Clinical demo dataset - FMT

Fecal Microbiome Transplants
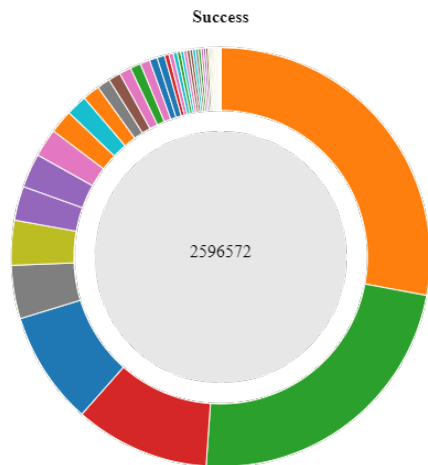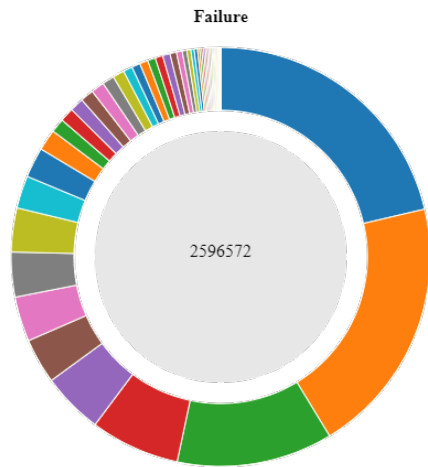
BIOMÉRIEUX

For clinical pathogens

QC Step	S1	S2	S3	S4	S5	S6
Basic Statistics	PASS	PASS	PASS	PASS	PASS	PASS
Per Base Sequence Quality	PASS	PASS	PASS	PASS	PASS	PASS
Per Sequence Quality Scores	PASS	PASS	PASS	PASS	PASS	PASS
Per BaseN Content	PASS	PASS	PASS	PASS	PASS	PASS
Adapter Content	PASS	PASS	PASS	PASS	PASS	PASS

Abundance by group

Click on a donut slice to display abundance by sample.
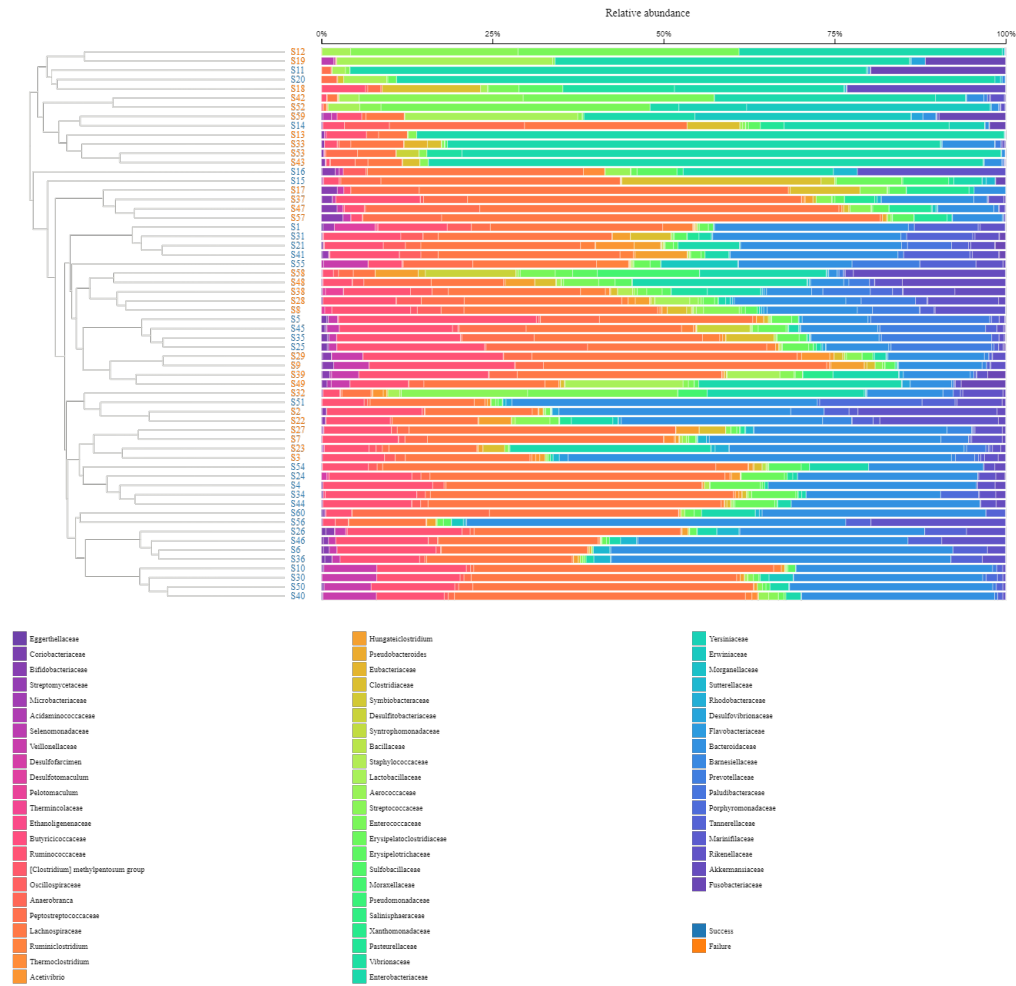
Failure

2596572

Success

2596572

Abundance view for each group composing the "FMT status group" metadata for every "family level" taxa. The bar plots on the right show the normalized counts for each sample in each group.

Fusobacteriaceae	Moraxellaceae	Oscillospiraceae
Akkermansiaceae	Sulfobacillaceae	[Clostridium] methylpentosum group
Rikenellaceae	Erysipelotrichaceae	Ruminococcaceae
Marinifilaceae	Erysipelatoclostridiaceae	Butyricicoccaceae
Tannerellaceae	Enterococcaceae	Ethanoligenenaceae
Porphyromonadaceae	Streptococcaceae	Thermincolaceae
Paludibacteraceae	Aerococcaceae	Pelotomaculum
Prevotellaceae	Lactobacillaceae	Desulfotomaculum
Barnesiellaceae	Staphylococcaceae	Desulfofarcimen
Bacteroidaceae	Bacillaceae	Veillonellaceae
Flavobacteriaceae	Syntrophomonadaceae	Selenomonadaceae
Desulfovibrionaceae	Desulfitobacteriaceae	Acidaminococcaceae
Rhodobacteraceae	Symbiobacteraceae	Microbacteriaceae
Sutterellaceae	Clostridiaceae	Streptomycetaceae
Morganellaceae	Eubacteriaceae	Bifidobacteriaceae
Erwiniaceae	Pseudobacteroides	Coriobacteriaceae
Yersiniaceae	Hungateiclostridium	Eggerthellaceae
Enterobacteriaceae	Acetivibrio	
Vibrionaceae	Thermoclostridium	
Pasteurellaceae	Ruminiclostridium	Failure
Xanthomonadaceae	Lachnospiraceae	Success
Salinisphaeraceae	Peptostreptococcaceae	
Pseudomonadaceae	Anaerobranca	

Stacked bar chart showing relative abundance profiles at "family level" for every selected samples. Sample labels are colored by group composing the "FMT status group" metadata.

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Sample clustering

Eggerthellaceae	Hungateiclostridium	Yersiniaceae
Coriobacteriaceae	Pseudobacteroides	Erwiniaceae
Bifidobacteriaceae	Eubacteriaceae	Morganellaceae
Streptomycetaceae	Clostridiaceae	Sutterellaceae
Microbacteriaceae	Symbiobacteraceae	Rhodobacteraceae
Acidaminococcaceae	Desulfitobacteriaceae	Desulfovibrionaceae
Selenomonadaceae	Syntrophomonadaceae	Flavobacteriaceae
Veillonellaceae	Bacillaceae	Bacteroidaceae
Desulfofarcimen	Staphylococcaceae	Barnesiellaceae
Desulfotomaculum	Lactobacillaceae	Prevotellaceae
Pelotomaculum	Aerococcaceae	Paludibacteraceae
Thermincolaceae	Streptococcaceae	Porphyromonadaceae
Ethanoligenenaceae	Enterococcaceae	Tannerellaceae
Butyricicoccaceae	Erysipelatoclostridiaceae	Marinifilaceae
Ruminococcaceae	Erysipelotrichaceae	Rikenellaceae
[Clostridium] methylpentosum group	Sulfobacillaceae	Akkermansiaceae
Oscillospiraceae	Moraxellaceae	Fusobacteriaceae
Anaerobranca	Pseudomonadaceae	
Peptostreptococcaceae	Salinisphaeraceae	
Lachnospiraceae	Xanthomonadaceae	Success
Ruminiclostridium	Pasteurellaceae	Failure
Thermoclostridium	Vibrionaceae	
Acetivibrio	Enterobacteriaceae	

Average-linkage clustering of the Canberra distances between abundances at "family level". Samples are colored by group composing the "FMT status group" metadata. Relative abundance profiles of the corresponding samples are displayed on the right part.

## Alpha diversity, Richness (ACE)

Box plots show the ACE estimated alpha-diversity distribution among groups for the FMT type metadata based on the OTU identified at a 97% similarity level.
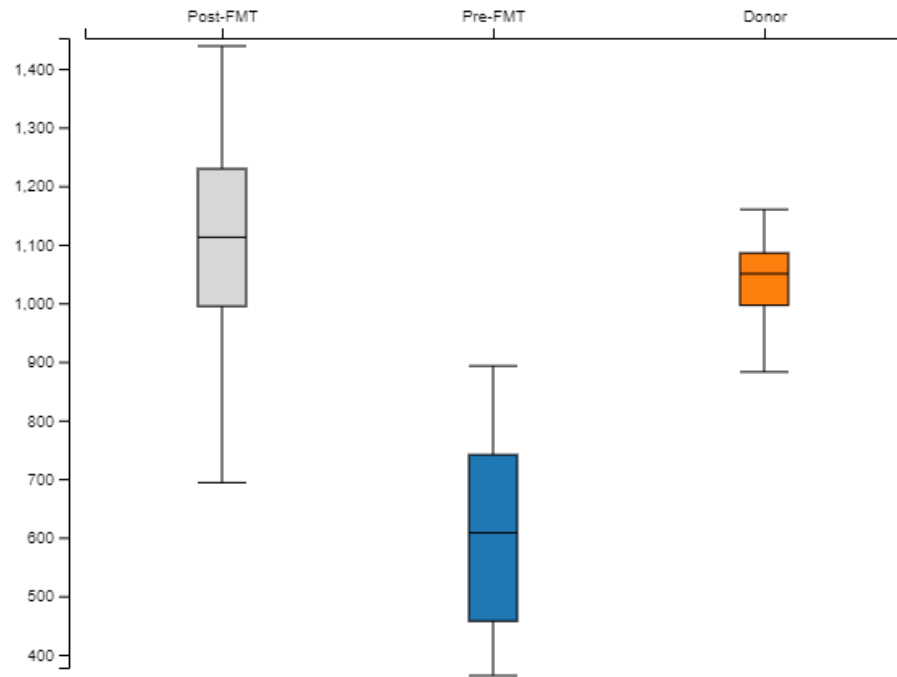
Comparison	P-value	Significance
Donor_vs_PostFMT	9.5143e-2	
Donor_vs_PreFMT	1.3073e-5	***
PostFMT_vs_PreFMT	2.2013e-6	***

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Alpha diversity, Evenness (Shannon index)

Box plots show the Shannon estimated alpha-diversity distribution among groups for the FMT type metadata based on the OTU identified at a 97% similarity level.
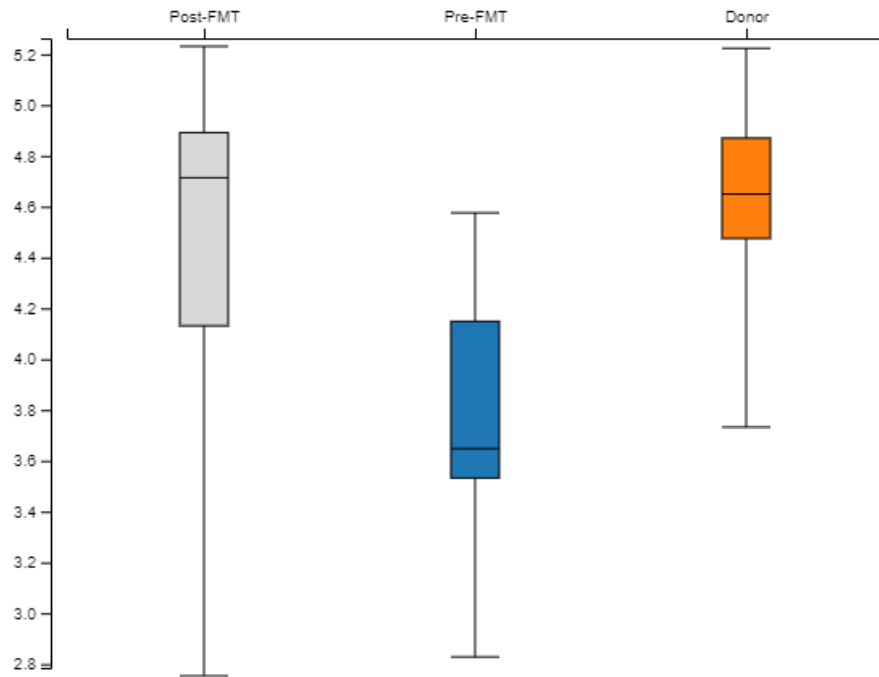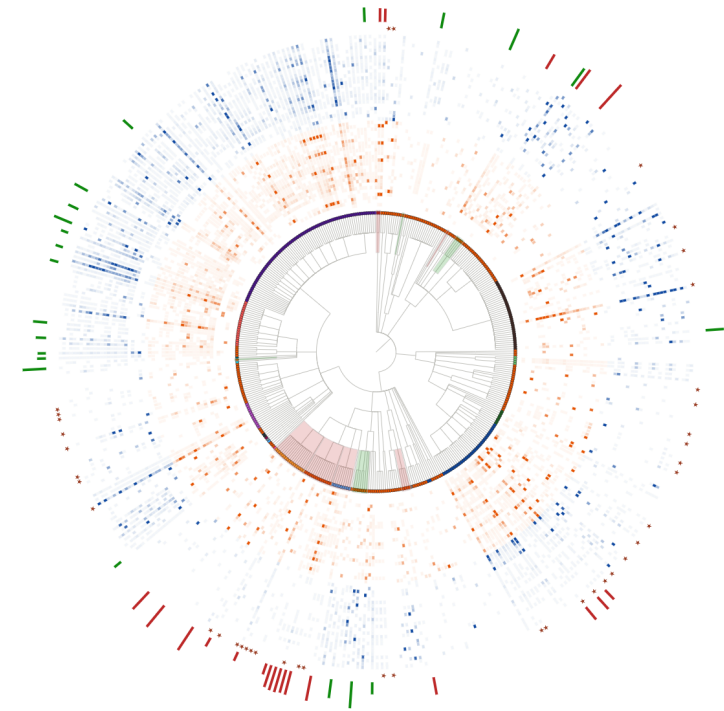
Comparison	P-value	Significance
Donor_vs_PostFMT	2.4888e-1	
Donor_vs_PreFMT	9.6488e-4	***
PostFMT_vs_PreFMT	4.3755e-3	**

Beta diversity, Bray-Curtis dissimilarity (p-value = 0.001)
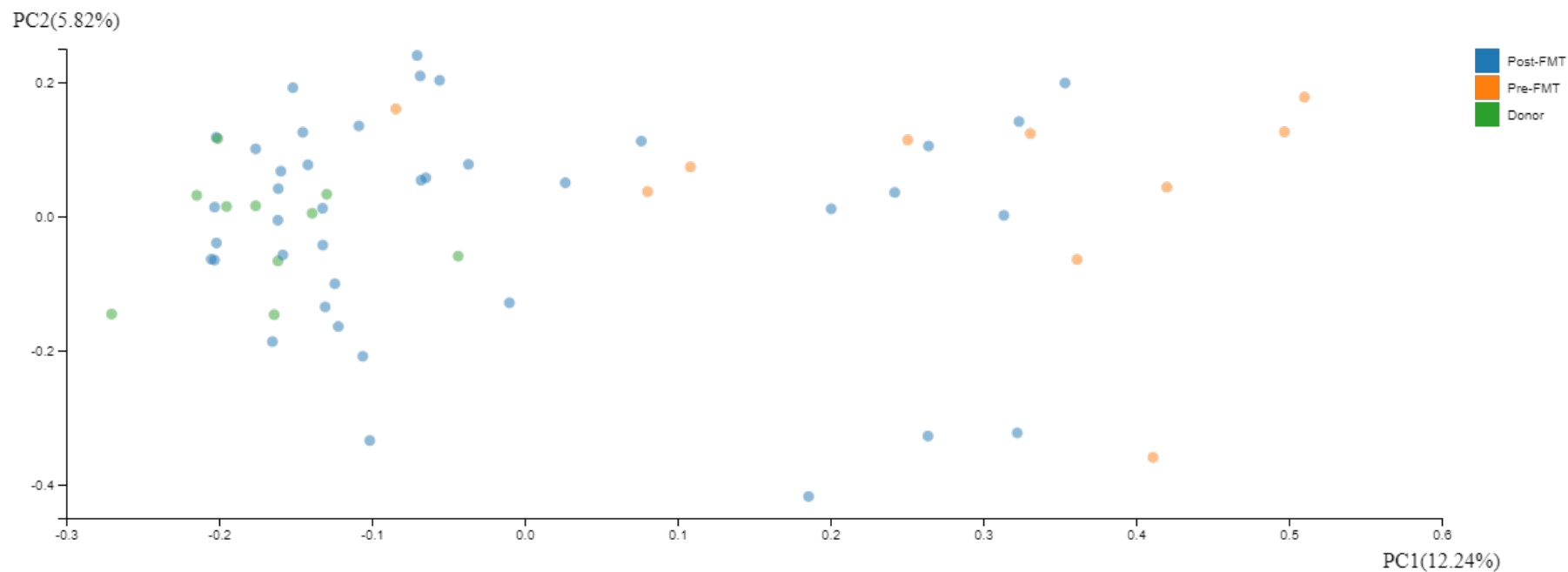
Principal Coordinates Analysis (PCoA) visualization of the beta diversity (estimated using the Bray-Curtis distance). Beta diversity was calculated based on the OTU identified at a 97% similarity level. Each dot represents a sample and is colored by group composing the FMT type metadata. The distance between the dots represents the similarity of the samples. The closer together, the more similar the diversity between the samples.
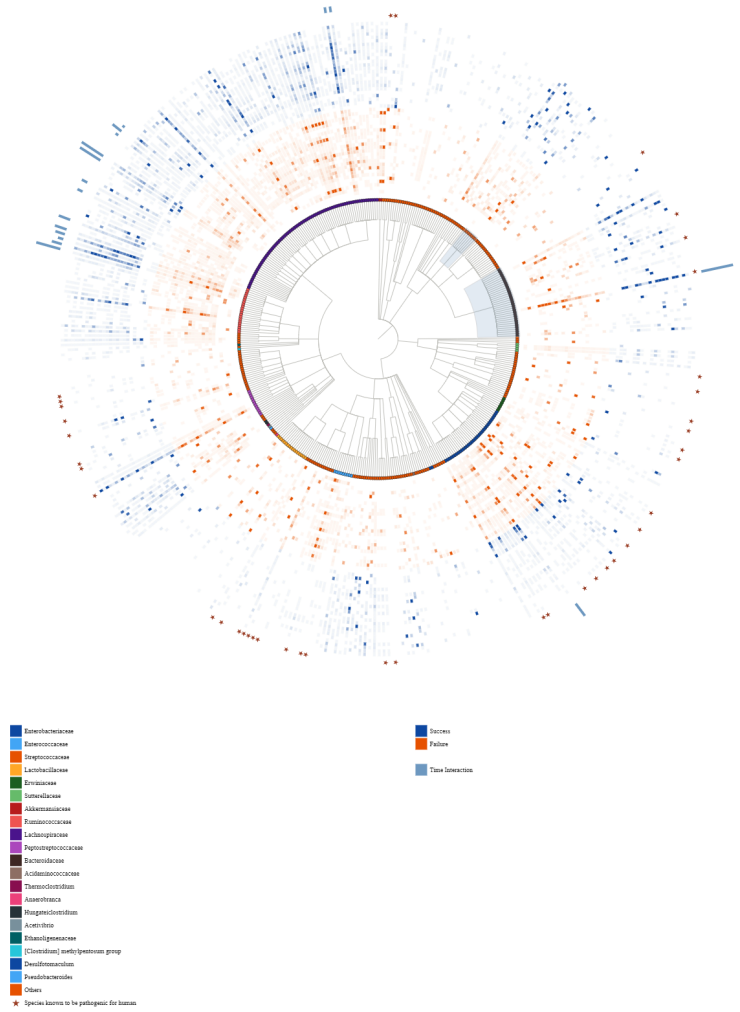
Circular dendrogram

Enterobacteriaceae
Enterococcaceae
Streptococcaceae
Lactobacillaceae
Erwiniaceae
Sutterellaceae
Akkermansiaceae
Ruminococcaceae
Lachnospiraceae
Peptostreptococcaceae
Bacteroidaceae
Acidaminococcaceae
Thermoclostridium
Anaerobranca
Hungateiclostridium
Acetivibrio
Ethanoligenenaceae
[Clostridium] methylpentosum group
Desulfotomaculum
Pseudobacteroides
Others

★ Species known to be pathogenic for human

Success
Failure

Over-detected
Under-detected

Tree of organisms present in all samples. The color intensity of external cells corresponds to the abundance of taxa in a sample (heatmap). There is one circle of cells per sample, colored by group composing the FMT status group metadata. Leaves are colored by "family level". Stars indicate potential pathogens. In case of successful differential abundance analysis comparing "Success vs Failure", external bars show the log(FC) of significantly different abundances at the level of the leaves (no matter the taxonomic level) and inside pie layers show taxa having significantly different abundances for the "family level".

Circular dendrogram

Enterobacteriaceae
Enterococcaceae
Streptococcaceae
Lactobacillaceae
Erwiniaceae
Sutterellaceae
Akkermansiaceae
Ruminococcaceae
Lachnospiraceae
Peptostreptococcaceae
Bacteroidaceae
Acidaminococcaceae
Thermoclostridium
Anaerobranca
Hungateiclostridium
Acetivibrio
Ethanoligenenaceae
[Clostridium] methylpentosum group
Desulfitomaculum
Pseudobacteroides
Others
★ Species known to be pathogenic for human

Success
Failure

Time Interaction

Tree of organisms present in all samples. The color intensity of external cells corresponds to the abundance of taxa in a sample (heatmap). There is one circle of cells per sample, colored by group composing the FMT status group metadata. Leaves are colored by "family level". Stars indicate potential pathogens.In case of successful time interaction analysis comparing Success vs Failure, external bars show the interaction log(FC) of significantly different abundances at the level of the leaves (no matter the taxonomic level) and inside pie layers show taxa having significantly different abundances using time interaction for the "family level".

Not for diagnostic use

Bacteroidaceae longitudinal analysis
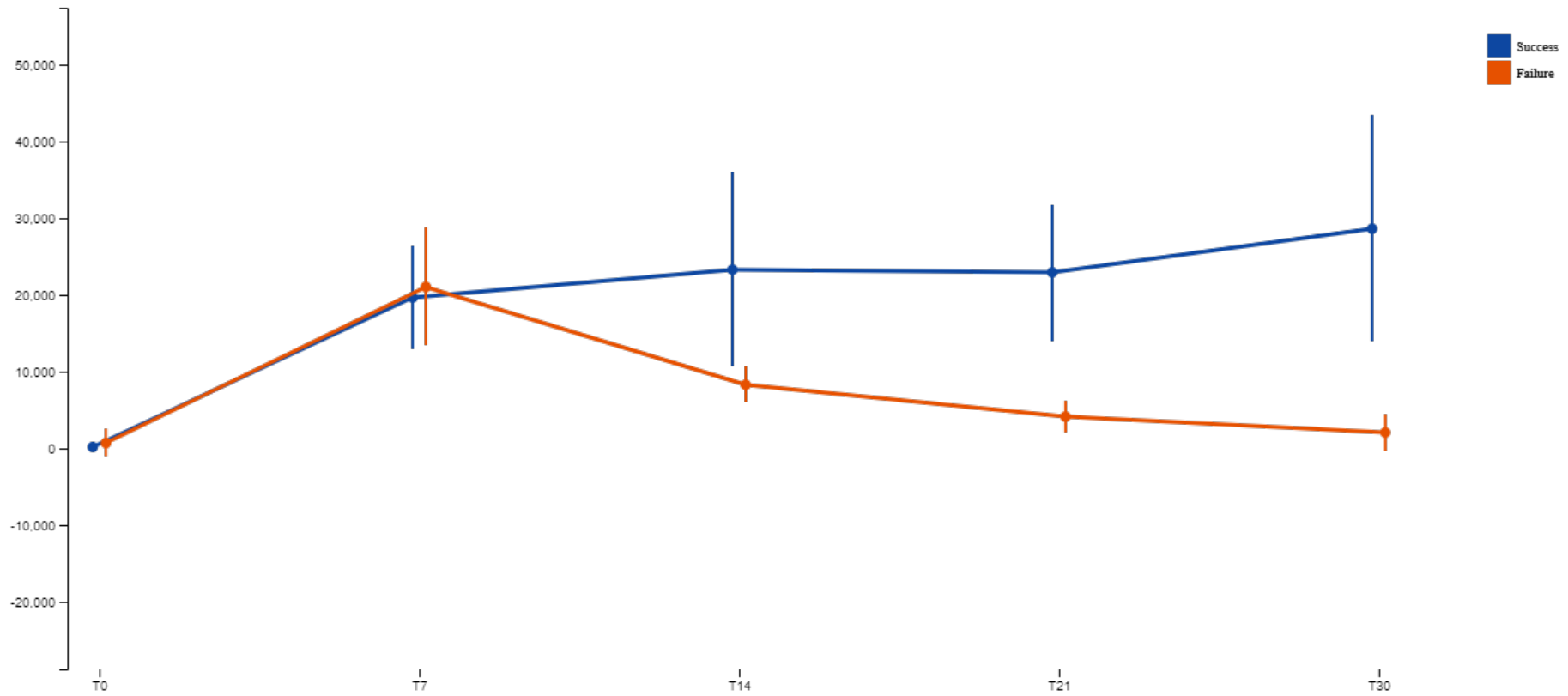
Graph showing the evolution of the abundance (normalized counts) of "Bacteroidaceae" over time, for "Success vs Failure".