Master project at Karolinska Institutet, Department of Epidemiology and Biostatistics in Stockholm

Purpose is to study how a sustainable lifestyle promotes good health and contributes to sustainable development. The specific aim for this project is:

To study potential associations between a healthy food index and presence and abundance of each bacterial species, genes and pathways in the gut microbiome diversity in different geographical areas in the America Gut study (n= 2000).

Data from the American Gut: <u>http://humanfoodproject.com/americangut/</u>

It is a collection of more than 15,000 human microbiome samples from more than 10,000 individuals, along with survey data describing self-reported measures of health, diet and lifestyle. The population is diverse: participants range in age from 0 to 99 years of age, and are primarily from the United States, Great Britain, Canada and Australia. Sample collect processing was performed under the ethics approval of the University of Colorado, Boulder and the University of California, San Diego and funded by crowed sources citizen science project De-identified data has been made publicly available for re-use. The current citation is a bioarchives pre-print is found here:

https://www.biorxiv.org/content/early/2018/03/07/277970

A subset of participants (n= 2000) have supplied answers to a validated food frequency questionnaire. In this study the quality of diet will be evaluated using a quality dietary index. In brief, we propose an index where increasing number of daily servings of

fruits/vegetables/legumes and wholegrain bread, respectively, will give increasing number of points (range 1-3), whereas increasing number of daily servings of red meat/processed meat 4 and sweets/cookies/soda, respectively, will give decreasing number of points (range 3-1). These 4 measures of diet quality will give 1-3 points each, in total 4-12 points.

The microbiome data have already been analyzed and is available. We will study potential associations between healthy food habits and presence and abundance of each bacterial species, genes and pathways in the gut microbiome diversity.

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