



Figure 4: Example of the NEAT encoding scheme on a four node network. The connection list showing from top to bottom the innovation number, the input/output nodes, w denoting the weight, and the enable bit. In this example the connection from node 3 to 4 is disabled, while this connect with no longer be active in the network, it remains important as a historical marker for computing the genetic distance and performing crossover.

A significant issue that is important to consider when designing a genetic encoding methods, in particular with respect to crossover, is the problem of competing conventions or the permutation problem [1][4]. This occurs when there are multiple genomes which refer to the same phenotype. This can lead to loss of information, inefficient allocation of computational resources and irregularities during crossover operations.

NEAT makes use of an innovation number which is a core component to the overall NEAT system. The innovation number tracks the appearance of specific genes within the system. When a unique mutation occurs, it is allocated an innovation number, this number is incremented globally each time this occurs. Any subsequent occurrences of the same mutation are given the same innovation number. It is important to note that NEAT is not initialised randomly and rather all networks begin as a single connection between the input and output node, thus all networks effectively have a common ancestor and innovation numbers do not need to be assigned during initialisation.