



Alzheimer's Diagnostics Tool

A PROJECT TO DIAGNOSE ALZHEIMER'S IN PATIENTS USING BAYESIAN NETWORKS

DEADLOCK

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ABSTRACT

The aim of the project is to provide an efficient Bayesian Network that can take into account various factors like exposure to chemicals, age, genetic mutations, symptoms and other medical conditions to determine if a patient has Alzheimer's or not. **Alzheimer's is a type of dementia that causes problems with memory, thinking and behavior.** Symptoms usually develop slowly and get worse over time, becoming severe enough to interfere with daily tasks. So, it becomes vital to diagnose it as early as possible. This Network tries to come close to that aim.

FEATURES:

1. The first dimension taken into account is exposure to hazardous materials. Here, pesticides, heavy metals, Aspartame, AGEs etc. are provided with a contributory probability towards causing Alzheimer's.
2. Age is another important factor. People generally develop the symptoms after 65 yrs of age but it can still occur between the ages of 35 to 65.
3. Genetic mutations have a huge role to play in determining if a patient has Alzheimer's or not. If a patient has a mutated APP and Presenilin 2 gene, he or she has a 100% chance of Alzheimer's. On the other hand, if a patient has a mutated Presenilin 1 gene, he has a 95% probability. APOE-e4 getting mutated also ups his or her chances of getting Alzheimer's. The probability also rises if a first degree relative has Alzheimer's.
4. Conclusions can also be drawn by checking the past medical record of the patient. Mild Cognitive Impairment, Cardiovascular diseases or a Traumatic Brain Injury also ups a patient's chances of getting Alzheimer's.
5. **Note:** While some of the probabilities are as close to reality as possible, many have been formulated with hypothesizing and following the general trend defined.
6. Finally, symptoms like dementia, mood swings, trouble understanding visual and spatial relationships are defined in the network.

USAGE MANUAL:

Download and place the “deadlock.dne” file in any directory and open it through NETICA application. Compile the project and after the network is initialized, modify and set the values accordingly and see how the network adapts to the change robustly and follows the trend as correctly as possible.

Note: There may arise a situation where the application throws an “Inconsistency” error. This might be an error programmatically, but it is intentional and logical. The error is thrown when one tries to toggle any mutation to “Yes” but tries toggling “Alzheimer’s” and “Genetic_Mutations” to “Absent”. This is not possible since it defined that having a mutation guarantees that Alzheimer’s will be present. Hence, the notion behind it is correct.

