Narrative Dashboard Enables Unique Insights From Longitudinal Analysis of Preterm Infant Gut Microbiome, Feeding, Nutrition and Growth Data

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Problem

Numerous studies have sought to find associations among microbial impact factors, clinical practices, and the state of the preterm infant gut microbiome. Current longitudinal studies are limited in their ability to integrate the microbiome analysis with clinical data.

The Solution: Individual Visual Narrative

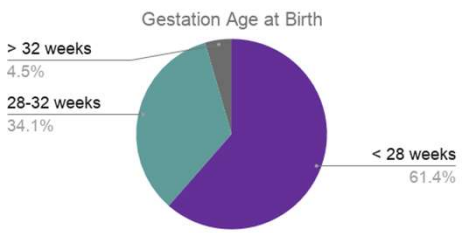
A dashboard has been developed to aid clinical researchers in identifying relationships between the microbiome and clinical factors for an individual infant. The dashboard presents **longitudinal** perinatal data and birth metrics **integrated** with feeding rates, diets, medications, diagnoses, and z-score for weight. It also includes selected microbiome-related measures: relative abundance, Preterm Gut Community Types (PGCT)[1] , and microbiota for age z-score (MAZ)[2] .

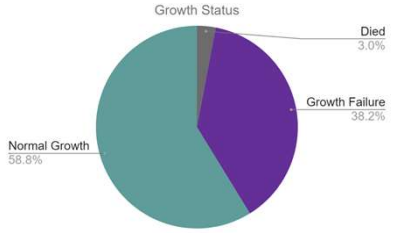
Machine Learning Predictions

Machine learning models were trained on a superset of infants (n=417) with clinical data to predict outcomes: growth failure (GF) defined as a birth-to-discharge weight z-score decline of ≥ 1.2, and non-typical development, defined as presenting with growth failure, NEC, and/or sepsis. The sensitivity of the training data is approximately 70% to predict GF over the first month.

Data Set

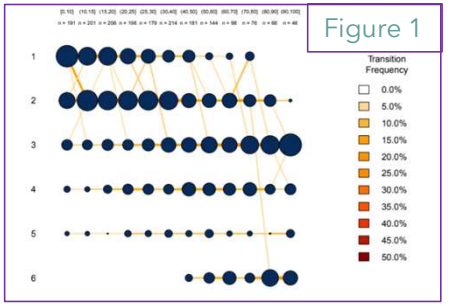
- **Collection:** We leveraged a large retrospective dataset of chronologically sampled infants (n=267) born under 34 weeks across 3 clinical sites.
- **Sequencing:** Infant stool samples were sequenced using shotgun metagenomic sequencing (n=2996 samples, Illumina NextSeq 2x150).





Preterm Gut Community Types (PGCT)

A summary of the underlying complex microbiome community structure based on the relative abundance of species in all samples (population). Figure 1 is an illustration of all samples across six distinct PCGTs over time.



References

1. Stewart CJ, Ajami NJ, O'Brien JL, et al. Temporal development of the gut microbiome in early childhood from the TEDDY study. Nature. 2018;562(7728):583-588. doi:10.1038/s41586-018-0617-x.
2. Subramanian S, Huq S, Yatsunenko T, et al. Persistent Gut Microbiota Immaturity in Malnourished Bangladeshi Children. Nature. 2014;510(7505):417-421. doi:10.1038/nature13421.

1. Patient snapshot at birth, with comparison between current and at-birth-weight values
2. Clinical events, fortification, and antibiotics tracking with option to distinguish between types
3. Longitudinal feed tracking across feed types and associated weight Z-score for each day
4. Machine-learning predictions of outcomes in real-time based on clinical and microbiome data

Clinical & Research Implications

- Integrated longitudinal display of microbial risk factors and microbiome analysis creates novel insights regarding impact of clinical decisions on a preterm infant's gut transitions
- Standardized gut health measurements enable comparison of variability across preterm infants
- Gut development trajectory establishes a personal baseline for a preterm infant and enables personalized interventions
- Predictive measures of growth failure allow for risk stratification and early interventions

Next Steps

1. Model validation on test data to improve models
2. Conduct clinical studies for researchers, integrating microbiome & clinical data
3. Identifying nutritional & microbiome phenotypes to stratify infants for precision care
4. UI/UX for rapid clinical decision making
5. Developing diagnostic measures to allow for clinically actionable interventions

5 Relative abundance of taxa identified with shotgun metagenomic sequencing for each sample

6 Preterm Gut Community Type (PGCT) with transitions over time allows interpretation of gut stability

7 Gut Maturity: Microbiota for Age Z-score (MAZ) allows personalization of an infant's care and feeding based on the gut maturity vs. chronological age