This analysis is on gene expression data from a National Center for Bioinformatics study (NCBI), GSE135223 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE135223>), on samples of blood and other tissue samples having relation to Irritable Bowel Syndrome (IBS) in the form of Chron's Disease (CD), Ulcerative Colitis (UC), or healthy samples. There are also some mock samples that are supposed to be by definition a placebo affect type sample of the in vitro or cell cultures, but the type of sample the mock sample was isn't clear. There are three mock samples, and there are three types of tissue: healthy or non IBS, UC, and CD. The original samples had to each individually be downloaded as zip files and loaded separately. The matrix methos of unloading and writing to a single long file as each is unzipped worked in segmenting or building the matrix of 6377X18 for genesXsamples, but froze up and made R crash or run for a very long time with no results when trying to make each 'list' of the original GSM sample into an integer column. There was also a meta list of 5 rows appended to the Ensembl ID fields for the probe extraction information that was saved separately.

The way this study was performed by a paraphrase of my own words of the summary, is that there were three healthy donors of blood, peripheral blood mononucleated cells (PBMC), that over the course of 7 days, the blood was separated into differnt samples with 5 samples of Chron's Disease, 5 samples of Ulcerative Colitis, and 5 samples of healthy or non IBS colon resections was added to in order to differentiate the macrophage activity. There were also 3 mock samples that are placebo effects without having added any viral like particles (VLP) of CD, UC, or non-IBS particles from colon resections to. The goal was to monitor the transcriptional responses of the macrophages in the PBMC of healthy cells in response to the VLP additions. The outcome was that the study claimed divergence was significant in the macrophage response of IBS colonic disorders in comparison to IBS colonic disorders.

This study was submitted August 2019, but made public almost a year later in June 2019. The human genome 19 and the Illumnina NovaSeq 6000 machine for capturing the blood sequences and the gene expression values from the samples.

A dashboard was created in Tableau that explores the same body system genes explored in the previous blog on Lyme Disease using GSE145974, and some genes in the COVID-19 dashboard using GSE152418 from the NCBI research and the Gene Expression Online (GEO) data repository. R was used to analyze these genes, and the exact fold change method was also a modified fold change because of the numerous 0 values when dividing the healthy mean values by the disease mean values. Previous studies have done the body system genes analysis after filtering for the top or least expressed genes in fold change, but this part of the study is saved for later so that we can see is some genes related to our systems in the body have an impact on Crohn's Disease (CD) or Ulcerative Colitis (UC) that a diet could improve symptoms of.

The body systems explored are the top 3 genes taken from genecards.org when searching for:

|  |
| --- |
| * lymphatic |
| * integumentary |
| * nervous |
| * circulatory |
| * musculature |
| * endocrine |
| * bone-structure |
| * reproductive |
| * tetanis |
| * alcohol |
| * ibuprofen |
| * aspirin |
| * tylenol |
| * nsaids |
| * cannabidiol |
| * melatonin |
| * calcium |
| * fish-oil |
| * omega-3s |
| * calcitonine |
| * magnesium |
| * estrogen |
| * testosterone |
| * vitamin-d |
| * adrenaline |
| * dopamine |
| * progesterone |
| * glucose |
| * glucagon |
| * iron |
| * corticosteroids |
| * insulin |
| * vitamin-b12 |
| * melanin |
| * prolactin |
| * vitamin-c |
| * zinc |

In the dashboard located on public.tableau.com, you can use the body sytem, gene, and group (healthy, mock, ulc. col., or Crohns) to see specific changes in the body, that will provide the genecards gene summary of those three genes related to the body system selected or the one gene, the fold change in the gene(s) in comparing disease/healthy sample values as a bar chart, the gene comparisions individually as the mean value in each group of CD or UC compared to healthy as a scatter plot, and the individual samples in each group side by side comparison of gene expression values to see which samples are far from their neighboring samples of each group as a bar chart. To select a gene, group, or system, just click it and to select multiple items press ctrl and scroll to the other item and click it. To deselect and go back to all genes to scroll through, just click each selected item again. You don't have to select an item from each filter to use the dashboard.

<https://public.tableau.com/profile/janis5126#!/vizhome/UlcerativeColitis-CrohnsDisease-GSE135223/Dashboard1?publish=yes>

