

1079-92-250

**Paola Bonizzoni\*** (bonizzoni@disco.unimib.it), Viale Sarca 336, 20126 Milan, Italy. *The binary perfect phylogeny model with persistent characters: applying the parsimony principle to discover genetic variations in individuals.*

The perfect phylogeny derives from a restriction of the parsimony methods used to reconstruct the evolution of the species (taxa). The model has several applications in computational biology. In particular, the binary perfect phylogeny has been used in mathematical formulations for the general problem of discovering the most common genetic variations in individuals. A central goal in the investigation of this model is to extend its applicability by taking into account the biological complexity of data and computational efficiency. The binary perfect phylogeny model is too restrictive to model common biological events such as recurrent and back mutations. In the talk we consider a natural generalization of the model that allows a special type of back mutation. We investigate the problem of reconstructing a near perfect phylogeny over a binary set of characters where characters are persistent: during evolution characters can be gained and lost once at the most. Based on this notion, we define the problem of the Persistent Perfect Phylogeny (referred as P-PPH). We restate the P-PPH problem as a special case of the Incomplete Perfect Phylogeny. Then by using a graph formulation of this last version, algorithmic solutions of the P-PPH problem are explored. (Received January 16, 2012)