



EMIF Deliverable 3.12: Integrative model of biomarkers from different modalities

Executive summary

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As part of EMIF-MBD it is planned to combine marker results from metabolomics, proteomics, genomics and other modalities to determine the optimal combined biomarker assay. The statistical analysis of such hugely multi-dimensionality data is complex. In order to progress this further, partners including KCL, European Bioinformatics Institute and Oxford have been working together to generate multimodal analyses. Using a novel approach to metabolomics data, mQTLs were identified and used to nominate both markers and novel genomic regions associated with AD. Such approaches will be further developed with the full datasets.

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