



Stool microbiome composition reflects post-menstrual age in preterm infants and differs between infants with and without typical development

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COI disclosure

I am a paid scientific consultant for Astarte Medical

Study design

3024 samples collected from **267 babies** across **3 sites**

- shotgun metagenomics on every sample
- generated ~12M paired-end reads/sample
- taxonomic and functional profiling

- ~ 10 samples/baby
- ~36% have growth failure (≤ -1.2 Z-score from birth to discharge)

- WashU St. Louis (Misty Good)
- Brigham and Women's (Kate Gregory)
- Newcastle University (Nicholas Embleton)

Analysis is a work-in-progress.
Completed for ~ 900 samples from 86 babies.

Objective

Can the preterm infant gut microbiome be used to predict gut health and identify infants at risk for growth failure?

Random forest classifier

Typically developing (TD) vs non-typically developing (NTD)

Train RF model on 70% of data.
Test on full dataset

		Predicted	
		NTD	TD
Actual	NTD	358 (true +)	13 (false -)
	TD	14 (false +)	448 (true -)

97% accuracy

Open questions

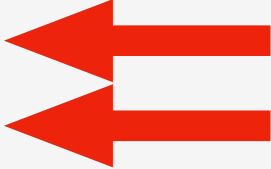
How robust is this model?

How early can accurate predictions be made?

Could key taxa be useful as a biomarker panel?

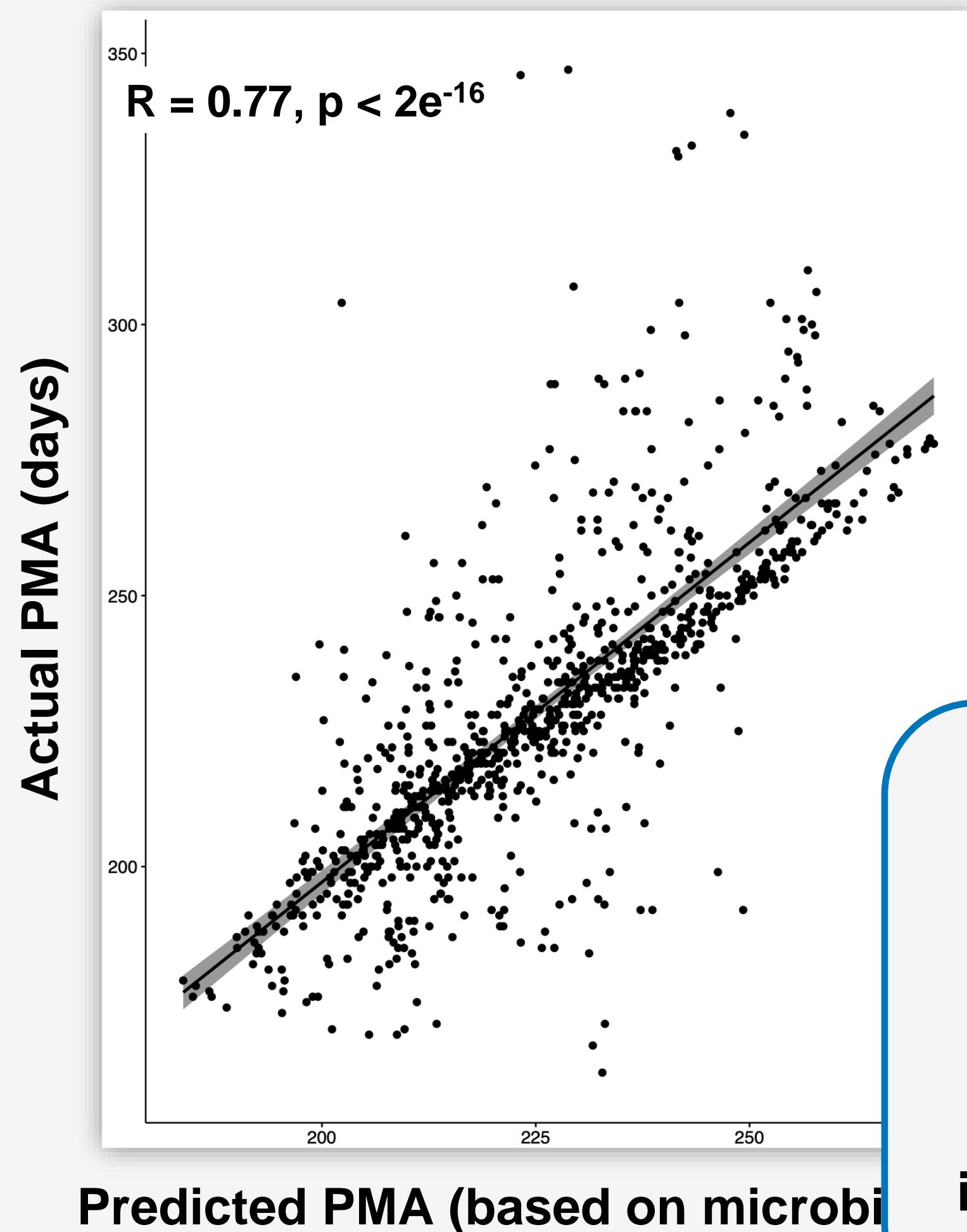
Increasing important to classifier

Species	Mean decrease in accuracy
Bifidobacterium_bifidum	0.067498595
Escherichia_coli	0.045797017
Lactobacillus_acidophilus	0.027465074
Bifidobacterium_longum	0.020643724
Staphylococcus_haemolyticus	0.019453886
Escherichia_unclassified	0.018946799
Propionibacterium_avidum	0.016515139
Bifidobacterium_animalis	0.015575921
Enterobacter_cloacae	0.012367224
Enterococcus_durans	0.009400138
Bifidobacterium_breve	0.009173547
Veillonella_unclassified	0.008977734
Veillonella_parvula	0.007807973
Klebsiella_oxytoca	0.007379208
Enterococcus_faecalis	0.00660995
Actinomyces_urogenitalis	0.006561894
Staphylococcus_lugdunensis	0.006337833
Klebsiella_pneumoniae	0.005498788
Streptococcus_thermophilus	0.005469943
Lactococcus_garvieae	0.004944994
Enterococcus_faecium	0.004306466
Citrobacter_koseri	0.004274305
Lactococcus_lactis	0.003944025
Pseudomonas_aeruginosa	0.003194776
Streptococcus_vestibularis	0.003104751



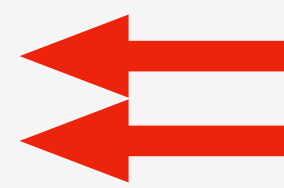
Random forest regression

Microbiome as predictor of post-menstrual age (PMA)



↑
portant to classifier

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Staphylococcus_aureus	0.016515139
Rothia_mucilaginosa	0.015575921
Clostridium_difficile	0.012367224
Staphylococcus_epidermidis	0.009400138
Bifidobacterium_breve	0.009173547
Lactobacillus_rhamnosus	0.00897734
Veillonella_atypica	0.007807973
Streptococcus_salivarius	0.007379208



Open questions

Could a microbiota-by-age Z score be a useful predictor of at-risk infants?

What are the key age-discriminatory taxa for preterm infants, and could these be the basis for better probiotics?

microbiomeDB: large-scale integration of maternal and infant microbiome studies



Explore the Studies

Table view | Find studies | Select a category | Grid view

Study Name	Category	DOI	Author	Key Findings	Action
Cross Study Analysis	M			Analyze multiple studies. Identify samples across two or more studies for a cross-study meta-analysis. Caution: cross-study analyses may result in conclusions that are invalid, confounded or otherwise misleading.	EXPLORE THE DATA
Bangladesh 5yr	H	10.1126/science.aau4735		Define the normal maturation of the gut microbiome during the first 5 years of postnatal life. 36 members of a birth cohort with consistently healthy anthropometric scores living within the Mirpur district of Dhaka, Bangladesh. Longitudinal design with monthly sampling for the first ~5 years of life. 2415 stool samples; V4 region of 16S rRNA gene.	Download Data EXPLORE THE DATA
Bee Microbiome	I		Dominguez-Bello, unpublished	Impact of social role and tetracycline application on the honey bee microbiome. 387 samples, including whole head, whole larva, whole pupa, whole gut and royal jelly. Honey bees (Apis mellifera) in Puerto Rico.	Download Data EXPLORE THE DATA
CAMP study	V	10.1101/2020.01.13.905604		The CAnine Microbiome during Parasitism (CAMP) study explores the impact of natural enteric parasite infection and diarrhea on the structure and composition of the microbiome. 155 canine cases with confirmed enteric parasite infection and 115 controls (parasites not detected). Case control design carried with the Clinical Parasitology Laboratory at PennVet's Ryan Hospital. 270 stool samples; V4 region of 16S rRNA gene.	Download Data EXPLORE THE DATA
ECAM	H	10.1126/scitranslmed.aad7121		The Early Childhood Antibiotics and the Microbiome (ECAM) study set out to identify the impact of antibiotics, delivery mode and diet on the infant gut Microbiome. 43 infants sampled during the first two years of life. Longitudinal design in healthy humans from USA. 1216 samples of various types; V4 region of 16S rRNA gene.	Download Data EXPLORE THE DATA
ENTICE study	V	10.1186/s40168-019-0740-4		The Effect of Nutritional Therapy on the microbiome in Canine Enteropathy (ENTICE) is a study leveraging a spontaneous dog model of diet-responsive chronic enteropathy to investigate the impact of therapeutic diet on the microbiome and remission. 459 stool samples, rectal swabs, and GI biopsies; V4 region of 16S rRNA gene. Longitudinal design carried at PennVet's Ryan Hospital.	Download Data EXPLORE THE DATA
Experimental cutaneous leishmaniasis	R	10.1016/j.chom.2017.06.006		This study explored the impact of infection with Leishmania major on the skin microbiome of WT mice or mice deficient in the cytokines IL10 or IL12. 641 skin swabs or stool samples; V4 or V1-V3 region of 16S rRNA gene. Longitudinal sampling at defined timepoints following infection.	Download Data EXPLORE THE DATA

News

MicrobiomeDB 17 Released
FRI APR 10 2020
We are pleased to announce the release of MicrobiomeDB 17 New data in this release There are no new datasets in this release New featu... read more

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THU FEB 06 2020
We are pleased to announce the release of MicrobiomeDB 16 New data in this release A study of a birth cohort of 271 children from the Amazonian lowlands near Iquitos... read more

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TUE NOV 05 2019
We are pleased to announce the release of... See all news

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Release 16 of our @microbiomeDB is live! Featuring new gut #microbiome data from Gordon lab from a birth cohort of >250 #Peruvian children with a high prev. of diarrhea & stunting. Part of the MAL-ED study; samples from 6, 12, 18 & 24mo. #malnutrition #globalhealth #DataScience

> 6000 samples from children during early life development (0-5yo)

MicrobiomeDB.org

Acknowledgements

Preterm Infant Microbiome

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MicrobiomeDB project

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