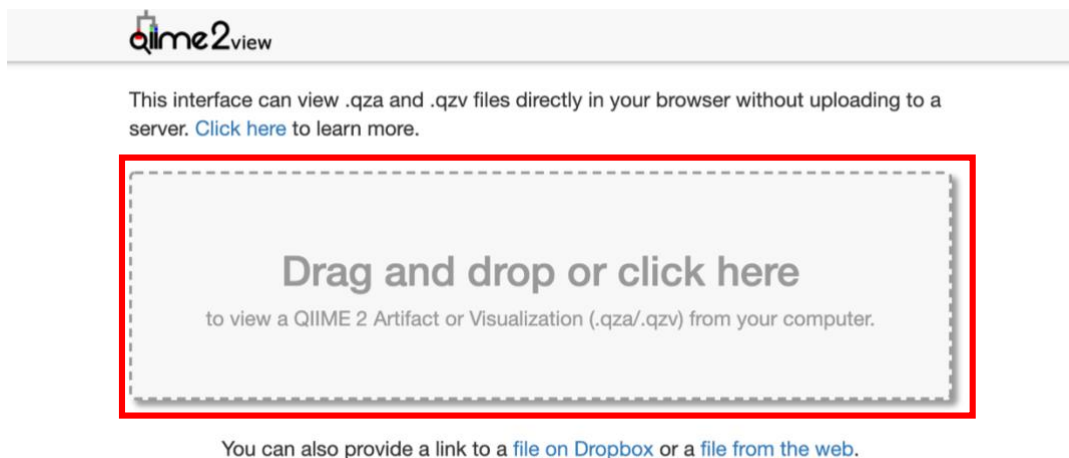


Supplementary File 2

Instructions to view QIIME2 Emperor Plot visualizations

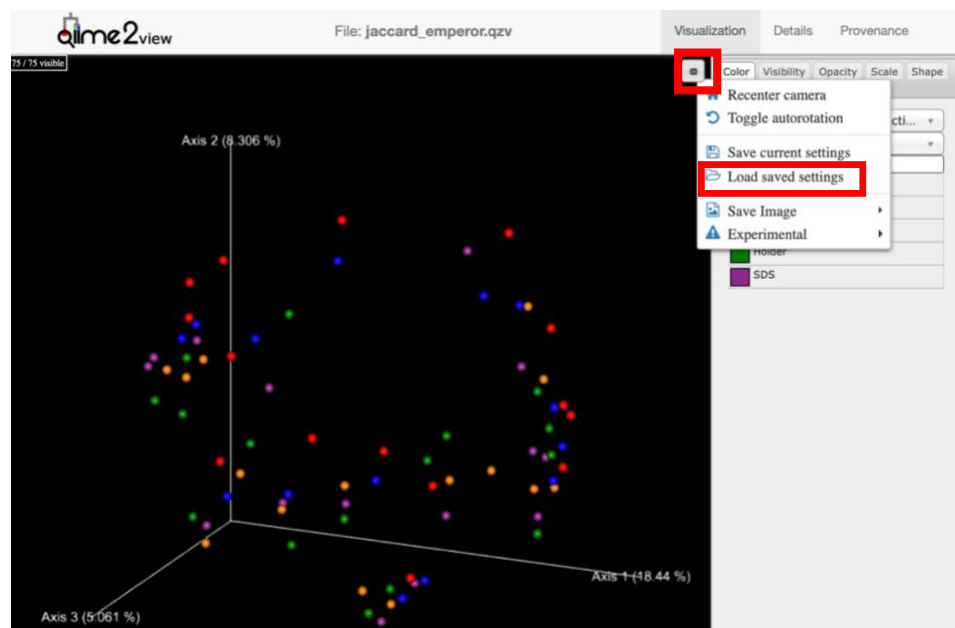
- Using Google Chrome, visit view.qiime2.org.
- Drag and drop **bray_curtis_emperor.qzv** or **jaccard_emperor.qzv** into the drag-and-drop box within the QIIME2 Viewer.

NOTE: QIIME2 Viewer will only open the "*.qzv" files.

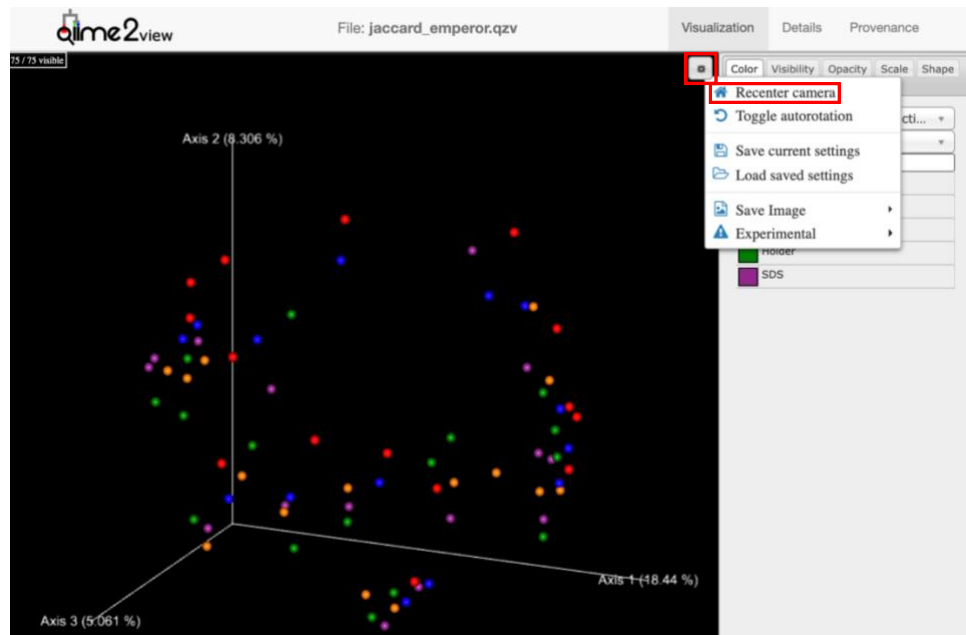


- After either .qzv file has been loaded, the sample groupings can be labeled with different metadata categories by selecting the settings button (gear) then **Load saved settings**.
 - To color samples by a metadata category, select a .json file specific to the similarity metric used to generate the plot.

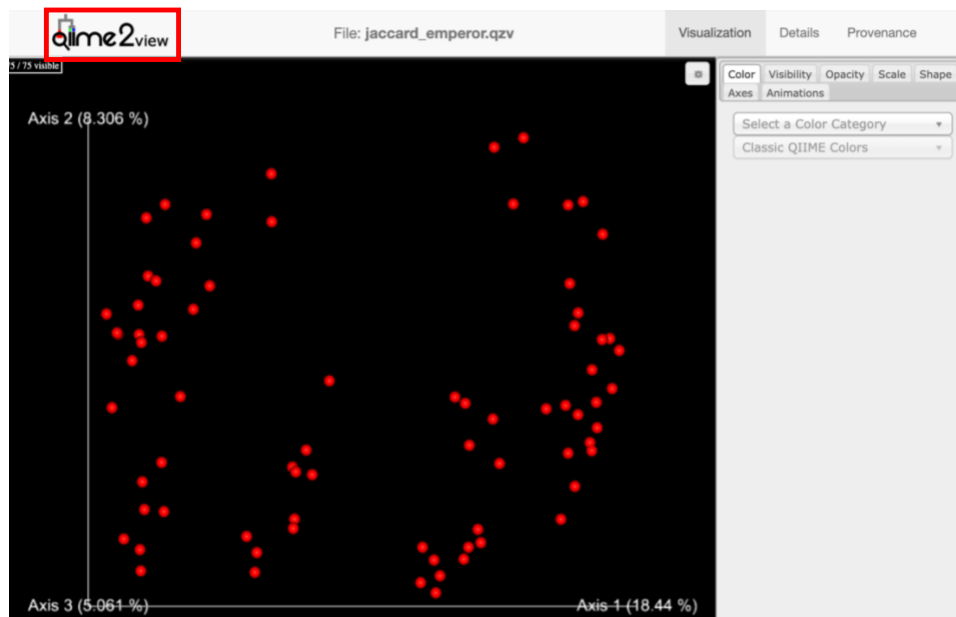
EX: Color samples by Method of Extraction in the Jaccard plot by selecting "Jaccard_Method_of_Extraction.json"



- Click and drag around the plot to see sample groupings in 3D. To recenter the view, select the settings button, then select **Recenter camera**.



- To view new a Q2 visualization, select the **Qiime2View** logo in the top-left corner.



References for Emperor PCoA Generation

Legendre, P., and L. Legendre. 2012. Numerical Ecology. In Null, (Elsevier), p. 499.

Jaccard, P. 1908. Nouvelles recherches sur la distribution floral. Bull. Soc. Vard. Sci. Nat 44:223--270.

Vázquez-Baeza, Y., M. Pirrung, A. Gonzalez, and R. Knight. 2013. EMPeror: a tool for visualizing high-throughput microbial community data. Gigascience 2:16.

Vázquez-Baeza, Y., A. Gonzalez, L. Smarr, D. McDonald, J.T. Morton, J.A. Navas-Molina, and R. Knight. 2017. Bringing the dynamic microbiome to life with animations. Cell Host Microbe 21:7--10.

Halko, N., P.-G. Martinsson, Y. Shkolnisky, and M. Tygert. 2010. An algorithm for the principal component analysis of large data sets. ArXiv E-Prints.

Sørensen, T. 1948. A method of establishing groups of equal amplitude in plant sociology based on similarity of species and its application to analyses of the vegetation on Danish commons. Biol. Skr. 5:1--34.