

The CICIL tool: a Java-based user-friendly application for the analysis of individual tumor size lesion dynamics



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INTRODUCTION

Clinical models of tumor dynamics generally omit information on individual target lesions (iTl), and use the total tumor size (TS) as a continuous variable to model the tumor time-course. However, differences in lesion dynamics might be predictive of tumor progression. To extract this information from clinical databases and process it, we have integrated knowledge from signal processing and machine learning into a novel and flexible approach for the non-parametric analysis of iTl [1, 2]. We called this new methodology **Classification Clustering of Individual Lesions** (CICIL). In this work, we present the **CICIL tool**, a **Java-based cross-platform** implementation of the CICIL methodology, made available to the scientific community [2].

METHODS

Integrating existing techniques from other fields into CICIL

Classification of individual target lesions

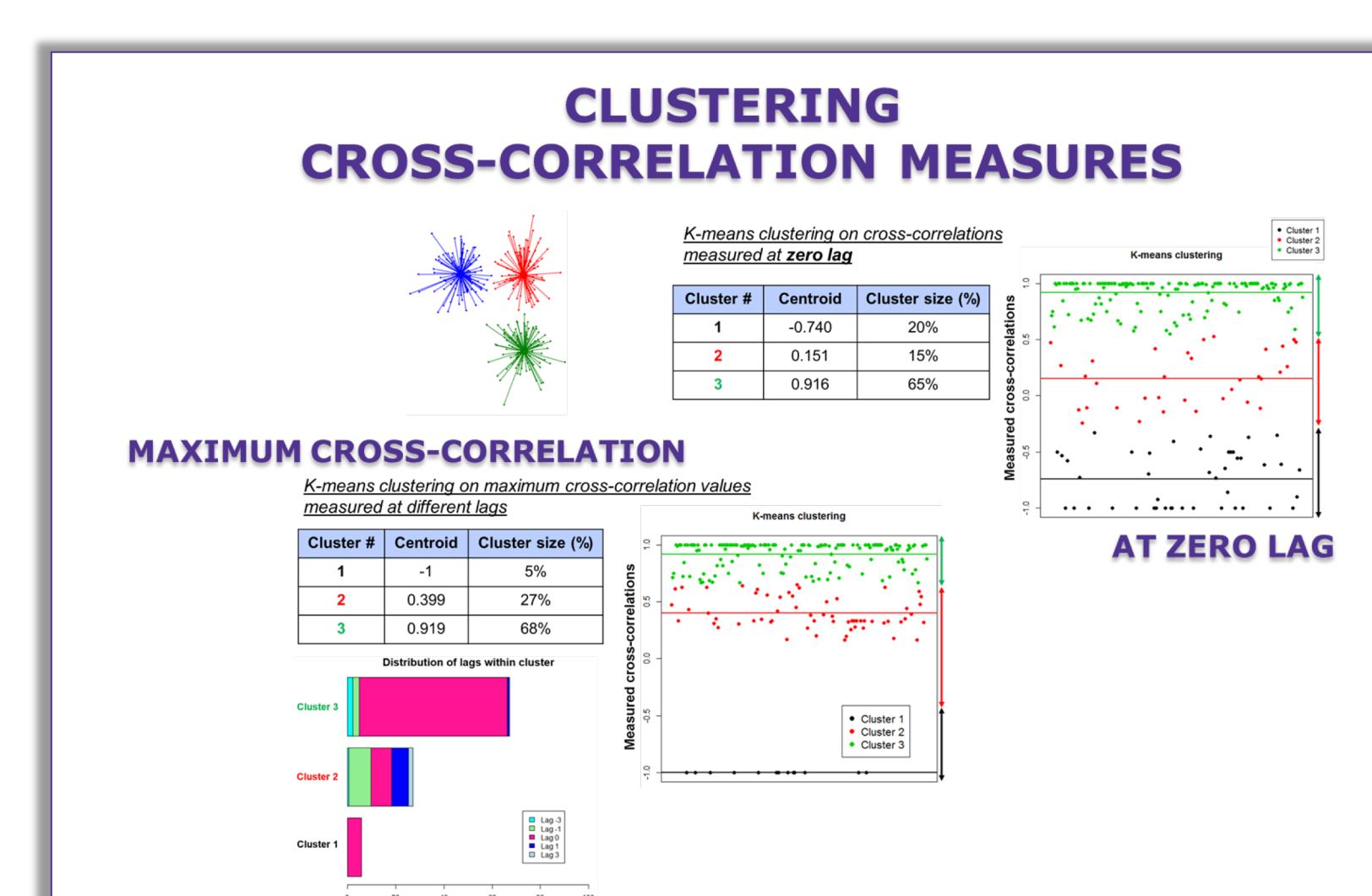
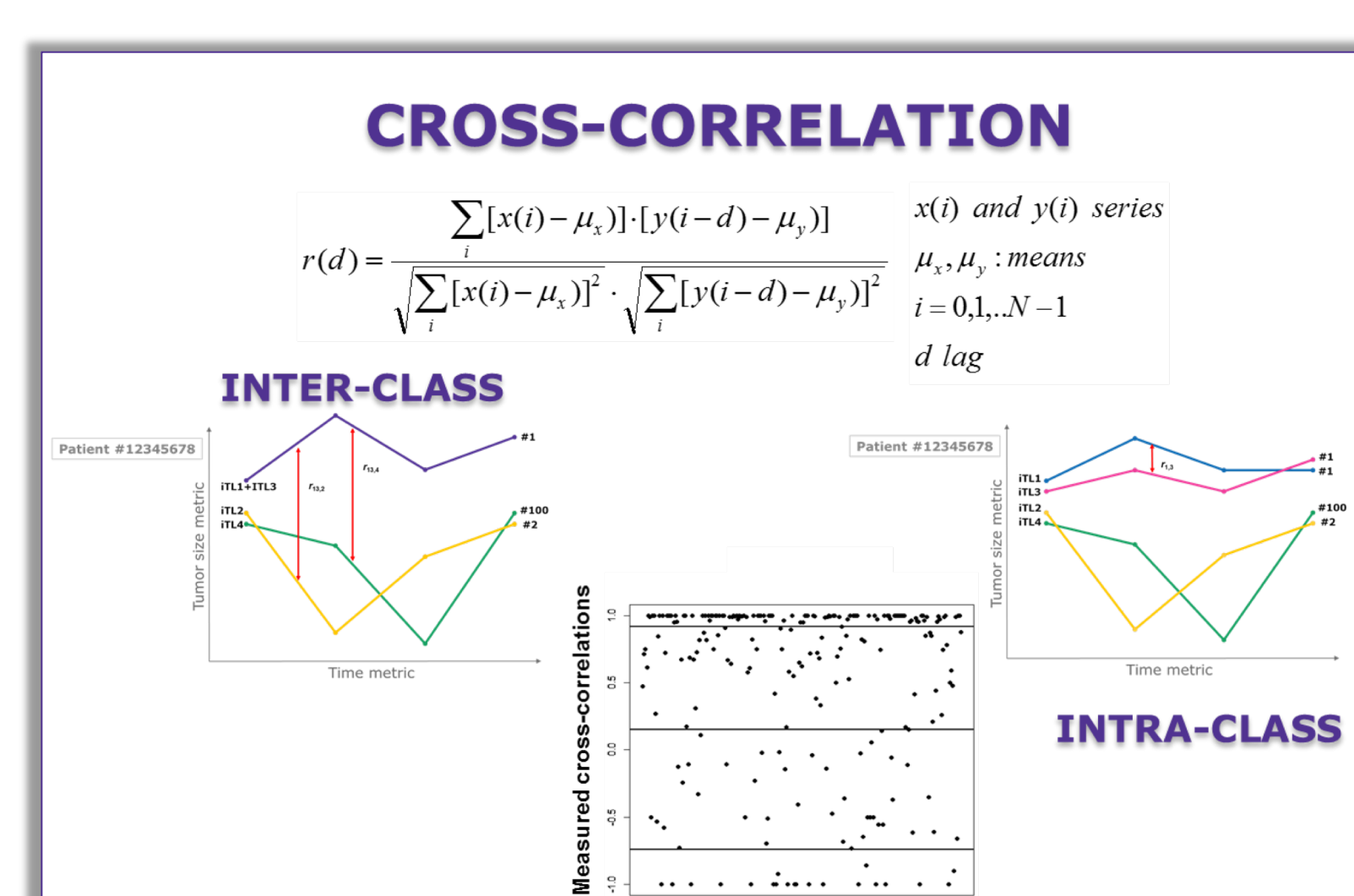
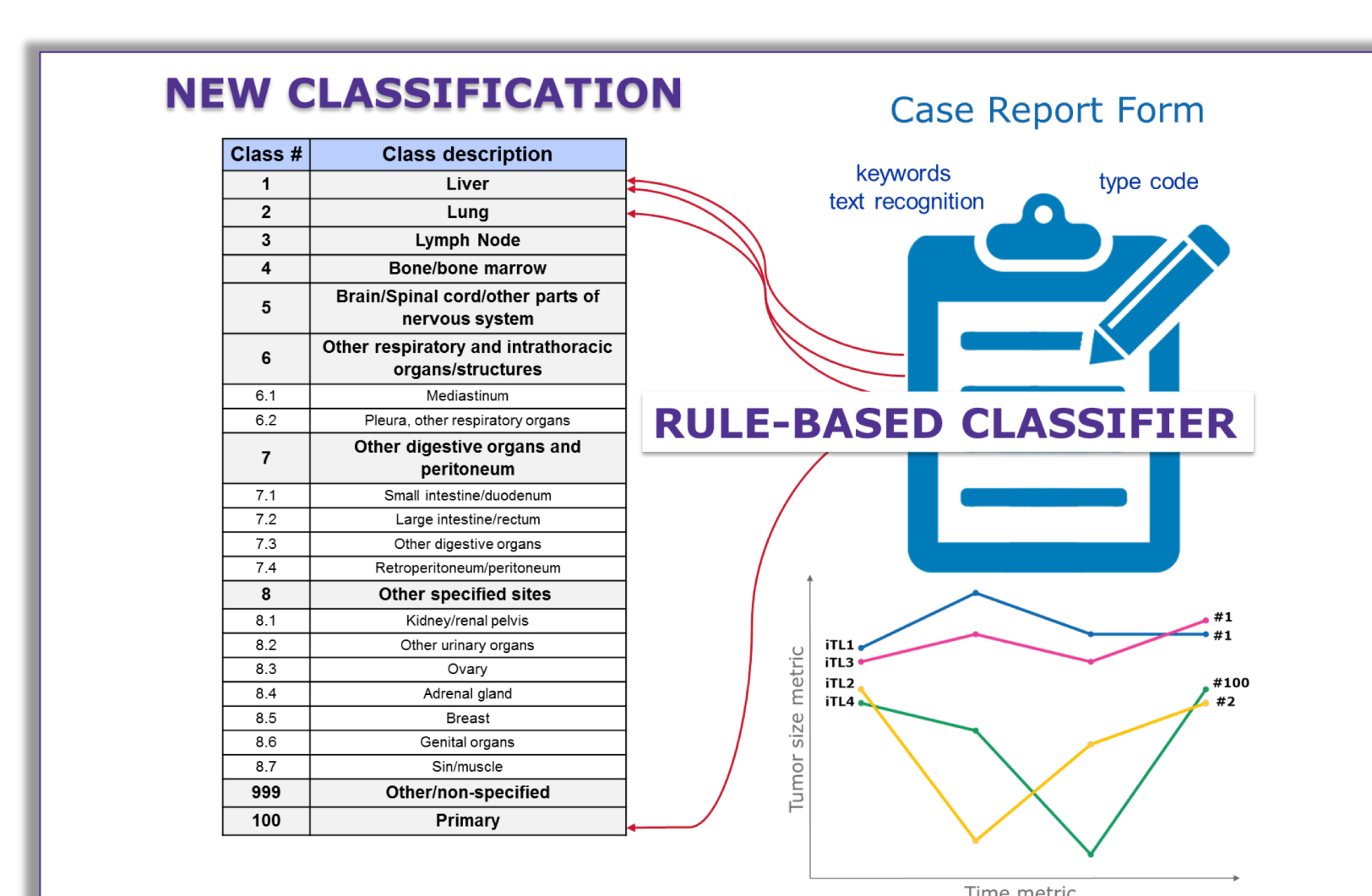
Rule-based classifier

Estimation of the degree of similarity

Cross-correlation

Result exploration and interpretation

K-means clustering



- Based on functional and location criteria, and medical evidences
- Automatic recognition of keywords
- At different lags to find the maximum cross-correlation
- Within the same class
- Among different classes
- Easy computation of similar tumor profiles proportion
- Quick assessment of lag effects
- Efficient results overview on large-scale datasets

A dedicated software tool implementing our methodology

Customizable classification definition

Java-based cross-platform implementation

Intuitive and user-friendly design

Easy methodology and knowledge sharing

Automatic report generation

RESULTS

- The CICIL tool's executable (JAR file) is publicly available along with a use case based on a mock dataset [2]. The tool can be executed on operating systems which contain a version of the Java Runtime Environment, minimum v1.7, and has been tested in Windows 7 and 8. System requirements and application features are described in the respective user guide embedded in the tool.

CONCLUSIONS

- The CICIL tool constitutes a user-friendly and flexible platform enabling data mining from TS clinical study databases.
- It allows a straightforward execution of CICIL to efficiently analyze and understand large-scale datasets prior to modeling.
- Results can guide the modeler in determining if a total TS evaluation might reasonably predict tumor lesion behavior, or potential differences in responses, within or across tumor classes, should be considered for a particular case study.

REFERENCES

1. Terranova, et al.. PAGE 2015; [Abstr 3399].
2. Terranova, et al.. CPT Pharmacometrics Syst. Pharmacol. 2018; 7, 228–236.

DISCLOSURES

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