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# Metagenome

Microbiome research for health improvement



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## METAGENOME Microbiome Analysis Toolchain:

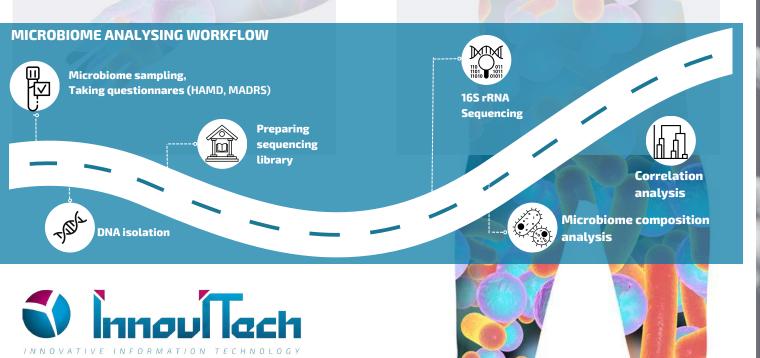
Advancing Diagnostics and Patient Care

#### **MICROBIOME AND MENTAL HEALTH**

- The composition of the intestinal flora, known as the microbiome, forms intricate connections with our body. Disruptions in microbial homeostasis have been implicated in various diseases, including major depressive disorder (MDD).
- MDD affects approximately **6% of the adult** population, posing significant challenges for clinicians in terms of treatment.

#### WHY IS MICROBIOME ANALYSIS BENEFICIAL?

- Secure storage of patient data and questionnaires (HAMD/MADRS -Depression Rating Scales)
- Determination of microbiome composition through next-generation sequencing of the 16S rRNA gene
- Streamlined sequencing workflow
  tracking
- Support for bioinformatic analysis and determination of patients' microbial status
- Correlation analysis: automated evaluation of the links between clinical data and microbiome composition



#### **DRIVING INNOVATION**

- Imbalances in the microbial ecosystem are increasingly linked to the development of various diseases. Analyzing the composition of intestinal flora can provide a new dimension in diagnosing patients with mental illnesses.
- METAGENOME software offers userfriendly support for bioinformatic analysis, covering everything from preprocessing raw sequencing files to phylogenetic classification. Our software stands out by automating the correlation analysis between intestinal flora composition and clinical data.
- This software provides clinicians with an exceptional opportunity to explore the underlying microbial changes associated with their patients' diseases, paving the way for more targeted interventions and personalized care.

### **COOPERATING PARTNERS**



UD-GenoMed Medical Genomic Technologies Ltd.



Semmelweis University Department of Psychiatry and Psychotherapy

#### TO REQUEST MORE INFORMATION OR TO LEARN HOW OUR TECHNOLOGY CAN BENEFIT YOU, PLEASE CONTACT US.

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