Abstract:
Phylogenetic Diversity (PD) is a measure of biodiversity that takes into account the evolutionary relationships of organisms. Because phylogeny is the fundamental basis for measuring the distinctness of organisms, PD captures information on variety in form and function. The measurement of PD is simple in conception: for a given assemblage, PD is equal to the sum of the branch lengths that connect that set of organisms on a phylogenetic tree. Unlike traditional measures of biodiversity, PD is robust to uncertainty about species identity because the tips of the tree can represent unique sequences, individual organisms, populations or species. Information on branch length ensures that only discrete entities are counted and that the degree to which they are unique is incorporated directly into the measurement of diversity, without the need for arbitrarily defined Operational Taxonomic Units. This attribute is particularly valuable in situations where species boundaries are uncertain (such as in microbial communities), where many species are undescribed, or where environmental genomic samples are homogenised ‘soups’ of organisms. In recent years, PD has been mathematically extended to allow the measurement of both alpha and beta-diversity, to incorporate information on abundance, and to correct for differences in sample size. In this presentation, I will discuss the conceptual and mathematical basis of the ‘PD-calculus’, as this emerging body of methods is known, and demonstrate applications in biodiversity and conservation science.