Chronic lymphocytic leukemia (CLL) is the most common adult leukemia with still unclear etiology. Indications of antigenic pressure have been hinted, using sequence and structure-based reasoning. The accuracy of such approaches, and in particular of the ones derived from 3D models obtained from the patients' antibody amino acid sequences, is intimately connected to both the reliability of the models and the quality of the methods used to compare and group them. The proposed work provides a sophisticated method for the classification of CLL patients based on clustering the amino acid sequences of the clonotypic B-cell receptor immunoglobulin, which is the ideal clone-specific marker, critical for clonal behavior and patient outcome. A novel CLL patient clustering method is hereby proposed, combining bioinformatics methods with the extraction of 3D object descriptors, used in machine learning applications. The proposed methodology achieved an efficient and highly informative grouping of CLL patients in accordance to their biological and clinical properties.

General information
State: Published
Organisations: Department of Biotechnology and Biomedicine, Department of Bio and Health Informatics, Immunoinformatics and Machine Learning, Technical University of Denmark, Center For Research And Technology - Hellas, Carlsberg Research Laboratory
Authors: Mochament, K. (Ekstern), Agathangelidis, A. (Ekstern), Polychronidou, E. (Ekstern), Palaskas, C. (Ekstern), Kalamaras, E. (Ekstern), Moschonas, P. (Ekstern), Stamatopoulos, K. (Ekstern), Chailyan, A. (Ekstern), Overby, N. (Ekstern), Marcatili, P. (Intern), Hadzidimitriou, A. (Ekstern), Tzovaras, D. (Ekstern)
Pages: 139-150
Publication date: 2017
Conference: 5th International Work-Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2017, Granada, Spain, April 26–28, 2017, Granada, Spain, 26/04/2017 - 26/04/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Lecture Notes in Computer Science
Volume: 10209
ISSN (Print): 0302-9743
Ratings:
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.67 SJR 0.315 SNIP 0.552
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.328 SNIP 0.618 CiteScore 0.37
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.325 SNIP 0.678 CiteScore 0.42
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.329 SNIP 0.699 CiteScore 0.49
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.323 SNIP 0.708 CiteScore 0.49
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.325 SNIP 0.721 CiteScore 0.49
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.314 SNIP 0.634
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.305 SNIP 0.548
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1