Advancing our Understanding of Cancer and the Human Microbiome with QIIME 2

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

Choose the interface that meets your needs

a) QIIME 2 View

b) QIIME 2 Studio prototype

c) QIIME 2 CLI

d) QIIME 2 Artifact API

Related Software:
- Galaxy
- EBI Metagenomics Portal
- QiITA
- NIH Nephele

Related Software:
- Mothur
- QIIME 1

Related Software:
- phyloseq

Data analyst (clinician, policy maker, research subject)

Cancer researchers and other domain scientists

Power users

Data scientists

COMPUTATIONAL SOPHISTICATION
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](https://library.qiime2.org)) is the primary site for discovering and disseminating QIIME 2 plugins.
DEICODE
(pronounced /de.ko.de/) Robust Aitchison PCA for sparse omics datasets, linking specific features to beta-diversity ordination through the use of compositional biplots.

mmvec
A software package for learning microbe-metabolite interactions.

q2-aldex2
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
"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
Assembles taxonomic weights to increase classification accuracy with q2-feature-classifier. Can download data from Qiita or use your data.

q2-coordinates
A qiime2 plugin supporting methods for geographic mapping of qiime2 artifact data or metadata.

q2-dbotu

q2-feature-classifier
2019.1

q2-fragment-insertion
2019.1

CZI project description
(source: NAU News)
Retrospective data provenance tracking
(or “What did I do 5 months ago?”)

Example of “feature volatility” generated with q2-longitudinal.

Source: QIIME 2 q2-longitudinal tutorial.
Data originally published in Bokulich et al. (2016).
Retrospective data provenance tracking
(backup slide)
### Upcoming Workshops

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<thead>
<tr>
<th>Title</th>
<th>Location</th>
<th>Workshop Dates</th>
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<tr>
<td>Microbiome Bioinformatics with QIIME 2 - Online!</td>
<td>Online</td>
<td>Oct. 5, 2020 - Oct. 9, 2020</td>
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<tr>
<td>An Introduction to QIIME 2</td>
<td>Online (via World of Microbiome)</td>
<td>Nov. 4, 2020 - Nov. 4, 2020</td>
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<tr>
<td>Microbiome Bioinformatics with QIIME 2</td>
<td>Online (via FAES at the National Institutes of Health)</td>
<td>Jan. 4, 2021 - Jan. 8, 2021</td>
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### Past Workshops

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

- Microbiome (16S/18S)
- Metagenome (shotgun)
- Mycobiome (ITS?)
- Virome
- Absolute abundance data (qPCR?)
- Transcriptome (inc. host immune signatures)
- Host genome
- Metabolome

*Et cetera...*
Acknowledgements

**Caporaso Lab team**
Evan Bolyen
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Chloe Herman
Chris Keefe
Andrew Sanchez
Anthony Simard

**QIIME and QIIME 2 communities**
QIIME 1 Development Team
QIIME 2 Development Team

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- ITCR (1U24CA248454-01)
- Partnership for Native American Cancer Prevention (U54CA143925)
National Science Foundation (1565100)
Chan-Zuckerberg Initiative
Alfred P. Sloan Foundation

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**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

For updates on what’s going on in the Caporaso Lab, follow @CaporasoLab on Twitter, and see the lab website at caporasolab.us.
How did QIIME 2 know what happened?

*.qza and *.qzv files are just structured zip files*

- Data, in the usual formats (e.g., newick, fasta, tsv, ...), is in the `data/` directory.
- The rest is human-readable QIIME-specific metadata.
Completely Free and Open Source

- You have a *licensed right* to use, redistribute, and even modify QIIME 2
  - (Consider [contributing to the QIIME 2](https://github.com/qiime2/) project via GitHub Pull Requests!)
- You can audit every line of code
- **Tested** on every code change
  - Unit tests, code coverage, linting
  - Tutorial commands automatically tested
- World-wide [network of collaborators](https://github.com/qiime2/)

Find all of our code at: [https://github.com/qiime2/](https://github.com/qiime2/)