



<https://qiime2.org>

Greg Caporaso
(project PI and speaker)

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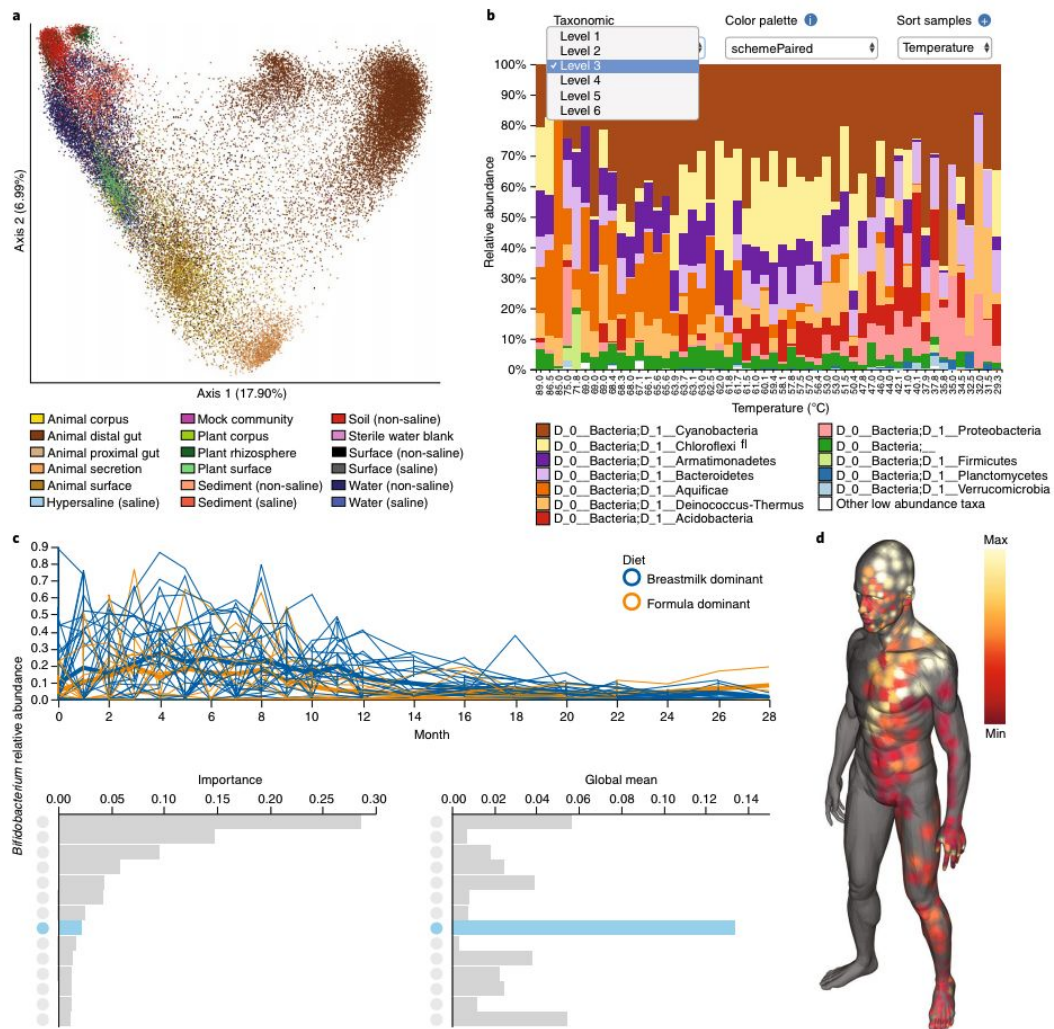


Figure source: [Bolyen et al., 2019](#) (Nature Biotechnology)

Please read the QIIME 2 community [Code of Conduct](#).

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

Category

Topics

Latest

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.

98 / month

1 unread

2 new

Technical Support

Post to this Category if you are experiencing a technical difficulty while running QIIME 2. Examples of difficulties include installation errors, help deciphering error messages, etc. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.

21 / month

2 new

Community Plugin Support

Post to this category if you have a question (bug report, technical detail, etc.). Content distributed in the QIIME 2 Core Distribution, we are planning on moving away from "Distribution," where all pl...

General Discussion

Post to this category if you have a general question about science, bioinformatics, or other general topics. Examples of posts include general discussions, etc. Posts in this category will not be...

Developer Discussion

Post to this category if you are a developer or have a suggestion. Posts in this category will be triaged by a QIIME 2 Moderator and responded to promptly.

Community Contributions

QIIME2中文帮助文档 (Chinese Manual)

Community Translations in progress initial



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 track 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.



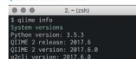
Easily share results with your team, even those members without QIIME 2 installed.



Plugin-based system — your favorite microbiome methods all fit in one place.

Choose the interface that fits your needs

q2cli the command line interface



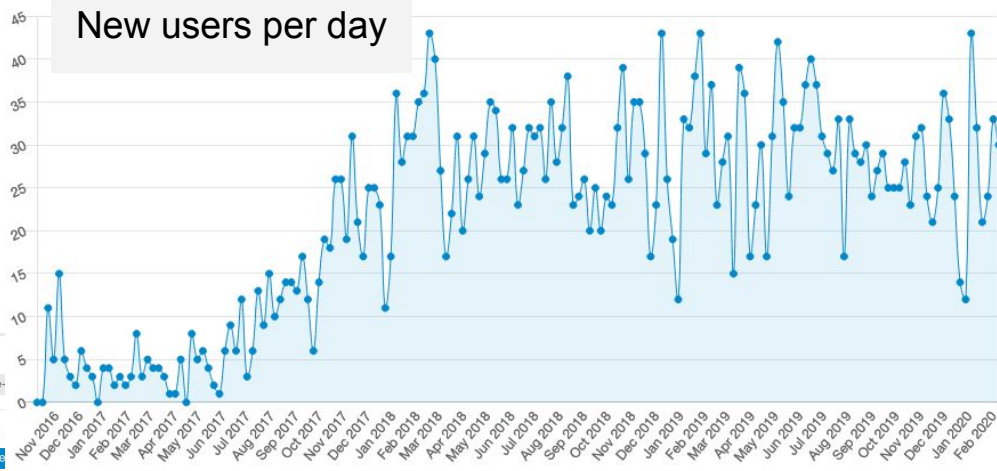
q2studio the graphical user interface



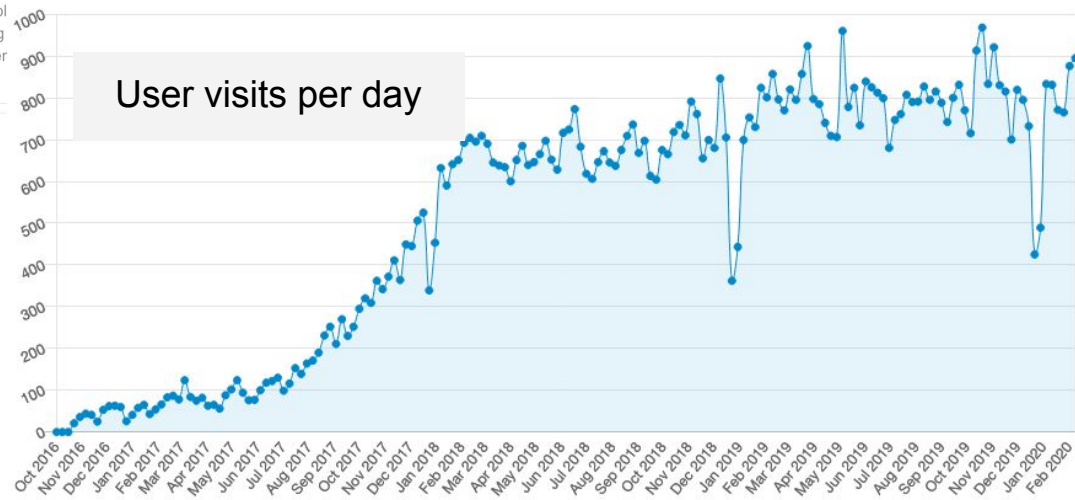
声明：本文为QIIME2官方帮助文档的中文版，由中科院遗传发育所刘永鑫博士翻译并亲测有效。文档翻译已获QIIME2团队官方授权。由于QIIME2更新频繁，如使用中遇到问题请访问QIIME2官方论坛阅读最新中文帮助。如中文翻译没有及时更新，新闻原文英文版 <https://docs.qiime2.org>

本人只习惯使用命令行模式分析数据，图形界面和python模式下载使用暂不介绍。本系列的教程主要以命令行方式为主，如需要图形界面或python模式的使用教程，请参考官方论坛或相关资源。

New users per day



User visits per day



Developers get:

- Package building and testing
- Documentation generation
- Interface-agnostic tutorials and usage examples



Plugins

Tutorials

User Interfaces

Documentation

Users get:

- Plugin discovery and installation mechanisms
- Up-to-date documentation
- Interface-specific tutorials and usage examples

<https://library.qiime2.org>

The screenshot shows the QIIME2 library homepage with a navigation bar (Home, Plugins, About, Resources) and an 'Add new plugin' button. The main content area displays a grid of plugin cards, each with a title, version number, description, and author information. The visible plugins are:

- DEICODE** (v0.2.3): Robust Altichison PCA for sparse omics datasets, linking specific features to beta-diversity ordination through the use of compositional biplots.
- mmvec** (v1.0.1): A software package for learning microbe-metabolite interactions.
- q2-aldeX2** (v0.1.1): Compositional differential abundance analysis. ALDEx2 provides a framework that encompasses essentially all high-throughput sequencing data types by modelling the data as a log-ratio transformed probability distribution rather than as counts.
- q2-breakaway** (v1.0): 'breakaway' is the premier package for statistical analysis of microbial diversity. 'breakaway' implements the latest and greatest estimates of richness, as well as the most commonly used estimates. The 'breakaway' philosophy is to estimate diversity, to put error bars on diversity estimates, and to perform hypothesis tests for diversity that use those error bars.
- q2-clawback** (v0.0.3): Assembles taxonomic weights to increase classification accuracy with q2-feature-classifier. Can download data from QIITA or use your data.
- q2-coordinates** (v2019.11): A qime2 plugin supporting methods for geographic mapping of qime2 artifact data or metadata.
- q2-dbotu** (v2018.4.2)
- q2-feature-classifier** (v2019.1)
- q2-fragment-insertion** (v2019.1)

The screenshot shows the QIIME2 library plugin submission form. The form includes fields for Title, Version, Source url, and Short summary. It also has a table for Plugin Authors with columns for Author, List position, and Remove. The form is titled 'q2-aldeX2' and includes a 'Publish to site?' checkbox. The Short summary field contains the following text:

Compositional differential abundance analysis. ALDEx2 provides a framework that encompasses essentially all high-throughput sequencing data types by modelling the data as a log-ratio transformed probability distribution rather than as counts.

The form also includes an 'Install Guide' section and a '# Directions' section.

Chan
Zuckerberg
Initiative

[CZI project description](#)
(source: NAU News)

qiime2 workshops

<https://workshops.qiime2.org>

Upcoming Workshops

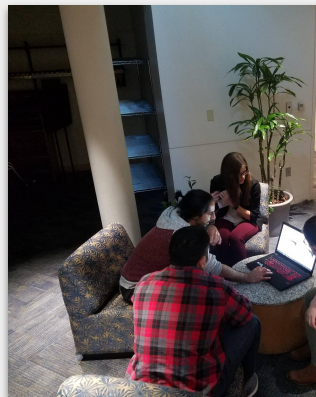
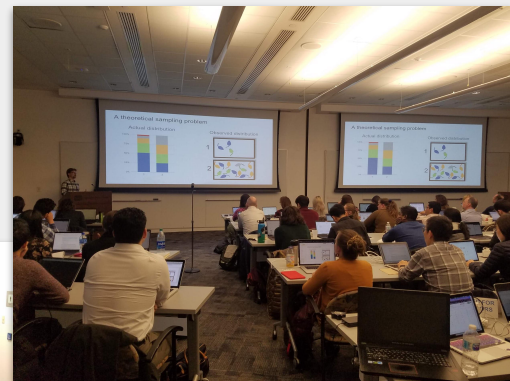
Title	Location	Workshop Dates
Advanced Topics in Microbiome Bioinformatics with QIIME 2 (not open to the public)	University of Bergen Bergen, Norway	March 16, 2020 - March 20, 2020
Microbial Communities Profiling via QIIME 2 and Qiita	NYC, USA	June 24, 2020 - June 25, 2020

Past Workshops

Title	Location	Workshop Dates
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

And [dozens more...](#)

NIH/FAES QIIME 2 workshop, Jan 2020
(90 students, 8 instructors, 3 days hands-on)



Where did you travel from?

