Dr. Sharon Browning is a Research Associate Professor in the Department of Biostatistics at the University of Washington. She earned her PhD in Statistics from the University of Washington under the supervision of Elizabeth Thompson. She has previously held positions at North Carolina State University, GlaxoSmithKline, and the University of Auckland in New Zealand.

Dr. Browning’s research involves development of statistical methods for analyzing large-scale genetic data, with a particular focus on models for haplotype frequencies. With Dr. Brian Browning, she developed the methodology implemented in the BEAGLE software package. This methodology includes haplotype phase inference, genotype imputation, inference of identity by descent segments, and haplotypic association testing. Dr. Browning was also co-developer (with Dr. Bo Madsen) of the weighted-sum method for rare variant association testing.

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