Brain Networks Constructed via Cross Recurrence Quantification Analysis

Anastasia Pentari[1,2], George Tzagkarakis[2], Panagiotis Tsakalides[1,2], 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
[4]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.

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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Method's Perspectives

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

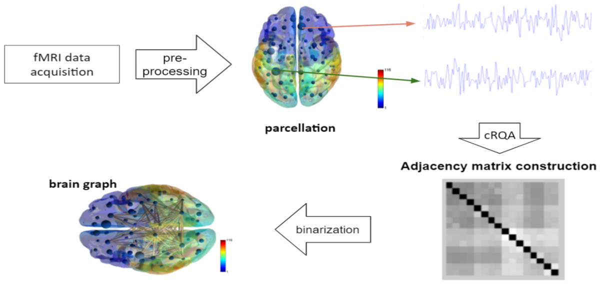
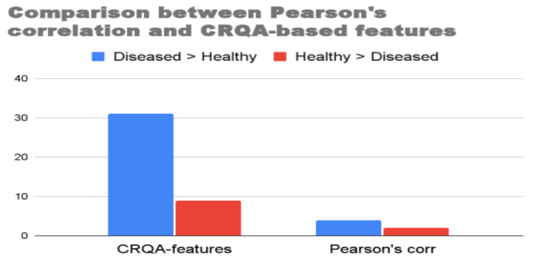


Figure 1. Pipeline of our proposed method: (a) rs-fMRI data acquisition; (b) Brain regions definition; (c) Application of CRQA to each regional pair of time series; (d) Integration of the CRQA features into a network (i.e., adjacency matrix computation); (e) Construction of the brain graph.



- 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

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