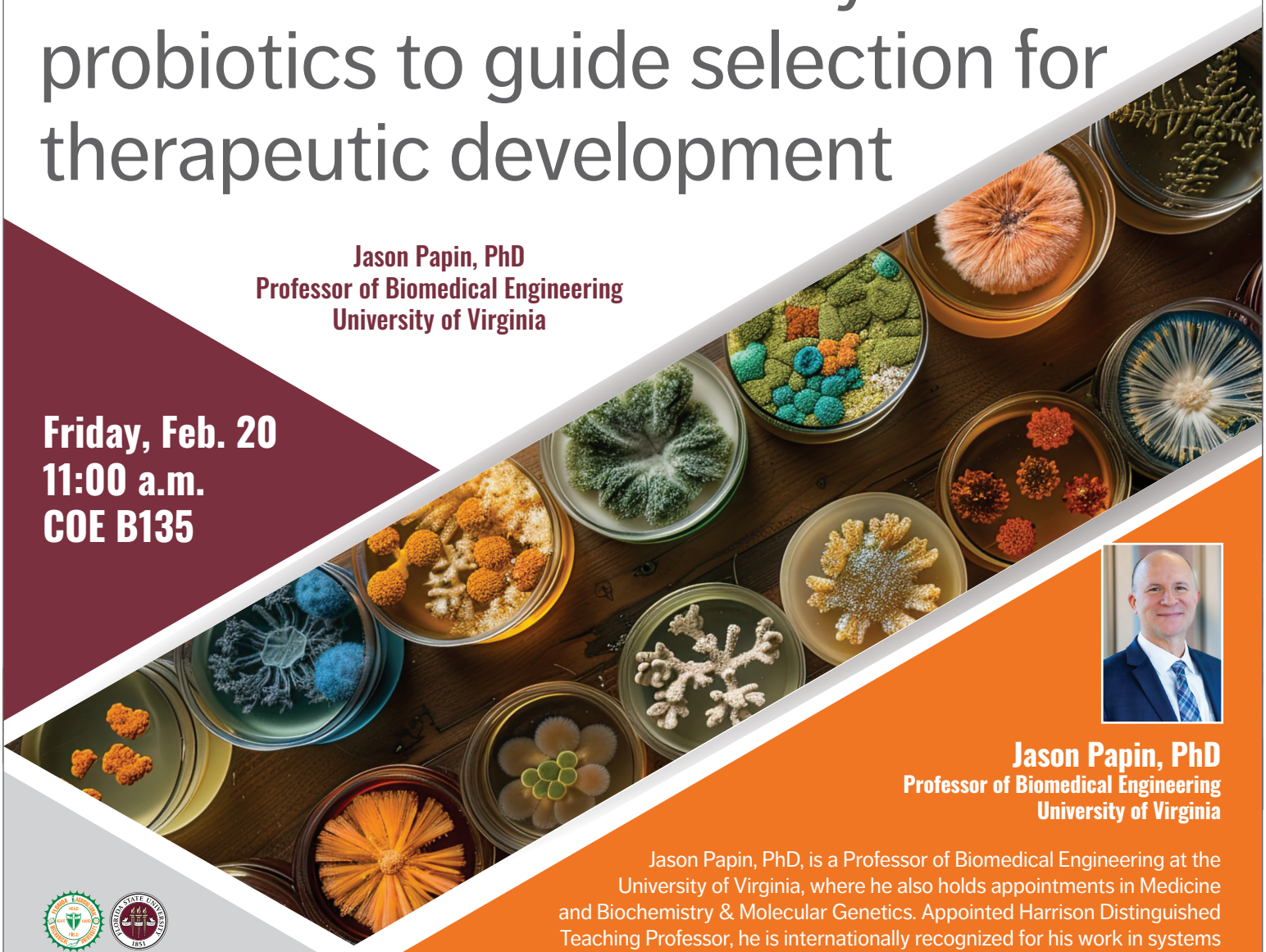
CHEMICAL & BIOMEDICAL ENGINEERING SEMINAR ANNOUNCEMENT

Metabolic network analysis of probiotics to guide selection for therapeutic development

Jason Papin, PhD
Professor of Biomedical Engineering
University of Virginia

Friday, Feb. 20
11:00 a.m.
COE B135



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Jason Papin, PhD, is a Professor of Biomedical Engineering at the University of Virginia, where he also holds appointments in Medicine and Biochemistry & Molecular Genetics. Appointed Harrison Distinguished Teaching Professor, he is internationally recognized for his work in systems biology, metabolic network analysis, and computational modeling of host–microbe interactions in infectious disease.

Dr. Papin has authored over 160 publications with more than 15,000 citations and serves on the editorial board of Cell Systems. He was Co-Editor-in-Chief of PLOS Computational Biology for nearly a decade and helped lead major initiatives in model reproducibility and code sharing. A dedicated educator and mentor, he has received numerous teaching and mentorship awards and is a Fellow of both the Biomedical Engineering Society and the American Institute of Medical and Biological Engineering. He is also co-founder and Chief Product Officer of Cerillo, Inc.

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Probiotic supplements are marketed for diverse health benefits, yet species inclusion often lacks functional rationale. We surveyed 352 U.S. probiotic products and found 36 unique microbial species, with most supplements containing only one species and no clear link between species and intended health benefit. To evaluate probiotic function, we developed a collection of 1,012 genome-scale metabolic models spanning pathogenic, probiotic, and host-associated bacteria. Flux balance analysis revealed that current probiotic species fail to capture the metabolic diversity of native microbes. Focusing on vaginal health, we identified vaginal microbes with metabolic profiles overlapping Gardnerella vaginalis, a key pathobiont. In vitro spent media assays using 11 vaginal isolates showed some inhibition of G. vaginalis. These findings demonstrate a scalable framework integrating metabolic modeling with experimental validation for function-based probiotic design.