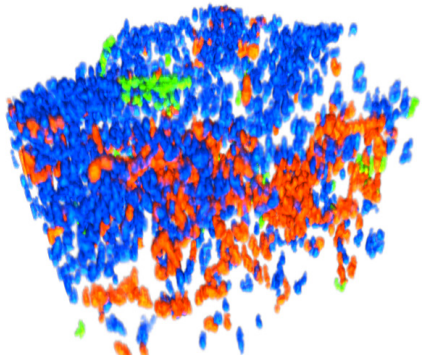
Faculty research interests

James Antaki's lab is involved in three application areas related to synthetic biology: heart-assist support systems for children and adults, development of a blood-purification system for severe malaria and multi-scale computer simulation of thrombosis in artificial circulation.

Ilana Brito's lab pioneers systems-level methods to examine horizontal gene transfer within the human microbiome, the predominant mechanism by which pathogens acquire antibiotic resistance. The Brito Lab studies the transmission of commensal microbes between people and their environments. They employ a combination of microbial engineering, single-cell sequencing approaches, and novel computational algorithms applied to metagenomic data to better understand the relationship between human health and the microbiome.



Bayesian statistical model to predict 90-day survival after receiving a ventricular assist device to treat advanced heart failure. (Antaki)



HiPR-FISH enables the discovery of novel microbial consortia from human oral plaque. The volumetric rendering shows one example of such a novel consortia formed by microbial cells from the genera of *Pseudopropionibacterium*, *Cardiobacterium*, and *Schwartzia*. (De Vlaminck).

(Over)

v. August 2022

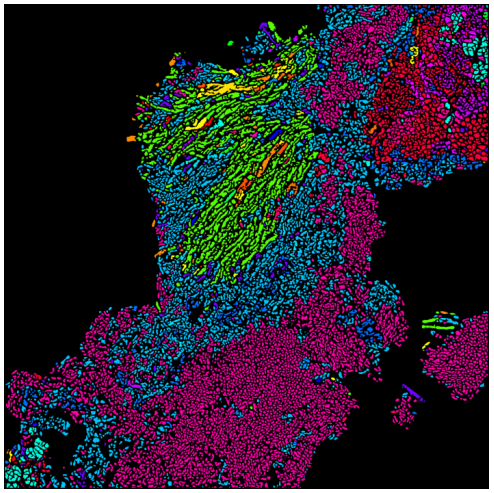
Jonathan Butcher's lab develops and utilizes multi-scale systems modeling to analyze molecular and cellular decisions necessary to grow and organize embryonic cardiovascular tissues. They incorporate finite-element-based growth mechanics simulation with population-based systems modeling to identify key signaling and emergent cellular decision bottlenecks that predict appropriate and malformed heart valves. These computational approaches inform bio-hybrid intervention strategies to repair congenital heart defects.

Nate Cira's lab is interested in understanding emergent properties in multipart biological systems. Currently this involves microbial communities and traveling networks. These investigations are aided by the lab's work developing high throughput fluidic tools.

Ben Cosgrove's lab studies how aging influences a decline in the ability of resident stem cells to regenerate adult tissues. His lab explores how alterations in intercellular communication and intracell signal transduction pathways are altered in aging. His research uses computational and experimental approaches to better understand these signaling networks at the single-cell level, and to target aberrant network functions to rejuvenate stem cells in aged tissues.

Iwijn De Vlaminck lab's mission is to improve human health through the development of genomics-based medicine technologies to study and diagnose infectious, immune and microbiome-associated disease. The lab pursues research in two areas: i) investigating technologies and applications of circulating cell-free DNA for the monitoring of infection, host tissue injury due to infection, organ and bone marrow transplant complications and microbiome-associated diseases. ii) investigating single-cell and spatial sequencing technologies, including technologies developed in-house, to study infection in native, complex tissues and to spatially profile host-microbiome interactions.

An overlaid time-lapse image of the slime mold, Physarum polycephalum. (Cira)



A digitized image of microbial communities in the human oral plaque from the HiPR-FISH workflow. HiPR-FISH enables highly multiplexed spatial mapping and quantitative analysis of complex microbial communities. (De Vlaminck)

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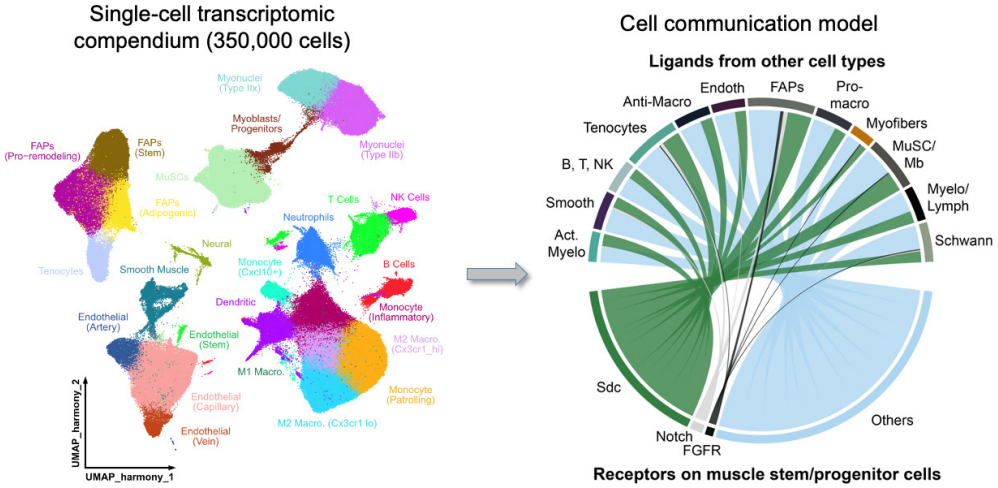

Large-scale single-cell transcriptomic atlas of skeletal muscle used to identify new cell communication factors. (Cosgrove)

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