

# GUSTO

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## Chapter 1

# Introduction



## Chapter 2

# Information

### 2.1 Summary

This wiki includes information, notes and protocols on the BABLAB's secondary analysis of data from the GUSTO study.

#### 2.1.1 Abstract

#### 2.1.2 Aims

Taken from the proposal submitted by Bridget describing the project.

Aim 1a: Identify changes in the microbiome across the first 8 years of life.

Aim 1b: Determine how these changes vary as a function of maternal childhood adversity, maternal prenatal mental health, maternal postpartum stressful life events, and child stressful life events in a community sample.

#### 2.1.3 Background

GUSTO (Growing Up in Singapore Toward Healthy Outcomes) is a large birth cohort study conducted in Singapore. The primary aim of GUSTO is to understand how conditions in pregnancy and early childhood influence the health and development of women and children. The study now includes data on the children up to 8 years of age. Bridget learned about this study through Michael Meaney, and the BABLab was granted access to some of the data to analyze.

Early life stress in both parents and children is associated with a higher incidence of youth mental health disorders, cognitive dysfunction, and altered neurobiology (Green et al. 2010; McLaughlin et al. 2010; Schickedanz et al. 2018;

Callaghan et al. 2016; Callaghan et al. 2019; Gee et al. 2013). Studies in animals have indicated that early life stress also influences the gastrointestinal microbiome (Bailey and Coe 1999; Pusceddu et al. 2015), which is itself associated with emotionality, cognition and the brain (Vuong et al. 2017). (from the proposal submitted by Bridget describing this project)

### 2.1.4 Collaborators

The BABLab has been communicating with the following GUSTO researchers about the data:

- Li Ting

The following people/groups have requested acknowledgement in publications with these data:

- The GUSTO Nutrition Team (for scoring child feeding practices, processing microbiome data)

Research mentors for Fran's 251 project include:

- Bridget Callaghan
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## 2.2 Measures

### 2.2.1 Stress

### 2.2.2 Gut Microbiome

### 2.2.3 Parenting

### 2.2.4 Diet Information

### 2.2.5 Covariates

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## 2.3 Analyses

In aim 1, we will use 16s rRNA sequencing to determine the taxonomic composition of microbiota. First we will map how richness (number of observed operational taxonomic units; OTUs) changes across age, and as a function of maternal childhood adversity and prenatal stress using mixed effects modelling. We will also examine how diversity (differences in composition between individual – using Unifrac phylogenetic distance metrics) differs as a function of within-individual age change, maternal childhood adversity and maternal prenatal stress using an unsupervised Principal Coordinates Analysis clustering approach. Finally, we will use Spearman rank correlation to determine which bacteria change monotonically with age, and maternal childhood and prenatal adversity. (from the proposal submitted by Bridget describing this project)

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