E.O. Wilson – one of the most distinguished biologists of the 20th century – said at the end of a life spent in service of living things, “*If I could do it all over again, and relive my vision in the twenty-first century, I would be a microbial ecologist. Ten billion bacteria live in a gram of ordinary soil, a mere pinch held between thumb and forefinger. They represent thousands of species, almost none of which are known to science.”* The ecosystem service contributions of soil microbiomes are tremendous (mediating, driving, and supporting the function of all plant communities on Earth for one) but poorly understood: the perennial problem of microbiology was for decades the “Great Plate Count Anomaly” wherein the number of bacteria that appear in culture is orders of magnitude smaller than that of a natural sample. However, the exponentially declining cost of “multi-omics” (genomic, proteomic, and transcriptomic) techniques coupled with the increasing quality of imaging techniques such as single cell stable isotope probing (SC-SIP) now allow for both coarse and fine-grained views of community-level microbial interactions. The latter permits insight into cellular activity and reproduction without the need for invasive fluorescent dyes which can disrupt cellular function. This is particularly significant because microbes can remain dormant for long stretches, indicating that mere detection via sequencing is insufficient to characterize a microbial ecosystem. SC-SIP, and similar techniques, enable detection of real-time metabolic changes. This study will also leverage EcoFab 2.0 – a high-throughput standardized, sterile environment developed for investigating plant growth and imaging – to investigate how symbiotic plant-microbe interactions tend to shift in grassland species under different IPCC warming scenarios (1.8 . We plan to use *Paspalum notatum*, a common grazing species which covers over 4 million acres in the southeastern United States alone, as our model organism. EcoFab permits the growth of only one small plant species at time. However, *P. notatum* generally grows in monocrops, making it strong candidate for inquiry into the species’ interactions with its soil microbiome. Specifically, we will address the following question: how will climate change impact the soil microbial community, both metabolically and compositionally? By leveraging both imaging and sequencing tools, we will provide novel insights into which functions of the soil microbiome (e.g. nutrient cycling, plant growth promotion, and organic matter decomposition) are at the greatest risk of disruption under a range of new climate patterns. In so doing, we will inform modifications of Earth Systems Models of the southeastern United States, shed light on the nature of microbial interactions (a growing field with implications from agriculture to human health), and offer avenues for further inquiry into the management of the soil microbiome.