

Project Summary for IgANN website

AI.IgAN

Primary Investigators

Prof. Peter Boor, PhD, Institute for Pathology, University Hospital RWTH Aachen, Aachen, Germany
Jun.-Prof. Roman Bülow, Institute for Pathology, University Hospital RWTH Aachen, Aachen, Germany

Brief Description

Pathology and particularly nephropathology diagnostics face challenges due to inter-observer variability, affecting patient treatment. Analysis of histology images currently utilizes only a small portion of available information, often qualitatively or semi-quantitatively. The integration of deep learning (DL) in image analysis offers new opportunities to enhance histopathology diagnostics. DL has demonstrated effectiveness in various medical fields, providing reproducible quantitative analysis and reducing observer variability. This includes segmenting, quantifying histology, classifying, and predicting survival and treatment outcomes. However, DL applications for IgA nephropathy (IgAN), particularly using large multicenter international datasets, are largely lacking. AI.IgAN collects such data from international collaborators within the IgAN-study group to develop AI tools for IgAN, aimed at automated quantification, outcome prediction, and augmenting diagnostic capabilities in digital nephropathology.

Project status

Continuous data collection & data analysis – please contact pboor@ukaachen.de to participate.

Published:

Hölscher, D.L., Bouteldja, N., Joodaki, M., Russo, M.L., Lan, Y.-C., Sadr, A.V., Cheng, M., Tesar, V., Stillfried, S.V., Klinkhammer, B.M., Barratt, J., Floege, J., Roberts, I.S.D., Coppo, R., Costa, I.G., Bülow, R.D., Boor, P., 2023. Next-Generation Morphometry for pathomics-data mining in histopathology. **Nat. Commun.** 14, 470.

Joodaki, M., Shaigan, M., Parra, V., Bülow, R.D., Kuppe, C., Hölscher, D.L., Cheng, M., Nagai, J.S., Goedertier, M., Bouteldja, N., Tesar, V., Barratt, J., Roberts, I.S., Coppo, R., Kramann, R., Boor, P., Costa, I.G., 2024. Detection of Patient-Level distances from single cell genomics and pathomics data with Optimal Transport (PILOT). **Mol. Syst. Biol.** 20, 57–74.

Hölscher, D.L., Goedertier, M., Klinkhammer, B.M., Droste, P., Costa, I.G., Boor, P., Bülow, R.D., 2024. tRigon: an R package and Shiny App for integrative (path-)omics data analysis. **BMC Bioinformatics** 25, 98.

Bouteldja, N., Hölscher, D.L., Bülow, R.D., Roberts, I.S.D., Coppo, R., Boor, P., 2022. Tackling stain variability using CycleGAN-based stain augmentation. **J. Pathol. Inform.** 13, 100140.