

# Trait-based community assembly and succession in the infant gut microbiome: Tables and Figures

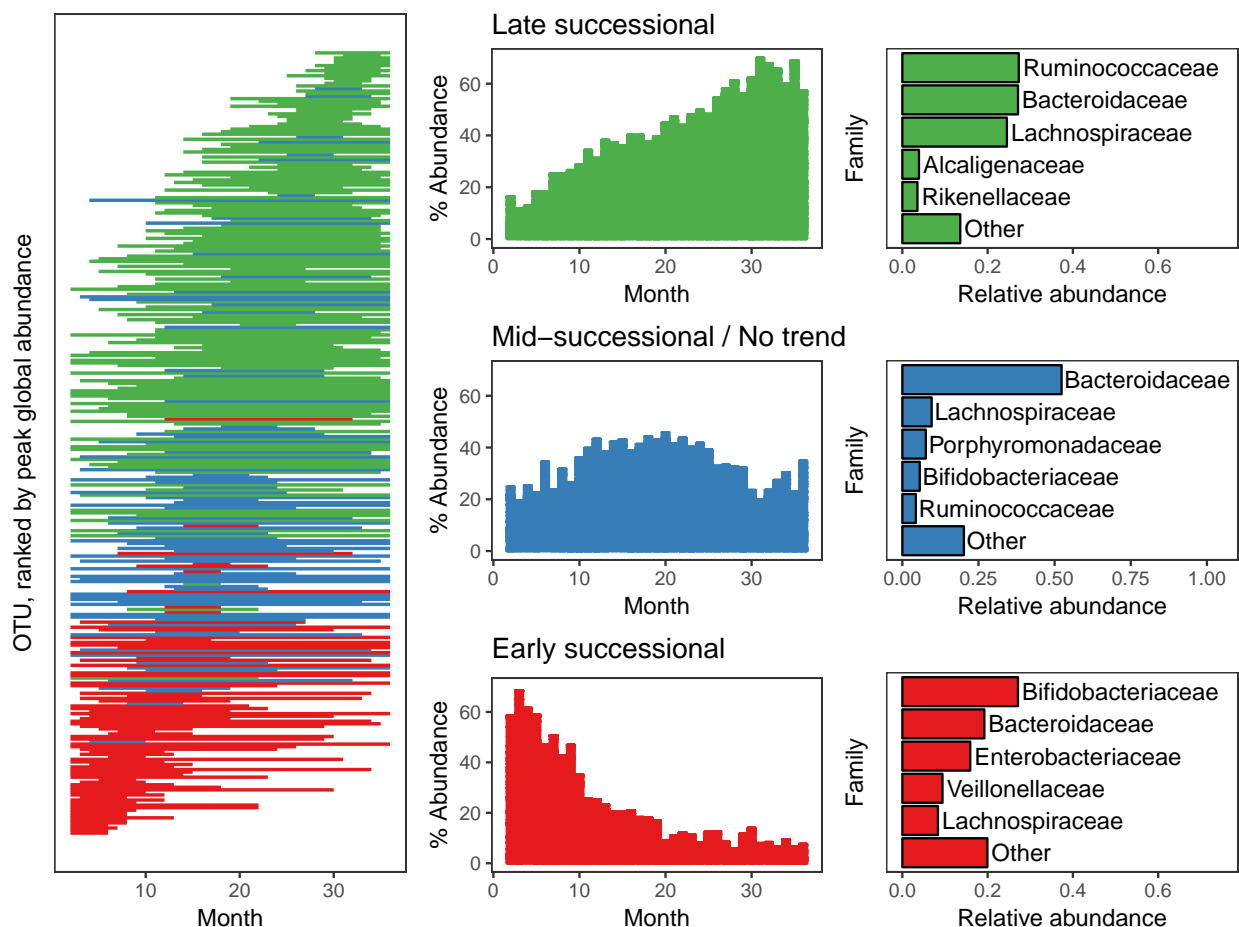
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## Tables and figures

Trait	Sources	Units	Range	Coverage
16S gene copies	PICRUSt, NCBI	No. in genome	1 - 12	0.68
Aggregation	IJSEM	0 or 1	0 - 1	0.34
B vitamins	Magnusdottir et al. 2015	No. pathways in genome	0 - 8	0.65
GC content	IJSEM, BacDive	Percent (%)	27 - 71	0.55
Genes	NCBI	No. in genome	1300 - 6300	0.53
Genome size	NCBI	Mb	1.3 - 6.7	0.53
Gram positive	IJSEM, BacDive	0 or 1	0 - 1	0.33
IgA binding affinity	Palm et al. 2014	$\log ([\text{IgA+}]/[\text{IgA-}] + 1)$	0 - 4.3	0.59
Length	IJSEM, BacDive	$\log (\mu\text{m})$	-0.8 - 2.2	0.31
Motility	IJSEM	0 or 1	0 - 1	0.33
Oxygen tolerance	IJSEM, BacDive	Nominal score (1 - 5)*	1 - 5	0.65
pH optimum	IJSEM, BacDive	pH	4 - 8.3	0.30
Salt optimum	IJSEM, BacDive	g/l	0 - 8	0.25
Sporulation	Browne et al. 2016	Continuous score (0 - 1)	0 - 0.72	0.57
Temperature optimum	IJSEM, BacDive	°C	23 - 40	0.30
Width	IJSEM, BacDive	$\log (\mu\text{m})$	-1 - 1.3	0.33

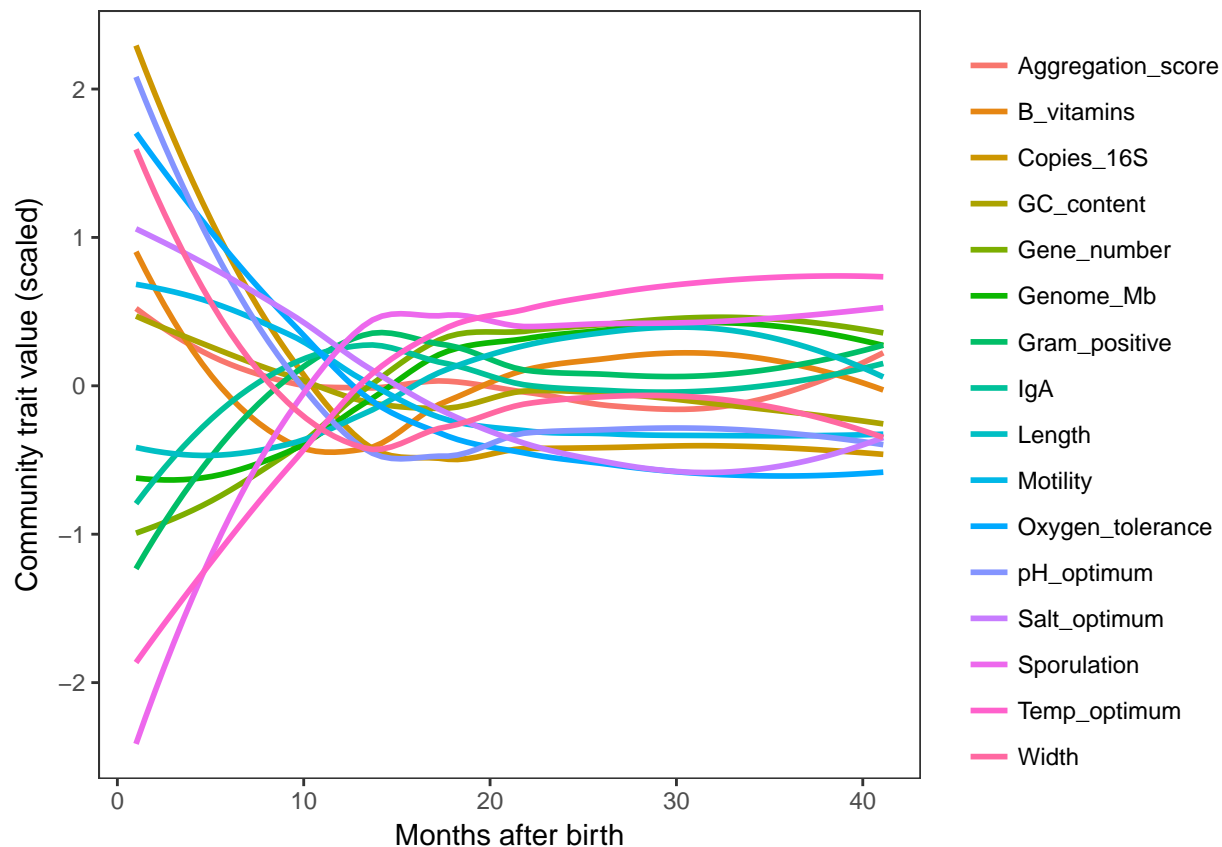
**Table S1.** Sources of trait data. Coverage refers to proportion of sequences with trait information.

\* 1: Anaerobe; 2: Facultative aerobe; 3: Facultative anaerobe; 4: Microaerophile; 5: Obligate aerobe.



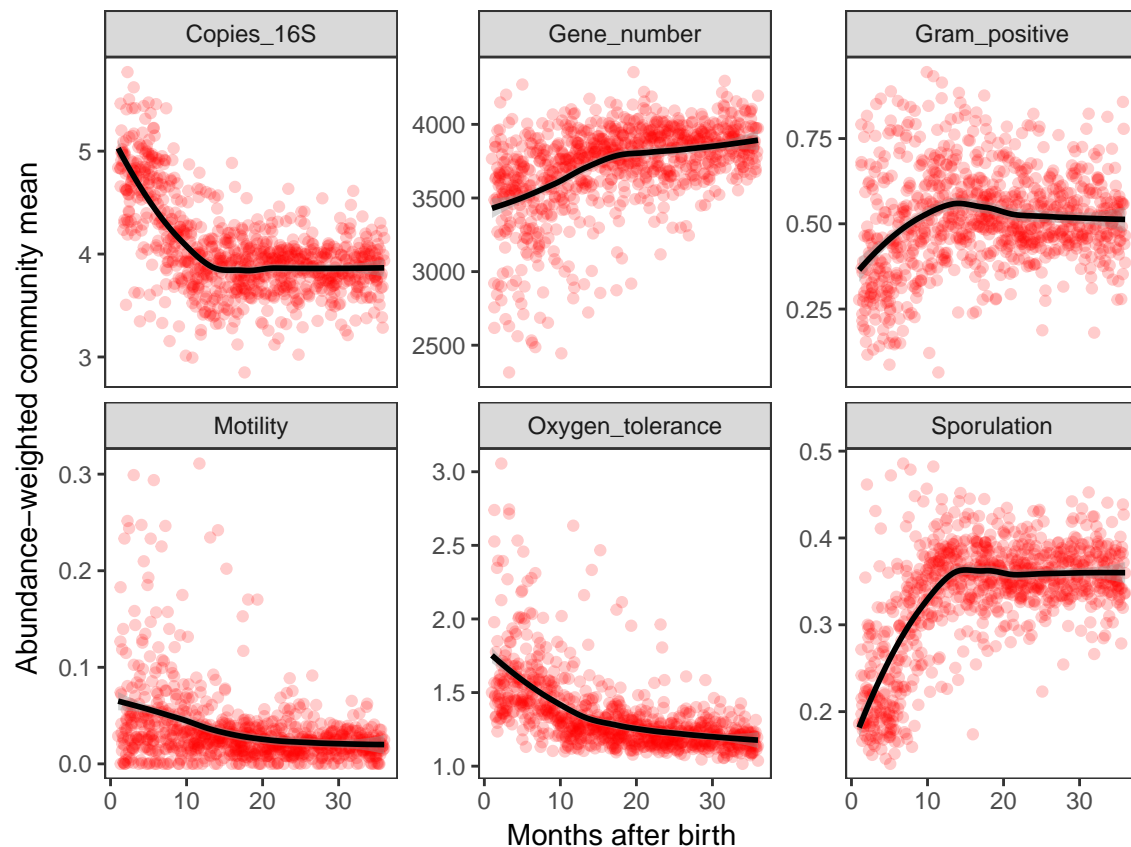
**Figure 1. OTU and family-level abundance patterns over time.**

Successional ranges of taxa (left), ranked by peak global abundance. Colored horizontal lines represent OTUs, and their ranges represent the first and last times their mean abundance surpassed 0.1% across infants. Taxa that never attained 0.1% mean abundance are not shown. OTU colors reflect their successional status. Taxa were categorized as early (red) or late (green) successional if their global abundances trended significantly ( $p < 0.05$ ) negative or positive over time based on linear regression. Center column panels reflect relative abundances across all infants. Right column panels show the top five most abundant families and their relative contributions.



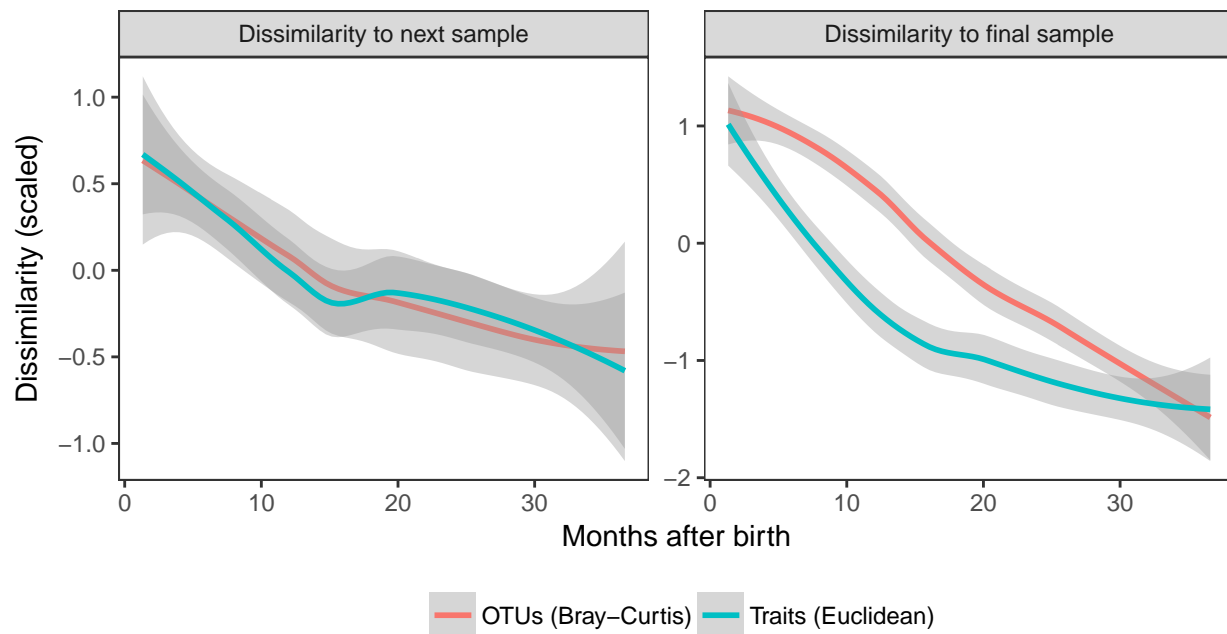
**Figure 2. Shifts in abundance-weighted trait values over time.**

Lines show community weighted mean trait values of gut microbiota over time across all infants. Trait values are scaled and centered to enable plotting on the same axis. Due to limited data, trait means represent only 25% (Salt optimum) to 68% (16S gene copy number) of the total community; for all coverage statistics see Table 1. Note that some traits are correlated, meaning that not each observation is statistically independent.



**Figure 3. Abundance-weighted trait patterns over time.**

Lines show community weighted mean trait values of gut microbiota over time across all infants. Grey shaded areas show 95% confidence intervals. Due to limited trait data, trait means represent only from 33% (Motility) to 68% (16S gene copy number) of the total community. For all trait-based trends see Supplementary Materials; for all coverage statistics see Table 1.



**Figure 4. Taxonomic and trait-based rates of community change within infants.**

Lines show the mean dissimilarity between gut microbiome community samples over infant development, and compare OTU-based composition with trait-based composition. At left, lines show how dissimilarity between subsequent samples generally decreases over time, highlighting the development of a more stable community both in terms of OTUs and traits. At right, lines show dissimilarity between samples and the final community sample for each infant, taken at around 36 months after birth. While both OTU-based and trait-based lines decrease monotonically, illustrating the gradual convergence in composition over early development, trait-based convergence occurs sooner than OTU-based convergence, suggesting that OTU turnover becomes more functionally redundant over time. In all cases, LOESS trendlines are scaled and centered around zero for comparability.

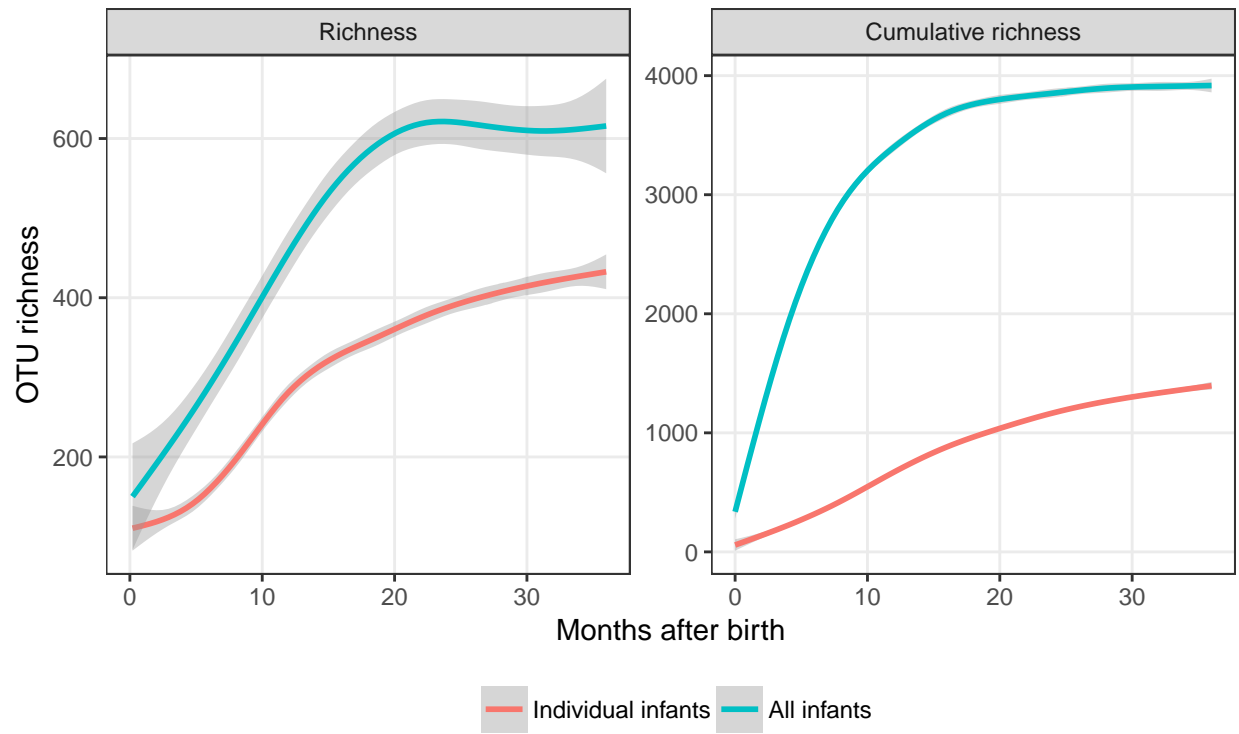
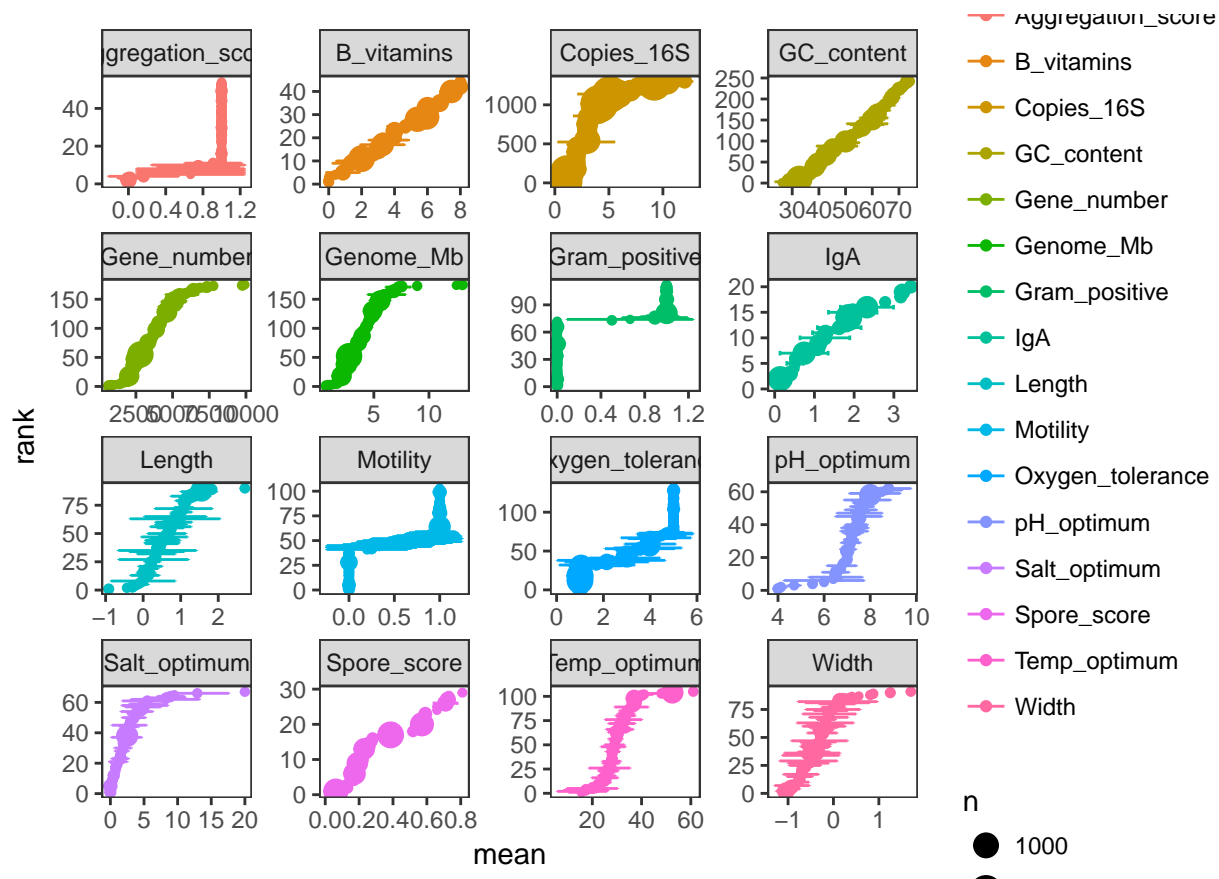
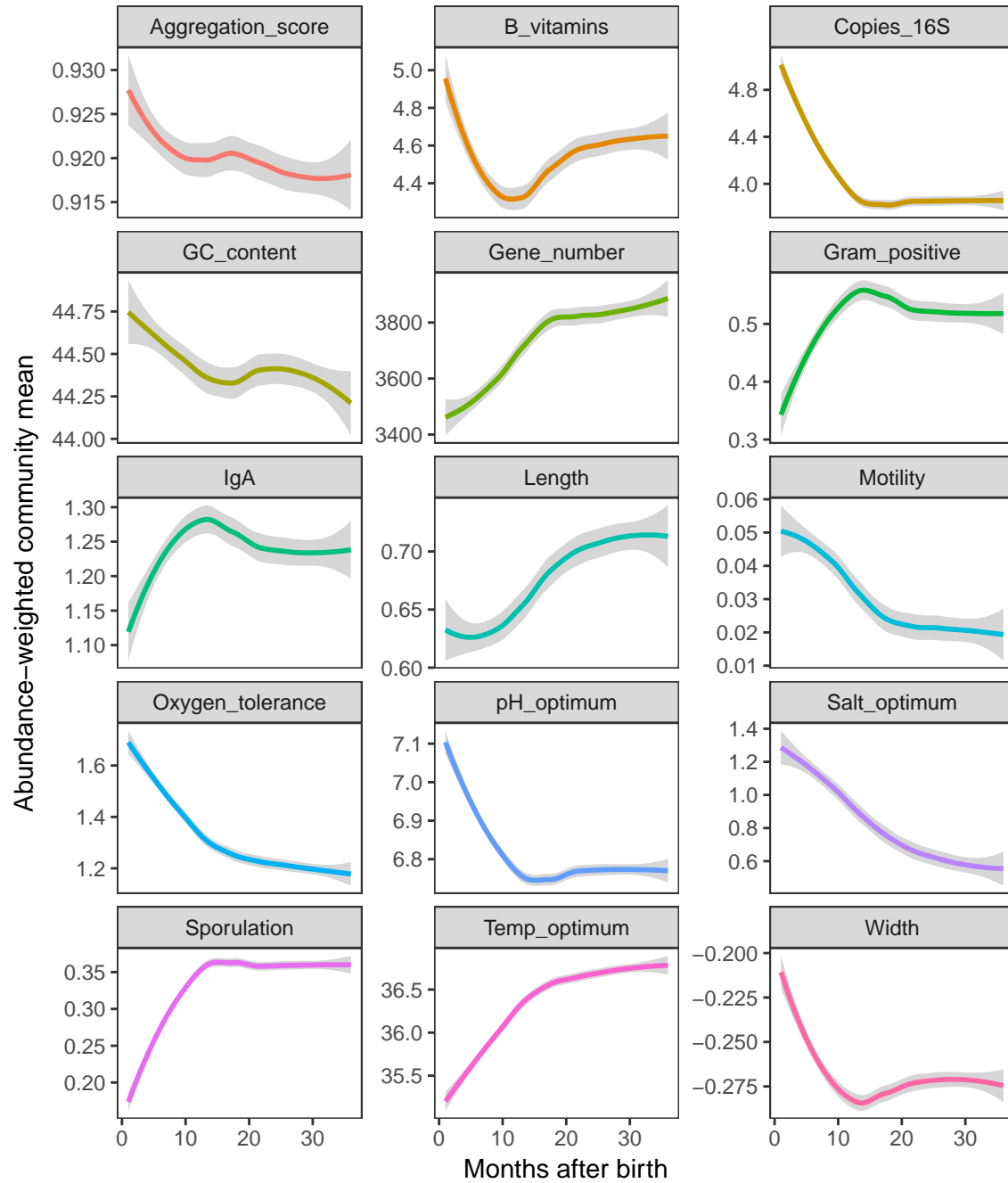


Figure 5. OTU richness in individual infants and across all infants.

# Supplementary figures

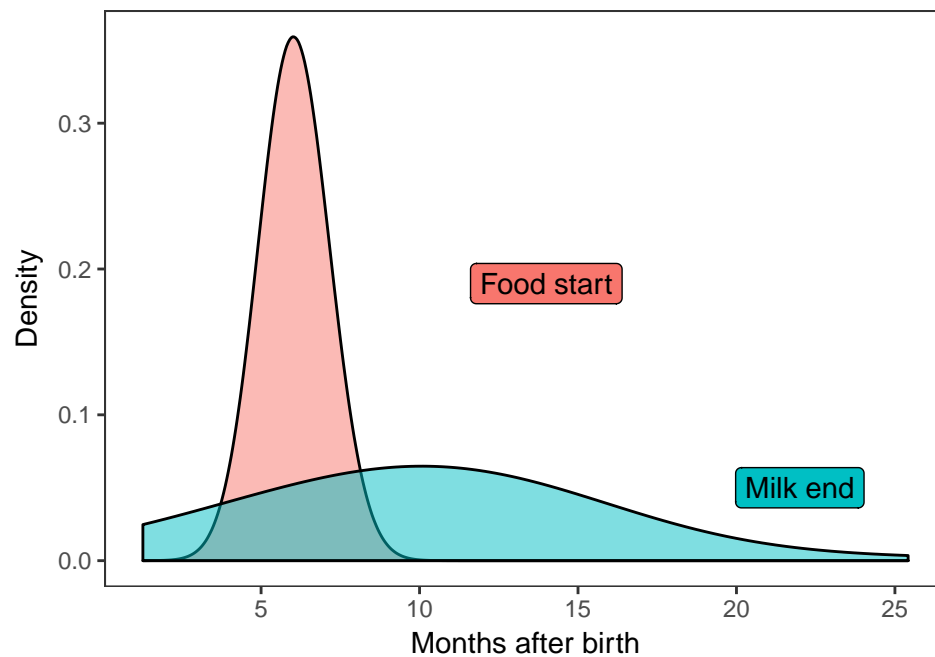






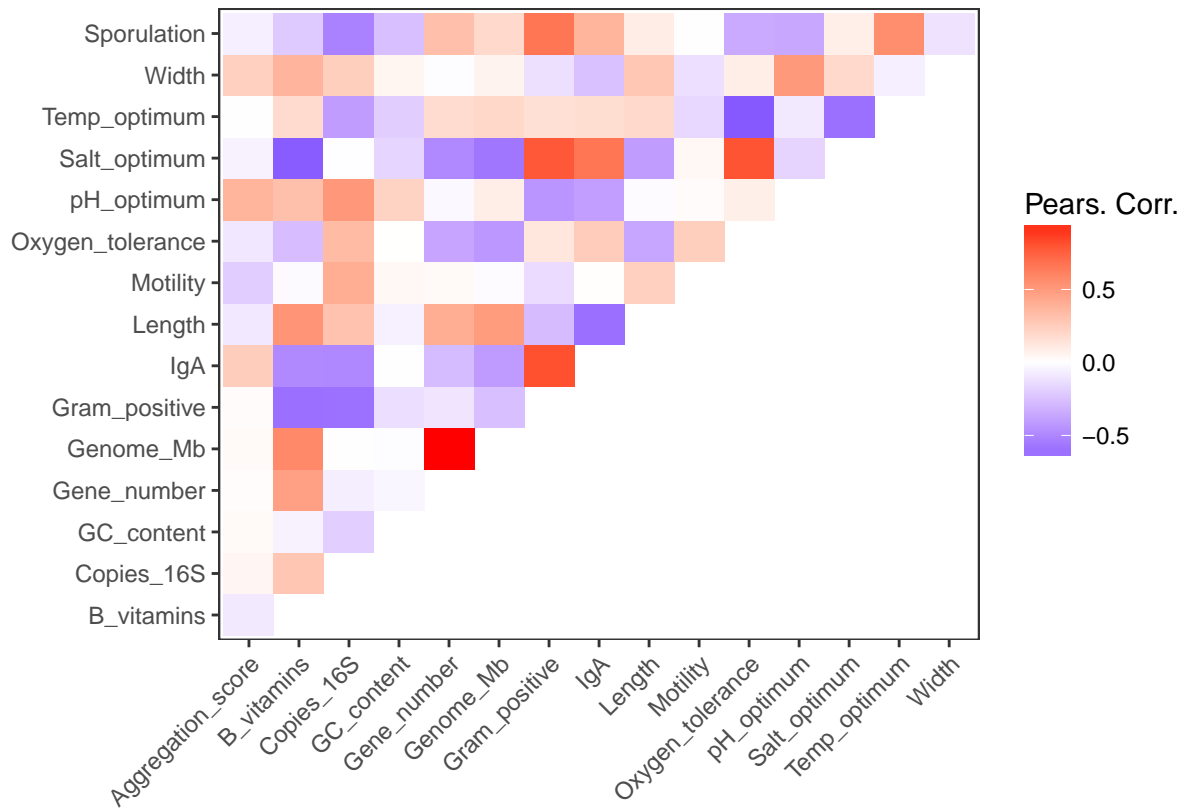
### Abundance-weighted trait patterns over time.

Lines show community weighted mean trait values of gut microbiota over time across all infants. Grey shaded areas show 95% confidence intervals. Due to limited trait data, trait means represent only from 33% (Motility) to 68% (16S gene copy number) of the total community. For all coverage statistics see Table 1.

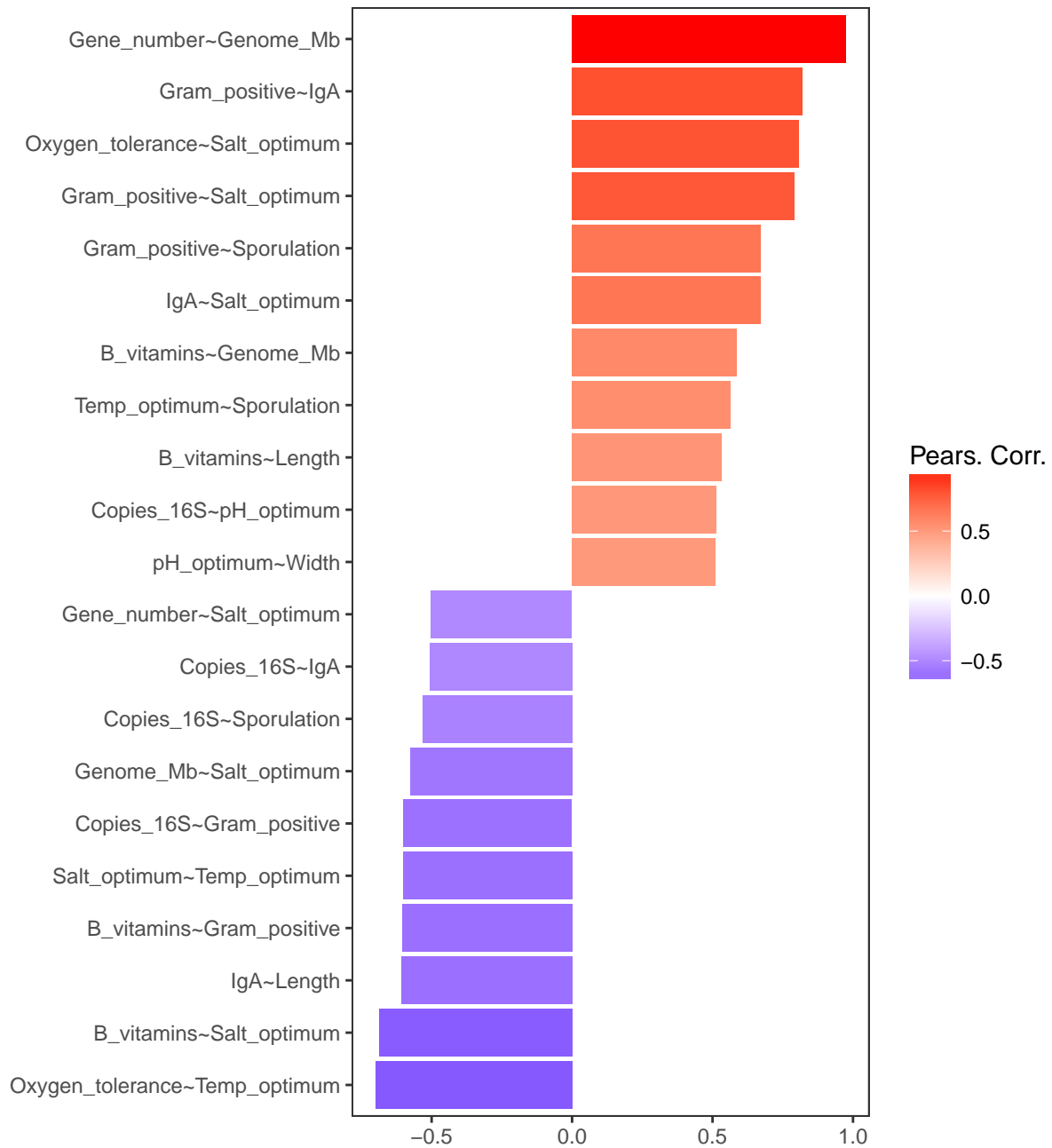


**Density of dietary transition times across infants.**

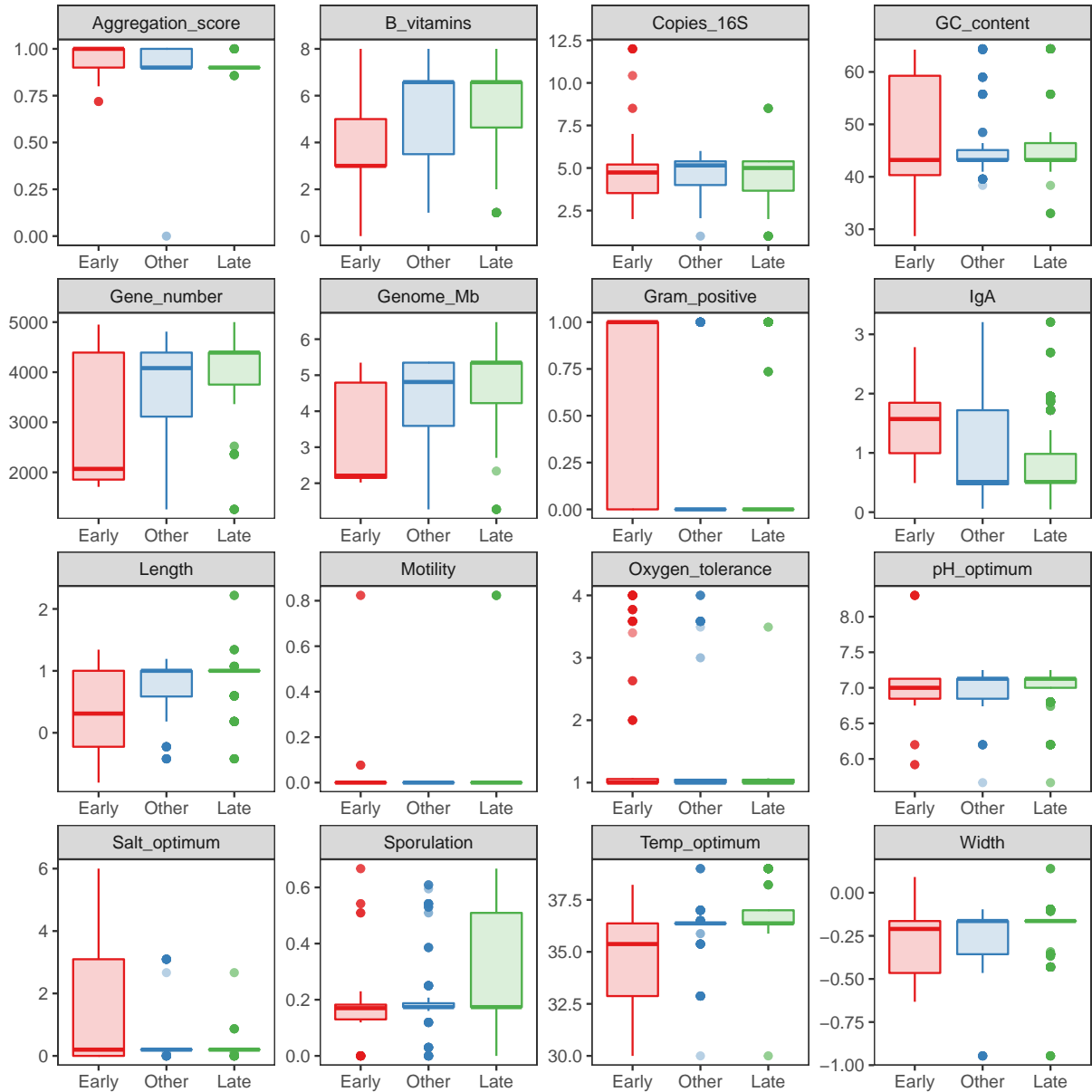
*Note:* For 'Milk', I included both formula and breastmilk.



**Pearson correlation coefficients among traits.**

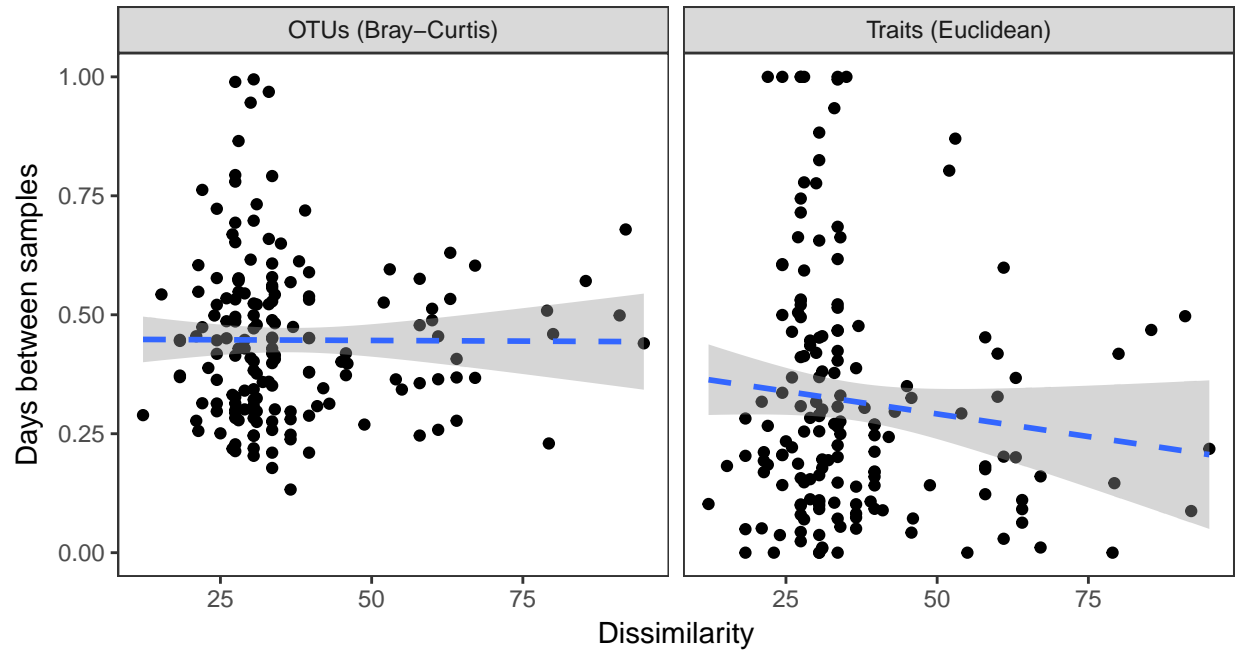


**Ranked pairwise Pearson correlations among traits  $> 0.5$ .**

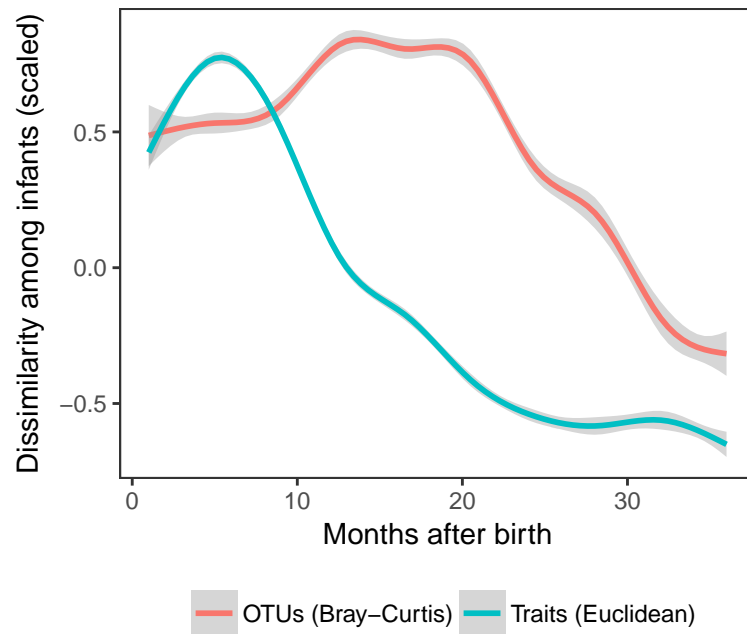


### Trait-based differences among OTUs, grouped by successional stage.

The early and late successional species should, given what we know about trait patterns over time (i.e., my brown bag talk). The interesting aspect is whether the 'Early and persistent' species exhibit different traits. *Note:* this plot does not consider abundances. It is simply a comparison of species traits among the groups. Other than that, it is conceptually similar to the continuous time plots below.



There is no relationship between the number of days between a sample (under 100 days) and the dissimilarity between community composition.

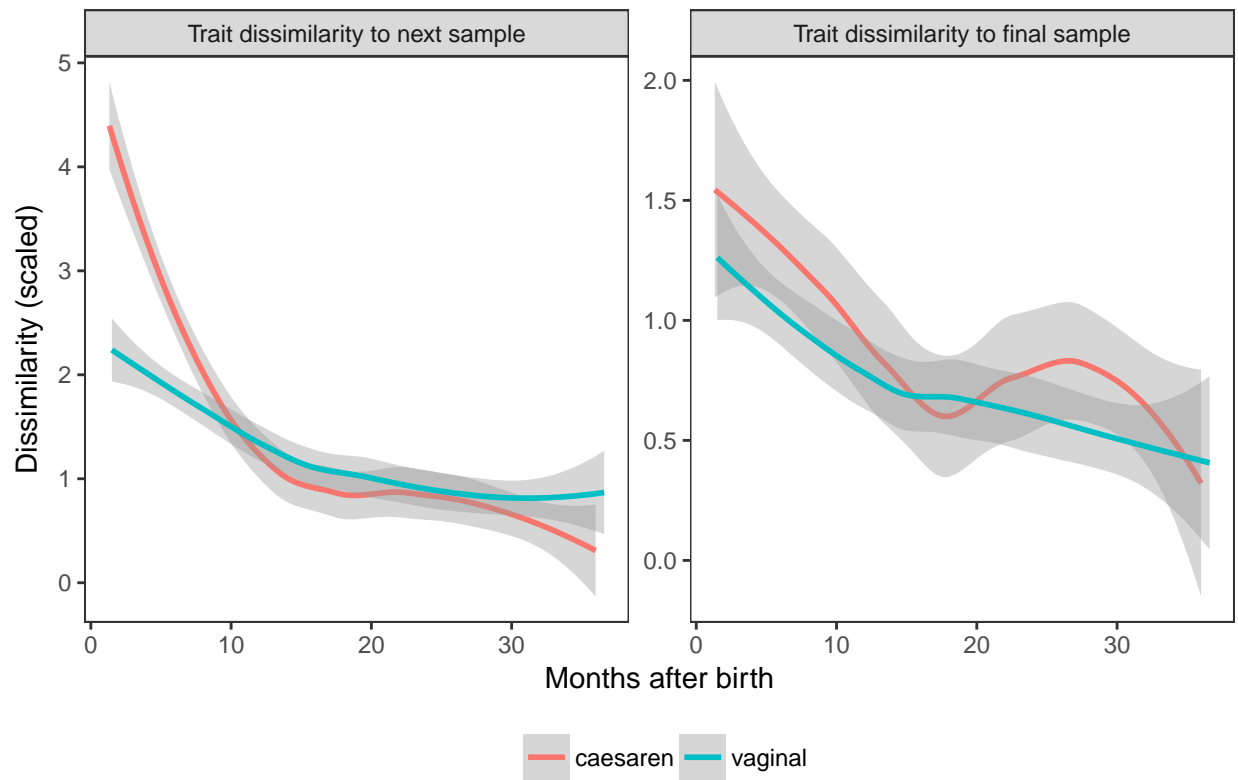


### Mean dissimilarity among infant gut microbiomes over early development.

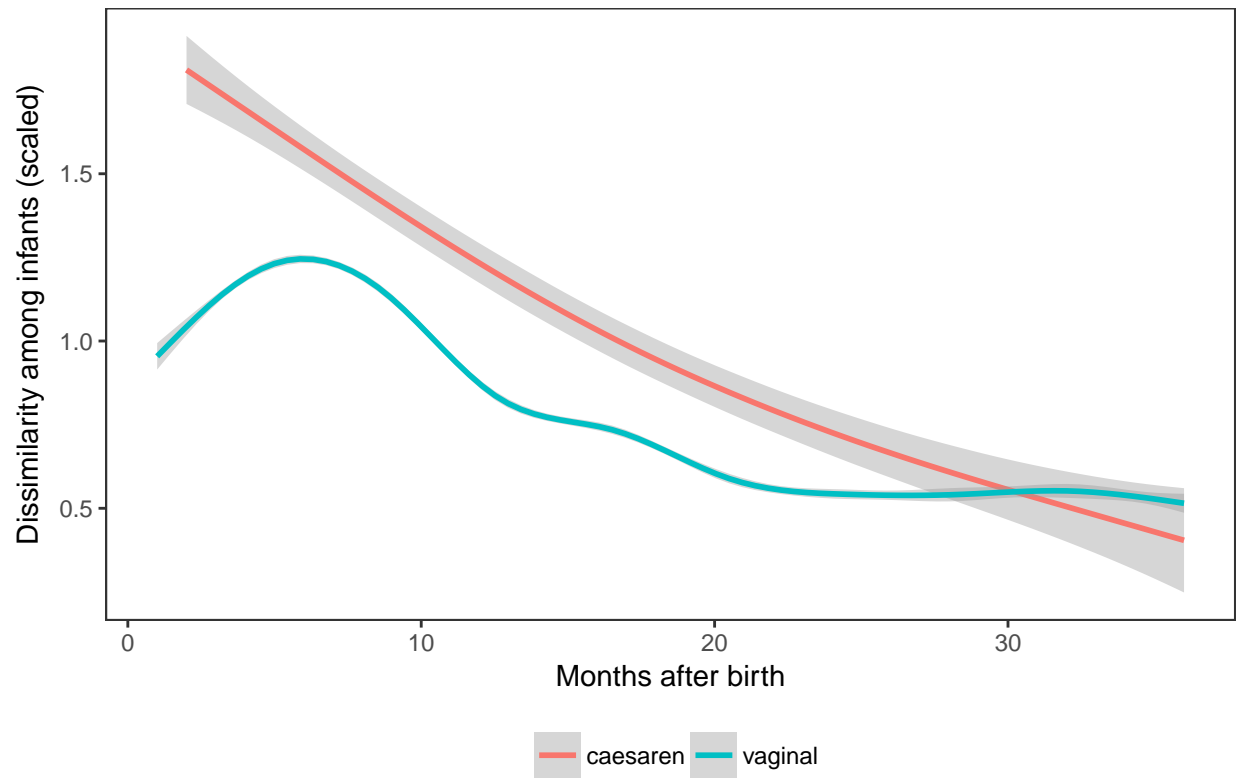
Community dissimilarity is calculated by grouping samples into one-month slices, and then calculating the average dissimilarity of all pairwise comparisons (except for samples from the same infant).



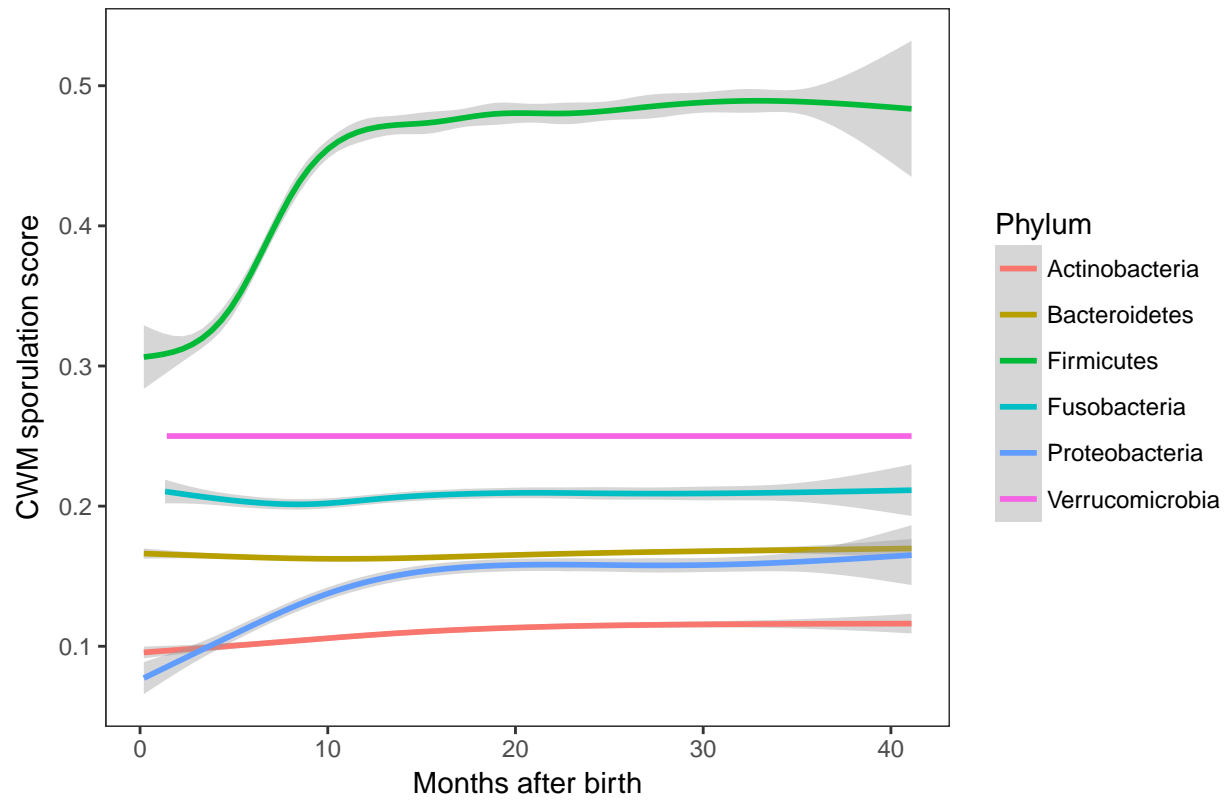
### Trait-based dissimilarity within babies, by birth mode



Trait-based dissimilarity among infants, by birth mode



Changes in sporulation score over time, by Phylum



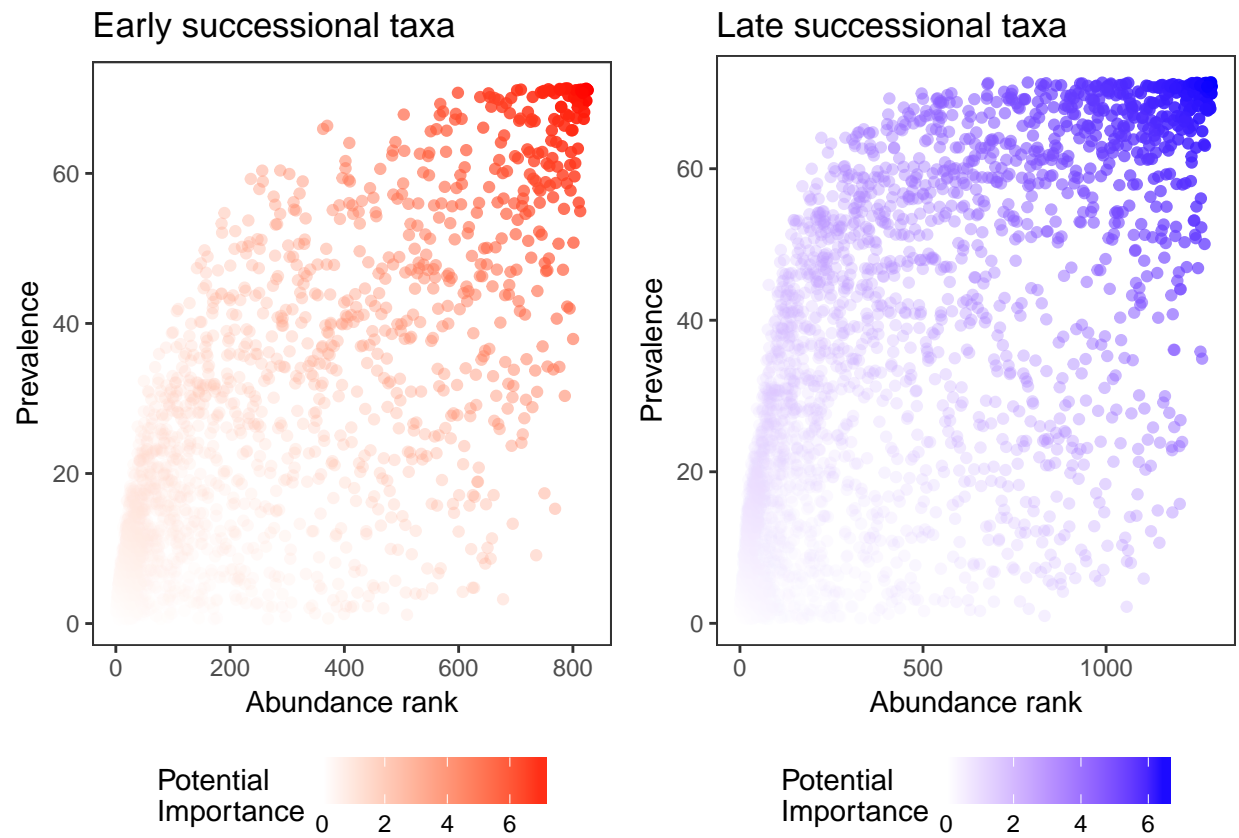


Table 1: Early successional taxa, by importance

Family	Genus	Species	OTU	Importance
Bifidobacteriaceae	Bifidobacterium	longum	otu72820	7.468
Bacteroidaceae	Bacteroides	unclassified	otu4381553	7.464
Bacteroidaceae	Bacteroides	unclassified	otu3600504	7.455
Enterobacteriaceae	unclassified	unclassified	otu782953	7.450
Lachnospiraceae	unclassified	unclassified	otu2724175	7.446
Bifidobacteriaceae	Bifidobacterium	unclassified	otu825808	7.428
Veillonellaceae	Veillonella	dispar	otu4388775	7.424
Veillonellaceae	Veillonella	dispar	otu4453501	7.419
Pasteurellaceae	Haemophilus	parainfluenzae	otu4477696	7.415
Bacteroidaceae	Bacteroides	fragilis	otu4343627	7.405
Bifidobacteriaceae	Bifidobacterium	adolescentis	otu4347159	7.402
Enterobacteriaceae	unclassified	unclassified	otu4425571	7.375
Enterobacteriaceae	unclassified	unclassified	otu2119418	7.352
Veillonellaceae	Veillonella	unclassified	otu4458959	7.329
Ruminococcaceae	unclassified	unclassified	otu265871	7.324
Streptococcaceae	Streptococcus	unclassified	otu4425214	7.313
Erysipelotrichaceae	unclassified	unclassified	otu4390365	7.307
Clostridiaceae	unclassified	unclassified	otu4434334	7.295
Enterobacteriaceae	unclassified	unclassified	otu668514	7.279
Clostridiaceae	Clostridium	neonatale	otu73000	7.278

Table 2: Late successional taxa, by importance

Family	Genus	Species	OTU	Importance
Bacteroidaceae	Bacteroides	unclassified	otu3600504	6.599
Bacteroidaceae	Bacteroides	unclassified	otu4381553	6.594
Lachnospiraceae	unclassified	unclassified	otu289734	6.586
Bifidobacteriaceae	Bifidobacterium	longum	otu72820	6.581
Bacteroidaceae	Bacteroides	uniformis	otu3327894	6.573
Bifidobacteriaceae	Bifidobacterium	unclassified	otu825808	6.565
Lachnospiraceae	unclassified	unclassified	otu2724175	6.559
Bacteroidaceae	Bacteroides	unclassified	otu4439360	6.557
Ruminococcaceae	unclassified	unclassified	otu265871	6.551
Bacteroidaceae	Bacteroides	fragilis	otu4343627	6.546
Bacteroidaceae	Bacteroides	caccae	otu193528	6.543
Pasteurellaceae	Haemophilus	parainfluenzae	otu4477696	6.535
Lachnospiraceae	Coprococcus	unclassified	otu182289	6.533
Bacteroidaceae	Bacteroides	uniformis	otu328617	6.530
Bifidobacteriaceae	Bifidobacterium	adolescentis	otu4347159	6.525
Verrucomicrobiaceae	Akkermansia	muciniphila	otu4306262	6.522
Enterobacteriaceae	unclassified	unclassified	otu782953	6.514
Streptococcaceae	Streptococcus	unclassified	otu4425214	6.501
Lachnospiraceae	Roseburia	unclassified	otu3926480	6.493
Erysipelotrichaceae	unclassified	unclassified	otu4390365	6.493