PhenoMeNal

e-infrastructure for clinical metabolomics data

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www.ebi.ac.uk
PhenoMeNa1
Large Scale Computing with Medical Metabolic Phenotyping Data

- H2020
- 3 Years
- 13 Partners
- €8 Million
- 830 PM
- Started in September
- EMBL-EBI leads
PhenoMeNal – Data Analysis Workflow

Metabolomics (NMR, MS) and other omic data
- Peak detection/alignment/quantification
- Drift/batch correction/normalisation
- Multiple cohort alignment
- Multiple assay comparison
- Long term stability reference

Data pre-processing

Univariate analysis
- linear or generalised linear models

Multivariate analysis
- PCA; PLS regressions

Dimension reduction
- Penalised regression; Bayesian variable selection

Metabolome wide significance level

External independent validation and large-scale replication

Cross validation

Marker Identification
- Statistical spectroscopy
- Database look up: Bayesian model fit
- MS: adduct/isotope pattern/fragmentation prediction/ & matching

Bioinformatics, cross-platform and multi-omics analyses
- Over representation
- Gene/metabolite enrichment analysis
- Induced network analysis
- Differential network analysis
- Pathway analysis/visualisation

Challenge studies and randomised control trials
PhenoMeNal – Knowledge Generation

Technologies
- Genomics
- Epigenomics
- Metagenomics
- Metabolomics
- Computational science

Resources
- Biobanking
- Industrial collaborations
- High Performance Computing

Methods
- Bayesian approaches
- Machine learning
- Network analysis

Enhanced knowledge base and novel approaches for data aggregation, integration, visualisation and analysis

Understanding aetiology, pathogenesis, pathways and mechanisms of common human disease
PhenoMeNal -

Data producer

PhenoMeNal Data VMI

Tool maker

PhenoMeNal Service VMI

GRID/Cloud (EGI)

PhenoMeNal Compute VMI

PhenoMeNal Portal VMI

User 1 – running public version of PhenoMeNal VMIs via portal

User 2 – running selected PhenoMeNal VMIs in a private cloud