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Statistical methods for harmonizing multi-scanner neuroimaging

Wednesday, March 23, 2022
11:45 AM

Zoom Meeting: Meeting ID: 963 9005 8784
Password: 606979

https://rutgers.zoom.us/j/96390058784?pwd=c3VGOFIvYUxRanV5Tk5kS2R0dTVsQT09

Light refreshments will be served

Abstract: While magnetic resonance imaging (MRI) studies are critical for the diagnosis, monitoring, and study for a wide variety of diseases, their use in quantitative analysis can be complex. An increasingly recognized issue involves the differences between MRI scanners that are used in large multi-center studies. To address this, the current state of the art is to "regress out" or "adjust for" scanner differences. Our group has found these methods to be insufficient, and have advocated for the adaptation of methods pioneered in genomics to help mitigate inter-scanner differences which can vary across the brain and result in both mean and variance shifts. We further study the implications of differences in correlation structures across and between images, and how this affects downstream inference.

Bio: Taki Shinohara is an Associate Professor of Biostatistics at the University of Pennsylvania. He directs the Penn Statistics in Imaging and Visualization Endeavor (PennSIVE), a Center of Excellence focusing on imaging statistics at the Perelman School of Medicine. His laboratory focuses on statistical methods and applications for neuroimaging data, with particular emphasis on multiple sclerosis research and neurodevelopmental studies.

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