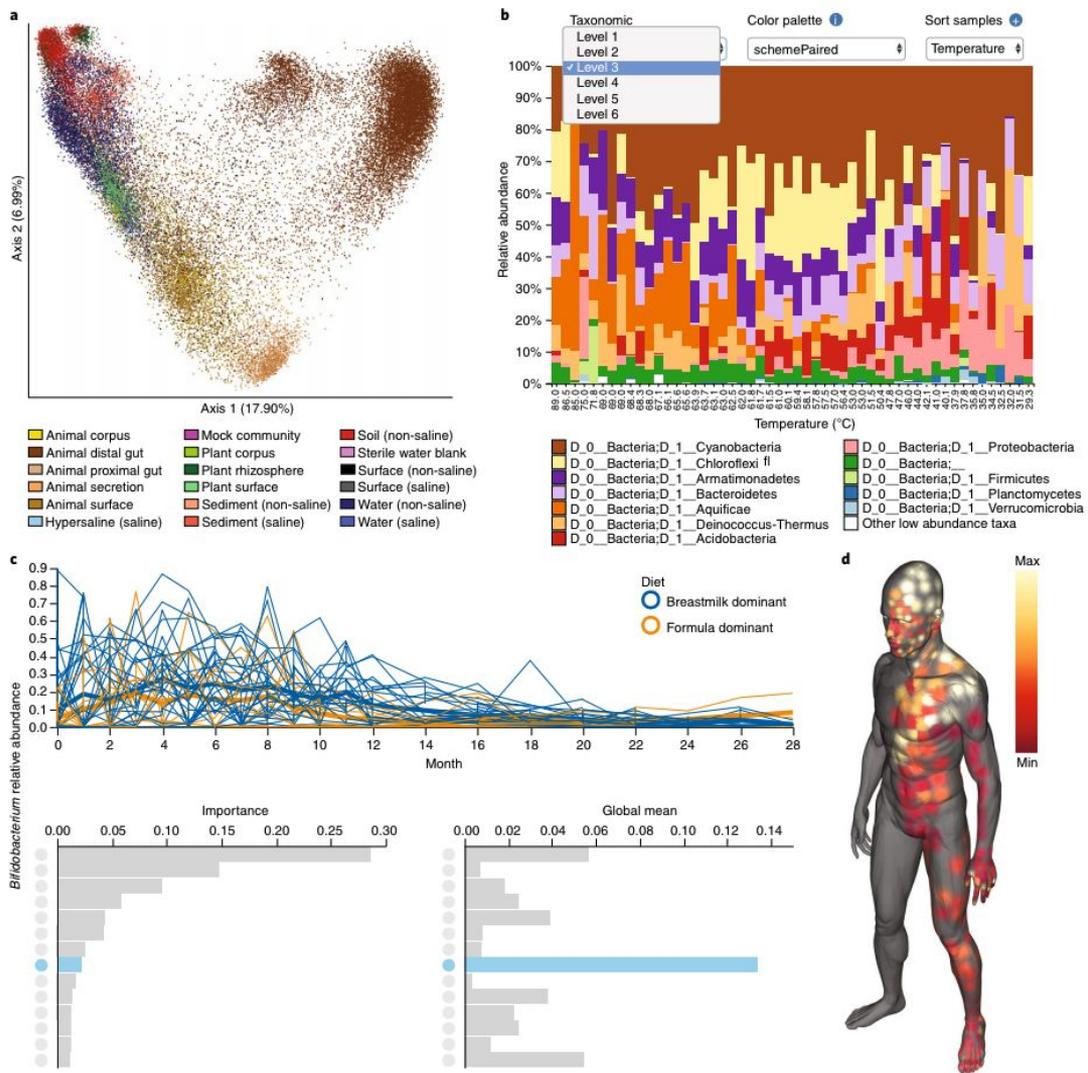




Greg Caporaso, Ph.D.
 Center for Applied Microbiome Science
 Pathogen and Microbiome Institute
 Northern Arizona University
 Flagstaff, Arizona
<http://caporasolab.us>





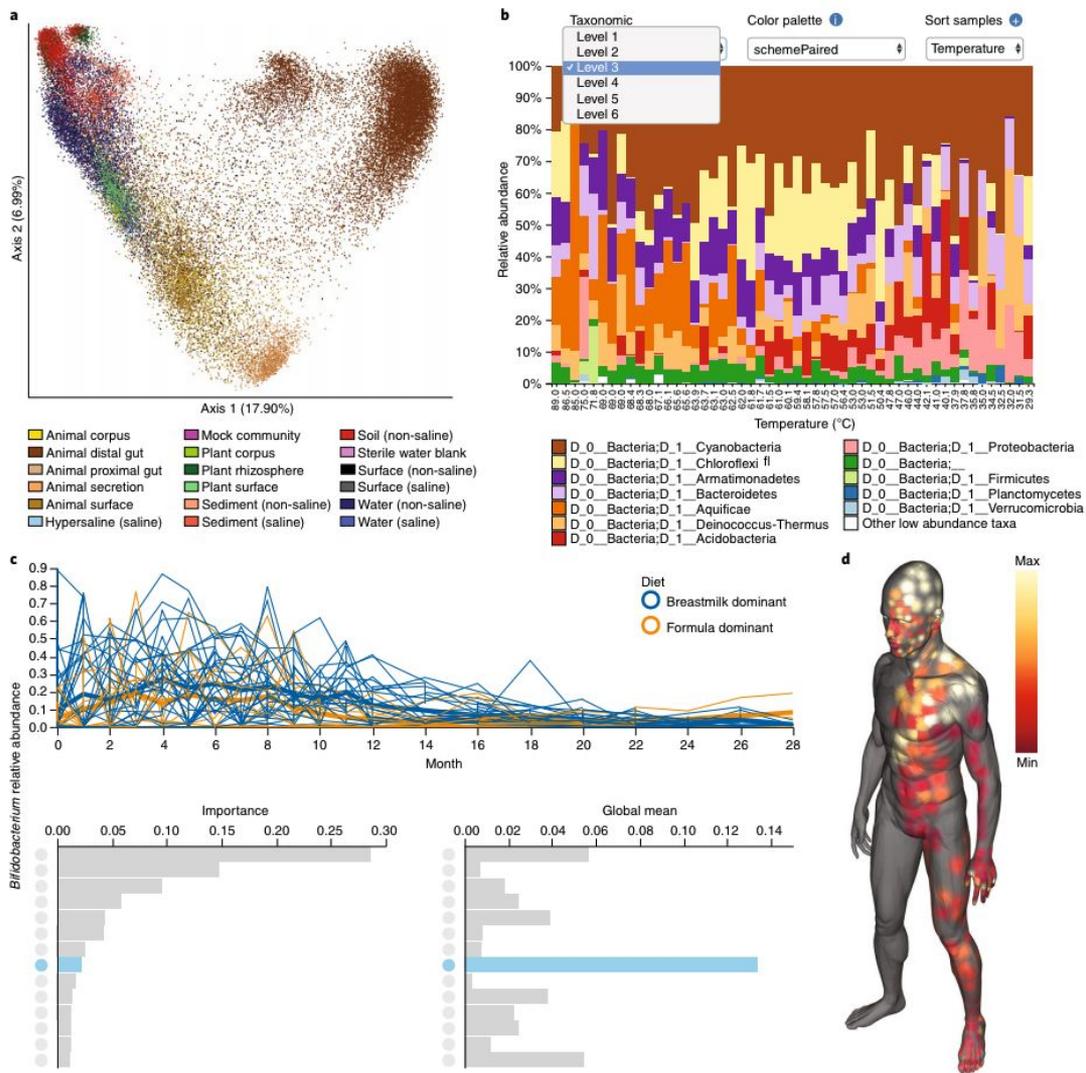
nature
biotechnology

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, Manimozhayan 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. Edwards, 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 Kosciolk, Jorden Kreps, Morgan G. I. Langille, Joslynn Lee, Ruth Ley, Yong-Xin Liu, Erikka Lofthfield, 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. 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

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



QIIME 2 microbiome (multi-omics*) bioinformatics platform

Geographic Information Systems layers:

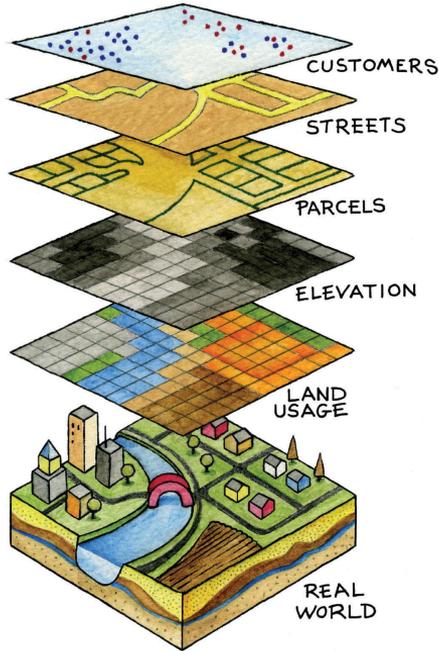


Image source: [Essentials of Geographic Information Systems, v. 1.0](#)
by Jonathan Campbell and Michael Shin

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.

```
8
9 import qiime2.plugin
10 from qiime2.types.per_sample_sequences import (
11     SequencesWithQuality, PairedEndSequencesWithQuality)
12 from qiime2.types.sample_data import SampleData
13 from qiime2.types.feature_data import FeatureData, Sequence
14 from qiime2.types.feature_table import FeatureTable, Frequency
15
16 import q2_dada2
17
18 plugin = qiime2.plugin.Plugin(
19     name='dada2',
20     version=q2_dada2.__version__,
21     website='http://benjjneb.github.io/dada2/',
22     package='q2_dada2',
23     description=('This QIIME 2 plugin wraps DADA2 and supports '
24                 'sequence quality control for single-end and paired-end '
25                 'reads using the DADA2 R library.'),
26     short_description='Plugin for sequence quality control with DADA2.',
27     citations=qiime2.plugin.Citations.load('citations.bib', package='q2_dada2')
28 )
29
30
31 plugin.methods.register_function(
32     function=q2_dada2.denoise_single,
33     inputs={'demultiplexed_seqs': SampleData[SequencesWithQuality |
34                                             PairedEndSequencesWithQuality]},
35     parameters={'trunc_len': qiime2.plugin.Int,
36                 'trim_left': qiime2.plugin.Int,
37                 'max_ee': qiime2.plugin.Float,
38                 'trunc_q': qiime2.plugin.Int,
39                 'chimera_method': qiime2.plugin.Str %
40                     qiime2.plugin.Choices(_CHIM_OPT),
41                 'min_fold_parent_over_abundance': qiime2.plugin.Float,
42                 'n_threads': qiime2.plugin.Int,
43                 'n_reads_learn': qiime2.plugin.Int,
44                 'hashed_feature_ids': qiime2.plugin.Bool},
45     outputs=[('table', FeatureTable[Frequency]),
46              ('representative_sequences', FeatureData[Sequence])],
47     input_descriptions={
48         'demultiplexed_seqs': ('The single-end demultiplexed sequences to be '
49                                'denoised.'),
50     },
51     parameter_descriptions={
52         'trunc_len': ('Position at which sequences should be truncated due to '
53                       '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 CuRatlon 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.

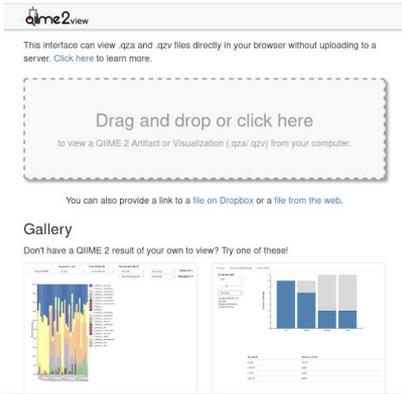


Chan Zuckerberg Initiative

[Project announcement \(via NAU News\)](#)

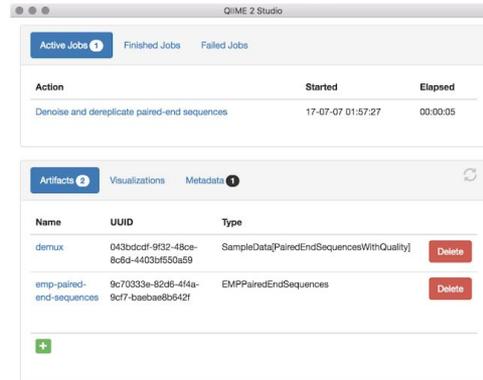
Multiple interface options increases accessibility, and plugin developers don't have to create any of these!

a) QIIME 2 View



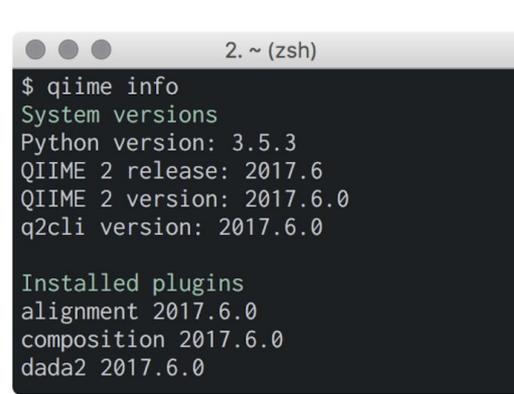
Related Software:
Galaxy

b) QIIME 2 Studio prototype



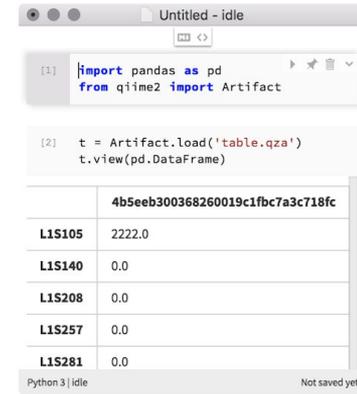
Related Software:
Galaxy
EBI Metagenomics Portal
QIITA
NIH Nephele

c) QIIME 2 CLI



Related Software:
Mothur
QIIME 1

d) QIIME 2 Artifact API



Related Software:
phyloseq

COMPUTATIONAL SOPHISTICATION

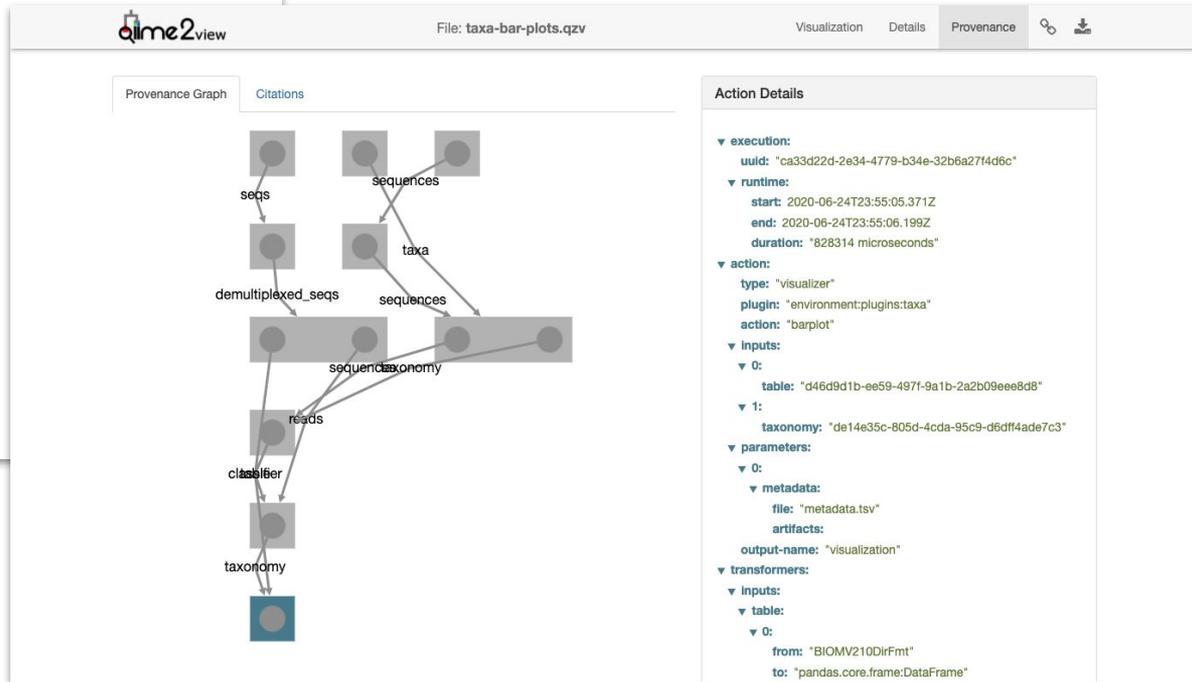
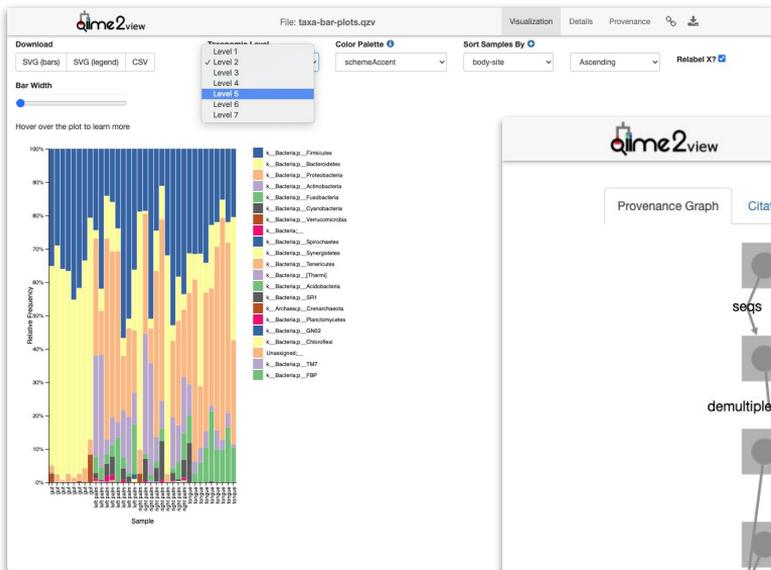
Data analyst (clinician, policy maker, research subject)

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.

all categories ▾ all tags ▾ **Categories** Latest New (6) Unread (1) Top Bookmarks My Posts

Category

User Support

Post to this category if you need help understanding output produced while running QIIME 2. Examples of this include help understanding plots labels, techniques that are used in QIIME 2, etc. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.

Technical Support

Post to this Category if you are experiencing errors, help deciphering error messages, or other technical issues. Posts in this category will be triaged by a QIIME 2 Moderator.

Community Plugin Support

Post to this category if you have a question about a community plugin (bug report, technical detail, etc.). Community plugins are distributed in the QIIME 2 Core Distribution. We are planning on moving away from the "Community Plugins" distribution, where all pl...

General Discussion

Post to this category if you have a general question about QIIME 2, bioinformatics, or other general topics. Examples of posts include sharing your work, asking for advice, etc. Posts in this category will not be...

98 / month

1 unread
2 new

F Form of OTU (ASV) • **User Support** **queued** featu

P Problems with importing data **import**

QIIME2中文帮助文档 (Chinese Manual)

Community Translations **In progress** **Install**



Yong-Xin Liu

20 Jul 17

QIIME 2 2017.7



QIIME 2™ is a next-generation microbiome bioinformatics platform that is extensible, free, open source, and community developed.

[Learn more >](#)



Automatically batch your analyses with hierarchical data processing — no more guesswork on what commands were used.



Interactively explore your data with beautiful visualizations that provide new perspectives.



Easily share results with your team, even those members without QIIME 2 installed.



Plugin-based system — your favorite microbe analysis methods all in one place.

Choose the interface that fits your needs

q2cli the command line interface

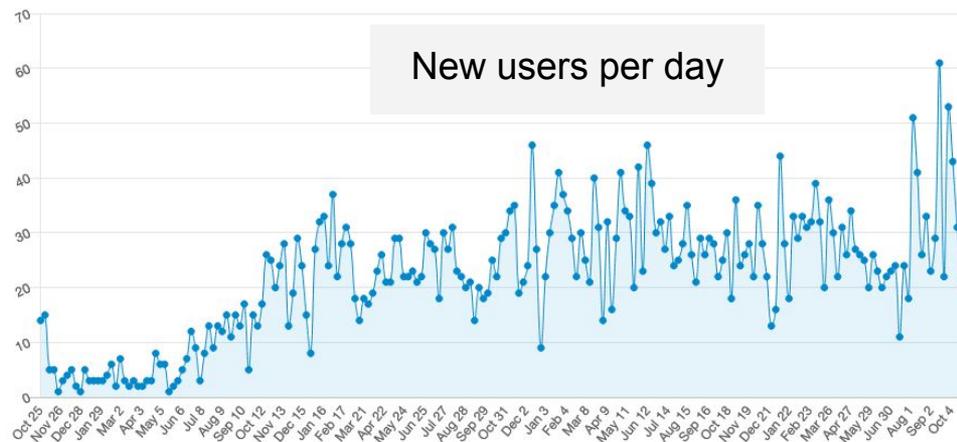
q2studio the graphical user interface



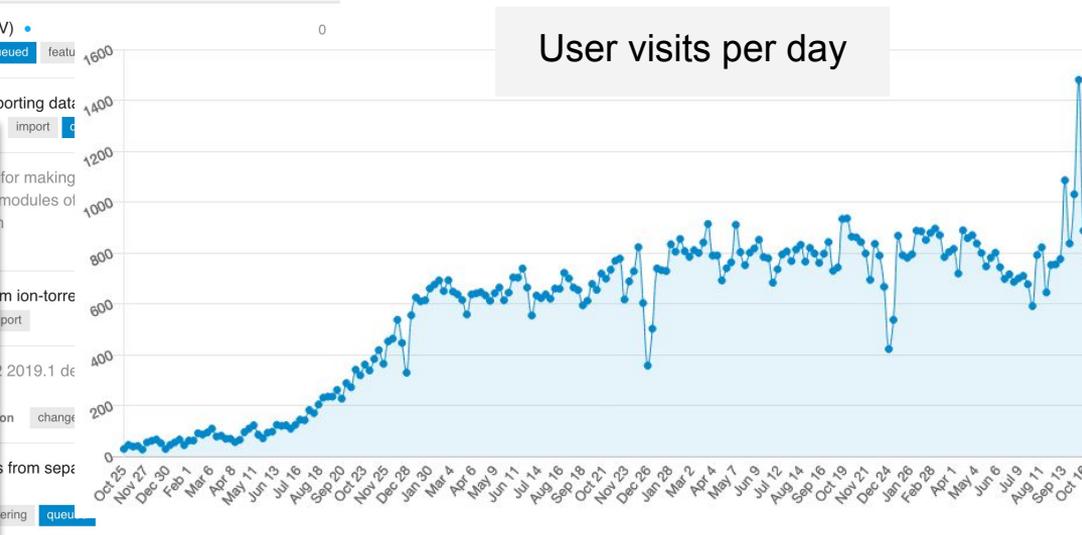
声明：本文为QIIME2官方帮助文档的中文版，由中科院遗传发育所刘永鑫博士翻译并亲测有效。文档翻译已获得QIIME2团队官方授权。由于QIIME2更新频繁，如使用中遇到问题请访问QIIME2官方论坛阅读最新版中文帮助。如中文翻译没有及时更新，新闻原文版本 <https://docs.qiime2.org>

本人只习惯使用命令行模式分析数据，图形界面和python模式下使用量不介绍。本系列的教程主要以命令行方式

Get an r² value when running a PERMANOVA



New users per day



User visits per day

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!

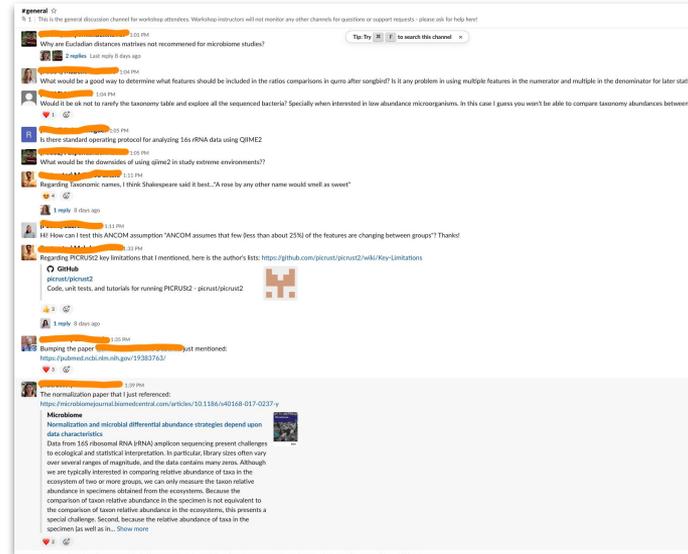
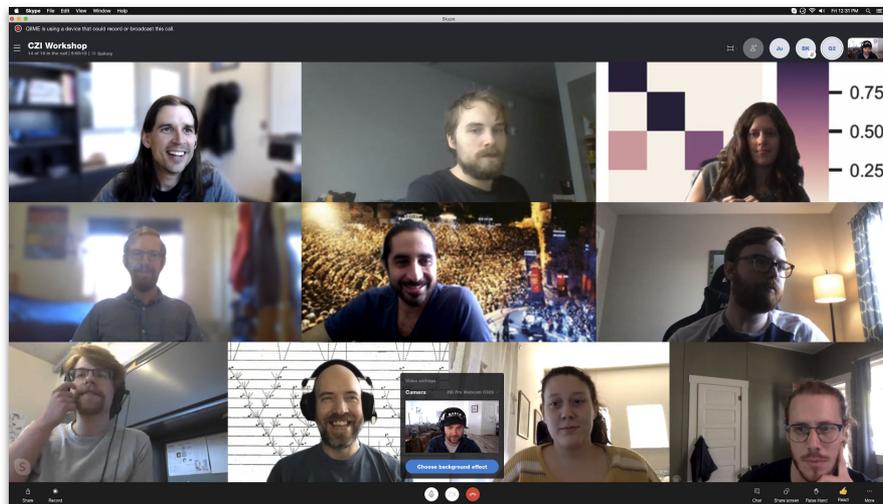
<https://workshops.qiime2.org/qiime-2-workshop-2017-06-21>



Fine art by Matthew Dillon (@thermokart).

CZI-CABANA Microbiome Bioinformatics with QIIME 2 Workshop

2020 October 5-9



Data Formats in QIIME 2

Data Formats are a way that data can be represented

Semantic Types keep the *formatting* separate from the *meaning*

Feat [BIOM, TSV, CSV, pandas DataFrame, etc.] [nc] [nc]

SampleData [FASTQ, FASTA+Qual, etc.] [nc] [nc]

Feat [TSV, CSV, pandas DataFrame, etc.] [nc] [nc]

Newick, scikit-bio, TreeNode, etc.

```

--output-dir PATH      Output unspecified results
                        directory
--verbose / --quiet    Display verbose output to
                        stdout and/or stderr during
                        execution of this action. Or
                        silence output if execution is
                        successful (silence is golden).
--examples             Show usage examples and exit.
--citations            Show citations and exit.
--help                Show this message and exit.
working directory: /mnt/home/migratory-mole/workshop
qiime diversity alpha-group-significance \

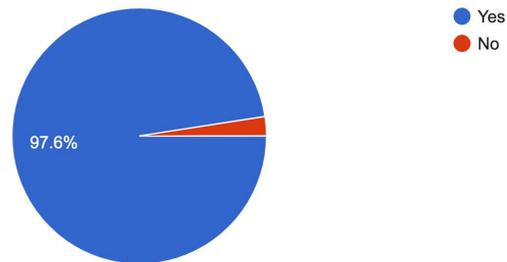
```



Select post-workshop questionnaire results

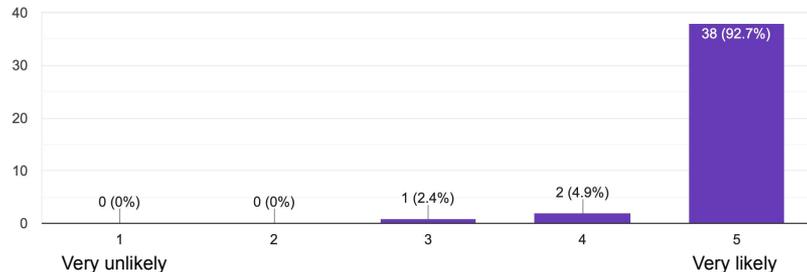
This workshop helped me learn what I most hoped to learn from participating in this workshop.

41 responses



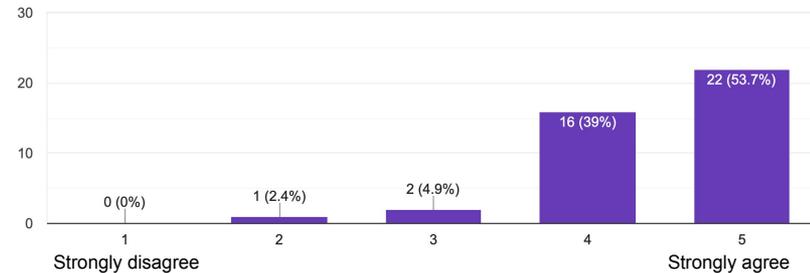
How likely are you to recommend this workshop to a friend or colleague?

41 responses



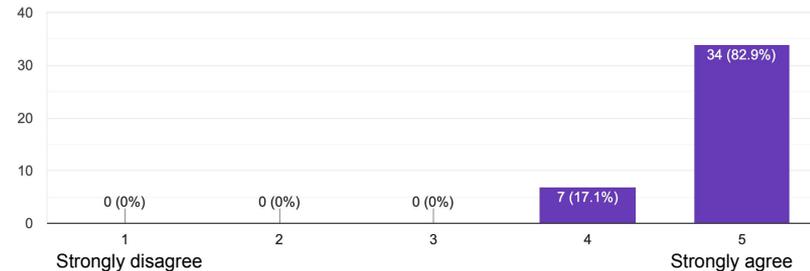
I can immediately apply what I learned at this workshop.

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>.

<u>Instructor</u>	<u>QIIME 2 Forum</u>	<u>Institutional affiliation</u>
Aeriel Belk	aeriel.belk	Department of Animal Sciences, Colorado State University
Alex Emmons	emmo1	Department of Animal Sciences, Colorado State University
Andrew Sanchez	andrewsanchez	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Anthony Simard	Oddant1	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
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
Greg Caporaso	gregcaporaso	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Heather Deel	hdeel	Department of Animal Sciences, Cell and Molecular Biology Special Academic Unit, Colorado State University
Jamie Morton	mortonjt	Center for Computational Biology, Flatiron Institute, Simons Foundation, New York, USA
Jessica Metcalf	jessicametcalf	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
Matthew Dillon	thermokarst	Center for Applied Microbiome Science, Pathogen and Microbiome Institute, Northern Arizona University, USA
Mehrbod Estaki	Mehrbod_Estaki	Department of Pediatrics, University of California San Diego, USA
Mike Robeson	SoilRotifer	Department of Biomedical Informatics, College of Medicine, University of Arkansas for Medical Sciences, Little Rock AR, USA
Nick Bokulich	nicholas_bokulich	Laboratory of Food Systems Biotechnology, Institute of Food, Nutrition, and Health, ETH Zürich, Switzerland
Renato Oliveira	reinator	Environmental Genomics, Instituto Tecnológico Vale, Belém, Pará, Brazil
Yoshiki Vazquez-Baeza	yoshiki	Center for Microbiome Innovation, Jacobs School of Engineering, University of California San Diego, USA

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Caporaso Lab

Evan Bolyen

Matthew Dillon

Chloe Herman

Chris Keefe

Andrew Sanchez

Anthony Simard

and [former lab members...](#)

QIIME and QIIME 2 communities

[QIIME 1 Development Team](#)

[QIIME 2 Development Team](#)

QIIME 2 project funding

National Cancer Institute

- ITCR ([1U24CA248454-01](#))
- [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>

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).



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

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