Molecular Cognition Group Strategy

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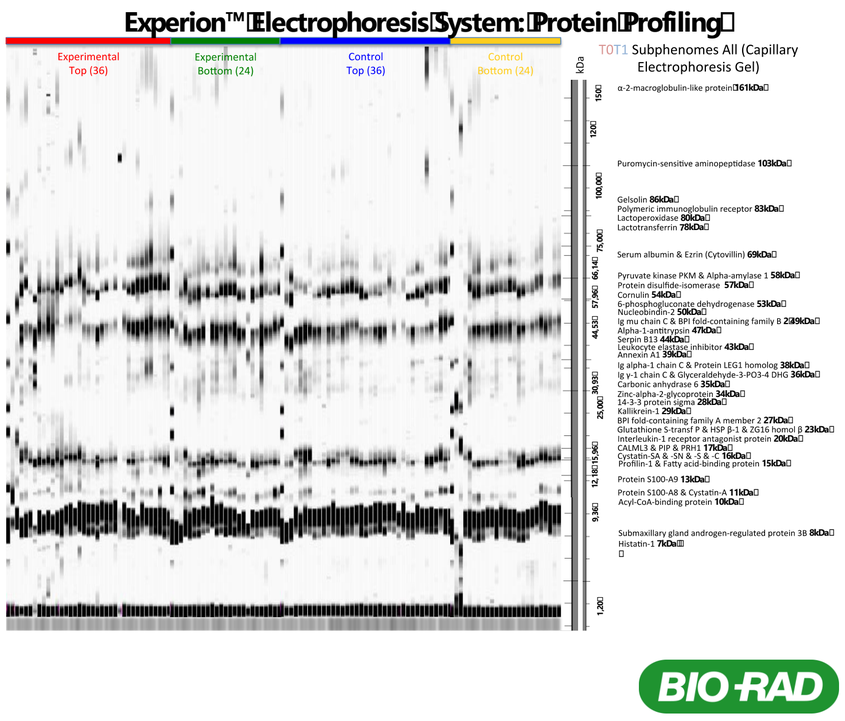
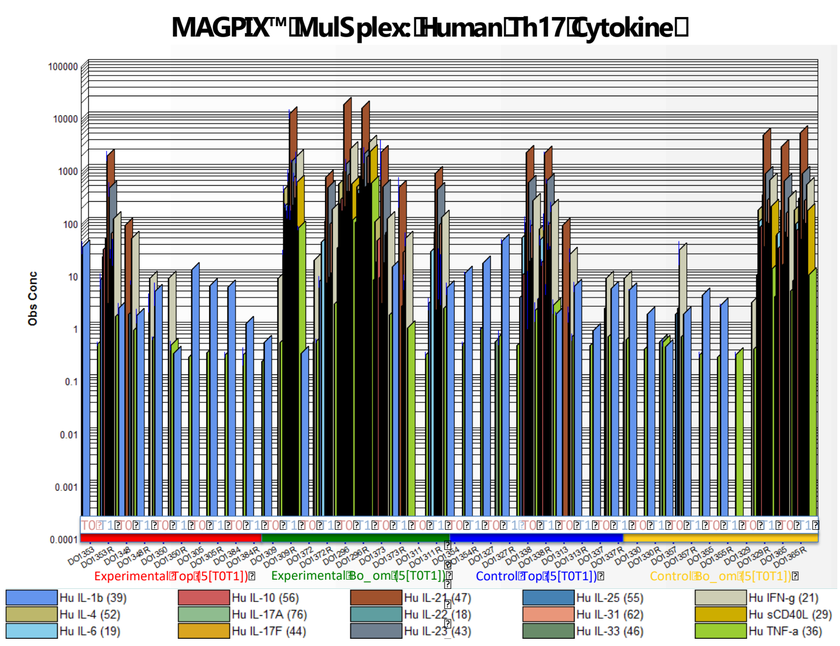
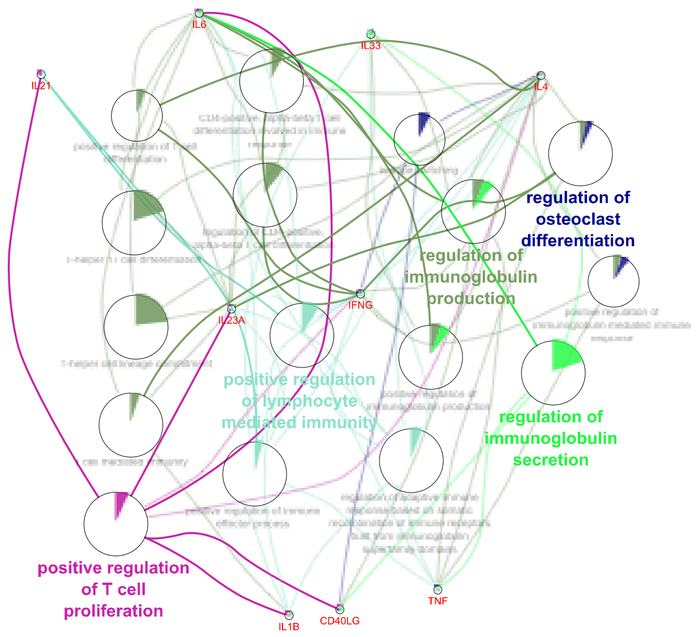
Introduction

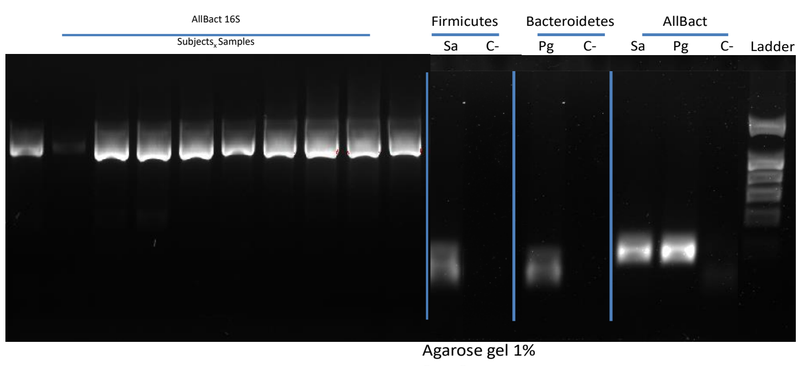
Neuronal functional protein networks found in the oral proteome are possibly useful to characterize a healthy phenome state and trait. Proteomics have extensively and objectively epitomized the understanding of healthy and pathological physiological states or conditions.[1] Our group aims at the molecular characterization of cognition.

Strategy









Agarose gel 1%
Sa – *Streptococcus aureus*
Pg – *Porphiromonas gingivalis*

Functional and physiological network profiling of cognition: A conceptual analysis [2]

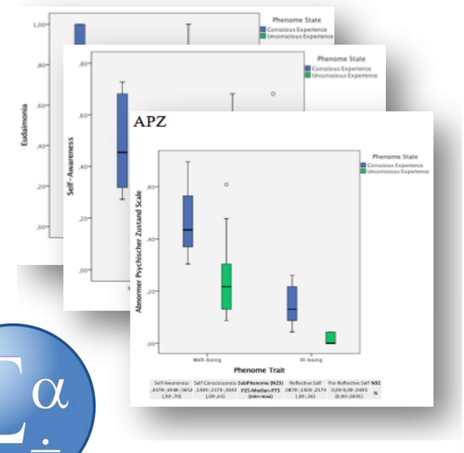
Characterization and stratification of cognitive functional profiles [3]

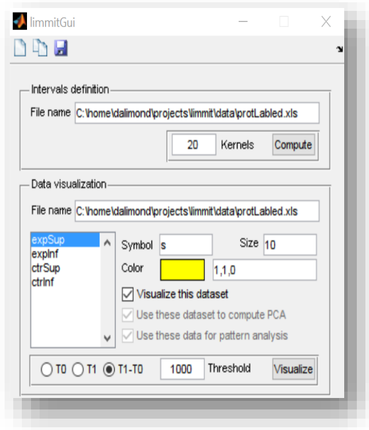
Protein Profiling of Cognition and GUI Toolbox Development [4]

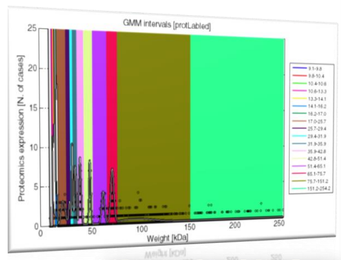
Anti/pro T-helper cell type 17 *equilibrium* in cognitive functional profiling [5]

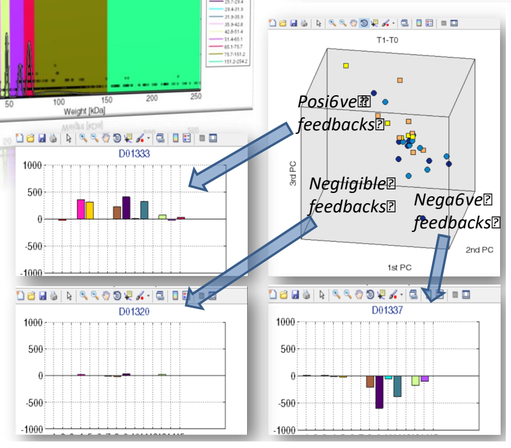
In silico characterization of the Neuronal Proteome and bioinformatic tool development [6]

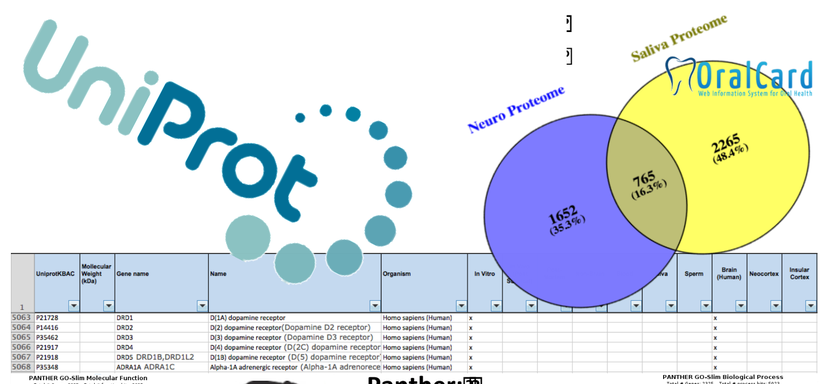
Oral microbiome interactomics with cognition: *Firmicutes Bacteroidetes* ratio as indicator of health [7]

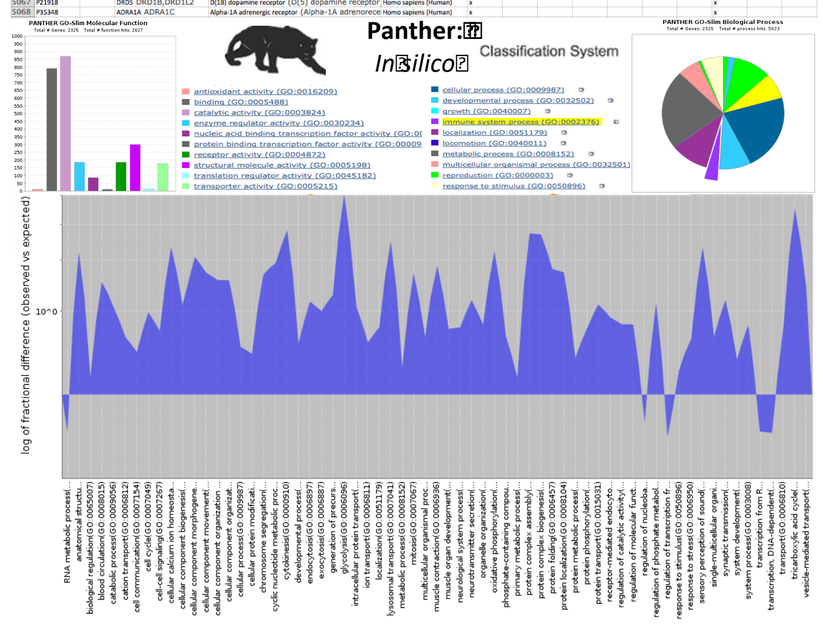












Discussion/Conclusion

The molecular method, conducted in 150 healthy 19-25 year-old university students, is composed by the objective, subjective and bioinformatics tasks. The objective is a proteomic evaluation of total proteins profiles and protein functional networks, and identification of saliva molecular profiles of cognitive states. The subjective assessment focuses on the phenome stratification, i.e. the psychological and phenomenological characterization. The bioinformatics assessment is a systems biology data correlation between the objective and subjective assessments, thru the development of a graphical user interface toolbox for data exploration and visualization.

The main outcomes of this study are the neuronal-oral proteome characterization, the identification of salivary healthy cognitive molecular networks and multi-omics data-mining solutions. [8]

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