Event title	WORKSHOP: Introduction to Metabarcoding using QIIME2
Event type	Workshop
Date of event	22/02/2022
Time of event	12:30-5pm AEDT
Topic description	Metabarcoding has revolutionised the study of biodiversity science. By combining DNA taxonomy with high-throughput DNA sequencing, it offers the potential to observe a larger diversity in the taxa within a single sample, rapidly expanding the scope of microbial analysis and generating high-quality biodiversity data. This workshop will introduce the topic of metabarcoding and how you can use Qiime2 to analyse 16S data and gain simultaneous identification of all taxa within a sample. Qiime2 is a popular tool used to perform powerful microbiome analysis that can transform your raw data into publication quality visuals and statistics. In this workshop, using example 16S data from the shallow-water marine anemone E. diaphana, you will learn how to use this pipeline to run essential steps in microbial analysis including generating taxonomic assignments and phylogenic trees, and performing both alpha- and beta- diversity analysis. This workshop is presented by the Australian BioCommons and Melbourne Bioinformatics with the assistance of a network of facilitators from the national Bioinformatics Training Cooperative.
Format description	Workshop, online via Zoom as described in https://zenodo.org/record/4158583 Ashley Dungan and Gayle Philip led the training by introducing key concepts and demonstrating the steps involved in the analysis. Participants then moved into breakout rooms where they had the chance to apply these skills with support from facilitators. The workshop followed the tutorial linked in the 'Related work' section. A breakdown of timings and topics is provided in the schedule. Participation was free but subject to application with selection. Applications were reviewed by the organising committee.
Identifier(s)/URL	https://www.biocommons.org.au/events/metabarcoding-qiime2
Licence	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials

Keywords	Bioinformatics http://edamontology.org/topic_0091 Analysis http://edamontology.org/operation_2945 Workflows http://edamontology.org/topic_0769 Microbial ecology http://edamontology.org/topic_3697 Metabarcoding QIIME2 Microbiome
Contact	Melissa Burke (melissa@biocommons.org.au)
Audience	This workshop is for Australian researchers who are performing or will perform hybrid genome assembly as part of their projects.
Prerequisites	The workshop will be conducted in a Unix environment so basic command line knowledge (e.g. logging in to a remote machine, navigating the directory structure and copying files between the computers) is a prerequisite. You should be familiar with the concepts of microbial analysis, however no previous experience with Qiime2 is required.
Technical requirements	● Slack was used to facilitate discussions. ● Access to the internet, speakers, a webcam, microphone and Zoom. ● Participants were provided with access to virtual machines via a Nectar Cloud instance

Learning outcomes	By the end of this workshop you should be able to:
	● Understand data and metadata formats required for Qiime2
	● Use Qiime2 to:
	  ○ Create and interpret sequence quality data
	  ○ Generate taxonomy reports/tables and phylogenic trees based on amplicon sequence variants
	  ○ Compare Alpha and Beta data analysis
	  ○ Develop publication quality graphics and statistics using 16S sequencing data
	● Assess the results to determine the influence of genotype (an intrinsic factor) and environment (an extrinsic factor) on anemone-associated bacterial communities

Lead Trainer	Dr Ashley Dungan, University of Melbourne Dr Gayle Philip, Melbourne Bioinformatics
Facilitators	Dr Andrew Perry, Monash Bioinformatics Platform Ms Rania Ismail , University of Melbourne Ms Laura Geissler, University of Melbourne Dr Kshitij Tandon, University of Melbourne Dr Igor Makunin, QCIF Bioinformatics/Galaxy Australia
Related work	This workshop follows the tutorial 'Introduction to metabarcoding with QIIME2' which has been made publicly available by Melbourne Bioinformatics.

	https://www.melbournebioinformatics.org.au/tutorials/tutorials/qiime2/qiime2/