Using Cross Reactivity in an AIS For Prediction of Outcome of Similar Diseases

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Identify Datasets

- Find datasets for similar diseases
- Datasets should have the same features
 - Ag, Ab should be in the same shape-space for both diseases
- Most datasets have statistics and not patient data

Implementation

• Using existing architectures - ARTIS [1]

ARTIS

- Proteins strings of length /
 - either self or non-self
- Receptors and Epitopes are fixed-length strings in HIS
- Detectors (antibodies) present at the vertices of a graph and move along the edges

ARTIS

- Detector activated when number of bindings above threshold
- These bindings decay with time
 - \bullet Match count reduces by 1 with probability $\gamma_{\it match}$ at each timestep

Detector Lifecycle

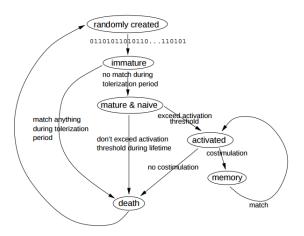


Figure: Detector Lifecycle [1]





Steven A Hofmeyr and Stephanie Forrest.

Architecture for an artificial immune system.

Evolutionary computation, 8(4):443-473, 2000.