Bradyrhizobium spp. have been economically valued, and well characterized, for their ability to form symbiotic relationships with legume plant rhizospheres. Symbiotic Bradyrhizobium form and live within legume root nodules where they chemically alter atmospheric nitrogen, through a process called ‘N-fixing’, into molecular forms that the legume can utilize for nutrition. It’s been thought that N-fixation was Bradyrhizobium spp.’s only function, as this symbiosis results in Bradyrhizobium receiving carbon sources from legume roots. Yet in recent studies, Bradyrhizobium has also been found at high abundances at various depths in bulk soil, outside of the influence of legume rhizospheres. More interest is being put into studies that quantify the relative amount of non-N-fixing, non-symbiotic Bradyrhizobium living both within legume and non-legume rhizospheres and within bulk soil. By studying non-symbiotic Bradyrhizobium in bulk soil, we can begin to hypothesize where these species are receiving their growth and energy sources. Due to their high abundances in bulk soil, these studies could also uncover important implications in Bradyrhizoibum spp.’s role in soil carbon and nitrogen cycling, and in our understanding of climate change on a global scale, as soil is becoming more appreciated for its ability to act as a carbon sink. My proposed project will use a mix of methods; including culturing Bradyrhizobium spp. from various bulk soil ecosystems, selecting genetically diverse non-symbiotic Bradyrhizobium spp. from those cultures, then culturing those chosen species under different carbon and nitrogen-source growing conditions. By analyzing the resulting transcriptomes of gene expression and exometabolites formed as a result of nutrient limitations, we can gain a better understanding of the influence that non-symbiotic Bradyrhizobium spp. have on biogeochemical cycling.