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The Phenotypic Basis of CT-derived Kidney Traits and Their Utility in Predicting Estimated Glomerular Filtration Rate

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Introduction/Background

The volume of imaging data, necessity of accurate and consistent granular imaging traits defined across the lifespan, and need to support underserved communities require novel end-to-end automation strategies, especially for kidney evaluation. To address this challenge, we developed and applied AI to CT scans and analyzed the clinical relevance of imaging traits with disease. We hypothesized that kidney imaging-derived phenotypes (IDPs) could be used to predict estimated glomerular filtration rate (eGFR).

Methods/Intervention

We extracted thorax, abdomen, and/or pelvis CT scans for 20,289 individuals in the Penn Medicine Biobank, segmented the kidneys using TotalSegmentator, and derived quantitative imaging traits to perform association studies, controlled for sex, age, age^2, BMI, and population stratification. A simple feed-forward neural network was also trained to predict eGFR using the kidney traits as well as age and sex. The dataset was split into 70%/15%/15% training/validation/testing.

Results/Outcome

We performed phenome-wide association studies against multiple quantitative kidney IDPs. For kidney volume, we observed strong significant negative associations with end-stage renal disease as well as related circulatory conditions such as hypertension and congestive heart failure, with similar trends also identified for kidney surface area and mean attenuation. Our neural network model for predicting eGFR from kidney traits, age, and sex was trained on eGFR values documented within 7 days of a CT scan. The model exhibited robust predictive ability and had a mean squared error of 413.93 on the testing dataset. Using a cutoff of 60 mL/min/1.73m2 for chronic kidney disease, our model had a sensitivity of 61.7% and specificity of 87.3%.

Conclusion

Our association studies demonstrate not only strong correlations between CT imaging-derived kidney traits and health conditions, but also granularity in how different kidney diseases affect certain kidney traits and not others. We will also perform genetic association studies to study the genetic architecture of our kidney IDPs. Furthermore, the quantitative IDPs showed strong predictive potential for estimating eGFR.

Statement of Impact

Our results not only validate the biological relevance of our IDPs, but also demonstrate the clinical utility of predicting eGFR from imaging traits that could be integrated into a clinical workflow and used to indicate further testing in relevant patients.

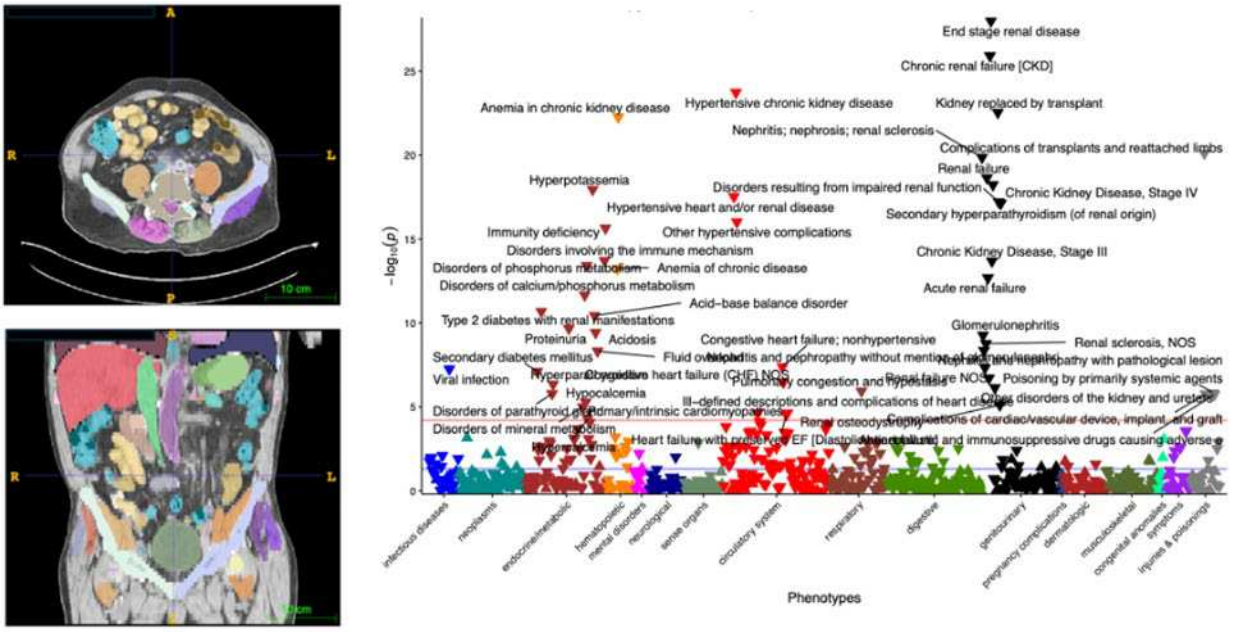

Figure 1. Example segmentation of abdominal structures (left) and phenome-wide association study (right) of electronic health records-derived diagnoses and estimated kidney volume. The red line is the Bonferroni-corrected phenome-wide significance threshold of 6.25E-05 and the blue line is the suggestive significance threshold of 0.05. The orientation of the triangles represents the direction of the associations.

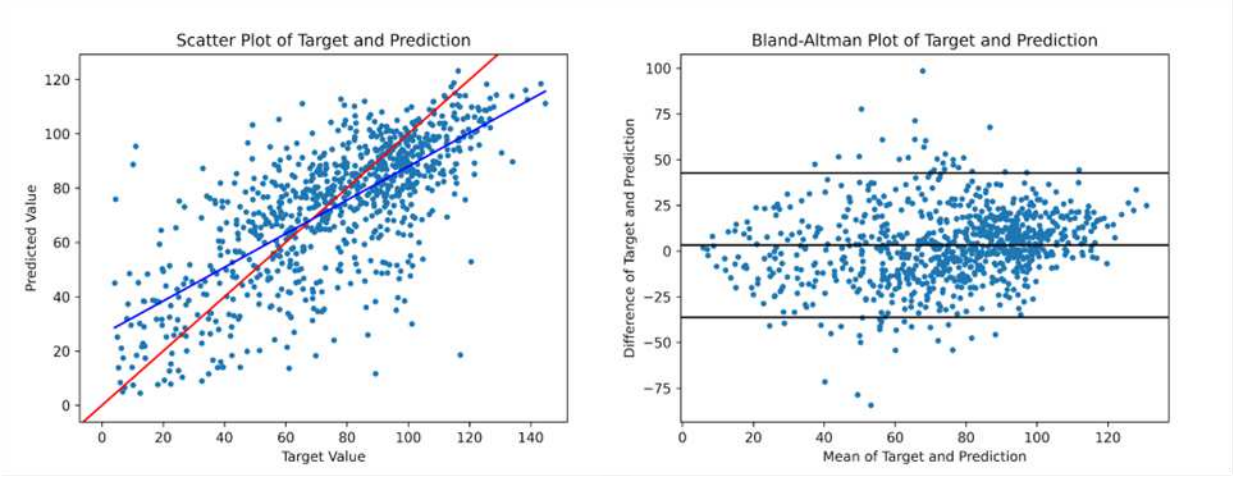

Figure 2. A scatter plot (left) and Bland-Altman plot (right) showing the neural network predictions for eGFR. In the scatter plot, the red line indicates the line where the prediction and target are equal, and the blue line indicates the line of best fit of the actual target-prediction pairs. In the Bland-Altman plot, the middle black line indicates the mean of the difference in the target and predicted values, while the top and bottom black lines represent the 95% confidence interval of the difference in the target and predicted values.

Keywords

imaging; deep learning; phewas; genomics; kidney