CIRC Symposium Series 2026-2027

Decoding the “Dark Genome” in the Cancer–Immune Arms Race During Tumor Evolution

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Nearly half of the human genome consists of repetitive DNA sequences scattered throughout our 3.2 billion letter genome. Often considered part of the “dark genome,” these sequences remain poorly understood and are challenging to study using conventional genomic approaches because of their repetitive nature. Once dismissed as “junk DNA,” they are increasingly recognized for their important roles in cancer development and evolution. When repetitive DNA sequences become active, they can produce molecules that resemble those generated during viral infections. This phenomenon, known as viral mimicry, can trigger immune responses that limit tumor growth. However, cancer cells can also evolve strategies to suppress these signals and evade immune detection, creating an evolutionary arms race between cancer and the immune system. In this talk, I will discuss how we use computational genomics, large-scale sequencing data, and mathematical modeling to decode the activity of the dark genome and uncover its hidden roles in cancer evolution. Using pancreatic cancer as an example, I will highlight how repetitive DNA shapes the balance between immune activation and tumor survival, and how understanding these interactions may reveal new opportunities for cancer treatment.

How the Brain Makes Sense of Music and Speech

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Music and speech unfold over time, yet we recognize meaningful patterns across substantial changes in their acoustic form. How does the human auditory cortex combine information over time, and which aspects of a sound does it preserve? Using intracranial recordings, our research addresses these questions through two complementary projects. The first compares temporal integration in music and speech. By presenting the same sound segments in different surrounding contexts, we measure how long preceding information influences neural responses and test whether different sound categories engage different integration timescales. The second examines the neural representation of song through controlled changes in melody, lyrics, and singer. Comparing responses when one feature remains constant and the others change allows us to ask which aspects of song neural populations encode independently of their acoustic realization. Together, these studies investigate how auditory cortex balances sensitivity to acoustic detail with stable representations of meaningful sound structure. CIRC’s BlueHive and BHWard resources support the computational analyses underlying this work.

Friday, November 20, 2026
11:30 am - 1 pm
Wegmans Hall 1400

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