**PROJECT SUMMARY**

Autism spectrum disorder (ASD) is a developmental disability associated with significant social, communication and behavioral challenges, and there is a distinct need for tools that help identify children with ASD as early as possible. Despite being highly heritable, the etiology of autism is still unclear. Our current incomplete understanding of ASD pathogenesis and the lack of reliable biomarkers hampers early detection, intervention and patient outcomes. The currently available questionnaire based screening tools suffer from vast number of false positives which create long wait-times for diagnostic evaluations. Additionally, standardized checklists are vulnerable to socio-economic and interpretational biases that disproportionately impact diagnosis in diverse communities. Borderline cases with children with average to above average cognitive abilities might be left undiagnosed till start of school.  In this study, we operationalize a documented aspect of ASD symptomology in that it has a wide range of co-morbidities occurring at much higher rates than in the general population. The ASD Co-morbid Risk (ACoR) methodology we propose in this grant can address the aforementioned complicated challenges of ASD screening, by distilling incipient predictive patterns of elevated risk from past medical history of individual patients.  In the setting of a pediatric primary care clinic at the Department of Pediatrics, University of Chicago, we plan to carry out a comparative study of ACoR with M-CHAT/F, which is the most common screening tool in current use. Via a direct comparison, we specifically aim to 1) estimate how much earlier we can trigger interventions, 2) the possibility of combining the scores for significant improvements in either Positive Predictive Value or the sensitivity while not losing specificity, 3) the superior performance in diverse cohorts, and 4) shed light on the ASD pathobiology by classifying patterns of co-morbidities that predict distinct presentations.