



Session 1 NMPB



METHYLATION BASED BIOMARKER IN CLINICAL PRACTICE

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in Szczecin, Poland



Topic and objectives



We are a new group in PUM (led by Dr Tomasz Wojdacz) founded by NAWA.

We are focusing on the development of biomarkers for early cancer diagnosis and personalised medicine.

Our objectives: We are looking for consortium that join as a partner in the Horizon 2020 grant application (e. g. Multi-omics for genotype-phenotype associations (RIA) ID: BIOTEC-07-2020).

Existing partnerships: MethylDetect; Aarhus University, Denmark; Serum Institute, Denmark.



Expertise

(of your institution/company)



Bioinformatic analysis of epigenomics data, including: genome wide methylation profiling, development of pipeline for the large-scale data analysis, processing the obtained data to identify the molecular processes affected by methylation changes.

Bioinformatic platforms and tools: ToppGene Suite (gene list enrichment analysis (GSEA) and candidate gene prioritization), GREAT platform (prediction functions of cis-regulatory regions), Cytoscape platform (analysing of functional interactions between genes and pathways affected by methylation changes), EpiExplorer and EpiGRAPH (exploring epigenetic significance of the data), etc.

Involvement in previous projects: Wojdacz, T.K. et al. Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials *Blood Adv* 3, 2474-2481 (2019); Engstrom, K. et al. Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. *Arch Toxicol* 91, 2067-2078 (2017); Morris, T. J. et al. ChAMP: 450k Chip Analysis Methylation Pipeline. *Bioinformatics* 30, 428-430 (2014).

Key words: Epigenomics, methylation, biomarker, cancer research



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