Prenatal exposure to toxic metals is linked to numerous adverse perinatal outcomes, such as preterm birth, as well as later-in-life outcomes, such as impaired neurocognition. During pregnancy, metals pass through the placental barrier to reach the developing fetus. In doing so, metals may alter placental gene expression, in turn dysregulating the biological functioning of a critical organ for fetal growth and development. This pathway may underly adverse health outcomes; however, few studies have evaluated genome-wide gene expression changes in response to metals in a human population to test this hypothesis. To make matters more complicated, research is increasingly demonstrating that pregnant women are exposed to multiple metals simultaneously, thus it is no longer adequate to investigate gene expression in response to single-metal exposure; rather, we must use mixtures-based approaches. But how can we assess the effect of multiple metals simultaneously in one model? Especially when the outcome of interest involves 35,000+ endpoints (i.e. expression levels of all detectable genes)! Join for this week’s seminar to find out! In this week’s presentation, you’ll learn about an ongoing study evaluating genome-wide placental gene expression in relation to cord tissue concentrations of eleven different metals/metalloids.

Through learning about this study, and the analytical challenges it poses, you’ll be able to:
1. Describe why analyzing environmental chemical mixtures is challenging
2. Identify different analytical approaches for different types of mixtures-related questions
3. Explain how to interpret a quantile-based g-computation regression model