**Abstract Title:** A blended exome and genome for scalable, low cost, and unbiased discovery through imputation and rare variant calling across the gene coding region

**Author Name:** Dr. Ricky Magner, Computational Scientist

**Author Institute:** Broad Institute, Cambridge, United States.

**Abstract:** Whole genome sequencing (WGS) is the gold standard for genetic analysis, but it can be expensive and time-consuming. Whole exome sequencing (WES) is a more cost-effective option, but it only sequences the protein-coding regions of the genome. To leverage the benefits of both WGS and WES, we developed a blended methodology that produces low-pass WGS and high-coverage WES data from the same sample. This allows us to generate data across the genome without the biases associated with pre-designed genotyping arrays. In this talk, we will present a performance assessment study of our blended genome/exome data modality. We will assess the accuracy of imputation using GLIMPSE across the genome and the performance of variant calling across the exome and clinically important gene regions. These evaluations include a side-by-side comparison of blended exome/genome data with high-coverage whole genome sequencing of the same samples, acting as a truth set, in order to systematically quantify the accuracy of the new data type. We share here the results as well as the methodology to carry out these evaluations in order to highlight the usefulness of a blended exome/genome approach for specific applications such as combined monogenic and polygenic risk estimation in a single assay.

**Area of expertise:** Computational Biology.