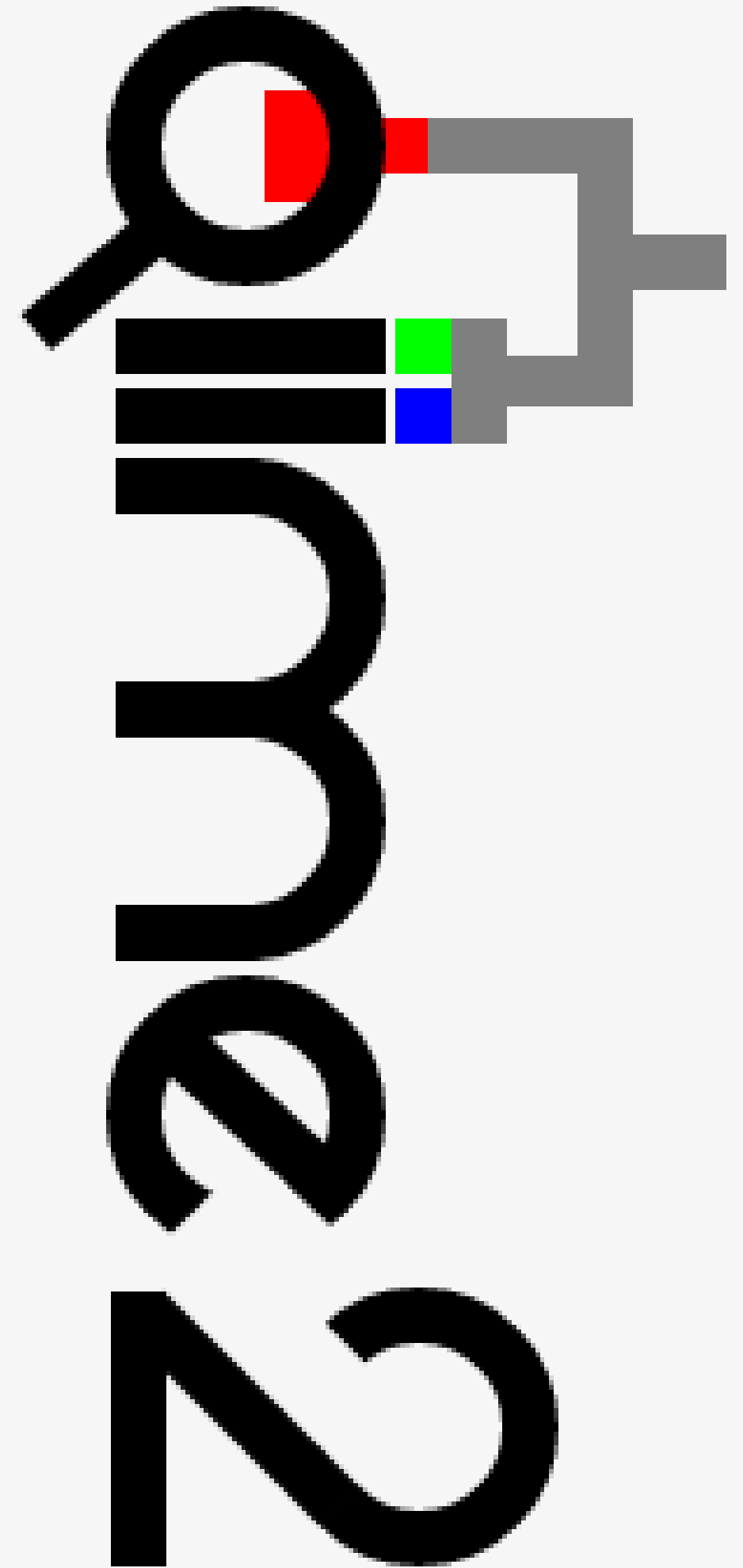


QIIME 2 - pipeline for performing metagenome analysis

presentation made by Anastasia Ramanchanka



Understanding of
microbiomes may
lead to...

**..insights into the role of
microorganisms in health and
disease.**

**..help in the development of
probiotics, prebiotics, and other
microbiome-based therapies.**

..more sustainable farming practices.

**..support the protection and
restoration of ecosystems.**

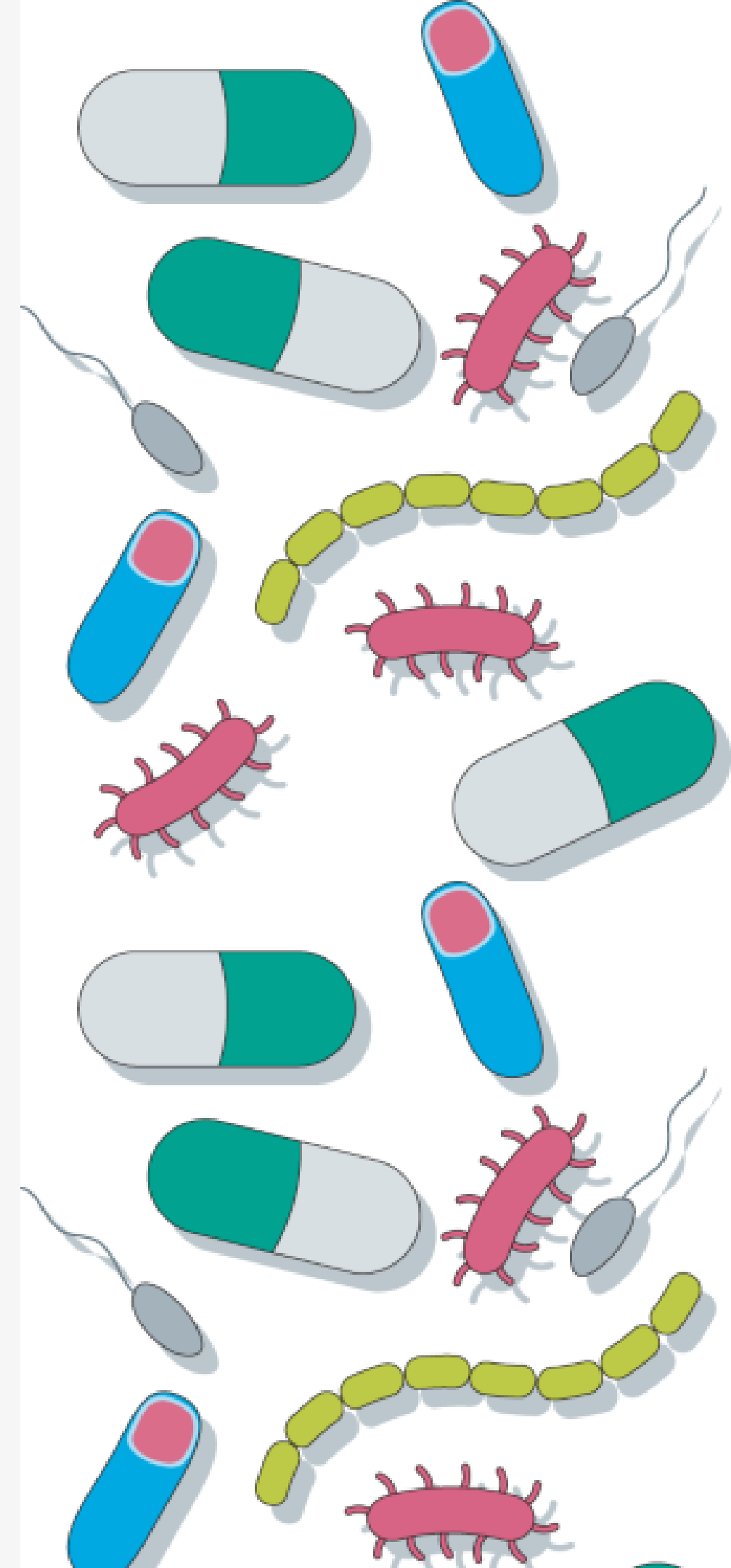
Our microbiomes impact the efficacy of medical treatment

Gut microbiome influences efficacy of PD-1–based immunotherapy against epithelial tumors

[BERTRAND ROUTY](#) ^{ID}, [EMMANUELLE LE CHATELIER](#) ^{ID}, [LISA DEROSA](#), [CONNIE P. M. DUONG](#) ^{ID}, [MARYAM TIDJANI ALOU](#),
[ROMAIN DAILLÈRE](#) ^{ID}, [AURÉLIE FLUCKIGER](#) ^{ID}, [MERIEM MESSAOUDENE](#), [CONRAD RAUBER](#), [...], AND [LAURENCE ZITVOGEL](#) ^{ID}

Good bacteria help fight cancer

Resident gut bacteria can affect patient responses to cancer immunotherapy (see the Perspective by Jobin). Routy *et al.* show that antibiotic consumption is associated with poor response to immunotherapeutic PD-1 blockade. They profiled samples from

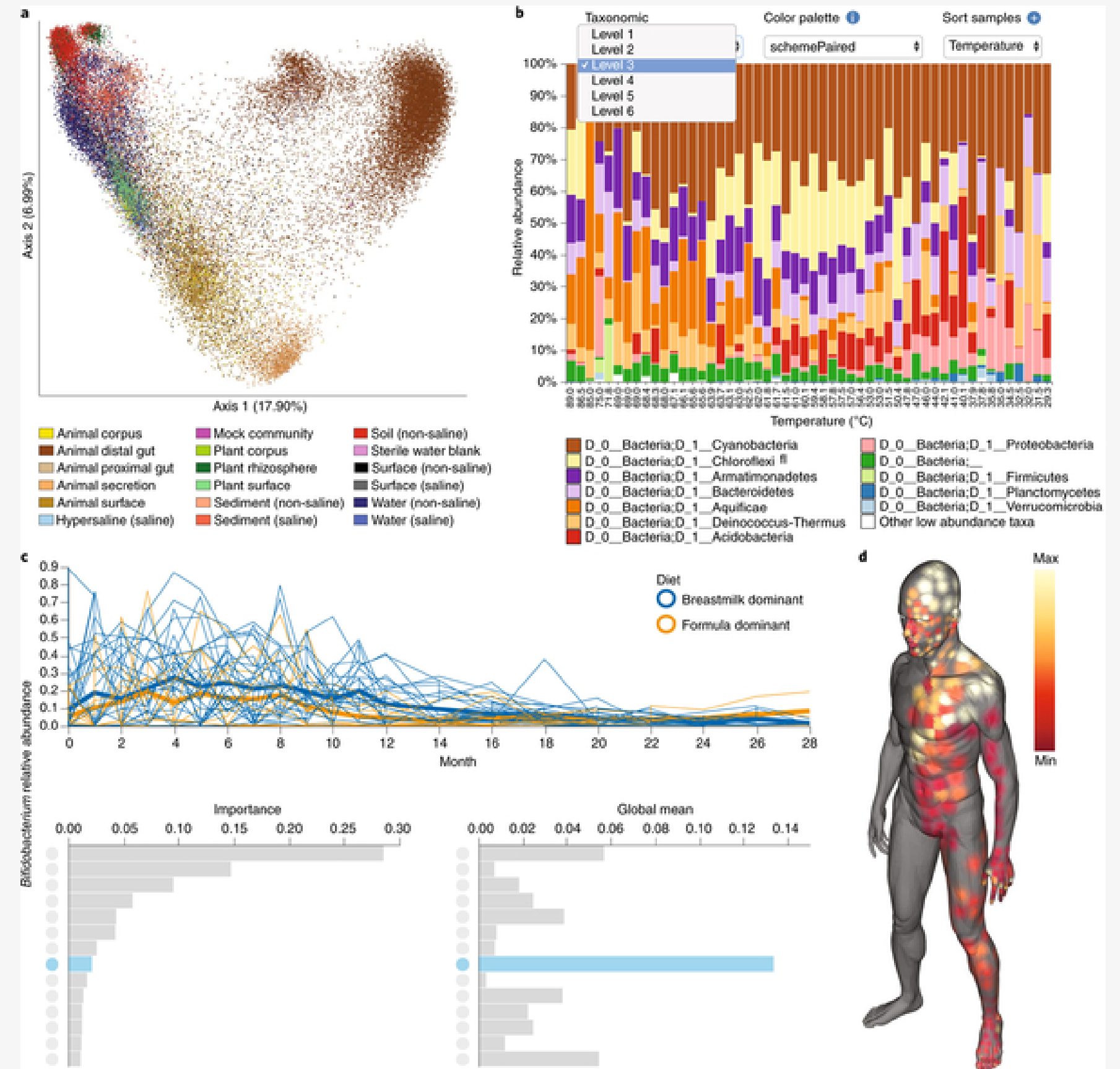


Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2

[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](#), ... [J. Gregory Caporaso](#) ✉

+ Show authors

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doi: 10.1038/s41587-019-0209-9

QIIME2 is completely free and Open Source



Users have a licensed right to use, redistribute and even modify QIIME2



Users can audit every line of code



World-wide network of collaborators

<https://github.com/qiime2>



Features that attract users to system

Latest microbiome bioinformatics methods and visualizations

Accessibility through detailed documentation and well-design interface

A community of microbiome scientists, developers and bioinformaticians

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

QIIME2 provides several interfaces for interacting with its platform and performing microbiome analysis.

Core concepts

● **QIIME 2 artifacts** as .qza files

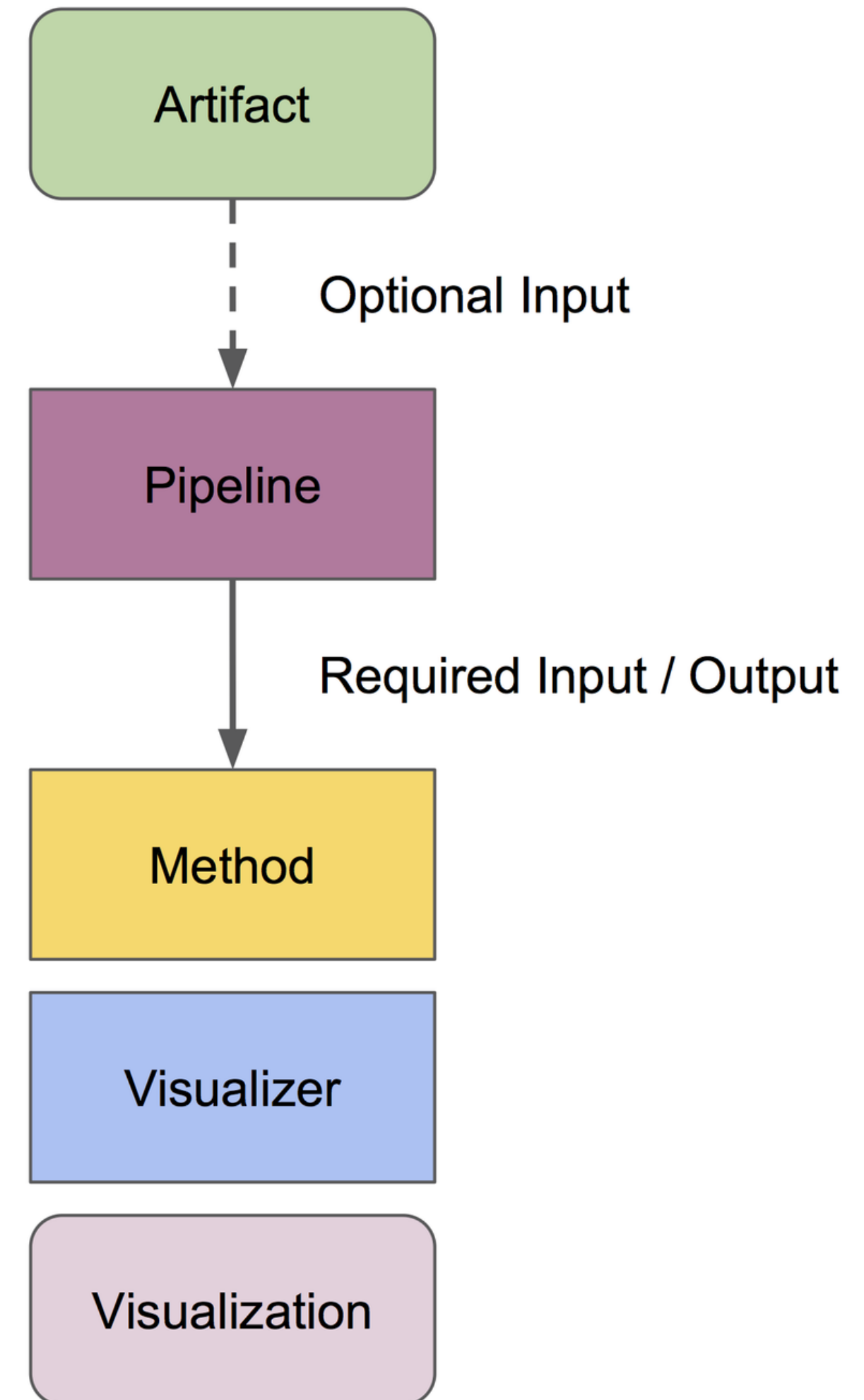
● **Visualizations** as .qzv files:

- statistical results table
 - interactive visualization
 - static images
 - any combination of visual data representations
-

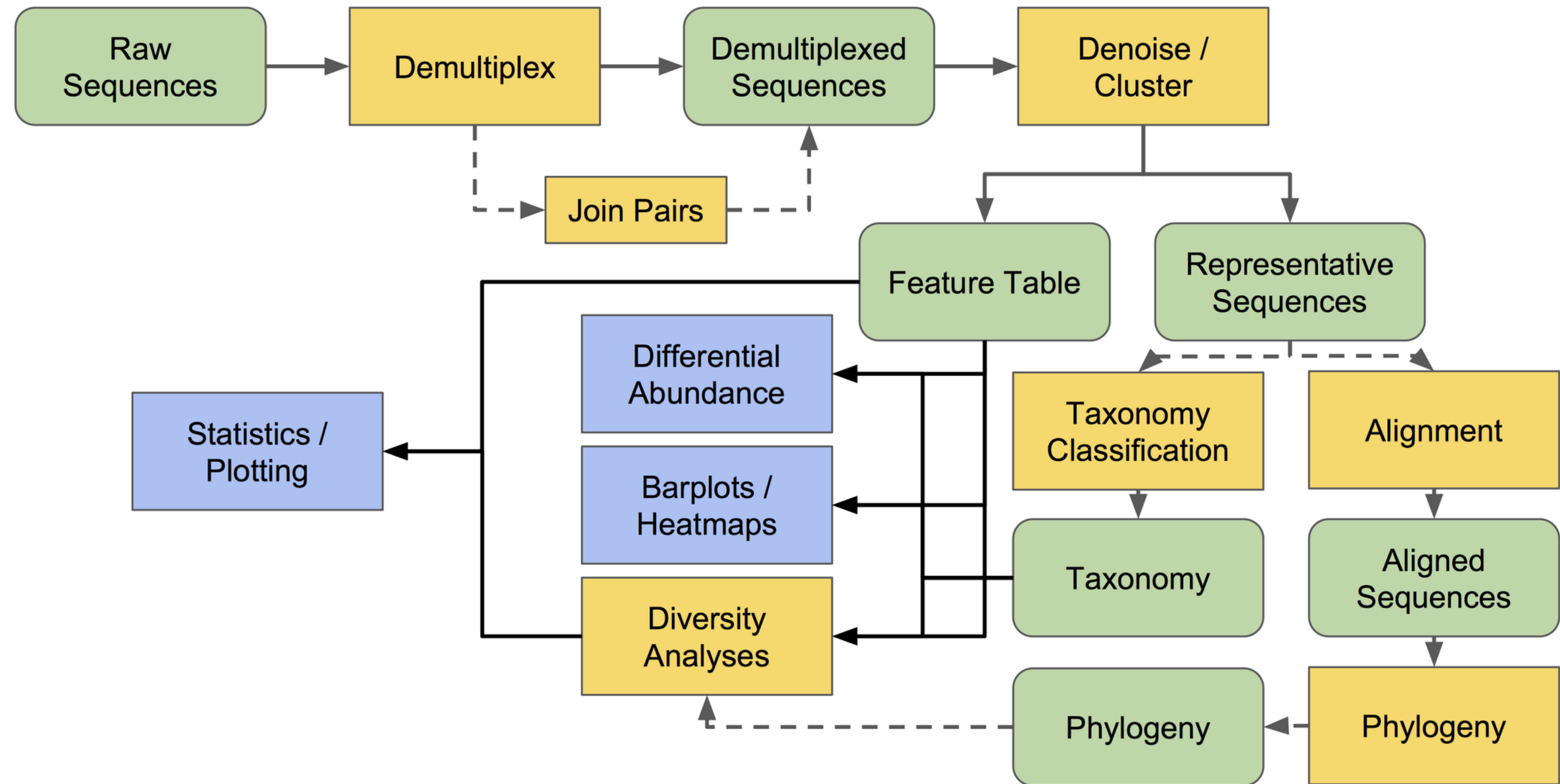
● **Semantic type**

● **Plugins**

● **Methods and visualizers**



Amplicon sequence data analyses



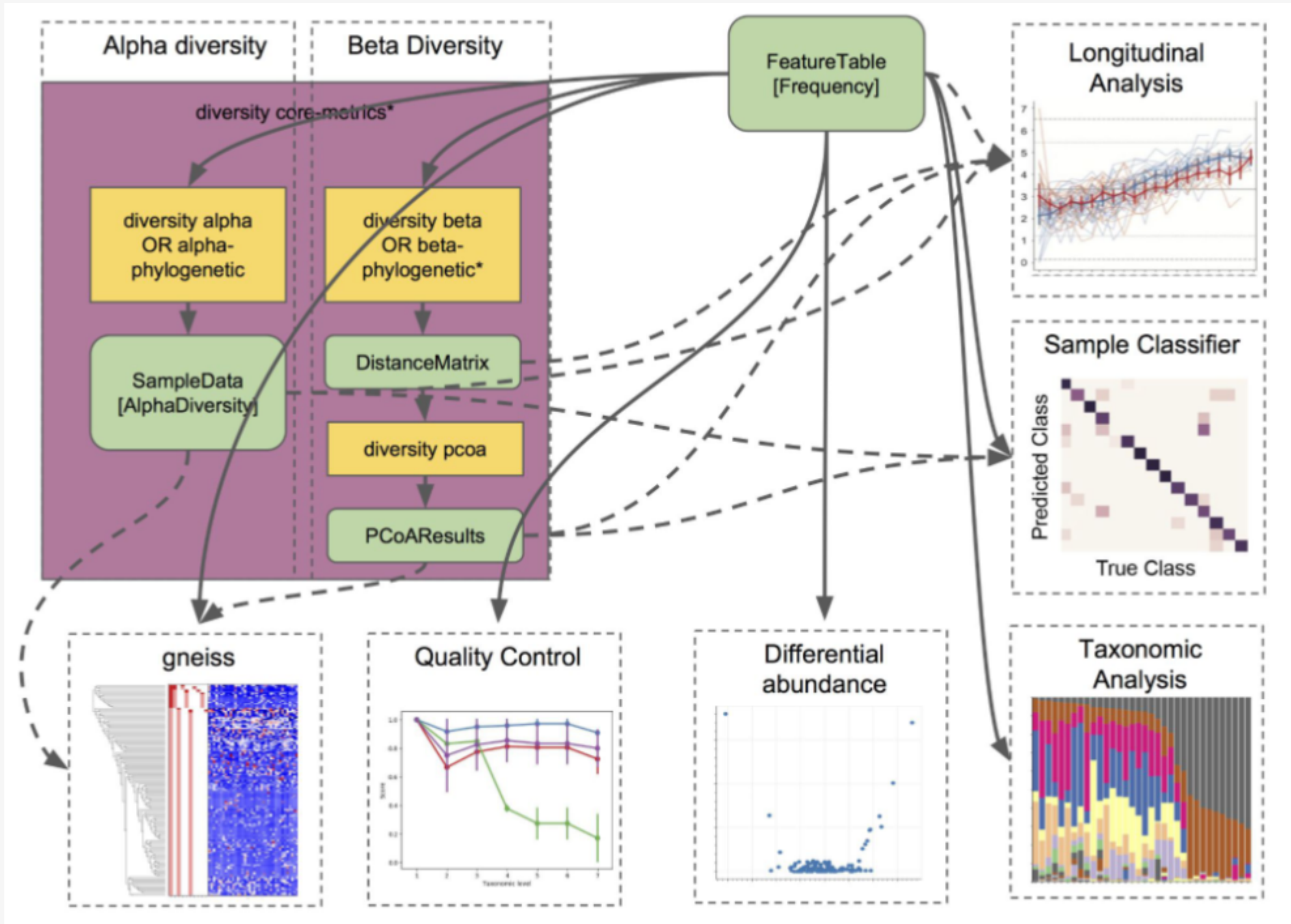
Sequence quality control and feature table construction

- **DADA2** - pipeline for detecting and correcting (where possible) Illumina amplicon sequence data
- **Deblur** - uses sequence error profiles to associate erroneous sequence reads with the true biological sequence from which they are derived
- **basic quality-score-based filtering**

Result: FeatureTable[Frequency]
FeatureData[Sequence]

Metric	Sample
Number of samples	34
Number of features	770
Total frequency	153,807

	Frequency	# of Samples Observed In
4b5eeb300368260019c1fbc7a3c718fc	11,373	13
fe30ff0f71a38a39cf1717ec2be3a2fc	8,929	16
d29fe3c70564fc0f69f2c03e0d1e5561	8,622	25
868528ca947bc57b69ffd83e6b73bae	7,663	10
154709e160e8cada6bfb21115acc80f5	7,412	13
1d2e5f3444ca750c85302ceee2473331	7,186	23



Tutorials

<https://docs.qiime2.org/2024.2/tutorials/>

● “Moving pictures”

● “Fecal microbiota transplant”

● “Atacama soil microbiome”

● “Parkinson’s mouse”

..and thank for your attention

