



Editor  
Science Advances

Dear Editor

Please find enclosed the manuscript entitled "**Reduced False Positives in Autism Screening Via Digital Bio-markers Inferred from Deep Co-morbidity Patterns**" for your consideration for publication in Science Advances as an original article.

Autism spectral disorder (ASD) is currently screened for in toddlers using standard questionnaires, .e.g. M-CHAT/F with a high number of false positives (85%) and a low sensitivity (38%) – translating to long wait-times for confirmatory diagnosis ( $\approx 1$  year). Children lose crucial time within which interventions are the most effective. Additionally, questionnaires are prone to interpretive biases leading to systematic under-diagnosis in diverse communities.

Here we report an orthogonal methodology that requires **no questionnaires or blood-work**. Using novel stochastic learning on individual diagnostic codes already recorded during past doctor's visits, we design a risk estimator significantly out-performing the state-of-the-art. Without pre-selecting co-morbid disorders, we learn hidden patterns in medical histories to enable cutting down false positives by upto half without losing specificity. Additionally, we get new insights into co-morbid risk that might shed light into ASD pathobiology.

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We are led by a multi-disciplinary team of machine learning experts (Chattopadhyay PH. 8145315312) and clinical practitioners with substantial scholarly work in pediatric developmental psychology and autism: 1) Peter J. Smith, Professor of Pediatrics and **Executive Committee Chair, American Academy of Pediatrics' Section on Developmental & Behavioral Pediatrics**, and 2) Prof. Michael Msall, **Section Chief of Developmental & Behavioral Pediatrics, UChicago, and Fellow of Joseph P. Kennedy Research Center on Intellectual & Neurodevelopmental Disabilities, UChicago**.

We look forward to, and humbly hope for, your positive response.

Sincerely,

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Chicago, IL

Thursday 22<sup>nd</sup> October, 2020