

# Robert Stehlin

## What is in your sample?

The table below shows the relative abundances of all of the organisms we observed in your sample. To produce this, we took the DNA sequences from your sample, and compared them against publicly available annotated reference databases. In some cases, a sequence may uniquely match a database record, in other cases a sequence may match may different records. To handle the uncertainty that can arise, we rely on a well used and publicly available microbiome software package called [QIIME 2](#). The exact approach taken is highlighted in the main tutorial on [feature-classification](#).

Show  entries

Search:

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.1304	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0753	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0566	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0519	Bacteria	Proteobacteria	Alphaproteobacteria	RF32		
0.0376	Bacteria	Tenericutes	Mollicutes	RF39		
0.0237	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
0.0235	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	
0.0235	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0232	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0228	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Sutterella
0.0179	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0175	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Butyrivibrio
0.0174	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0168	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0163	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0160	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0152	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0127	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0123	Bacteria	Tenericutes	Mollicutes	RF39		
0.0119	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0111	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0105	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0104	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.0097	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0096	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0093	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0092	Bacteria	Cyanobacteria	4C0d-2	YS2		
0.0089	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0088	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
0.0087	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0082	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0079	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.0076	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
0.0074	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0072	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0072	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0066	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0066	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	Paraprevotella
0.0059	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira
0.0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0057	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0056	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium
0.0054	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0054	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Paraprevotellaceae]	Paraprevotella
0.0053	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0053	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0052	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0051	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Gemmiger
0.0048	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	
0.0046	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium
0.0043	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0042	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0038	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0036	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0035	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Phascolarctobacterium
0.0033	Bacteria	Tenericutes	Mollicutes	RF39		
0.0030	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0028	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0028	Bacteria	Tenericutes	Mollicutes	RF39		
0.0027	Bacteria	Firmicutes	Clostridia	Clostridiales		

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0027	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
0.0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0026	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0025	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0025	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0025	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0025	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0024	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0023	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0023	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0023	Bacteria	Cyanobacteria	4C0d-2	YS2		
0.0022	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0022	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	
0.0022	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Butyricimonas
0.0020	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
0.0020	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Oribacterium
0.0018	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0017	Bacteria	Proteobacteria	Alphaproteobacteria	RF32		
0.0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
0.0016	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Odoribacter
0.0016	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira
0.0016	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0015	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0015	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
0.0014	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0014	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0014	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0013	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0013	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0012	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0011	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	

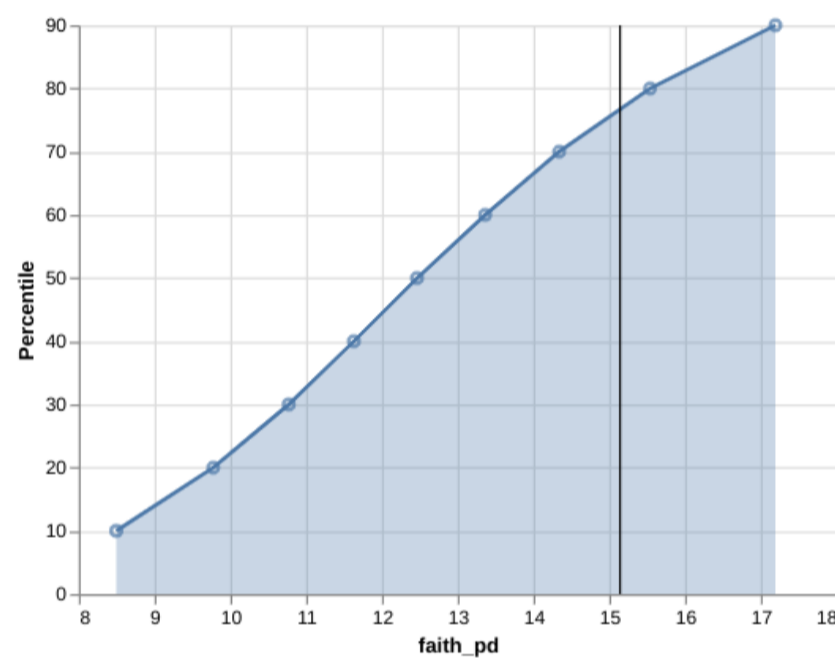
Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0011	Bacteria	Tenericutes	Mollicutes	RF39		

Showing 1 to 100 of 224 entries

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## Alpha Diversity

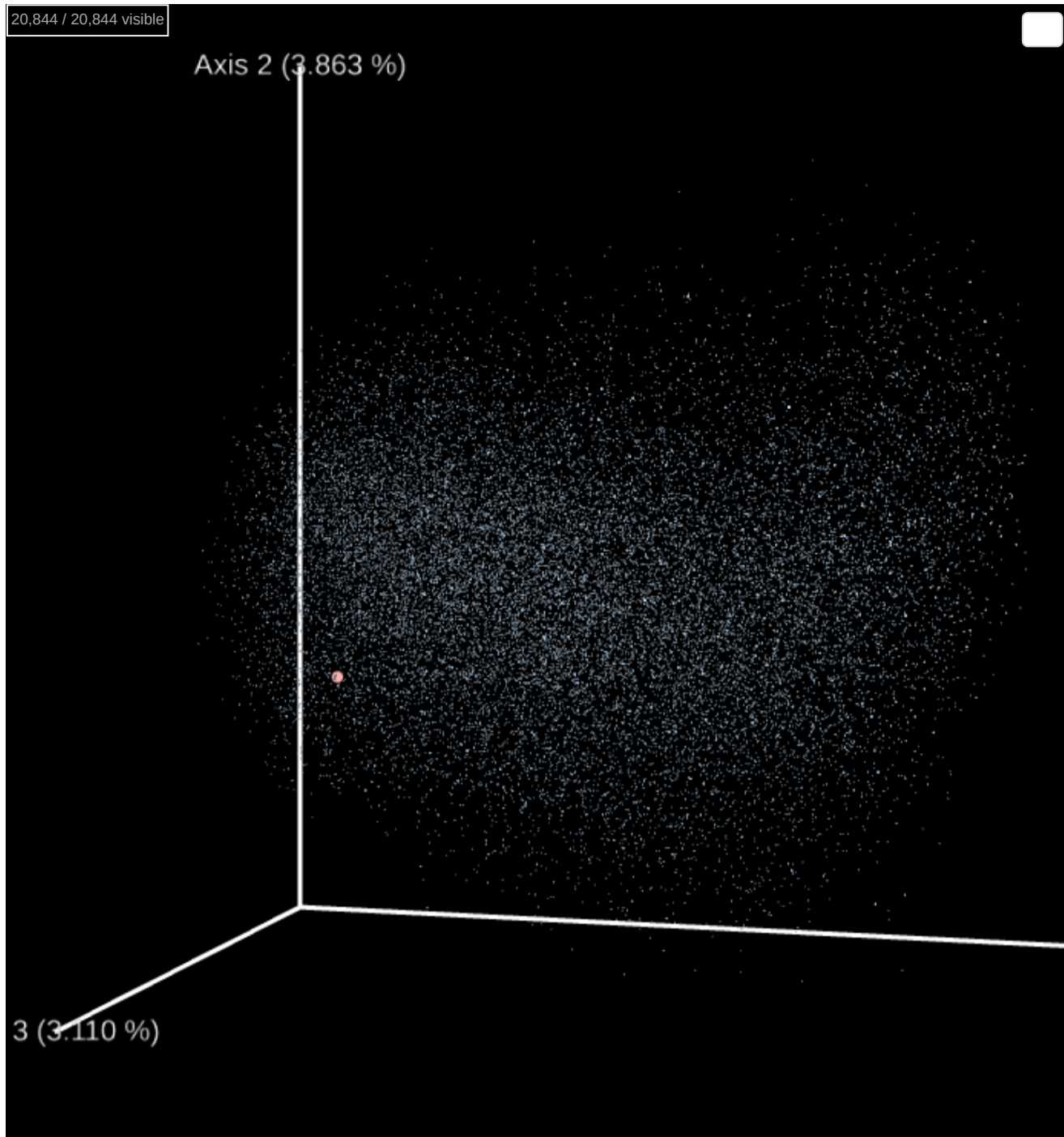
Here, we're providing a measure of the diversity of your sample, and how it compares to the diversities of all of the same type of samples in The Microsetta Initiative. There are many ways to calculate diversity. For instance, you could compute a diversity value by counting the number of unique organisms observed (i.e., the sample "richness"). Or, you might be interested in weighting the calculation by the relative abundance of the organisms (i.e., the sample "evenness"). The metric we're computing here is called Faith's Phylogenetic Diversity (originally defined [here](#)). Faith's Phylogenetic Diversity computes the "richness" of your sample as the amount of evolutionary breadth represented by your sample. The way we compute alpha diversity is also through [QIIME 2](#), and more information on it can be found in the alpha and beta diversity [sections](#) of the QIIME 2 tutorial.



## Beta Diversity

Here we display how your sample fits in among the other samples of The Microsetta Initiative in terms of shared microbes. There are many ways to calculate beta diversity, differing in how to weight the distance between any two microbes. We take evolutionary distance into account with the metric displayed here, known as Unweighted Unifrac. You can find an overview of this metric [here](#) or better understand its derivation [here](#). This computation is performed with [QIIME 2](#), and more information on it can be found in the alpha and beta diversity [sections](#) of the QIIME 2 tutorial.

20,844 / 20,844 visible



Color Visibility Opacity Scale Axes

Animations

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We will periodically update this site with minor revisions; we apologize if you encounter any temporary inconveniences.

Questions? Check out our [FAQ!](#)

Stuck? Please contact [microsetta@ucsd.edu](mailto:microsetta@ucsd.edu) for help.

# Robert Stehlin

## What is in your sample?

The table below shows the relative abundances of all of the organisms we observed in your sample. To produce this, we took the DNA sequences from your sample, and compared them against publicly available annotated reference databases. In some cases, a sequence may uniquely match a database record, in other cases a sequence may match many different records. To handle the uncertainty that can arise, we rely on a well used and publicly available microbiome software package called [QIIME 2](#). The exact approach taken is highlighted in the main tutorial on [feature-classification](#).

Show  entries

Search:

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0011	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0011	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0011	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0010	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Sutterella
0.0010	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0010	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales		
0.0010	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
0.0009	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0009	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0009	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0009	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0009	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0009	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0008	Bacteria	Tenericutes	Mollicutes	RF39		
0.0008	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Moryella
0.0007	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.0007	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
0.0007	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0007	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0007	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
0.0007	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira
0.0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	



Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Oribacterium
0.0006	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
0.0006	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0005	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Slackia
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Dialister
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0005	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Oxalobacter
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0005	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	
0.0005	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0004	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0004	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Adlercreutzia
0.0004	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	
0.0004	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Odoribacteraceae]	Odoribacter
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0004	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	Holdemania
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
0.0004	Bacteria					
0.0004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0003	Bacteria	Firmicutes				
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Shuttleworthia
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0003	Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae	
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0003	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	
0.0003	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0002	Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	Clostridium
0.0002	Bacteria	Tenericutes	Mollicutes	RF39		
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	
0.0002	Bacteria	Cyanobacteria	4C0d-2	YS2		
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0002	Bacteria	Firmicutes				
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0002	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0002	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0002	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Anaerotruncus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Dehalobacteriaceae	Dehalobacterium
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0001	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0001	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira



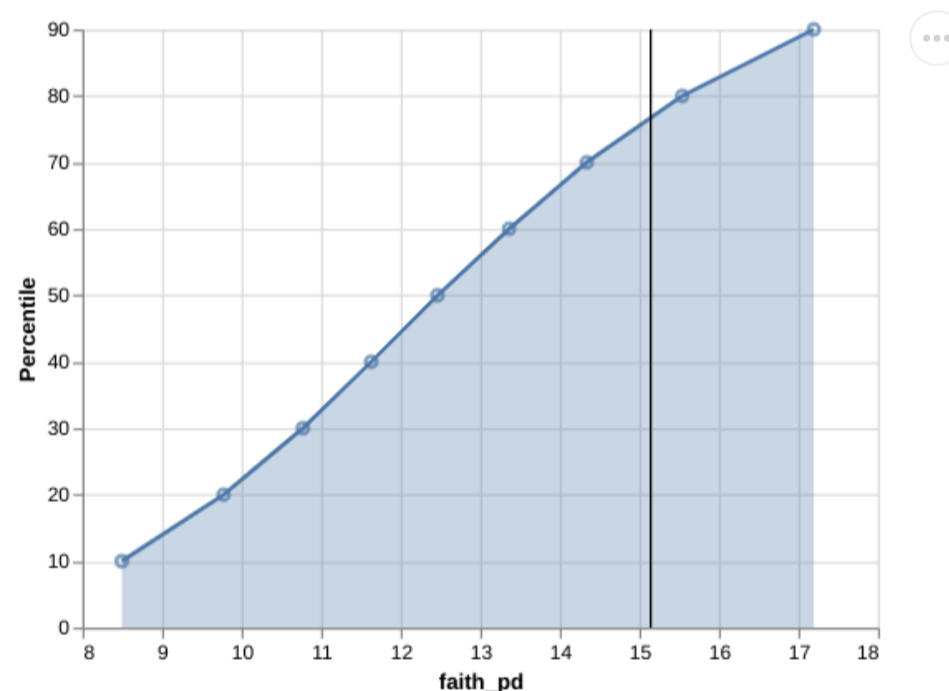
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0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		

Showing 101 to 200 of 224 entries

Previous 1 **2** 3 Next

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## Beta Diversity

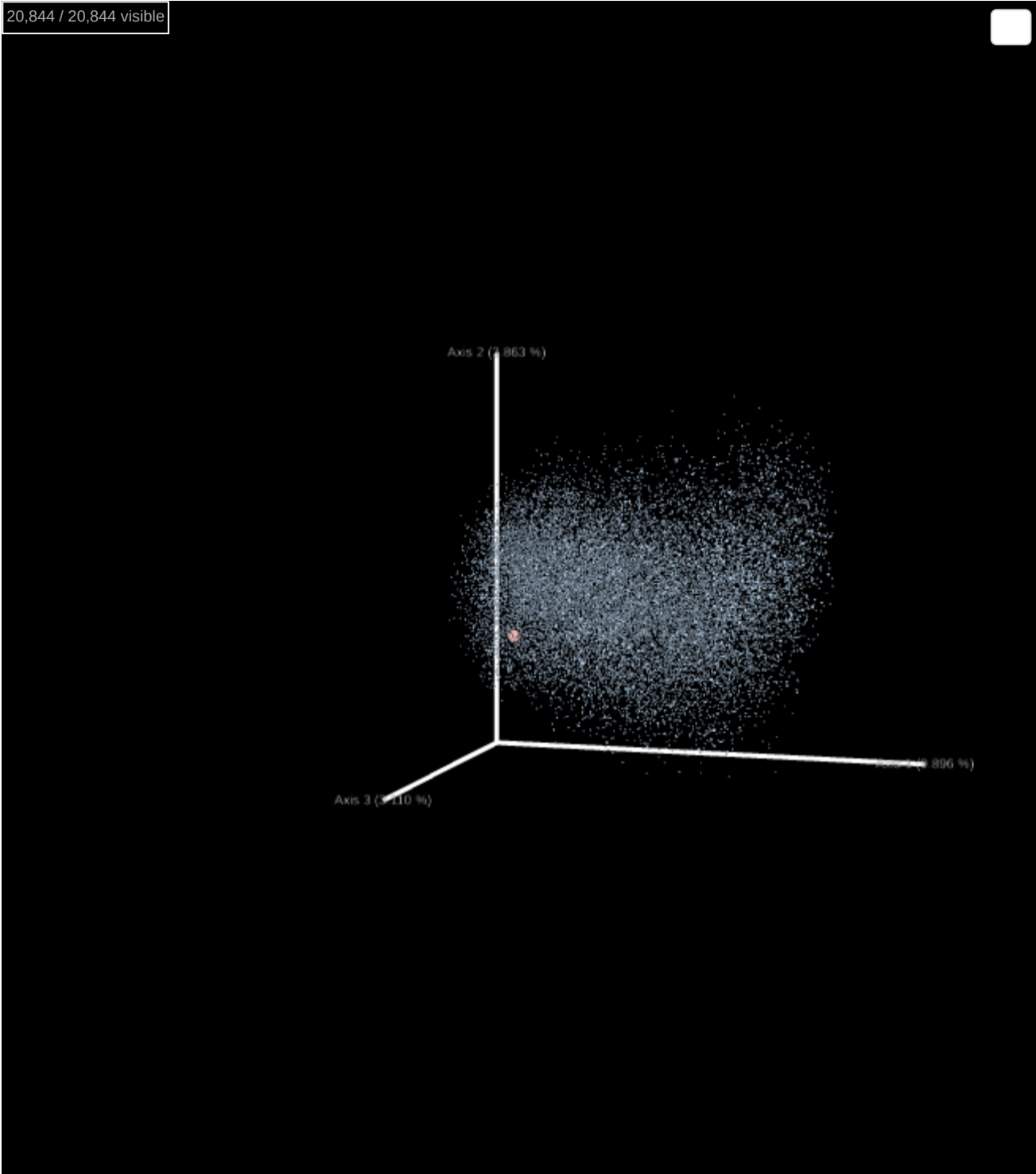
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scatter : My Data

Pastel1

Search for a value ...

- Me
- Not Me



Questions? Check out our [FAQ!](#)

Stuck? Please contact [microsetta@ucsd.edu](mailto:microsetta@ucsd.edu) for help.

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Search:

Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	
0.0001	Bacteria	Proteobacteria	Alphaproteobacteria	RF32		
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	
0.0001	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0001	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales		
0.0001	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	[Barnesiellaceae]	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
0.0001	Bacteria	Lentisphaerae	[Lentisphaeria]	Victivallales	Victivallaceae	
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
0.0001	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira

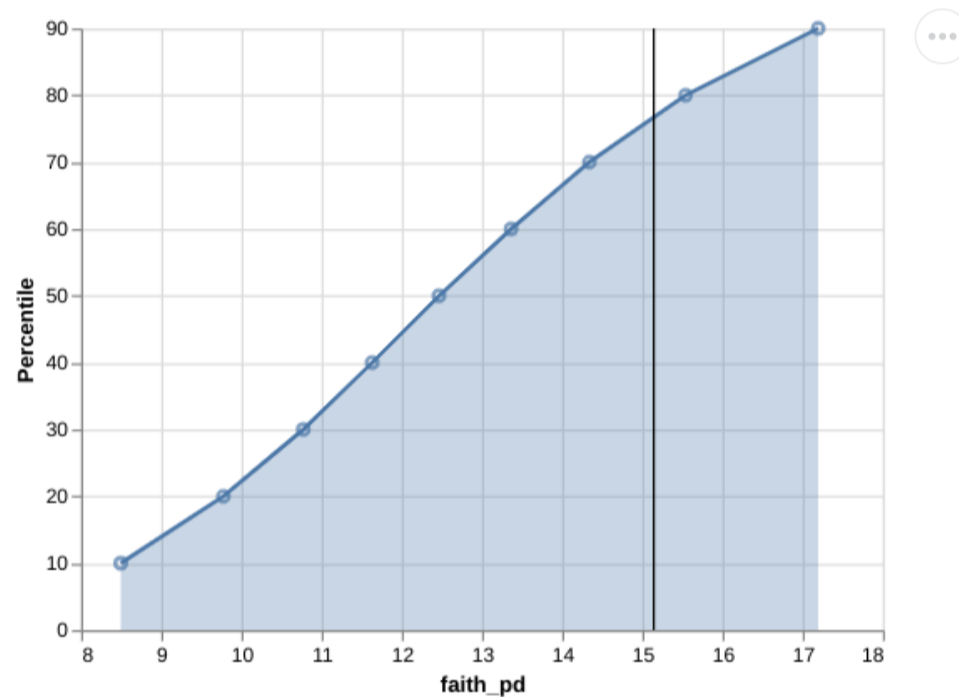
Relative Abundance	Kingdom	Phylum	Class	Order	Family	Genus
0.0001	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium

Showing 201 to 224 of 224 entries

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## Alpha Diversity

Here, we're providing a measure of the diversity of your sample, and how it compares to the diversities of all of the same type of samples in The Microsetta Initiative. There are many ways to calculate diversity. For instance, you could compute a diversity value by counting the number of unique organisms observed (i.e., the sample "richness"). Or, you might be interested in weighting the calculation by the relative abundance of the organisms (i.e., the sample "evenness"). The metric we're computing here is called Faith's Phylogenetic Diversity (originally defined [here](#)). Faith's Phylogenetic Diversity computes the "richness" of your sample as the amount of evolutionary breadth represented by your sample. The way we compute alpha diversity is also through [QIIME 2](#), and more information on it can be found in the alpha and beta diversity [sections](#) of the QIIME 2 tutorial.



## Beta Diversity

Here we display how your sample fits in among the other samples of The Microsetta Initiative in terms of shared microbes. There are many ways to calculate beta diversity, differing in how to weight the distance between any two microbes. We take evolutionary distance into account with the metric displayed here, known as Unweighted Unifrac. You can find an overview of this metric [here](#) or better understand its derivation [here](#). This computation is performed with [QIIME 2](#), and more information on it can be found in the alpha and beta diversity [sections](#) of the QIIME 2 tutorial.

20,844 / 20,844 visible

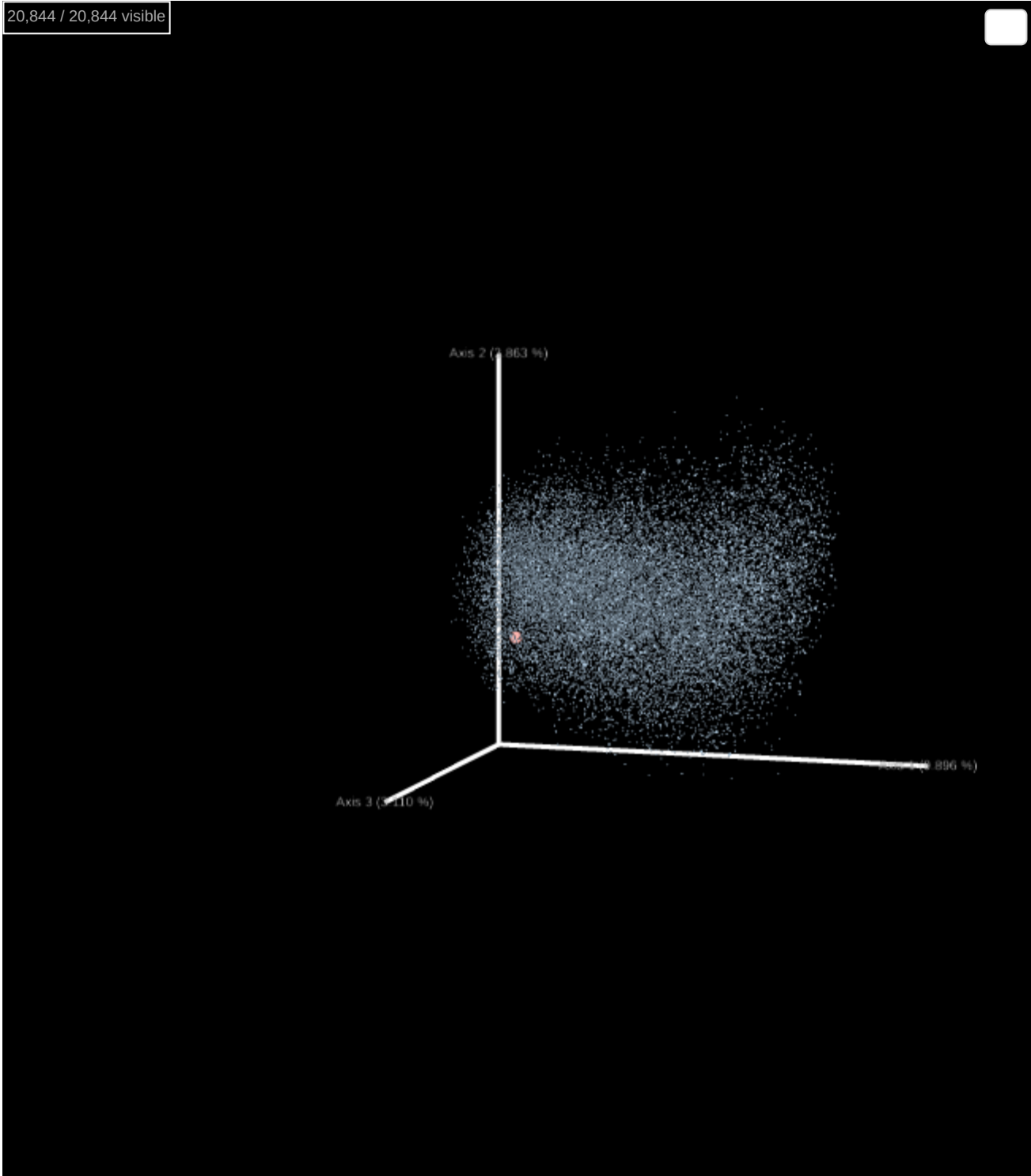
Color Visibility Opacity Scale Axes Animations

scatter : My Data

Pastel1

Search for a value ...

- Me
- Not Me



We will periodically update this site with minor revisions; we apologize if you encounter any temporary inconveniences.

Questions? Check out our [FAQ!](#)

Stuck? Please contact [microsetta@ucsd.edu](mailto:microsetta@ucsd.edu) for help.