The Influence of Different Normalization Methods on Cross Recurrence Quantification Analysis

Mohammadreza Rezaie, MSc and Farzaneh Haghighat, PhD
Rehabilitation Sciences Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

OBJECTIVE

To compare the effect of different normalization methods on the Cross Recurrence Quantification Analysis (CRQA) variables. More methods were also introduced based on the central tendency and dispersion in Statistics in order to achieve the most possible coupling stability.

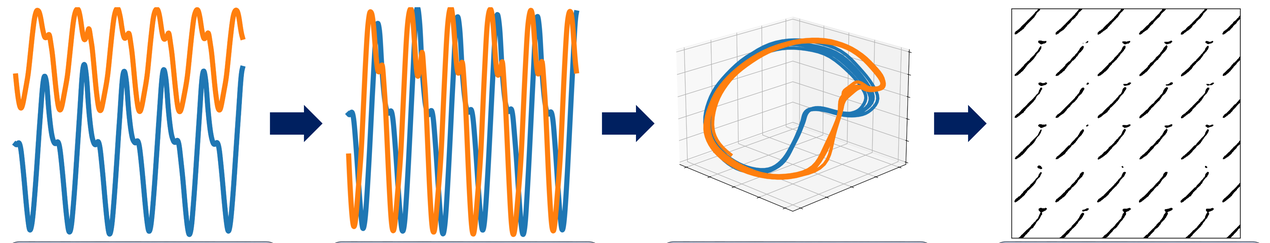
METHODS

Initial time-series of pelvis, thigh, and shank kinematics in sagittal plane for 10 healthy individuals during 30s treadmill running at a fixed velocity of 3.5 m/s were used [1]. 40 consecutive heel strikes were interpolated to 3900 points and normalized by:

- **M0**: no normalization,
- **M1**: amplitude between 0 and 1,
- **M2**: zero mean & unit amplitude,
- **M3**: zero mean & unit standard deviation,
- **M4**: zero mean & unit interquartile range,
- **M5**: zero median & unit median absolute deviation,
- **M6**: zero median & unit interquartile range.

REC: Recurrence rate
DET: % Determinism
DMAX: max diagonal length
DMEAN: mean diagonal length
ENT: Shannon entropy

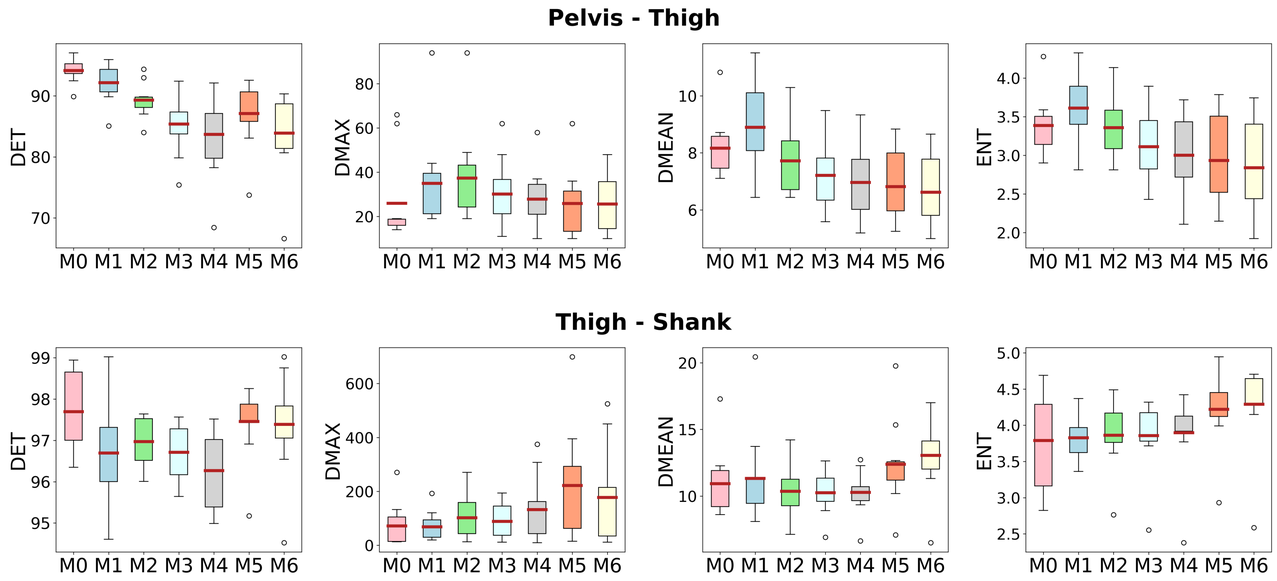
Optimal time delay and dimension were estimated for each signals using Average Mutual Information (AMI) and False Nearest Neighbors (FNN) algorithms, respectively. For each couple, both signals were embedded in a common state space reconstructed by the average of time delay and the maximum of dimension values [2]. Methods were compared using Repeated-measure ANOVA for DET, DMAX, DMEAN, and ENT variables.



Initial time-series (Pelvis - Tight) (Thigh - Shank) → **Normalized by M1 - M6** → **State Space Delay (AMI) Dimension (FNN)** → **Euclidean norm 2.5% fixed REC 4 min diagonal line**

RESULTS

Significant differences (p<0.05) were observed between the methods in all CRQA variables for both couples. The largest stability was obtained by M1 and M6 methods for Pelvis-Thigh and Thigh-Shank couplings, respectively.



DISCUSSION AND CONCLUSION

CRAQ variables were subject to normalization methods and there was no one-size-fits-all solution in terms of coupling stability. Since the radius is permitted to fluctuate as much as necessary in the fixed REC thresholding, reasonable results still can be obtained by ignoring normalization (M0) compared with other methods, even if no overlap exists.

This study suggests examining several normalization methods on pilot data in order to find the one (or none) that results in the most stable coupling between the input signals; this may lead to a more sensitive and robust CRQA.

REFERENCES

1. Fukuchi et al. (2017), *PeerJ*, PMID: 28503379
2. McCamley et al. (2017), *Comput. Math. Methods Med.*, PMID: 29201135