

Creating a web app to study human
gut microbiome variation across
geographic region of the world

Challenges

- Integrate the comparisons and contrasts of the gut microbiome diversity across human populations
- Lack of simple tools to analysis and visualize the differences of microbiome community for people who lack experience working on microbiome data

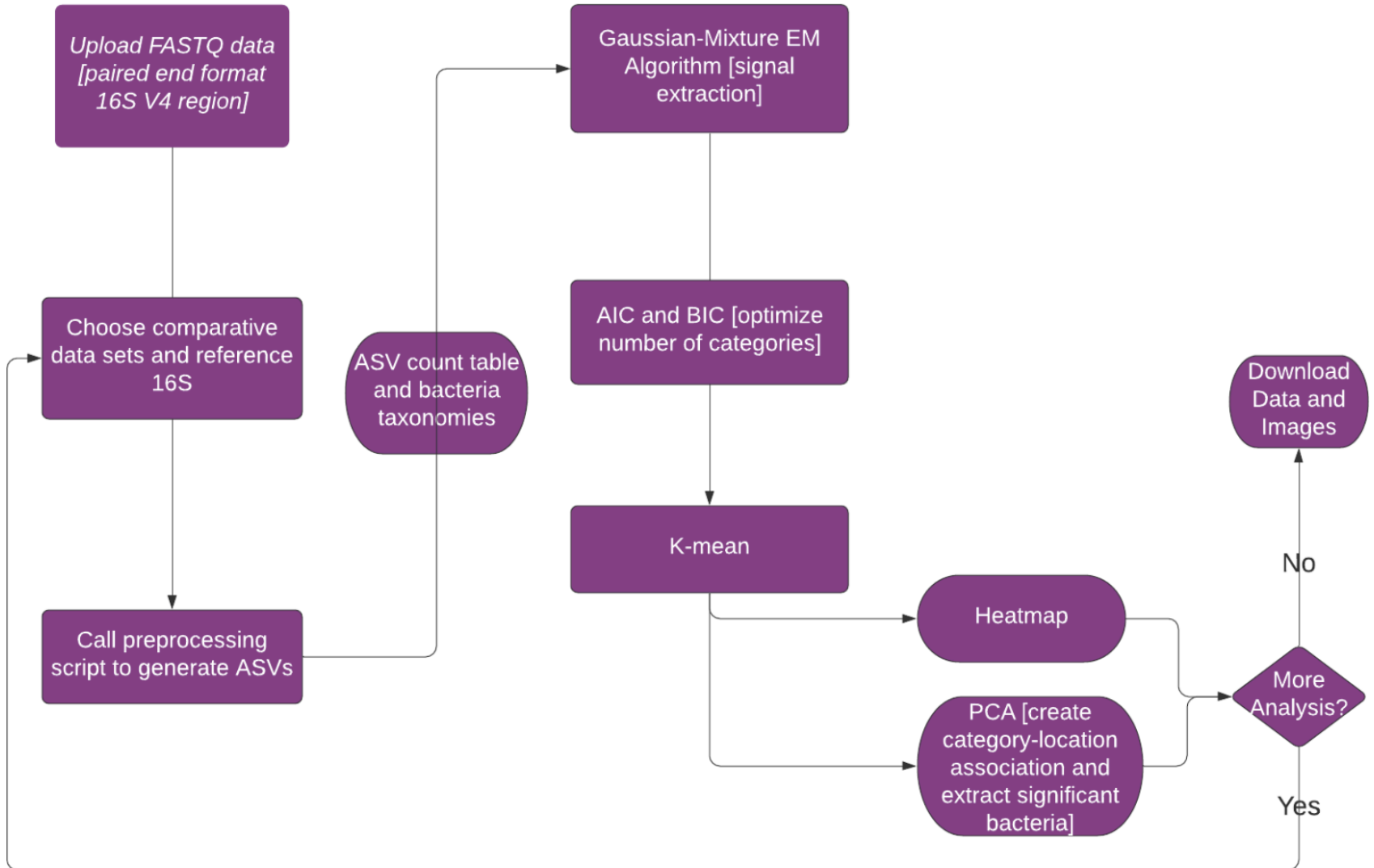
Data set

Acquired human gut microbiome data from public repositories for 16S V4 region

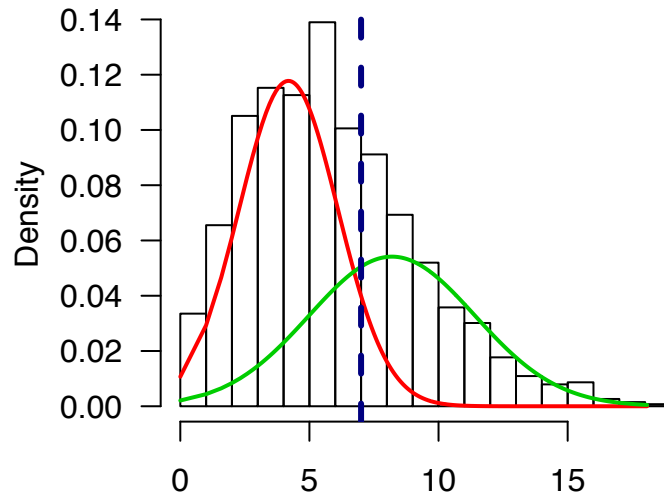
At present, we have samples (1,428) from India, Europe and Brazil

Project Zero

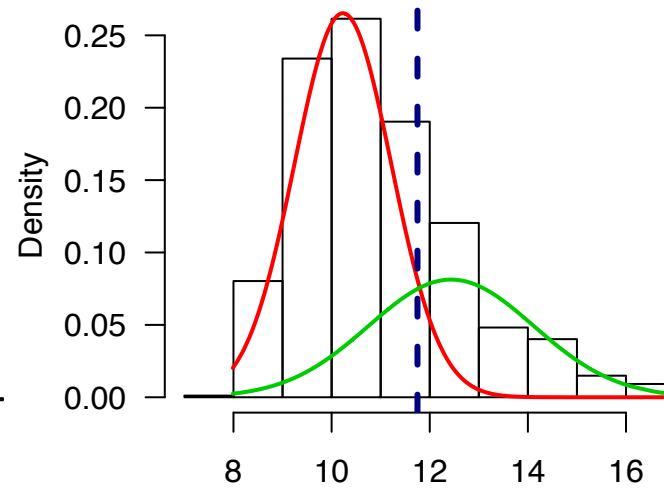
Team Zero | February 28, 2020



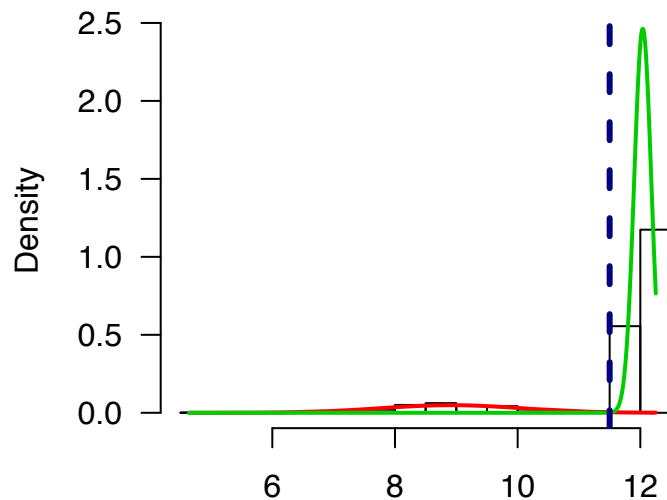
The Gaussian Mixtures - EM Algorithm to extract informative bacteria groups



$\log_2(\text{\#reads for bacteria})$

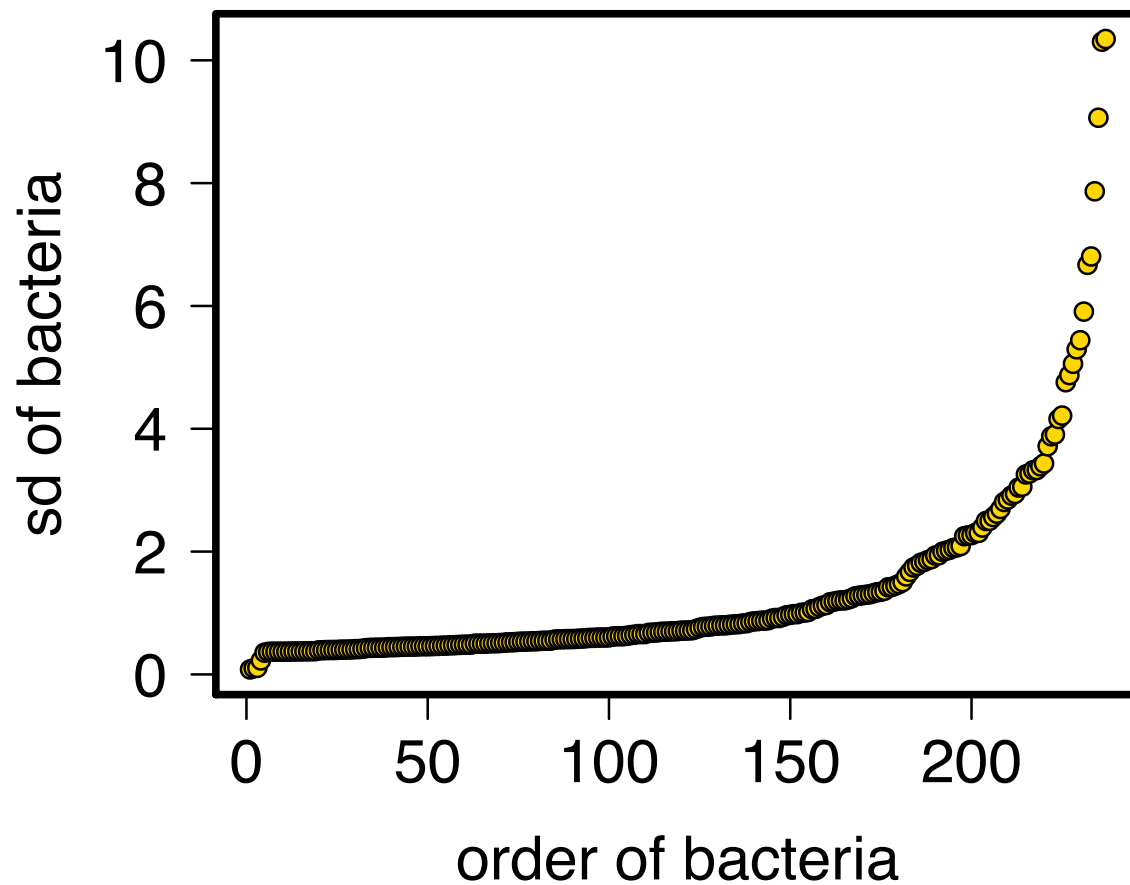


$\log_2(\text{sd of bacteria})$

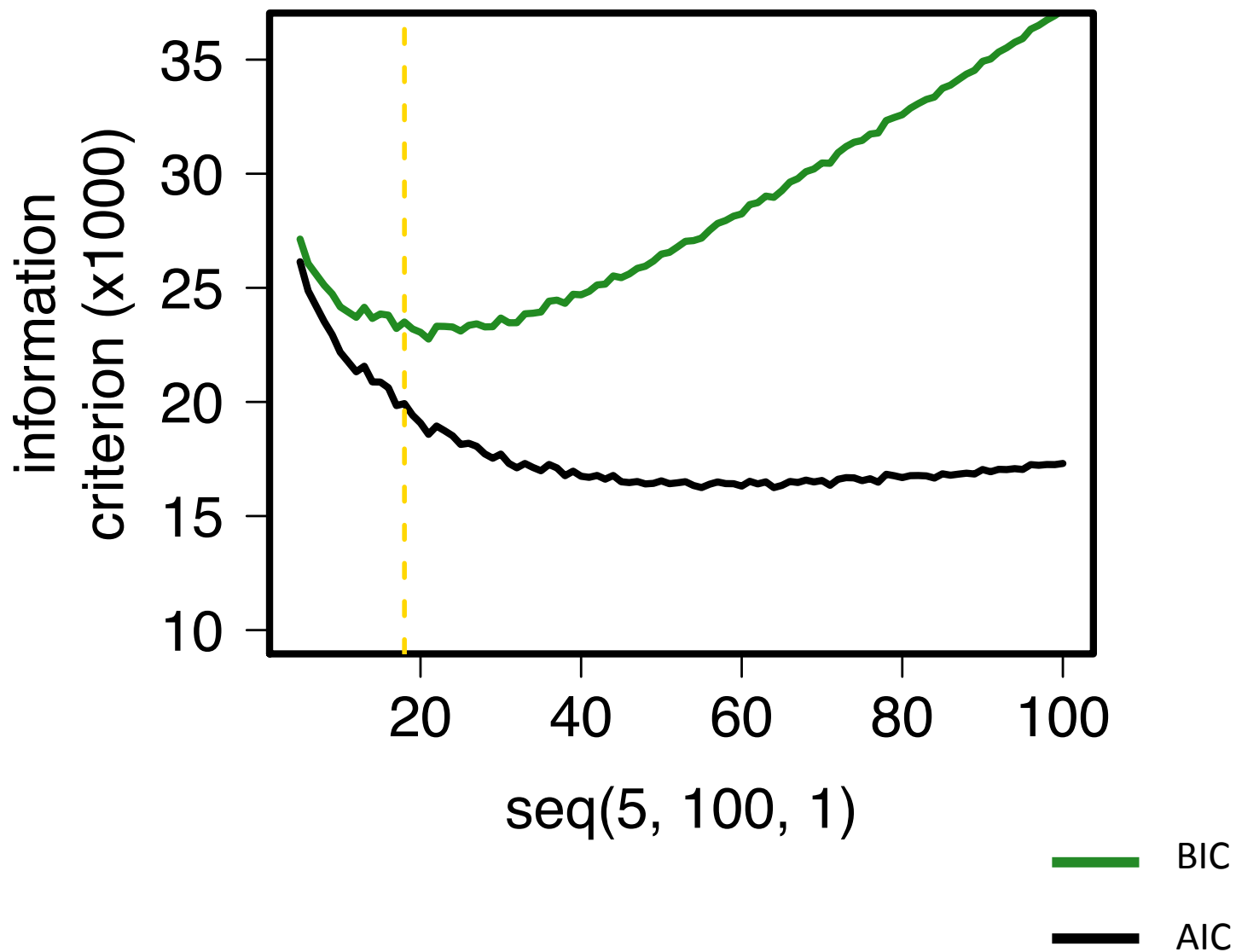


$\log_2(\text{\#reads for sample})$

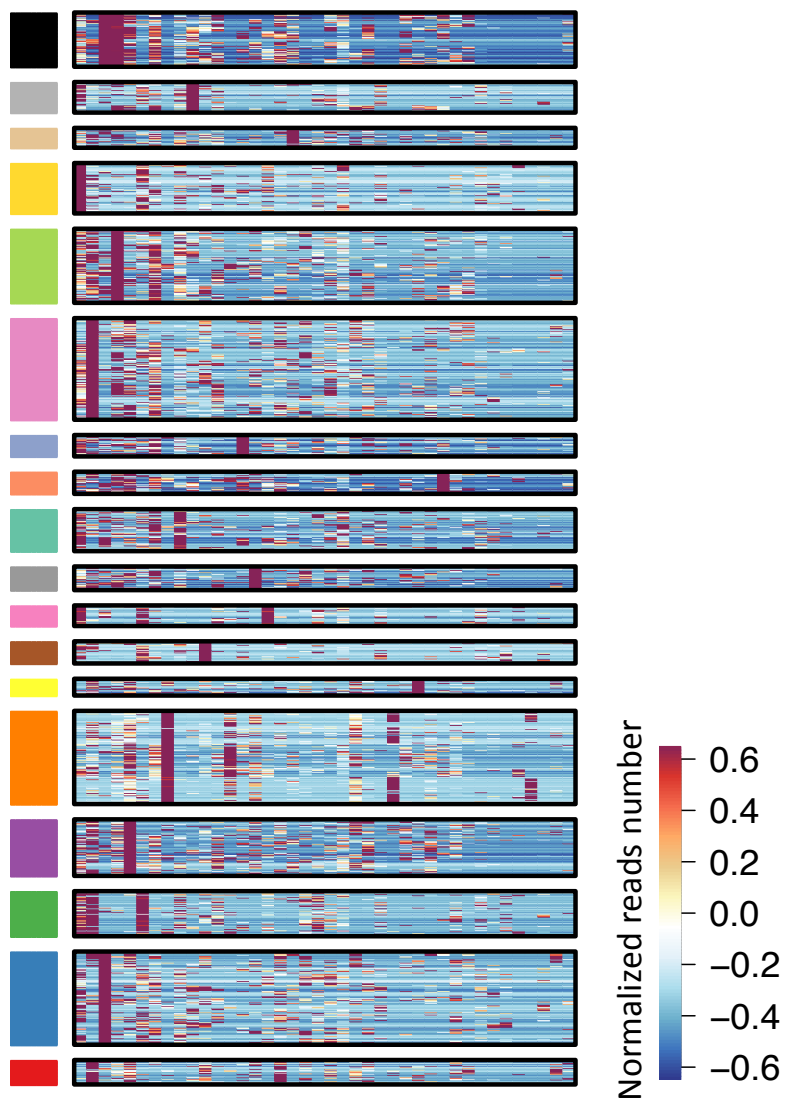
Bacterial group extraction with significant vibration between samples



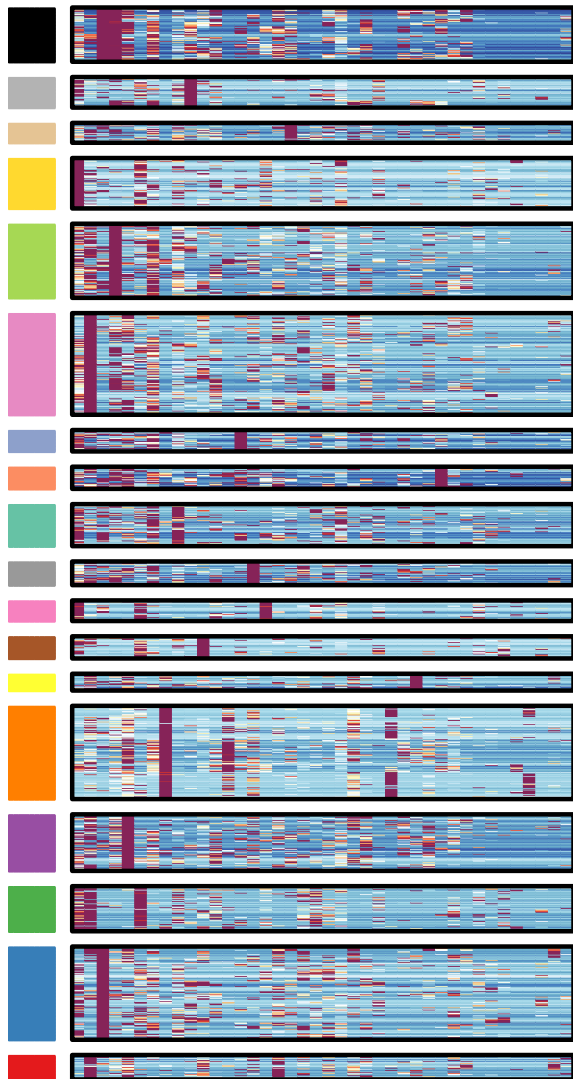
Optimized categories selection based on AIC and BIC



18 categories were used to train k-mean

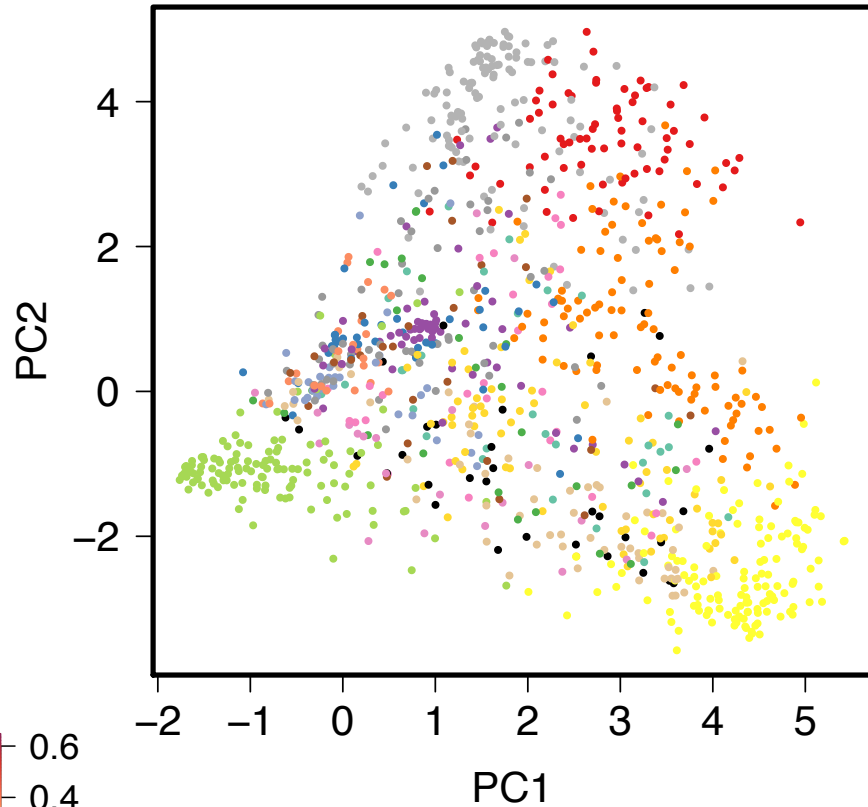


18 categories were used to train k-mean



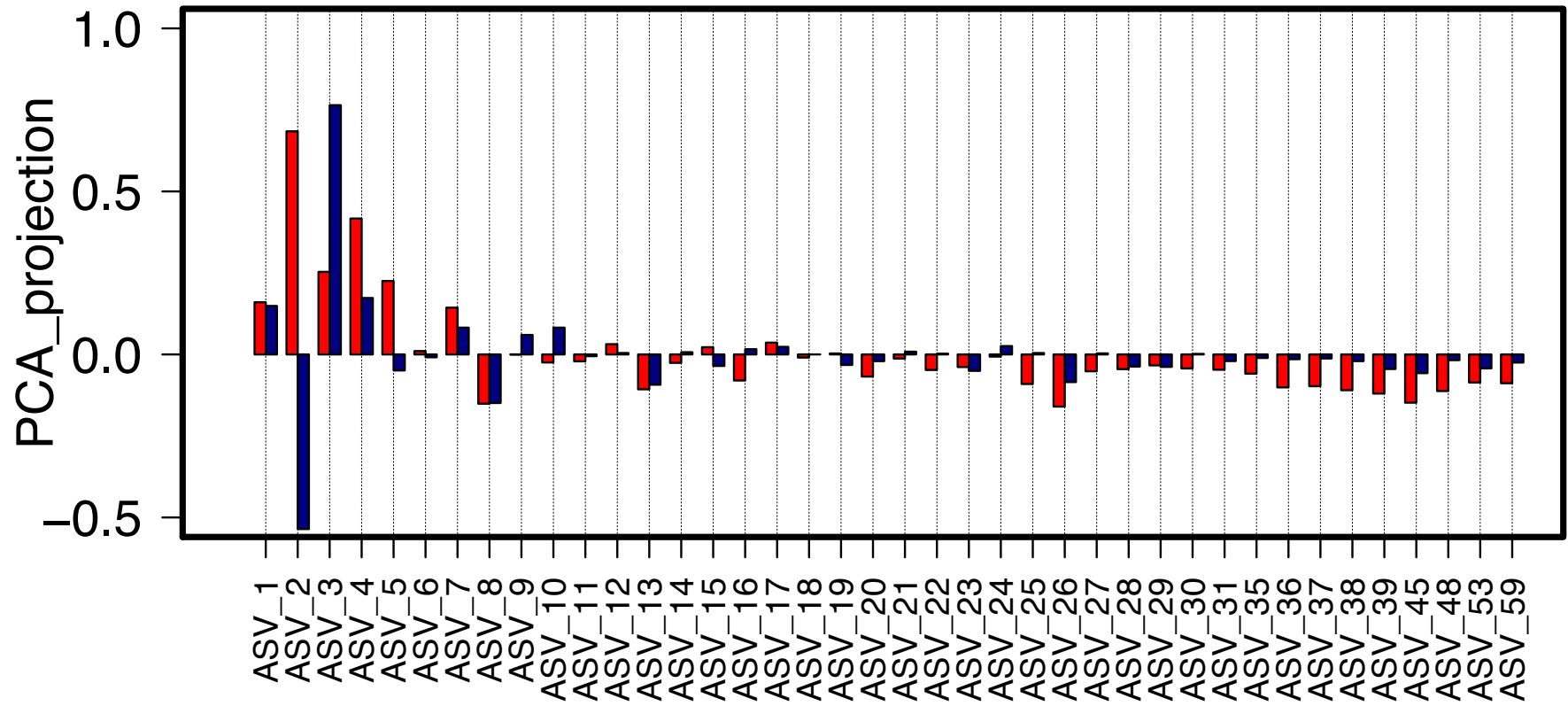
Normalized reads number

0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6



- class1
- class2
- class3
- class4
- class5
- class6
- class7
- class8
- class9
- class10
- class11
- class12
- class13
- class14
- class15
- class16
- class17
- class18

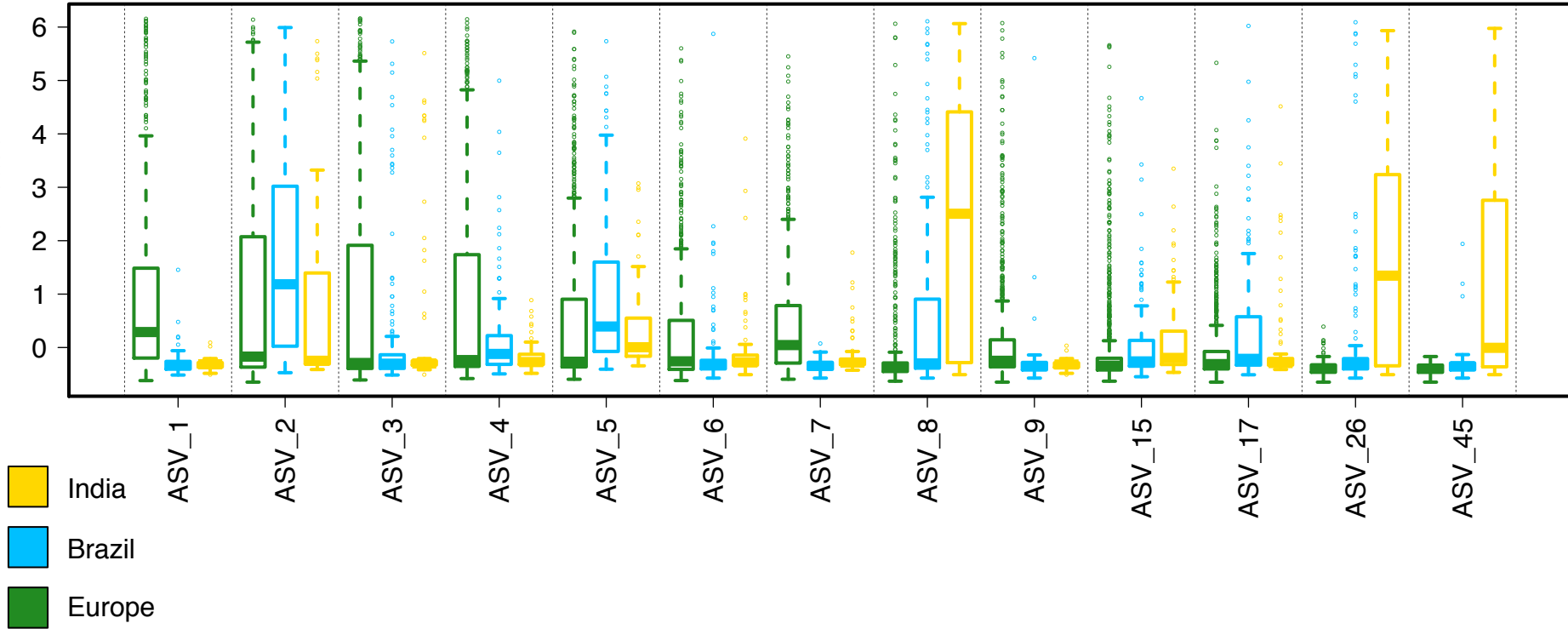
PCA loading indicates geographic preference of microbiota



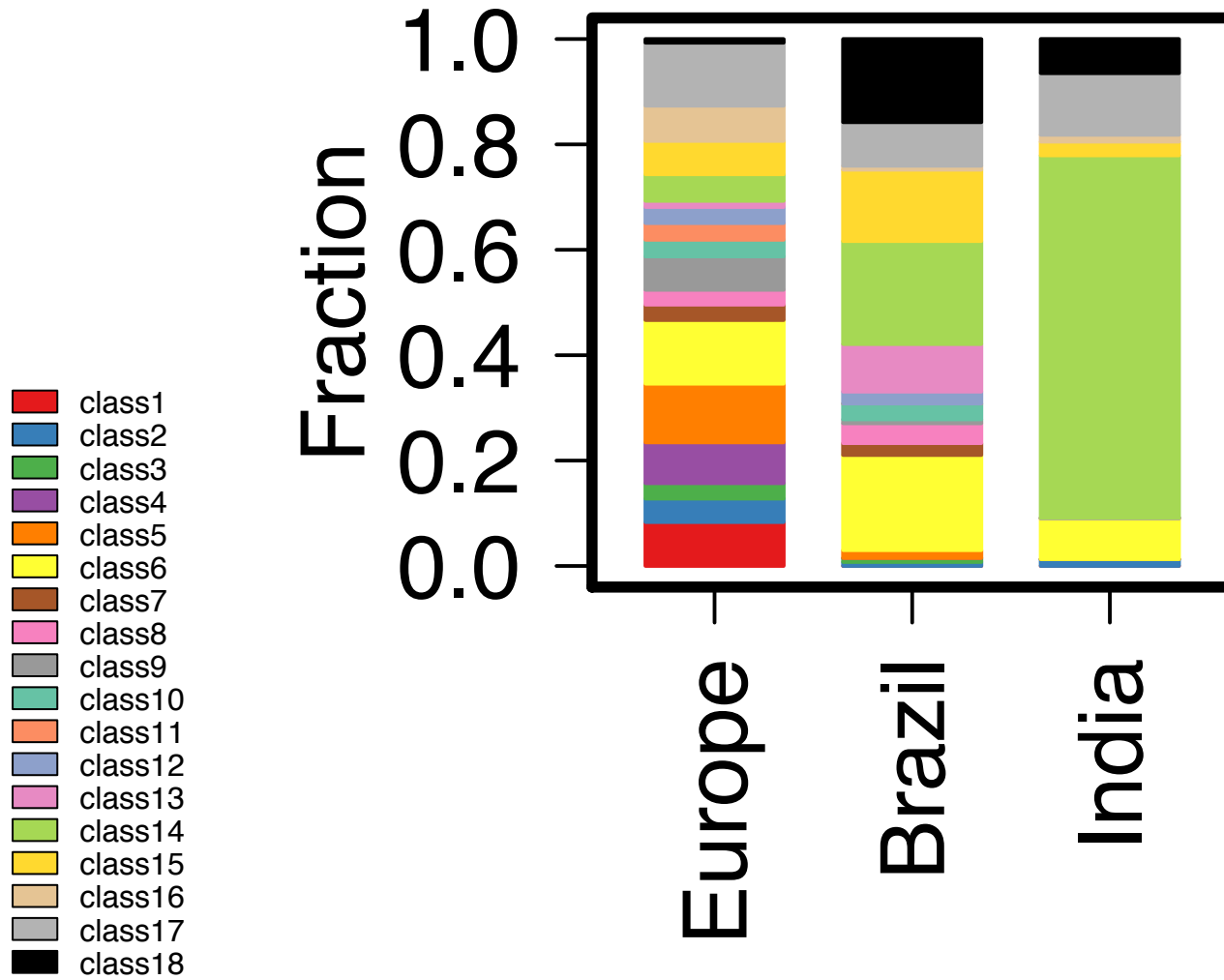
First direction

Second direction

geographic preference for specific bacterial species



Geographic preference for specific bacterial species



Conclusion

- Observed patterns based on gut microbiome differences across geographic regions
- Developed novel techniques to identify bacterial signatures which differentiate populations based on geography
- Developed a web app providing a GUI interface for users to upload/download resources and make plots on the server