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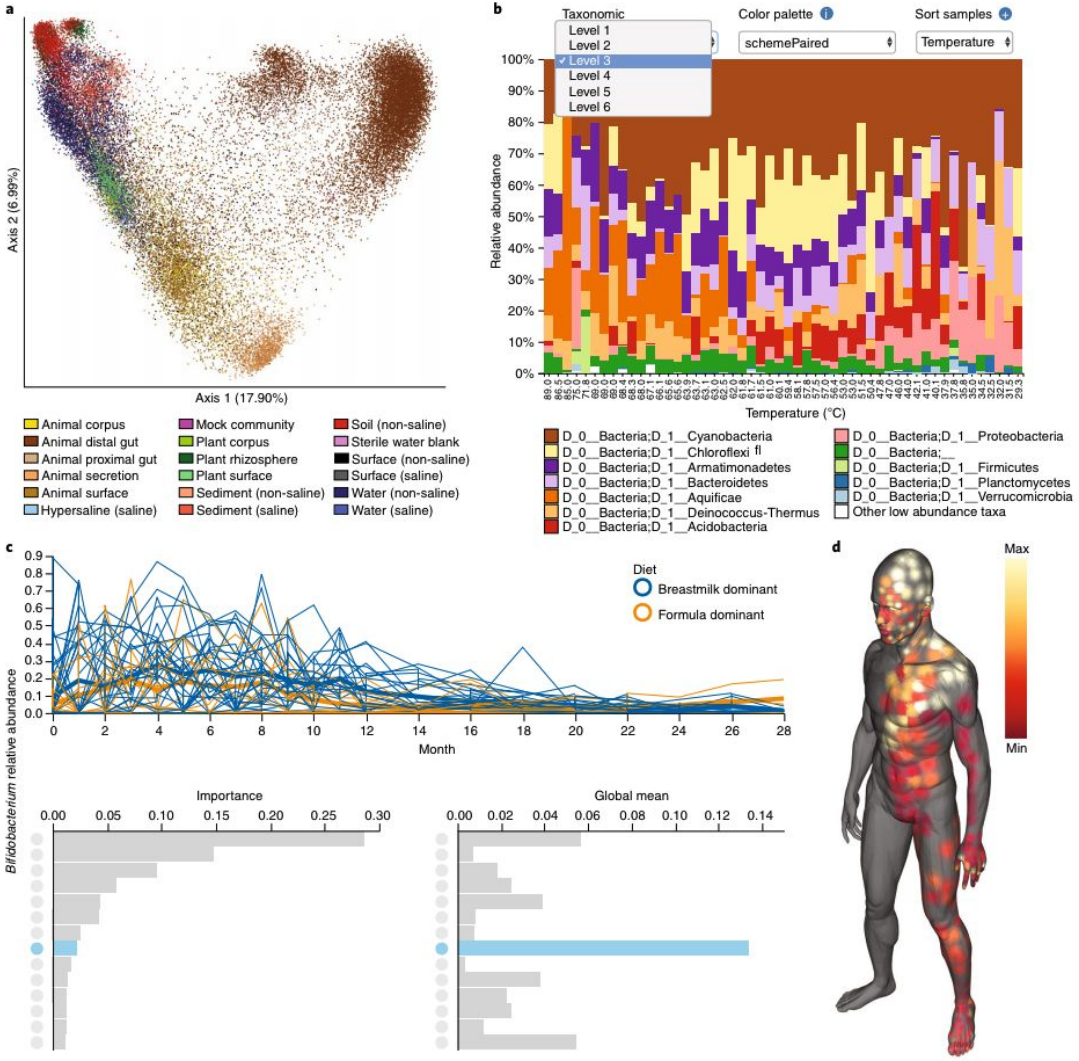
These slides: https://bit.ly/q2-dec20-eoss



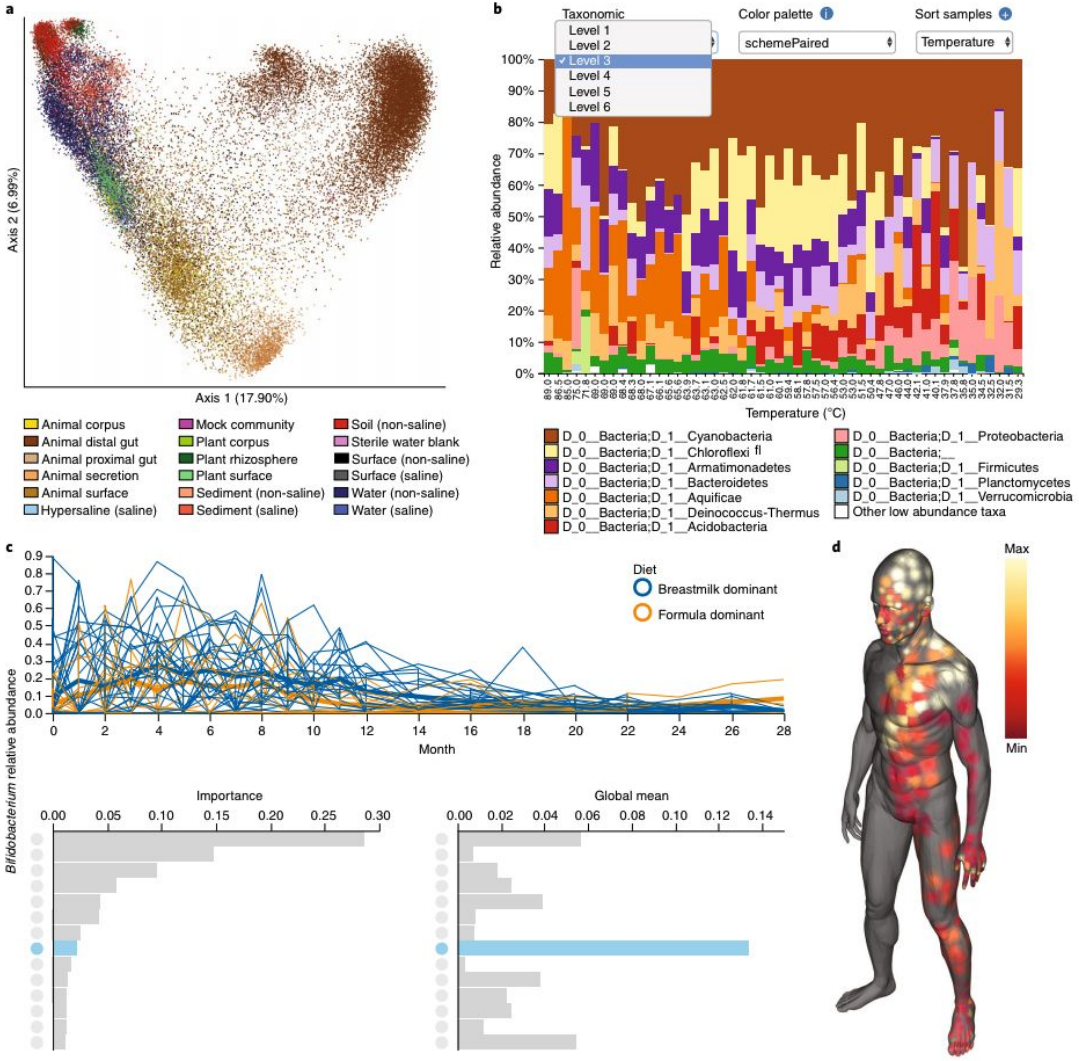
qiime 2

nature biotechnology

Correspondence | Published: 24 July 2019

Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2

Evan Bolyen, Jai Ram Rideout, Matthew R. Dillon, Nicholas A. Bokulich, Christian C. Abnet, Gabriel A. Al-Ghalith, Harriet Alexander, Eric J. Alm, Manimozhiyan Arumugam, Francesco Asnicar, Yang Bai, Jordan E. Bisanz, Kyle Bittinger, Asker Brejnrod, Colin J. Brislawn, C. Titus Brown, Benjamin J. Callahan, Andrés Mauricio Caraballo-Rodríguez, John Chase, Emily K. Cope, Ricardo Da Silva, Christian Diener, Pieter C. Dorrestein, Gavin M. Douglas, Daniel M. Durall, Claire Duvallet, Christian F. Edwardson, Madeleine Ernst, Mehrbod Estaki, Jennifer Fouquier, Julia M. Gauglitz, Sean M. Gibbons, Deanna L. Gibson, Antonio Gonzalez, Kestrel Gorlick, Jiarong Guo, Benjamin Hillmann, Susan Holmes, Hannes Holste, Curtis Huttenhower, Gavin A. Huttley, Stefan Janssen, Alan K. Jarmusch, Lingjing Jiang, Benjamin D. Kaehler, Kyo Bin Kang, Christopher R. Keefe, Paul Keim, Scott T. Kelley, Dan Knights, Irina Koester, Tomasz Kosciolek, Jorden Kreps, Morgan G. I. Langille, Joslynn Lee, Ruth Ley, Yong-Xin Liu, Erikka Loftfield, Catherine Lozupone, Massoud Maher, Clarisse Marotz, Bryan D. Martin, Daniel McDonald, Lauren J. McIver, Alexey V. Melnik, Jessica L. Metcalf, Sydney C. Morgan, Jamie T. Morton, Ahmad Turan Naimey, Jose A. Navas-Molina, Louis Felix Nothias, Stephanie B. Orchanian, Talima Pearson, Samuel L. Peoples, Daniel Petras, Mary Lai Preuss, Elmar Pruesse, Lasse Buur Rasmussen, Adam Rivers, Michael S. Robeson II, Patrick Rosenthal, Nicola Segata, Michael Shaffer, Arron Shiffer, Rashmi Sinha, Se Jin Song, John R. Spear, Austin D. Swafford, Luke R. Thompson, Pedro J. Torres, Pauline Trinh, Anupriya Tripathi, Peter J. Turnbaugh, Sabah Ul-Hasan, Justin J. J. van der Hooft, Fernando Vargas, Yoshiki Vázquez-Baeza, Emily Vogtmann, Max von Hippel, William Walters, Yunhu Wan, Mingxun Wang, Jonathan Warren, Kyle C. Weber, Charles H. D. Williamson, Amy D. Willis, Zhenjiang Zech Xu, Jesse R. Zaneveld, Yilong Zhang, Qiyun Zhu, Rob Knight & J. Gregory Caporaso - Show fewer authors



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QIIME 2 microbiome (multi-omics*) bioinformatics platform

Geographic Information Systems layers:

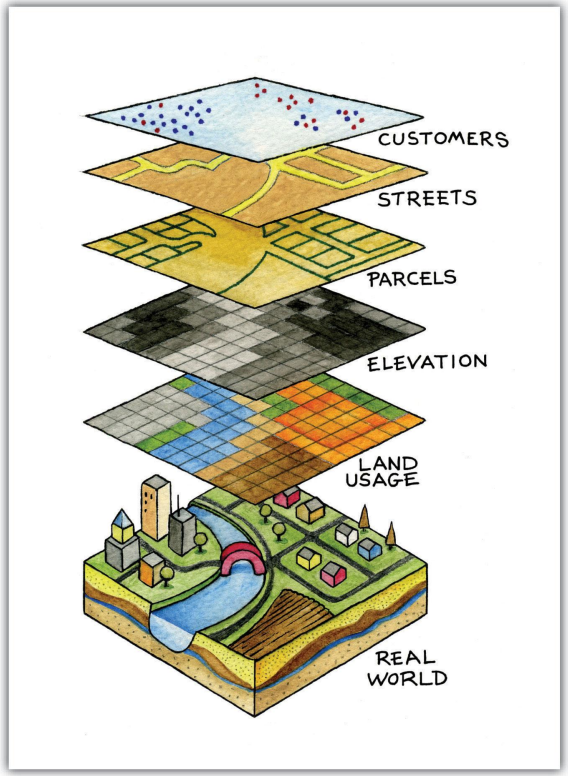


Image source: Essentials of Geographic Information Systems, v. 1.0 by Jonathan Campbell and Michael Shin

Microbiome layers:

Taxonomy:

- Bacteria and archaea (16S rRNA surveys)
- Fungus and other eukaryotes (ITS and 18S rRNA surveys)
- Phage and other viruses (shotgun surveys)

Functional potential via shotgun metagenome surveys

Functional activity:

- Metatranscriptome
- Metaproteome
- Metabolome

* Multi-omics support is funded and in a planning stage now, with limited support currently available. Learn more about where QIIME 2 is going here.

Anyone can create and distribute a plugin.

- They define *all* bioinformatics analysis functionality.
- They're Python 3 "method annotations" that QIIME 2 interprets.
- They can wrap methods not written in Python 3 (e.g., DADA2 is written in R, and mafft is a binary).
- The QIIME 2 Library (https://library.qiime2.org) is the primary site for discovering and disseminating QIIME 2 plugins.

```
import qiime2.plugin
from q2_types.per_sample_sequences import (
    SequencesWithQuality, PairedEndSequencesWithQuality)
from q2_types.sample_data import SampleData
from q2_types.feature_data import FeatureData, Sequence
from q2_types.feature_table import FeatureTable, Frequency

import q2_dada2

plugin = qiime2.plugin.Plugin(
    name='dada2',
    version=q2_dada2.__version__,
    website='http://benjjneb.github.io/dada2/',
    package='q2_dada2',
    description=('This QIIME 2 plugin wraps DADA2 and supports '
                 'sequence quality control for single-end and paired-end '
                 'reads using the DADA2 R library.'),
    short_description='Plugin for sequence quality control with DADA2.',
    citations=qiime2.plugin.Citations.load('citations.bib', package='q2_dada2')
)


plugin.methods.register_function(
    function=q2_dada2.denoise_single,
    inputs={'demultiplexed_seqs': SampleData[SequencesWithQuality |
                                             PairedEndSequencesWithQuality]},
    parameters={'trunc_len': qiime2.plugin.Int,
                'trim_left': qiime2.plugin.Int,
                'max_ee': qiime2.plugin.Float,
                'trunc_q': qiime2.plugin.Int,
                'chimera_method': qiime2.plugin.Str %
                qiime2.plugin.Choices(_CHIM_OPT),
                'min_fold_parent_over_abundance': qiime2.plugin.Float,
                'n_threads': qiime2.plugin.Int,
                'n_reads_learn': qiime2.plugin.Int,
                'hashed_feature_ids': qiime2.plugin.Bool},
    outputs=[('table', FeatureTable[Frequency]),
             ('representative_sequences', FeatureData[Sequence])],
    input_descriptions={
        'demultiplexed_seqs': ('The single-end demultiplexed sequences to be '
                               'denoised.')
    },
    parameter_descriptions={
        'trunc_len': ('Position at which sequences should be truncated due to '
                      'decrease in quality. This truncates the 3\' end of the '
```

qiime2 library

(https://library.qiime2.org)

Latest Plugins

q2-coremicrobiome 1.0

Qiime2 plugin of COREMIC: CORE MICrobiome [https://doi.org/10.7717/peerj.4395]. This plugin works with qza files from QIIME 2.

gemelli 0.0.5

Gemelli is a toolbox for running tensor factorization on sparse compositional omics datasets. Gemelli performs unsupervised dimensionality reduction of spatiotemporal microbiome data. The output of gemelli helps to resolve spatiotemporal subject variation and the biological features that separate them.

RESCRIPt 2020.11

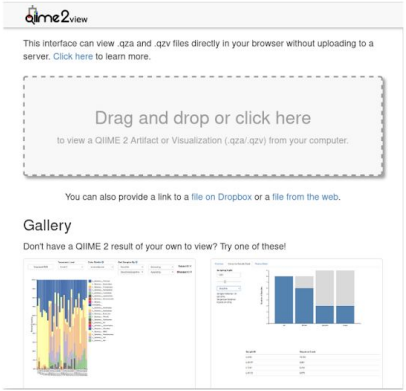
REference Sequence annotation and CuRatIon Pipeline RESCRIPt is a QIIME 2 plugin to support a variety of operations for managing and curating reference sequence databases, DNA/RNA sequence data, and taxonomic data.

Chan Zuckerberg Initiative

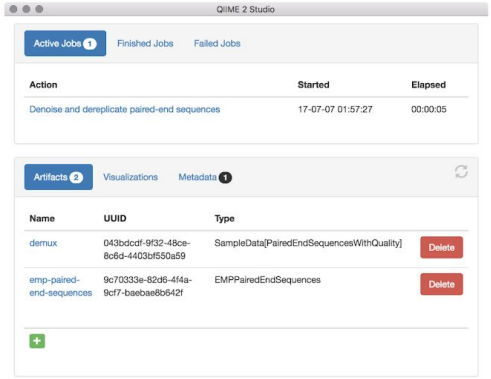
Project announcement (via NAU News)

Multiple interface options increases accessibility, and plugin developers don't have to create any of these!

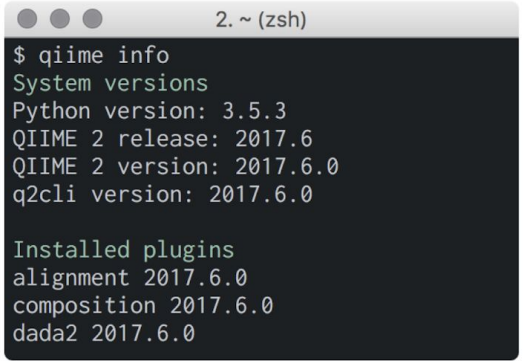
a) QIIME 2 View



b) QIIME 2 Studio prototype



c) QIIME 2 CLI



d) QIIME 2 Artifact API

Related Software:
Galaxy

Related Software:
Galaxy
EBI Metagenomics Portal
QIITA
NIH Nephele

Related Software:
Mothur
QIIME 1

Related Software:
phyloseq

COMPUTATIONAL SOPHISTICATION

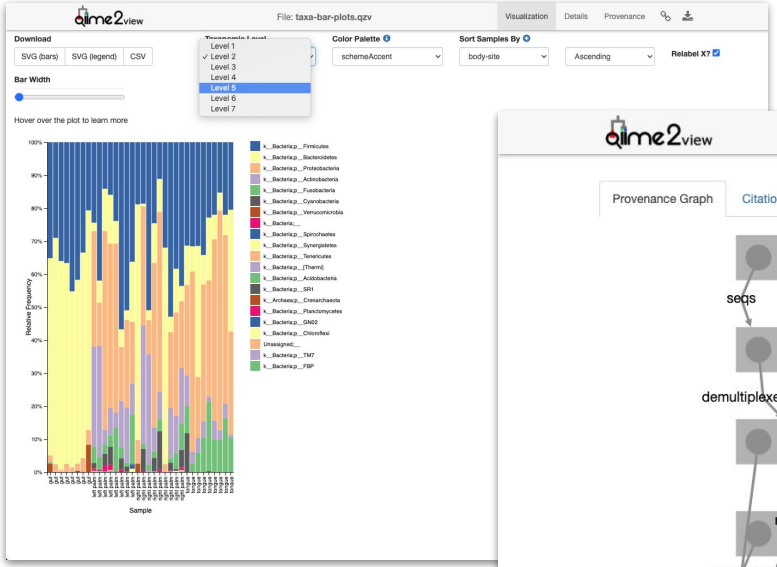
Data analyst (clinician, policy maker, research subject)

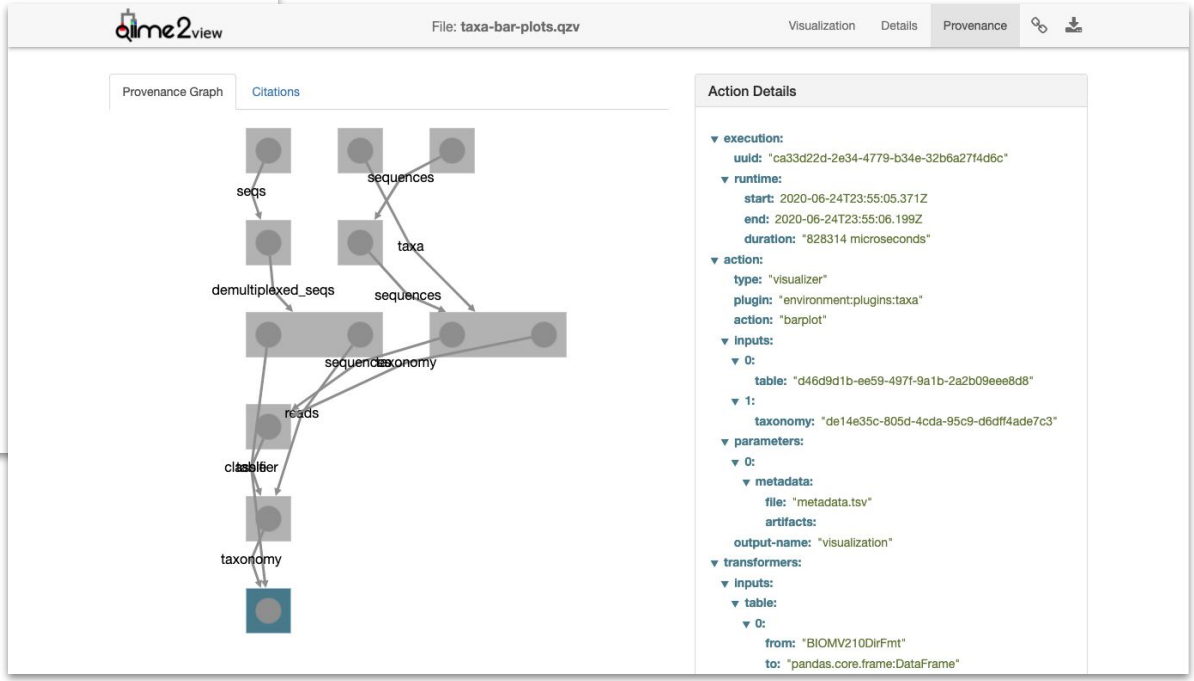
Cancer researchers and other domain scientists

Power users

Data scientists

QIIME 2's retrospective data provenance tracking system facilitates reproducibility, and plugin developers don't even have to know that this exists!





[Explore data provenance interactively here.]

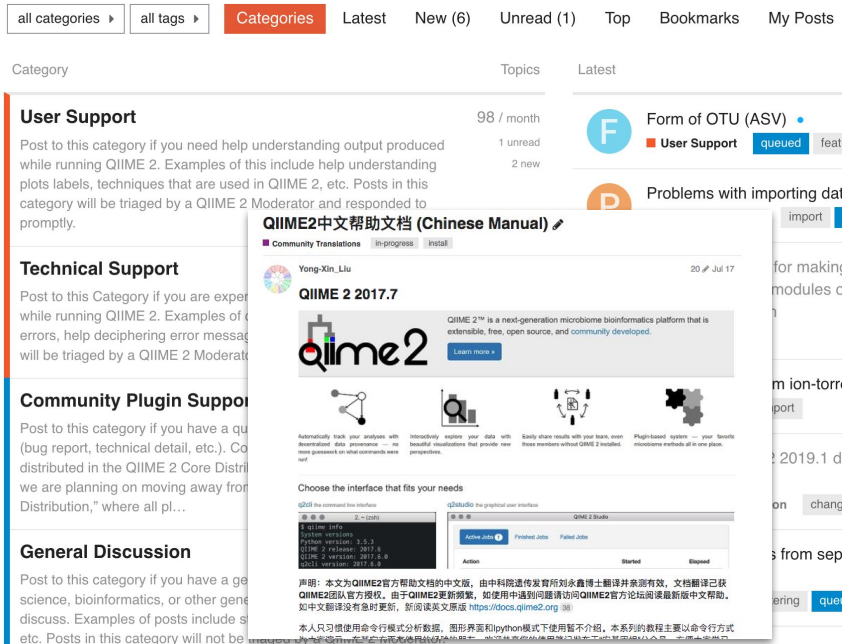
Source: QIIME 2 q2-longitudinal tutorial.

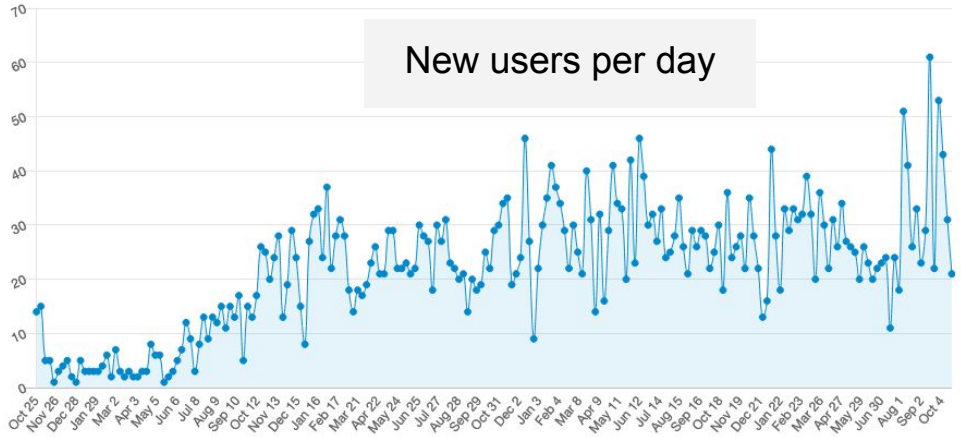
Data originally published in Bokulich et al. (2016).

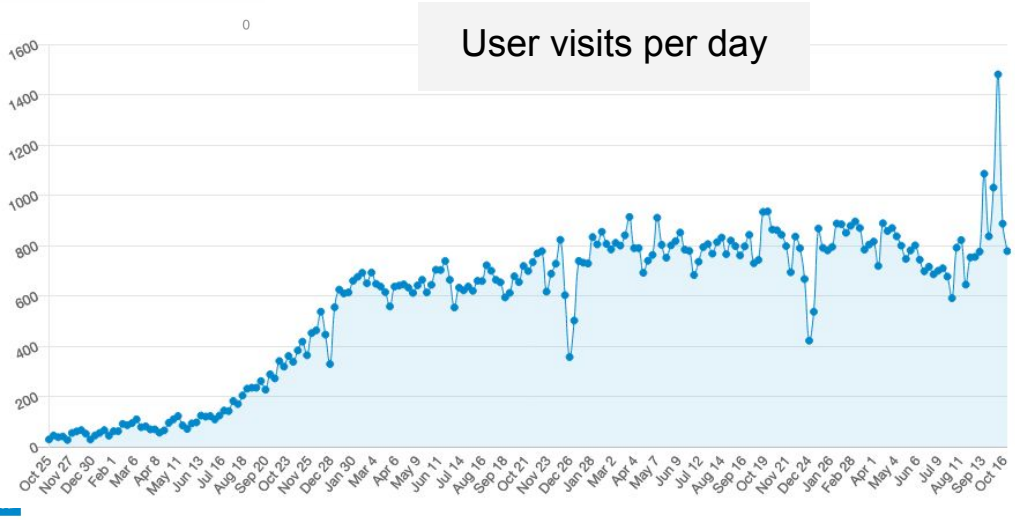
Plugin developers can provide (and receive!) support on the QIIME 2 Forum.

https://forum.qiime2.org

Please read our Code of Conduct when joining.







qiime2 workshops

https://workshops.qiime2.org

Upcoming Workshops

Title	Location	Workshop Dates
Microbiome Bioinformatics with QIIME 2 - Online!	Online	Oct. 5, 2020 - Oct. 9, 2020
An Introduction to QIIME 2	Online (via World of Microbiome)	Nov. 4, 2020 - Nov. 4, 2020
Microbiome Bioinformatics with QIIME 2	Online (via FAES at the National Institutes of Health)	Jan. 4, 2021 - Jan. 8, 2021

Past Workshops

Title	Location	Workshop Dates
Introduction to microbiome study design and analysis	Puerto Rico	Aug. 1, 2020 - Aug. 1, 2020
Microbiome Bioinformatics with QIIME 2	Bethesda, Maryland	Jan. 8, 2020 - Jan. 10, 2020
Microbiome Bioinformatics with QIIME 2 Workshop	Fort Collins, Colorado (USA)	Nov. 25, 2019 - Nov. 26, 2019
Microbiome Bioinformatics with QIIME 2 Workshop (not open to the public)	University of Wyoming	Oct. 24, 2019 - Oct. 25, 2019
Microbiome Bioinformatics with QIIME 2	Bangkok, Thailand	Sept. 11, 2019 - Sept. 12, 2019
QIIME 2 @ One Health Summer School	University of Bern, Switzerland	Aug. 14, 2019 - Aug. 14, 2019
Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS); (includes a QIIME 2 session)	Woods Hole, MA, USA	July 29, 2019 - July 29, 2019

Las Vegas Workshop, June 2017

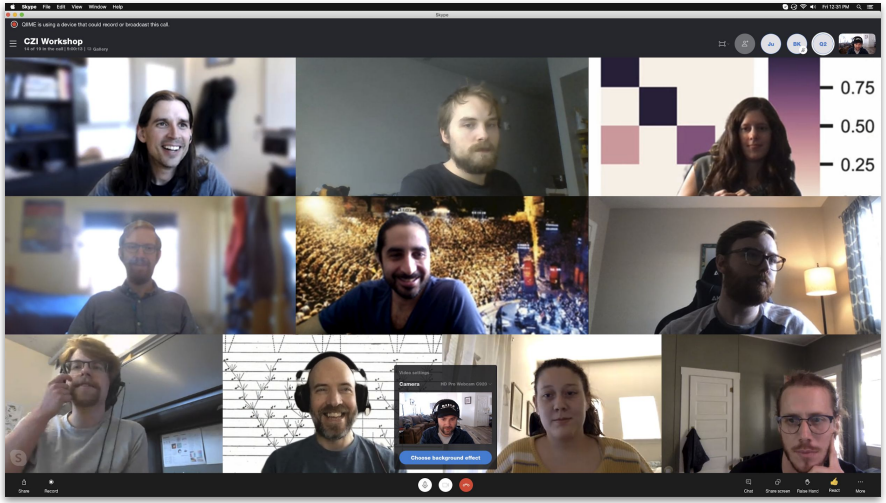
Register for the June 2017 *Microbiome Bioinformatics with QIIME 2* workshop in Las Vegas by 11:59pm Pacific Time on May 5th for a chance to win one of three limited-edition QIIME 2 cross-stitches. Be the envy of your lab by owning this beautiful piece of microbiome bioinformatics art!

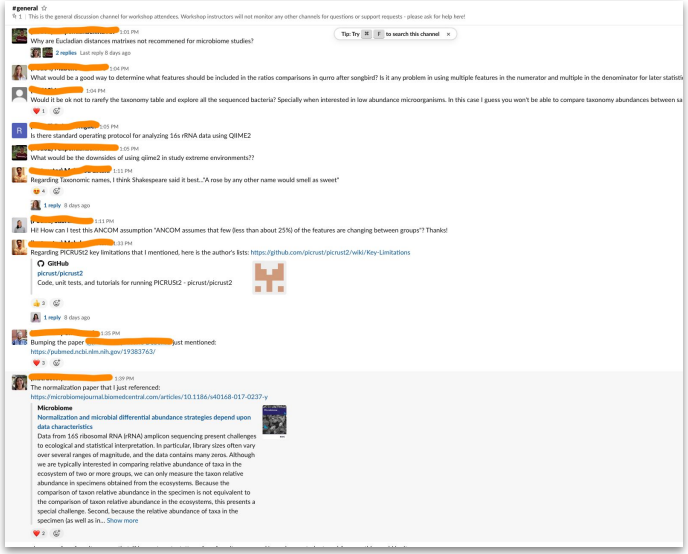
https://workshops.qiime.org/qiime-2-workshop-2017-06-21

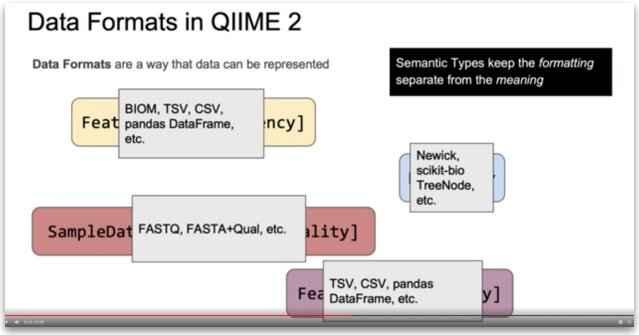
Fine art by Matthew Dillon (@thermokarst).

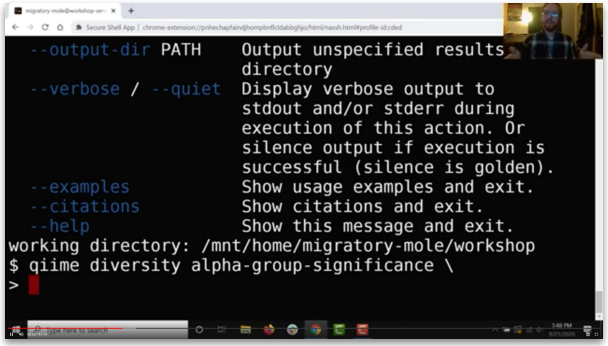
CZI-CABANA Microbiome Bioinformatics with QIIME 2 Workshop

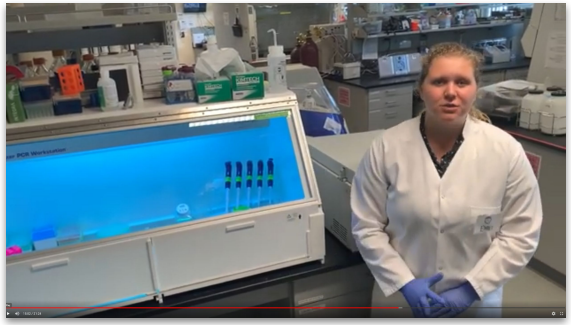
2020 October 5-9





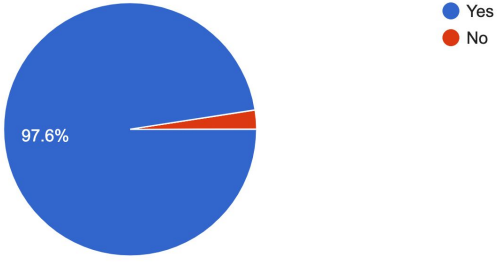




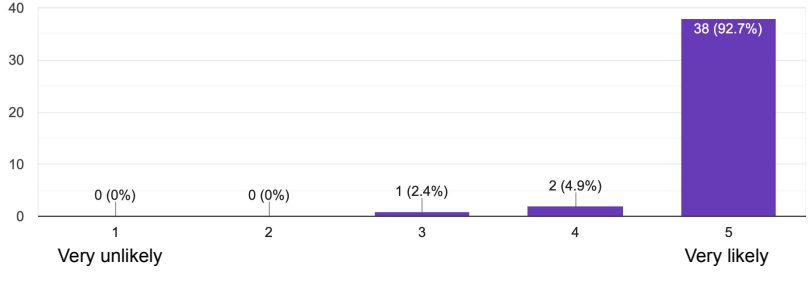


Select post-workshop questionnaire results

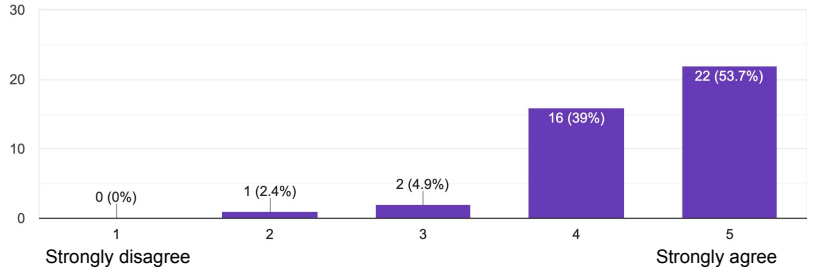
This workshop helped me learn what I most hoped to learn from participating in this workshop.
41 responses



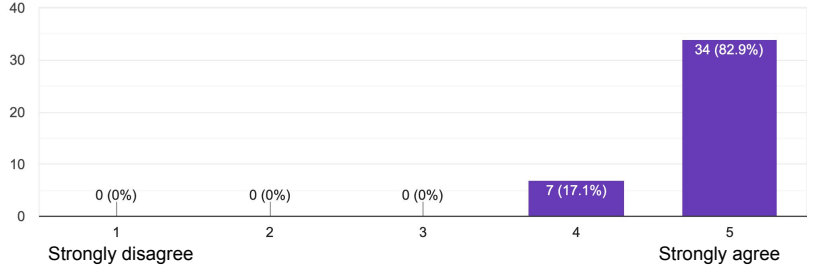
How likely are you to recommend this workshop to a friend or colleague?
41 responses



I can immediately apply what I learned at this workshop.
41 responses



I felt comfortable learning in this workshop environment.
41 responses



Pre and post-workshop questionnaires were derived from materials developed by *The Carpentries*, that are available under the CC-BY License. The original materials are available at https://github.com/carpentries/assessment.

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Ben Kaehler	BenKaehler	School of Science, University of New South Wales, Canberra, Australia
Chloe Herman	cherman2	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Chris Keefe	ChrisKeefe	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Emily Borsom	emilyborsom	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Emily Cope	Emily_Cope	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Evan Bolyen	ebolyen	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
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Jessica Metcalf	jessicalmetcalf	Department of Animal Sciences, Colorado State University
Justine Debelius	jwdebelius	Centre for Translational Microbiome Research, Department of Microbiology, Tumor, and Cancer Biology, Karolinska Institutet, Stockholm, Sweden
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QIIME 1 Development Team
QIIME 2 Development Team

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- Partnership for Native American Cancer Prevention (U54CA143925)

National Science Foundation (1565100)
Chan-Zuckerberg Initiative (2019-207342)
Alfred P. Sloan Foundation

QIIME 2 resources
Docs: https://docs.qiime2.org
Developer resources: https://dev.qiime2.org
Tech support: https://forum.qiime2.org
Twitter: @qiime2
GitHub: https://github.com/qiime2
Workshops: https://workshops.qiime2.org
YouTube: https://www.youtube.com/c/qiime2

These slides: https://bit.ly/q2-dec20-eoss

The Caporaso Lab is currently hiring software engineers, post-doctoral scholars, and graduate students to join the QIIME 2 team!

Watch the QIIME 2 Forum job board and/or @qiime2 on Twitter for announcement of these positions (and post your own job listings for free).

NAU NORTHERN ARIZONA UNIVERSITY

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