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Bonus Module
PICRUSt

Morgan Langille

Analysis of Metagenomic Data

June 24-26, 2015

bioinformatics.ca

16S rRNA gene

QIIME

Shotgun Metagenomics

MetaPhlAn

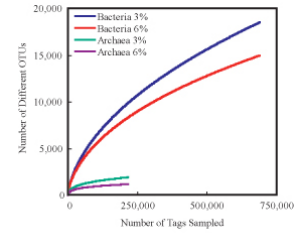
HUMAnN

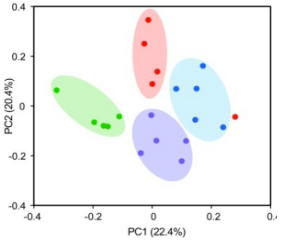
	Sample 1	Sample 2	Sample 3
OTU 1	4	0	2
OTU 2	1	0	0
OTU 3	2	4	2

PICRUSt

	Sample 1	Sample 2	Sample 3
K00001	20	15	18
K00002	1	2	0
K00003	4	5	4

STAMP





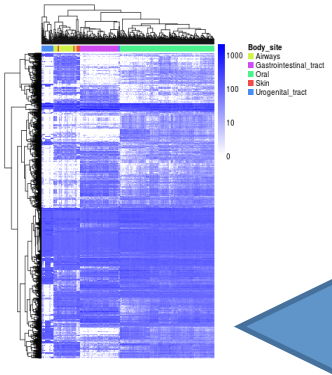
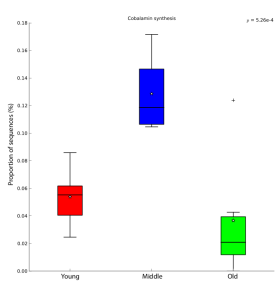
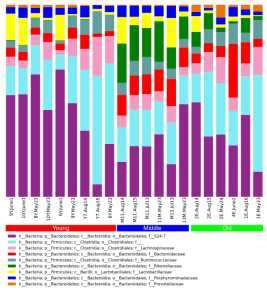


Figure 2





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PICRUSt

- **P**hylogenetic **I**nvestigation of **C**ommunities by **R**econstruction of **U**nobserved **St**ates
- http://picrust.github.com

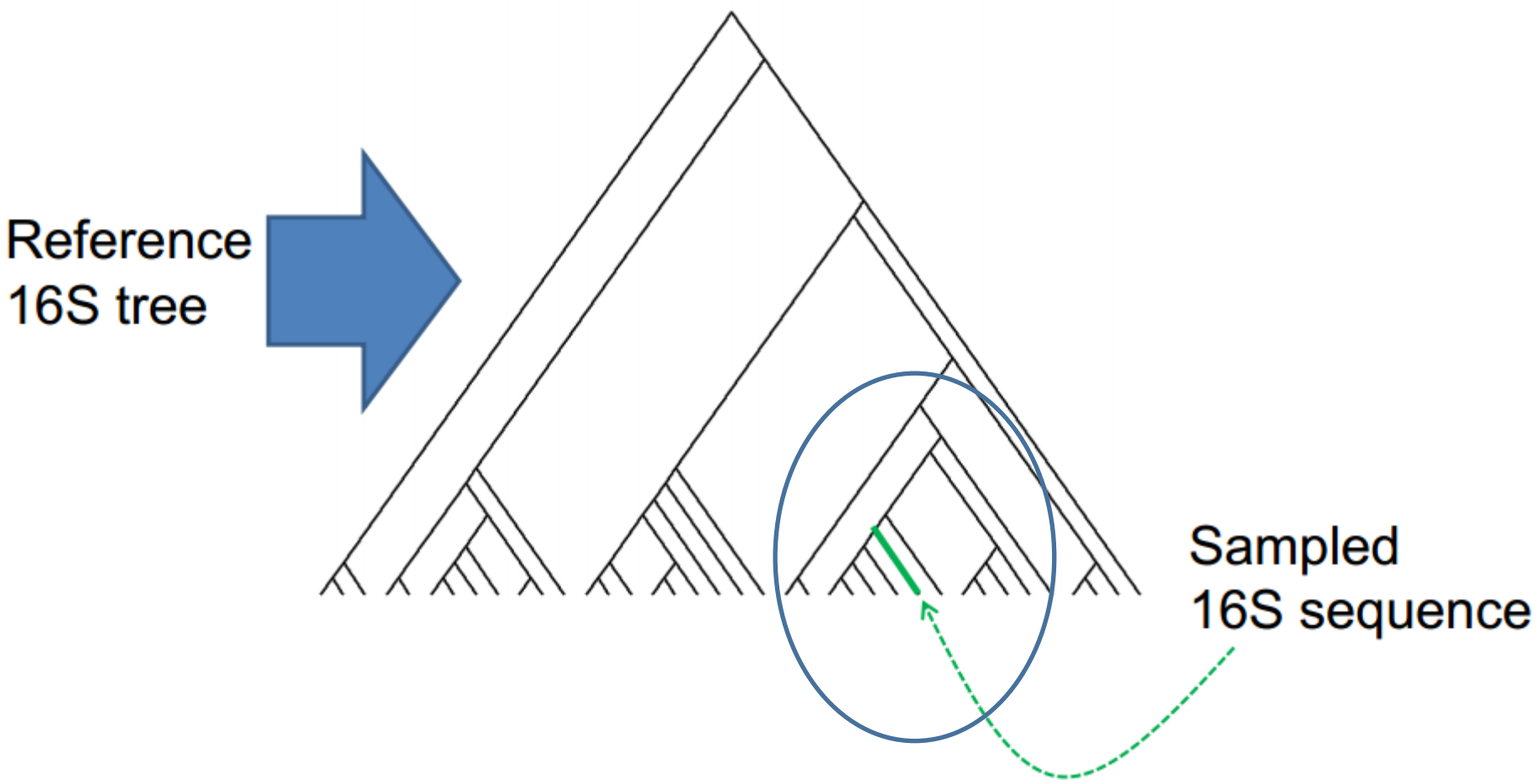
NATURE BIOTECHNOLOGY | COMPUTATIONAL BIOLOGY | ANALYSIS

日本語要約

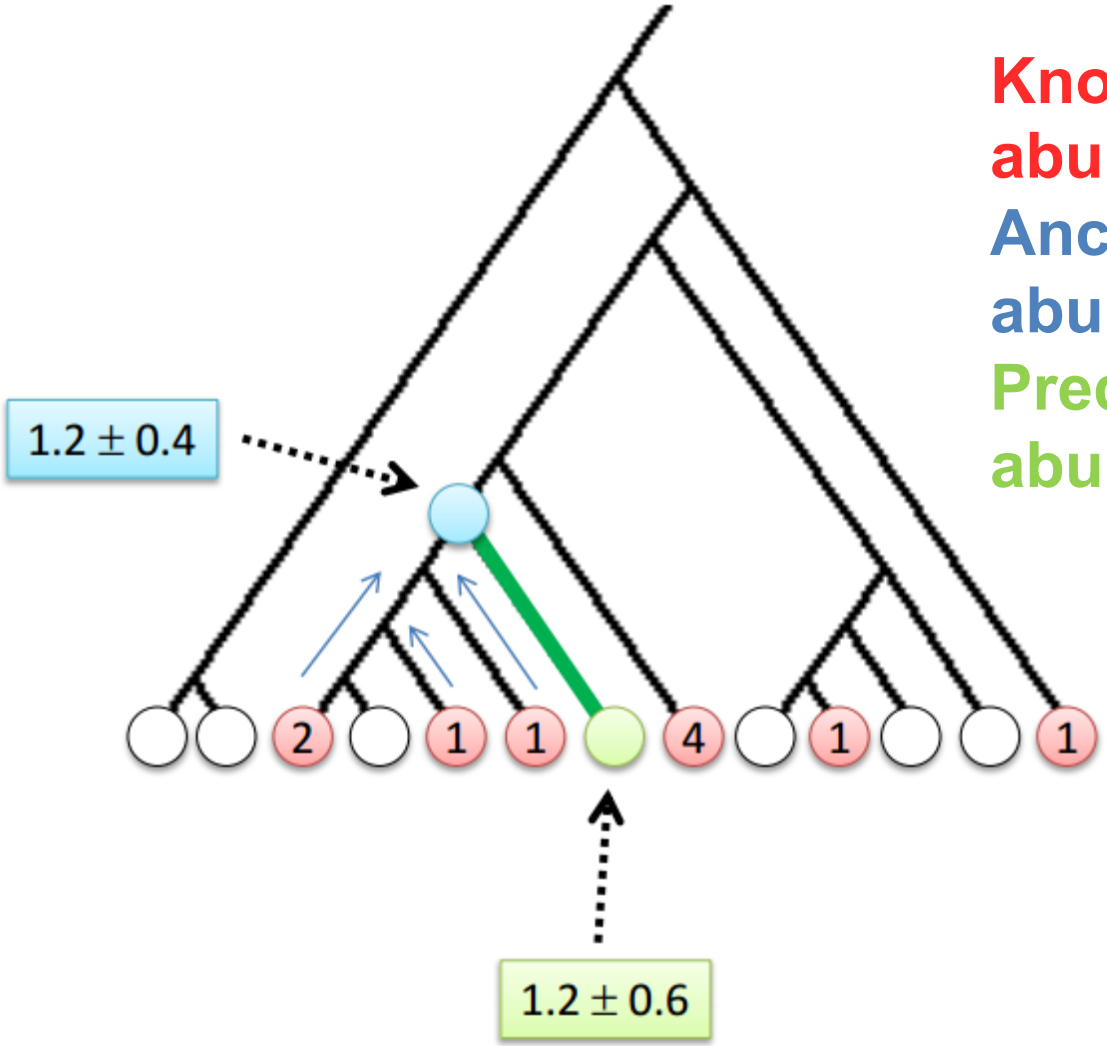
Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences

Morgan G I Langille, Jesse Zaneveld, J Gregory Caporaso, Daniel McDonald, Dan Knights, Joshua A Reyes, Jose C Clemente, Deron E Burkepile, Rebecca L Vega Thurber, Rob Knight, Robert G Beiko & Curtis Huttenhower

PICRUSt: How does it work?



Predicting the abundance of a single function

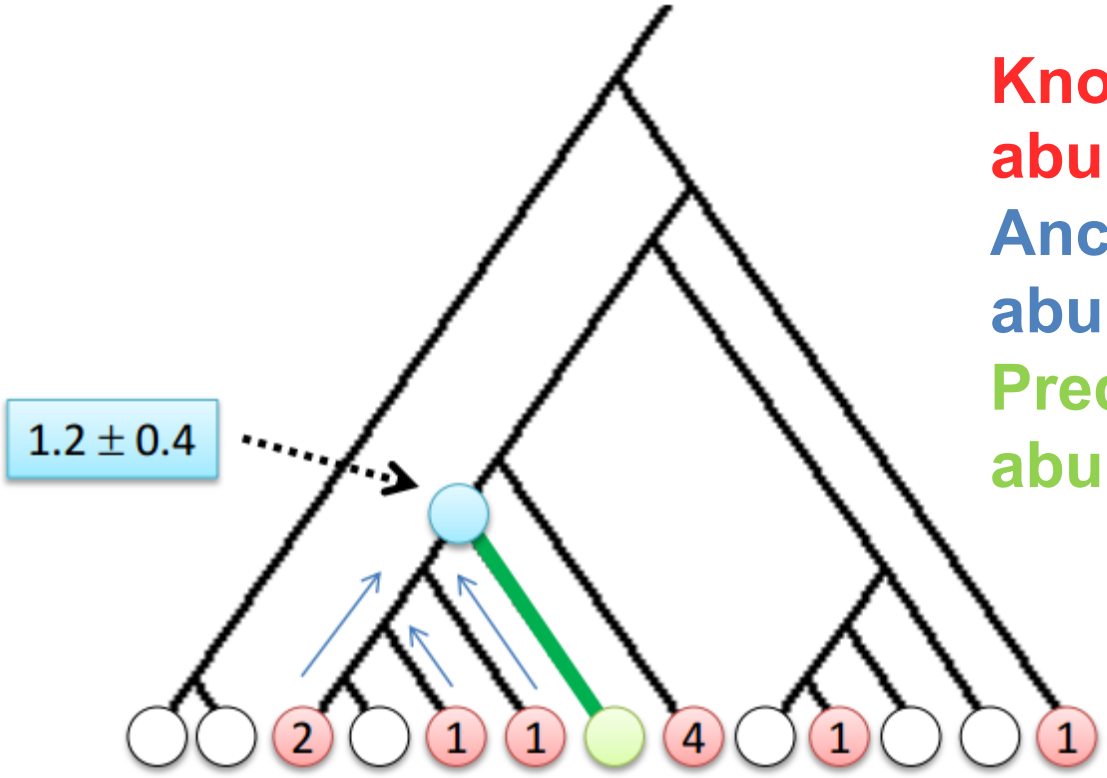


Known gene abundance

Ancestral gene abundance

Predicted gene abundance

Predicting the abundance of a single function



Known gene abundance

Ancestral gene abundance

Predicted gene abundance

Repeat for each function (~8000X)

Repeat for all unknown tips (>100,000)

PICRUST: Predicting Metagenomes

OTU Table

	S1	S2	S3
12345	10	0	5
67890	1	0	0
66666	4	8	2

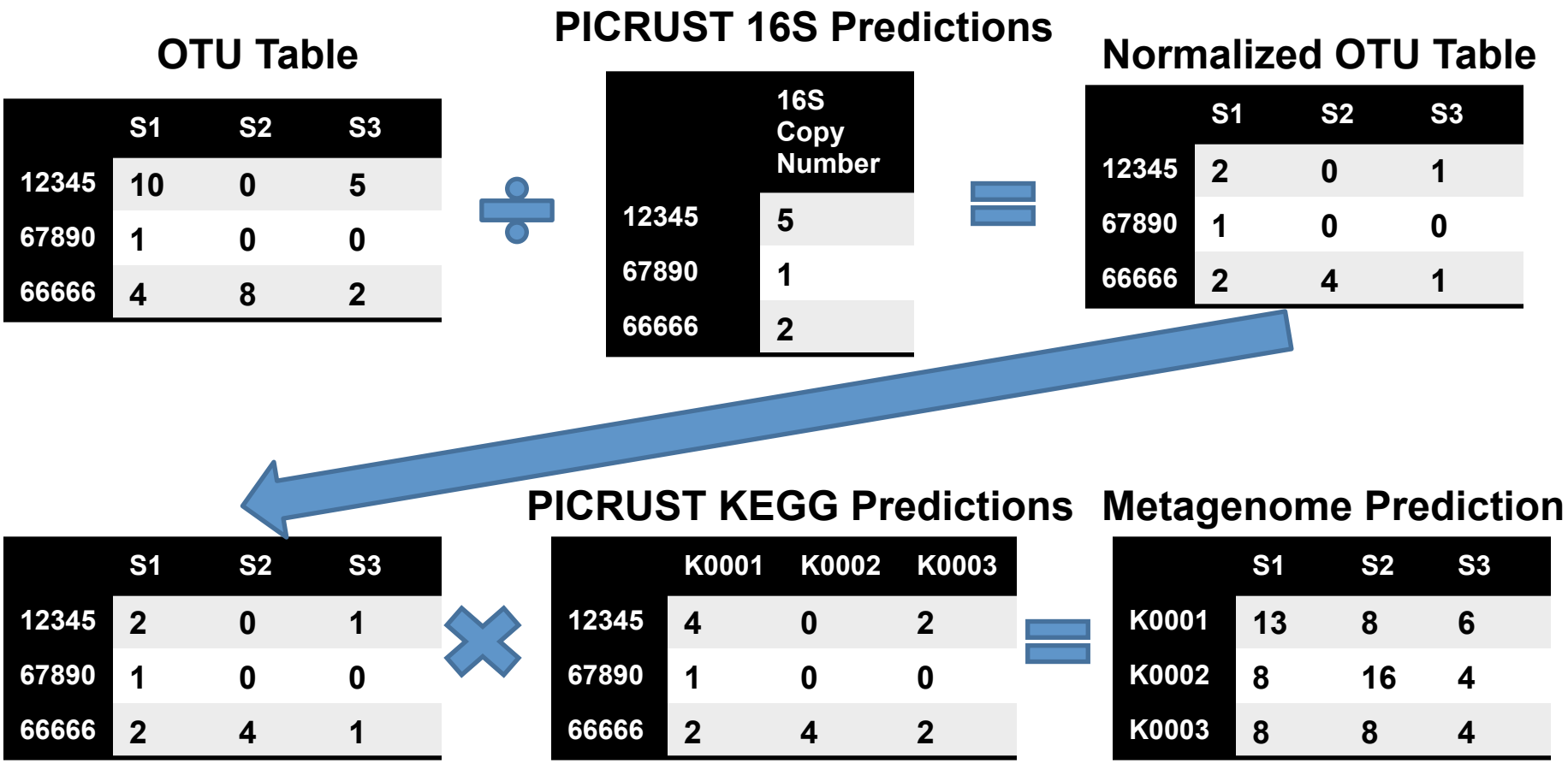
PICRUST 16S Predictions

	16S Copy Number
12345	5
67890	1
66666	2

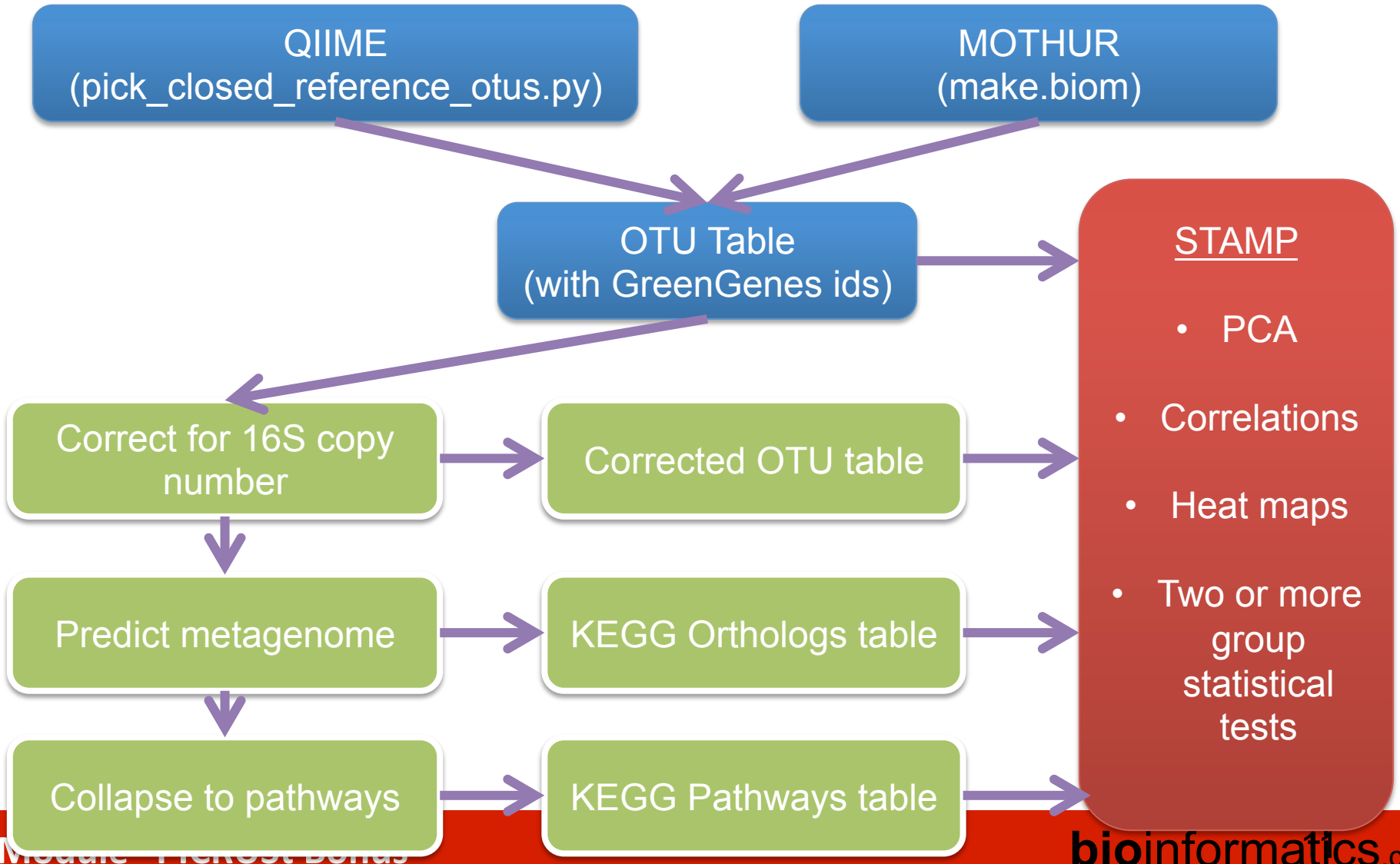
Normalized OTU Table

	S1	S2	S3
12345	2	0	1
67890	1	0	0
66666	2	4	1

PICRUST: Predicting Metagenomes



Tutorial Pipeline



Questions?

We are on a Coffee Break & Networking Session