



DATA ANALYTICS RESEARCH CENTER

# Computational intelligence methods applied to single and multiview neuroimaging data

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**Lecture Hall "G2" (Bldg. G, Level 0)**

The aim of this seminar is to discuss innovative approaches that exploit computational intelligence to infer new knowledge from neuroimaging data. The main challenge is to devise methods able to cope with the high dimensionality and the low signal-to-noise ratio that characterizes this kind of data

The first part of the talk is focused on functional neuroimaging and how clustering techniques can be used to derive robust sets of features from whole brain maps. The advantage of this approach compared to traditional univariate feature selection methods is that of preserving the information about the anatomical regions that form clusters and of taking into account relationships among features. Furthermore, for each subject, clusters are ranked according to their median value and a stochastic rank aggregation method, TopKLists, is applied to combine the individual rankings within each class of subjects. For comparison, the same approach was tested on an anatomical parcellation. We found parcels for which the rankings were different among control subjects and subjects affected by Parkinson's disease and amyotrophic lateral sclerosis and found evidence in literature for the relevance of top ranked regions in default-mode brain activity.

The second part of the talk will describe a multi-view learning framework that combines functional MRI and diffusion tensor imaging to study brain connectivity. In this approach, structural and functional connectivity features are extracted from multi-modal MRI images with a clustering technique, and used for the multi-view classification of different phenotypes of neurodegeneration by an ensemble learning method (random forest). The results highlight the potentials of mining complementary information from the integration of multiple data views in the study of neurodegenerative diseases.

The third part of the seminar involves connectome-wide analyses in normal and clinical populations by using functional and structural connectivity data from which high-density whole-brain networks. These analyses typically rely on a preprocessing step (pruning) to reduce computational complexity and remove the weakest edges that are most likely affected by experimental noise. However, weak links may contain relevant information about brain connectivity, therefore, the identification of the optimal tradeoff between retained and discarded edges is a subject of active research. We introduce a pruning algorithm to identify edges that carry the highest information content. The algorithm selects both strong edges (i.e. edges belonging to shortest paths) and weak edges that are topologically relevant in weakly connected subnetworks. The newly developed "strong-weak" pruning (SWP) algorithm was validated on simulated networks that mimic the structure of human brain networks. It was then applied for the analysis of a real dataset of subjects affected by amyotrophic lateral sclerosis (ALS), both at the early (ALS2) and late (ALS3) stage of the disease, and of healthy control subjects. SWP preprocessing allowed identifying statistically significant differences in the path length of networks between patients and healthy subjects.

## **SHORT BIO**

Roberto Tagliaferri is full professor in Computer Science at the University of Salerno. He has had courses in Computer Architectures, Artificial and Computational Intelligence, and Bioinformatics for computer scientists and biologists.

He has been co-organizer of international workshops and schools on Neural Nets, Computational Intelligence and Bioinformatics. He has been co-editor of special issues on international journals and of Proceedings of International conferences. He is senior member of the IEEE "Computational Intelligence" and "System, Man and Cybernetics" societies, and of INNS. He was chair of the Italy Chapter of the IEEE CIS from 2013 to 2017. He is Associate Editor of the IEEE Transactions on Cybernetics and of Source Code in Medicine and Biology of Biomed Central, and he has been co-editor of special issues on international journals and of proceedings of international workshops in the areas of Computational Intelligence and Bioinformatics. His research activity has been oriented to Computational Intelligence models and applications in the areas of Astrophysics, Biomedicine and Bioinformatics.

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