The study of injective envelopes of metric spaces, also known as metric trees (R-trees or T-theory), has its motivation in many subdisciplines of mathematics as well as biology/medicine and computer science. Its relationship with biology and medicine stems from the construction of phylogenetic trees. Concepts of “string matching” in computer science is closely related with the structure of metric trees. A metric tree is a metric space \((M, d)\) such that for every \(x, y\) in \(M\) there is a unique arc between \(x\) and \(y\) and this arc is isometric to an interval in \(\mathbb{R}\). In this talk, we examine convexity and compact structures in metric trees and show that nonempty closed convex subsets of a metric tree enjoy many properties shared by convex subsets of Hilbert spaces. Furthermore, we show that a setvalued mapping \(T^*\) of a metric tree \(M\) with convex values has a selection \(T : M \to M\) for which \(d(T(x), T(y)) \leq d_H(T^*(x), T^*(y))\) for each \(x, y \in M\). Here by \(d_H\) we mean the Hausdroff distance. We will mention some applications. (Received June 25, 2008)