## **CDCS Opening symposium**

CDCS
CENTER FOR DATA AND COMPUTING
IN NATURAL SCIENCES

## **OPENING SYMPOSIUM 2022**







Contribution ID: 105 Type: Poster

## sPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies

Meta-analysis has been established as an effective approach to combining summary statistics of several genome-wide association studies (GWAS). However, the accuracy of meta-analysis can be attenuated in the presence of cross-study heterogeneity. We present sPLINK, a hybrid federated and user-friendly tool, which performs privacy-aware GWAS on distributed datasets while preserving the accuracy of the results. sPLINK is robust against heterogeneous distributions of data across cohorts while meta-analysis considerably loses accuracy in such scenarios. sPLINK achieves practical runtime and acceptable network usage for chi-square and linear/logistic regression tests. sPLINK is available at https://featurecloud.ai/app/splink.

**Primary authors:** DOMINIK HEIDER; ESA PITKÄNEN; BAKHTIARI, Mohammad (Data scientist); DANIEL RUECKERT; GEORGIOS KAISSIS; NINA KERSTIN WENKE; TIM KACPROWSKI; JAN BAUMBACH; JULIAN SPÄTH; MARKUS LIST; STEFAN WEISS; TOBIAS FRISCH; UWE VÖLKER

**Co-authors:** JULIAN MATSCHINSKE; Mr NASIRIGERDEH, Reza (AI in Medicine and Healthcare, Technical University of Munich, Munich, Germany); TORKZADEHMAHANI, Reihaneh (AI in Medicine and Healthcare, Technical University of Munich, Munich, Germany)

Presenter: BAKHTIARI, Mohammad (Data scientist)

Session Classification: Poster session with buffet

Track Classification: CDL3 (Systems Biology)