Brain Networks Constructed via Cross Recurrence Quantification Analysis

Anastasia Pentari\(^1\), George Tzagkarakis\(^2\), Panagiotis Tsakalides\(^1\), Panagiotis Simos\(^2\)\(^3\), George Bertsias\(^3\)\(^4\), Eleftherios Kavroulakis\(^3\), Kostas Marias\(^2\)\(^4\) and Efrosini Papadaki\(^2\)\(^3\)

\(^1\)Department of Computer Science, University of Crete
\(^2\)Institute of Computer Science, Foundation for Research and Technology-Hellas
\(^3\)School of Medicine, University of Crete
\(^4\)Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology-Hellas

\(^3\)Department of Electrical and Computer Engineering, Hellenic Mediterranean University

apentari@csd.uoc.gr, gtzag@ics.forth.gr, tsakalid@ics.forth.gr,akis.simos@gmail.com, bertsias@uoc.gr
terryka21985@gmail.com, kmarias@ics.forth.gr, papada@otenet.gr

Abstract

There is a growing interest in developing new approaches aiming to approximate the dynamic functional connectivity (dFC) of human brain. Cross recurrence quantification analysis (CRQA) is an effective method for inferring the joint dynamics between pairs of time series corresponding to distinct dynamical systems. On the other hand, the resting-state functional magnetic resonance imaging (rs-fMRI) tool provides useful information about brain connectivity and functionality. In this work, we apply the CRQA-based features on brain networks and examine how well these characteristics can represent the brain’s dynamic behavior, by exploiting the rs-fMRI recordings.

Method’s Perspectives

- Extract specific brain subnetworks
- Evaluate dFC variations between healthy and diseased groups
- Classification

Main Procedure

Fig. 1 presents our method’s pipeline. Specifically:

- Take pair of time-series from brain regions
- Apply the CRQA method:
  - Extract the Cross Recurrence Plots (CRPs)
  - Extract the CRQA-based features from CRPs
- Quantification Analysis
- Construct the Adjacency matrix through features
- Thresholding the Adjacency matrix
- Construct the brain network

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Figure 1. Pipeline of our proposed method: (a) rs-fMRI data acquisition; (b) Brain regions definition; (c) Application of CRQA to each regional pair of time series; (d) Integration of the CRQA features into a network (i.e., adjacency matrix computation); (e) Construction of the brain graph.

Comparison between Pearson’s correlation and CRQA-based features

- 120 interrelations between rs-fMRI time-series were examined
- 16 regions out of the 90
- CRQA-based features proved to detect more statistically significant interrelations than the conventional Pearson’s correlation
- Specific CRQA features proved to be more effective