

Amplicon sequence analysis in QIIME2 and R

Mar 28 & Apr 1 1 - 4 PM

Learn to perform amplicon sequence analyses in QIIME2 using the command line. As well, import and process the generated data into R for common workflows via phyloseq and DESeq2.

New to R?
Check out the 2-hour Intro to R workshop
Jan 24 / Feb 14 / Mar 21

For more information: http://ecoscope.ubc.ca/events/