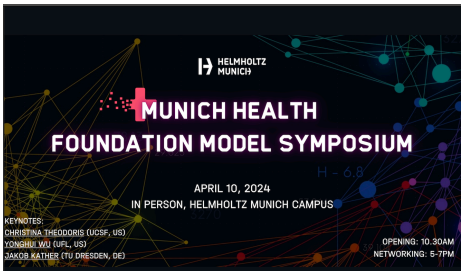

Contribution ID: **10** Type: **Poster**

ML-enabled genetic causal inference of biological aging

The aging process is a complex phenomenon intricately linked with the onset and progression of various age-related diseases. In this study, we propose a novel framework that synergistically combines machine learning techniques with genetic causal inference methods to elucidate the underlying mechanisms of biological aging and its association with disease susceptibility.

Our research employs deep learning algorithms to extract embeddings from medical data, capturing multi-faceted biological processes associated with aging. Leveraging these embeddings, we extend the Mendelian Randomization framework to jointly analyze multiple risk factors, enabling a comprehensive understanding of their influence on aging and disease onset.

In particular, our focus lies on the application of this methodology to fundus images and age-related macular degeneration (AMD). We employ a RETFOUND model, fine-tuned to optimize embeddings for age prediction using Rank N contrast loss, effectively delineating age-related changes within the latent space. By conducting genome-wide association studies (GWAS) on these embeddings, we identify genetic factors contributing to age-related ocular diseases.

The method extends beyond the study of AMD, demonstrating its adaptability to diverse diseases and data types. By elucidating the complex interplay between aging and disease susceptibility, our research aims to provide valuable insights into the aging process across various health conditions, facilitating targeted interventions and personalized healthcare strategies.

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Session Classification: Break + Posters session

Track Classification: Poster