

# **Meta-analysis and Large-scale Evidence in Molecular Epidemiology**

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## **Abstract:**

The advent of molecular epidemiology and molecular medicine has created unique opportunities and challenges. Meta-analytic techniques may be used to combine molecular data from various similar or even dissimilar studies. Assessing heterogeneity and biases is probably more important than arriving at (potentially spurious) summary estimates in the application of these techniques. The talk will discuss some of the insights into heterogeneity and biases that we have gained through the application of meta-analysis in molecular epidemiology with emphasis on human population genetics. We will also discuss efforts to minimize biases in large-scale designs and international consortia of investigators.