DBDS Workshop in Biostatistics
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<th>DATE:</th>
<th>April 1, 2021</th>
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<tr>
<td>TIME:</td>
<td>2:30-3:50pm</td>
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<tr>
<td>TITLE:</td>
<td><em>Leveraging local and polygenic signal for GWAS gene prioritization</em></td>
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| SPEAKER:| Hilary Finucane  
Co-Director of the Program in Medical and Population Genetics,  
Broad Institute of MIT and Harvard |

**Abstract:**
Prioritizing likely causal genes from GWAS data is a fundamental problem. There are many methods for GWAS gene prioritization, including methods that map candidate SNPs to their target genes, and methods that leverage patterns of enrichment from across the genome. In this talk, I will introduce a new method for leveraging genome-wide patterns of enrichment to prioritize genes at GWAS loci, incorporating information about genes from many sources. I will then discuss the problem of benchmarking gene prioritization methods, and I will describe a large-scale analysis to benchmark many different methods and combinations of methods on data from the UK Biobank. Our analyses show that the highest confidence can be achieved by combining multiple lines of evidence, and I will conclude by giving examples of genes prioritized in this way.

**Short Bio:**
Hilary Finucane is a faculty member at Harvard Medical School and Massachusetts General Hospital and the co-director of the Medical and Population Genetics Program at the Broad Institute of MIT and Harvard.

**Suggested Reading:**
- [10 Years of GWAS Discovery: Biology, Function, and Translation](#)