**Workshop in Biostatistics**  
MSOB X303

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<th>DATE:</th>
<th>May 16, 2019</th>
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<tbody>
<tr>
<td>TIME:</td>
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<tr>
<td>TITLE:</td>
<td>Construction and application of polygenic risk scores</td>
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<td>SPEAKER:</td>
<td>John Witte</td>
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<td>Professor of Epidemiology &amp; Biostatistics</td>
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<td>University of California, San Francisco</td>
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**Abstract:**

Over the past decade genome-wide association studies (GWAS) have found thousands of variants associated with hundreds of phenotypes. The conventional GWAS approach evaluates each variant individually. However, these almost always have a small effect on a given phenotype. To address this limitation, one can instead combine variants together into a polygenic risk score (PRS), which can be more strongly associated with phenotypes. This suggests that a PRS may be useful for predicting phenotypes. For example, indicating which individuals are at a substantially increased risk of cancer and should undergo more active screening. While there is much hope and excitement surrounding the potential use of PRS, there also remain a number of unanswered questions and concerns with this approach. I will consider some of the critical issues, including how to best construct PRS from GWAS data, with an application to multiple different cancers in the UK Biobank cohort.