

Techniques Involved in Artificial Immune System

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DESCRIPTION

Artificial Immune Systems (AIS) are a type of computationally intelligent, rule-based machine learning system inspired by the concepts and processes of the vertebrate immune system in artificial intelligence. Artificial Immune Systems is a field focused with abstracting the structure and function of the immune system to computer systems and examining how these systems might be used to solve computational issues in mathematics, engineering, and information technology.

AIS are a branch of Biologically Inspired Computing (BIC) and Natural Computation (NC), with a focus on Machine Learning and a place in the larger area of Artificial Intelligence.

Artificial Immune Systems are problem-solving adaptive systems based on theoretical immunology and observed immune functions, principles, and models. Although such models initiated the field of AIS and continue to provide fertile ground for inspiration, AIS is distinct from computational immunology and theoretical biology, which are concerned with simulating immunology using computational and mathematical models in order to better understand the immune system, unlike other topics such as DNA computing, AIS is not concerned with the examination of the immune system as a substrate for computation.

New AIS ideas, such as threat theory and algorithms inspired by the innate immune system, are now being investigated. Although some argue that these do not yet provide a truly "new" abstract over and above existing AIS algorithms, others claim that they do. This, however, is a contentious issue, and the discussion is currently one of the key driving reasons behind AIS development.

Another new area is the investigation of degeneracy in AIS models, which is inspired by its proposed role in open ended learning and evolution.

AIS was founded with the goal of finding efficient abstractions of immune system operations, but it has recently become interested in modelling biological processes and applying immune algorithms to bioinformatics challenges.

Techniques

Specific immunological hypotheses that describe the function and behaviour of the mammalian adaptive immune system inspired the prevalent approaches.

Clonal selection algorithm: Affinity maturation is a set of algorithms influenced by the clonal selection hypothesis of acquired immunity that explains how B and T cells enhance their antigen response over time. These algorithms concentrate on the Darwinian aspects of the theory, such as selection being influenced by antigen-antibody affinity, reproduction by cell division, and variation through somatic hyper mutation. Clonal selection methods, some of which resemble parallel hill climbing and the genetic algorithm without the recombination operator are most widely used in the optimization and pattern recognition areas.

Negative selection algorithm: T cell tolerance is inspired by the positive and negative selection processes that occur during the development of T cells in the thymus. Negative selection is the process of identifying and eliminating self-reacting cells, or T cells that may select or attack own tissues. This class of algorithms is commonly utilised in problem domains like as classification and pattern recognition.

Immune network algorithms: Algorithms based on Niels Kaj Jerne's idiotypic network theory, which describes how anti-idiotypic antibodies regulate the immune system. This class of algorithms focuses on network graph architectures involving antibodies as nodes, with the training method creating between nodes based on affinity. Immune network techniques are similar to artificial neural networks and have been utilised in clustering, data visualisation, control, and optimization.

Dendritic cell algorithms: The Dendritic Cell Algorithm (DCA) is an example of a multi-scale immune-inspired algorithm. This algorithm is based on a dendritic cell model that is abstract. The DCA is abstracted and implemented through a process of investigating and modelling numerous elements of DC activity, ranging from the molecular networks found within a single cell to the behaviour of a population of cells as a whole. Information is granulated at multiple tiers inside the DCA, which is accomplished using multi-scale processing.

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Received: 03-Feb-2022, Manuscript No. JCCI-22-16102; **Editor assigned:** 07- Feb-2022, PreQC No. JCCI-22-16102 (PQ); **Reviewed:** 21-Feb-2022, QC No. JCCI-22-16102; **Revised:** 28- Feb-2022, Manuscript No. JCCI-22-16102 (R); **Published:** 07- March-2022,

DOI:10.35248/2155-9899.22.13.654.

Citation: Sait H (2022) Techniques Involved in Artificial Immune System. J Clin Cell Immunol.13:654.

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