

# Utah Population based genetic and clinical feature in Colorectal cancer

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## **BASIC INFORMATION**

**Link to the project:** <https://github.com/seyoun209/dataviscourse-pr-coloncancer>

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## **BACKGROUND AND MOTIVATION**

Colorectal cancer is the third most common cancer diagnosed yearly, in both men and women, in the United States and the second leading cause of cancer-related deaths when men and women are combined. Colorectal cancer treatment is beneficial and reducing the number of incidences when removing the colon polyps. Also, early diagnosis and survival are better with detecting the polyps in the colon.

Interestingly, the asserted pedigree and twin studies indicate that 20-30% of colon cancer cases appear to arise in the inherited susceptibility. Also, 3-5% of colon cancer occurs in inherited syndrome. However, the risk of adenomatous polyps in men and women or different ages concerning the family history of colon cancer cases is not studied well.

Association studies reported genetic variants and exposure risk factors, including BMI, smoking, exercise, alcohol consumption, NASID, and hormone menopause.

This project will use the seven families with several patients (n=198)'s genetic information. We initiate genetic information to compared familial information. We will respectably sort out all exposure risk with ascending/descending method to understand which exposure risk is most relatively related to colon cancer. Lastly, we will try to understand the polyp size with the relationship with the family's inheritance. Therefore, in this visualization, we evaluated the polyp size with the location and the clinical factors in huge extended families with a strong family history representing the familial high-risk colorectal cancer classification.

## **PROJECT OBJECTIVE**

The objective is to utilize interactive plots to help viewers explore relations between polyps sizes and other biological and family-related factors. The plots allow users to sort and filter data such that the relations can be viewed from different perspectives. This would allow users draw conclusions on how the various factors affect the incidence of colon cancer.

## **DATA**

The Utah population database (UPDB) was used to identify the seven families. Colorectal cancer cases in the families were contacted by the Utah Cancer Registry through mail requesting them, or their next of kin, permission to be contacted by the study. In total, there are seven large kindreds with multiple colorectal cancer cases included in this study. The medical records were obtained on colorectal cancer cases. Published guidelines evaluated adenomatous and hamartomata's polyposis syndromes.

Due to the IRB, the data is not appropriated to provided.

## **DATA PROCESSING**

We obtain the raw data from UPDB. For effective display of information, we clean up the raw data such that data categories with many missing data are discarded from the plots. We

narrow down the data exposure risks for display as the following:

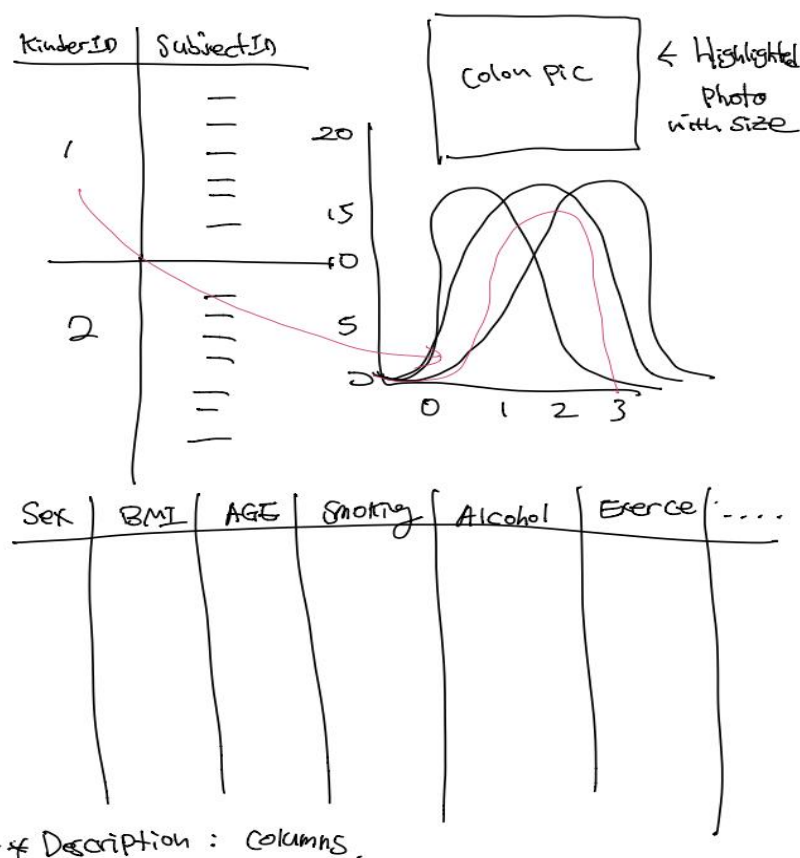
- Kinder ID, Subject ID, Sex, BMI, Age, Smoking, Alcohol, Exercise, NASID, HRT

In the second screen, we display the position and size of polyposis on the image of colon with the following information:

- Kinder ID, Subject ID, Site, Polytype, Size of Polyp.

## VISUALIZATION DESIGN

Brainstorming



Initial Design 1 (Not using): We are not using this design because it might confuse the audience. Since our data is relatively complicated due to multiple variants, it does not focus on our motivation, which compares each kinder IDs. We have to use lots of hovering tooltips that may cause the data even more complicated and not delivering well with our purpose. We are concerned that this is too much, just a data table instead of visualizing.

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Figure 1 displays a multi-panel visualization showing the relationship between genetic data, polygenic risk scores, and disease risk.

The top panel shows a table of genetic data with columns: Genetic & Multivariate, YouTube tutorial, Process Book, Contact, and a mouseover description.

The middle panel shows a table of subject data with columns: Sex, Age, BMI, Smoking, Alcohol, Exercise, NASID, and HRT.

The bottom panel shows a map of the human gut with a red dot indicating the location of the subject's gut.

The right panel shows a density plot of Polygenic Risk Score (PRS) for subjects with and without Crohn's Disease (CD). The x-axis is PRS (0 to 3) and the y-axis is Frequency of subjects (0 to 20). The blue curve represents subjects without CD, and the orange curve represents subjects with CD. The curves overlap significantly, indicating that PRS is not a strong predictor of CD risk in this dataset.

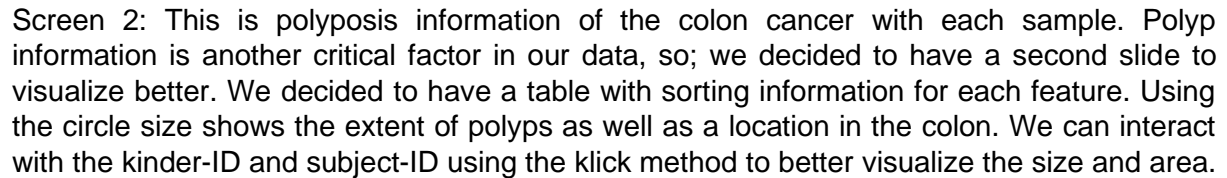
Initial Design 2 (Not Using): We are not using this design because all the data is compacted in one page. Every information will be average, including density plot and also all the multivariate features. In that case, we are not able to track down individual subject value. Nevertheless, we were trying to see the overall average of each family may be beneficial. We decided to split two slides to better visualize all the data by focusing on clinical and genetic information.

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[illegible]

Initial Design 3 (Using): We choose this design for our visualization. Since we have multiple clinical information, we decided to have two different slides to visualize our data.

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## Utah Population based genetic and clinical feature in Colorectal cancer

KinderId ▲	SubjectID ▼	S
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[illegible]

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