



- Multiple window high resolution DNA-SIP**
(16S rRNA gene amplicon based)
- Identify OTUs ¹³C-labeled by each C source on each sampling day.
 - Measure activity characteristics of each OTU based on ¹³C-labeling or population dynamics:
 - **C source bioavailability** averaged across all ¹³C-labeling sources.
 - **Maximum log₂ fold change** in abundance over sampling days.
 - **Latency of ¹³C assimilation** relative to the overall C mineralization

