Identify the relationship between referral rate and potential predictors using logistic regression

Elisa Zhang, Shicong Wang

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Introduction

In this section, we need to focus on building an inference model to evaluate what kind of parameters can exert effect on genetic referrals. Given on previous analysis, we list some of the features that seemingly related to the response: cancer stages, ECOG level, sex assigned at birth, ethnicity and age.

However, when consider both cancer stage and ECOG level, we wonder whether they are correlated. On behalf of that ECOG level serve as a public domain to classify a patient according to their well-being, which appear to relate to cancer stage. As a result, we mainly concern one model with both stage and ECOG, while the other two serve as a safeguard against this association and are shown in appendix.

Important concept

During the analysis, we faced a problem when estimating the standard error for the overall referral rate. Note that our response is binary, we deal with the proportion problem as below:

The random variable P' is the sample proportion:

$$P' = \frac{X}{n}$$

where X is the random variable for the number of acceptance, n is the sample size.

The standard deviation is found to be

$$\sigma_{p'} = \sqrt{\frac{p(1-p)}{n}}$$

where p is the probability of acceptance, p' is the sample proportion of acceptance, and n is the size of the sample.

Therefore, the confidence interval for a population proportion become as

$$p = p' \pm \left[Z_{\alpha/2} \sqrt{\frac{p'(1-p')}{n}} \right]$$

where $Z_{\alpha/2}$ is set according to our desired degree of confidence and $\sqrt{\frac{p(1-p)}{n}}$ is the standard deviation of the sampling distribution.

Visulization

Since visualizing the dependent variables in the model helps us anticipate and make sense of results, we try to generate a series of plots on each variable. In each plot, we generate error bars by using the formula in last section.

1. Cancer Stage

The figure below illustrates the relationship between referral rate and cancer stages. There are many overlaps among error bars. The cancer stage might not be related to the referral rate.

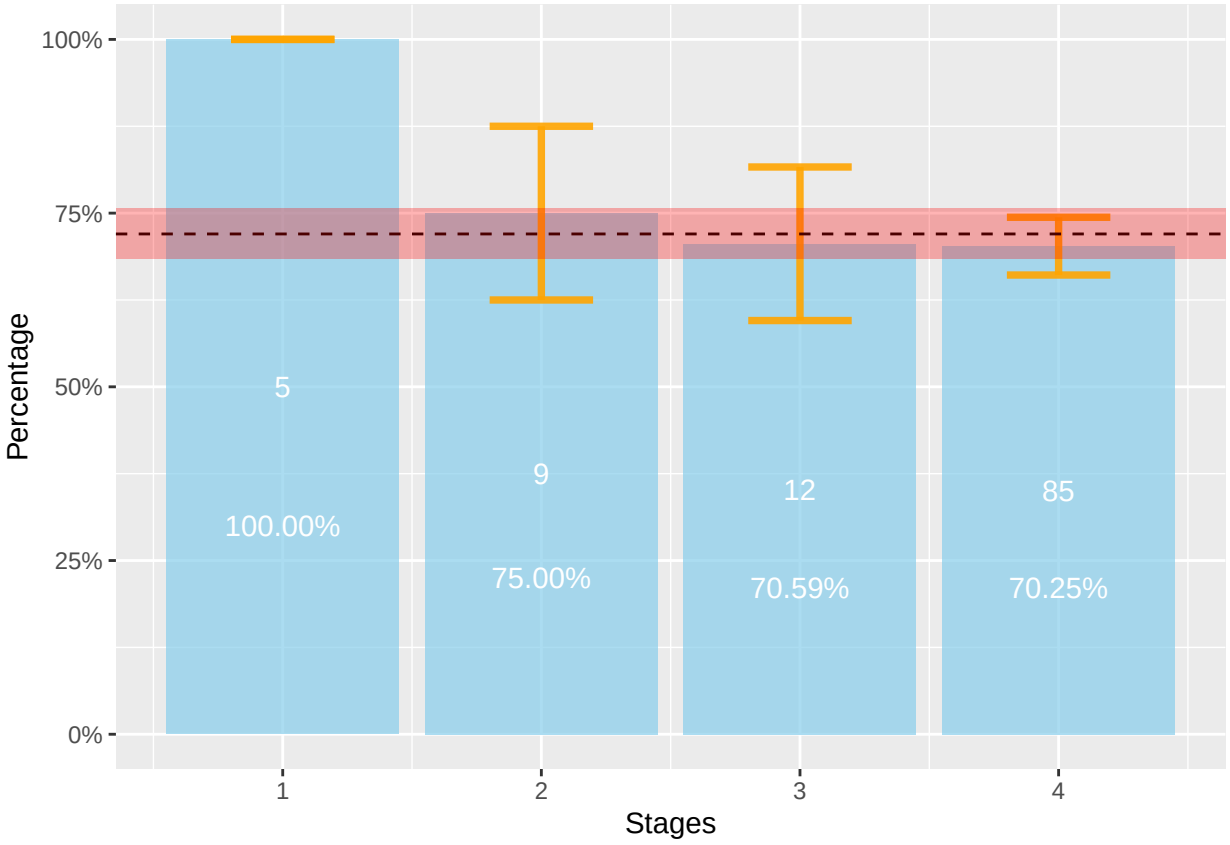


Figure 1: Proportion of Patients Who got referrals in each Cancer Stage

2. ECOG level

The figure below shows the relationship between ECOG status and referral rate. We can conclude that there is no obvious relationship between ECOG status and the referral rate.

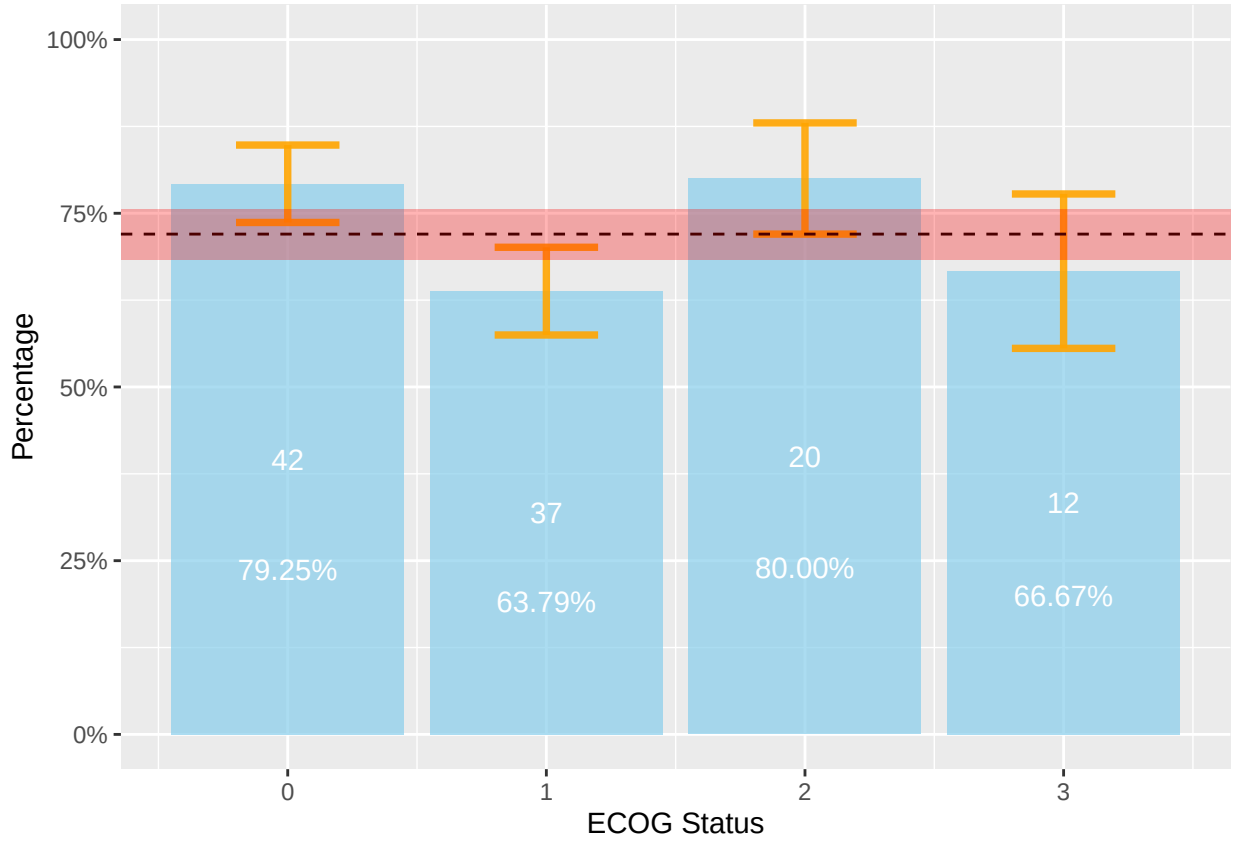
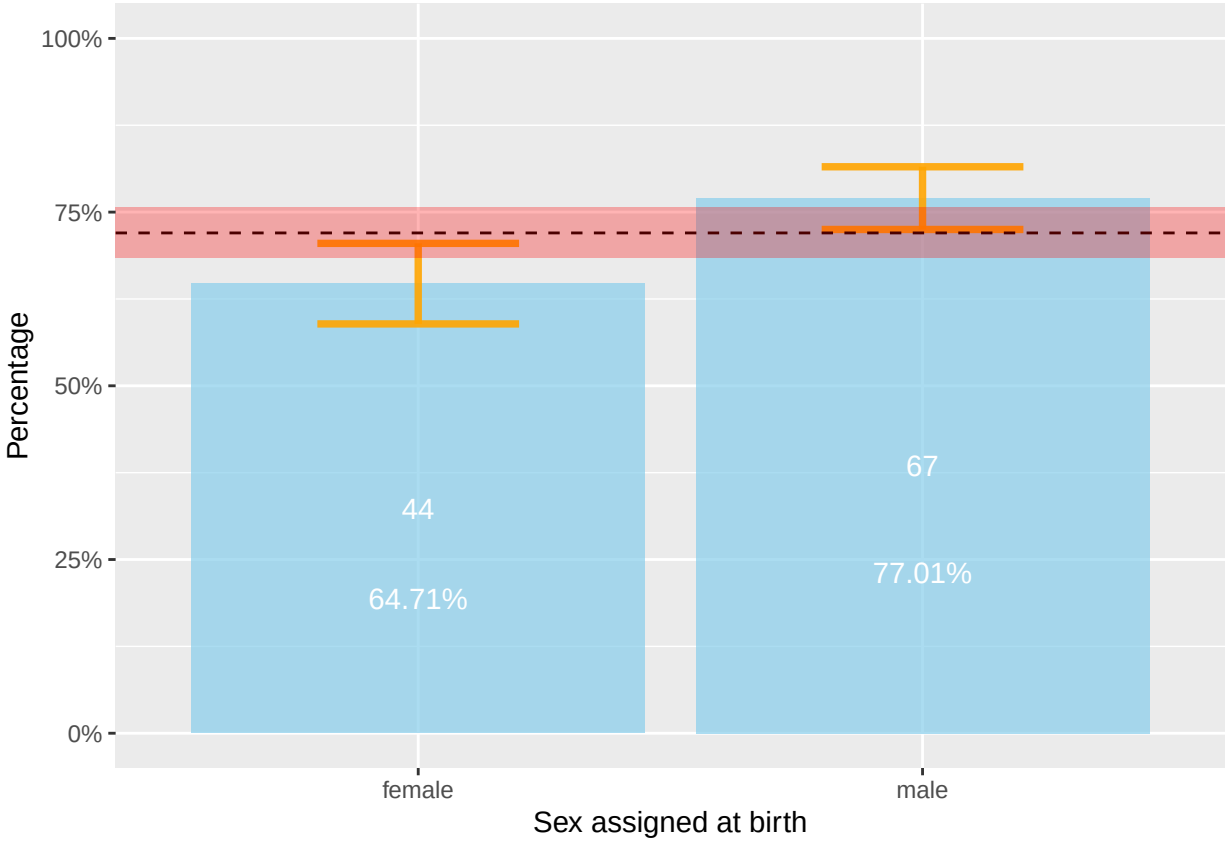


Figure 2: Proportions of Patients Who got referral rate in each ECOG Level

3. Sex Assigned at Birth

From the the plot below, we might conclude that gender is related to the referral rate.



4. Ethnicity

Since some ethnicity only contain few observations, we divide the race into white and not white and use as the new variable. And the figure below does not show that there is an obvious relationship between race and referral rate.

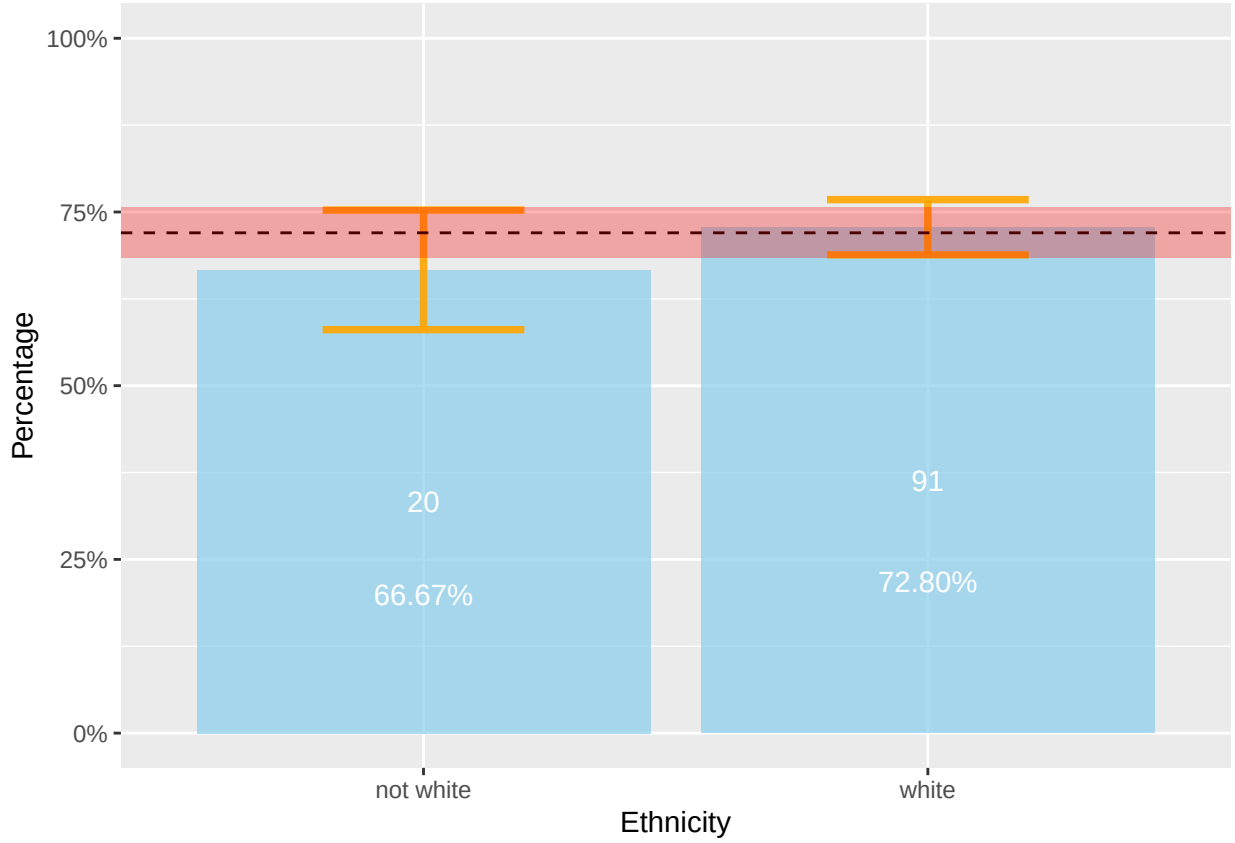


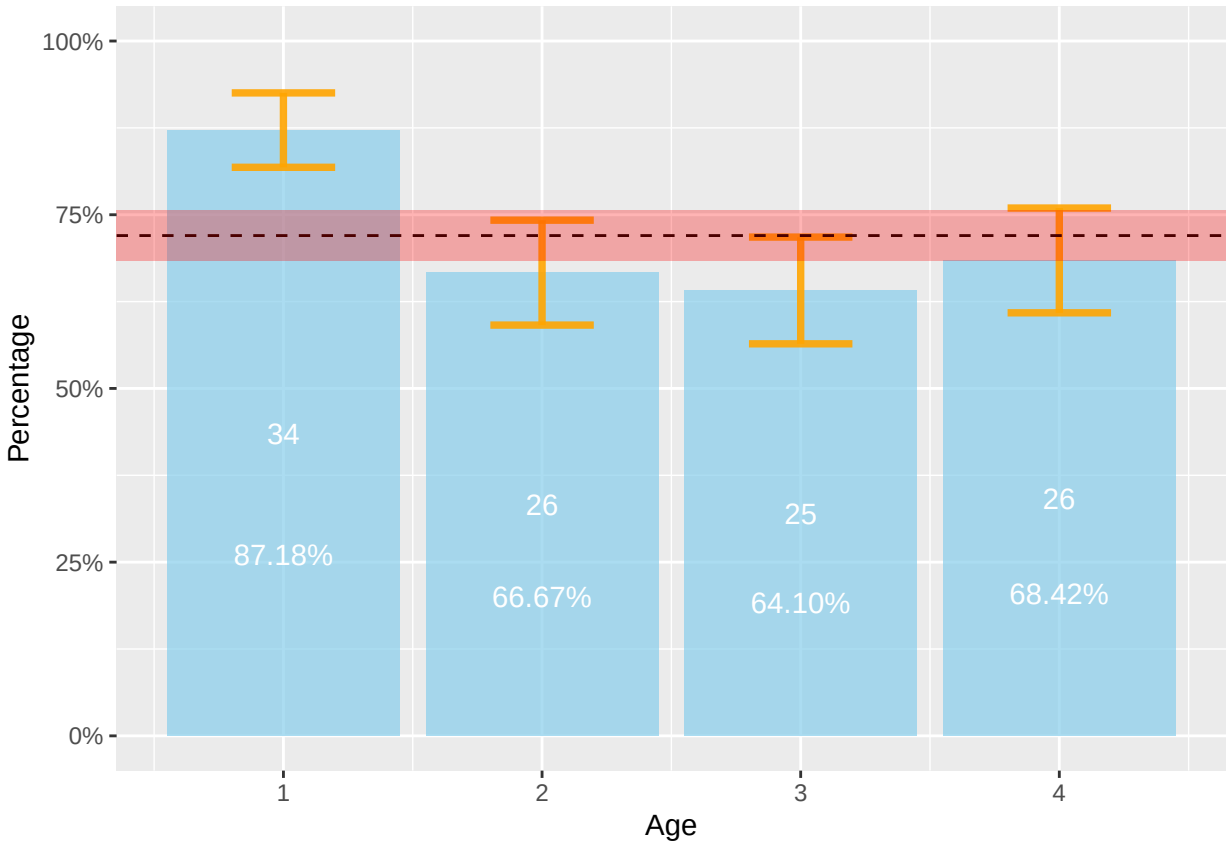
Figure 3: Proportions of Patients Who got referral rate among races

5. Age

We divide Age into groups using quantiles. The first group contains patients from 32 to 62 years old. And the second group contains patients aged from 62 to 68. And the third group include patients from 68 to 75.5 years old. And the last group include patients whose age are in the 4th quantile.

```
##   0%  25%  50%  75% 100%
## 32.0 62.0 68.0 75.5 96.0
```

From the plot below, there is no much difference for the referral rate among 2nd, 3rd and 4th groups.



Model Fit

We will use logistic regression to fit our data since we have binary outcome of whether the patients got a referral from GIM or not. We will fit three models. The full model will include both cancer stage and ECOG level. And the other two will only include either ECOG level or Cancer Stage which are put in appendix.

Below is the full model:

```
model1 <- glm(`Genetics Referrals` ~  `Stage at Dx (#0-4)` +
                `ECOG at Initial (#0-4)` +
                `Age at Dx (#)` +
                `Ethnicity/ Ancestry` + `Sex Assigned
at Birth (m/f)` , family = "binomial", data = dat_1)
summary(model1)
```

```
##
## Call:
## glm(formula = `Genetics Referrals` ~ `Stage at Dx (#0-4)` + `ECOG at Initial (#0-4)` +
##     `Age at Dx (#)` + `Ethnicity/ Ancestry` + `Sex Assigned\nat Birth (m/f)`,
##     family = "binomial", data = dat_1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8614  -1.3437   0.7106   0.8358   1.2903
##
## Coefficients:
##                                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)                       3.4843634  1.8067729   1.929   0.0538 .
```

```
## `Stage at Dx (#0-4)`                -0.2976799  0.2814298  -1.058   0.2902
## `ECOG at Initial (#0-4)`            -0.0003937  0.1960274  -0.002   0.9984
## `Age at Dx (#)`                     -0.0277649  0.0198487  -1.399   0.1619
## `Ethnicity/ Ancestry`white           0.2280004  0.4502499   0.506   0.6126
## `Sex Assigned\\nat Birth (m/f)`male  0.5031592  0.3687174   1.365   0.1724
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 184.94  on 154  degrees of freedom
## Residual deviance: 178.24  on 149  degrees of freedom
## AIC: 190.24
##
## Number of Fisher Scoring iterations: 4
```

Since the majority of p-values are greater than 0.05, we don't have enough confidence to reject the null hypothesis that the variables have no correlations with the dependent variable. Consequently, it's insufficient that these variables contribute significantly to genetic referrals.

Model selection

In case of the correlation between ECOG level and cancer stage, we consider to extract either of them from the full model and compare them to the full model. However, conclusions have not changed so far.

We consider the following results:

(1) According to the corresponding information from client, we note that many patients even with high cancer stage are asymptomatic. Since ECOG measures well being, it is reasonable that there might not be a relationship between these variables.

(2) By fitting three models, we checked whether the analysis is robust to possible association. Then we find the results of three models are quite similar that all of which are not significant enough. In that case, it's unnecessary to pay much attention on such association.

Therefore, we still maintain the full model in this section.

Diagnostic Plot

The diagnostic plot can be used to measure the goodness of fit of the model.

Binned residual plot

The binned residual plot can assess the overall fit of regression models for binary outcomes. Since most of points are within the grey line and there is no obvious pattern for the points, the model does not have much problem.

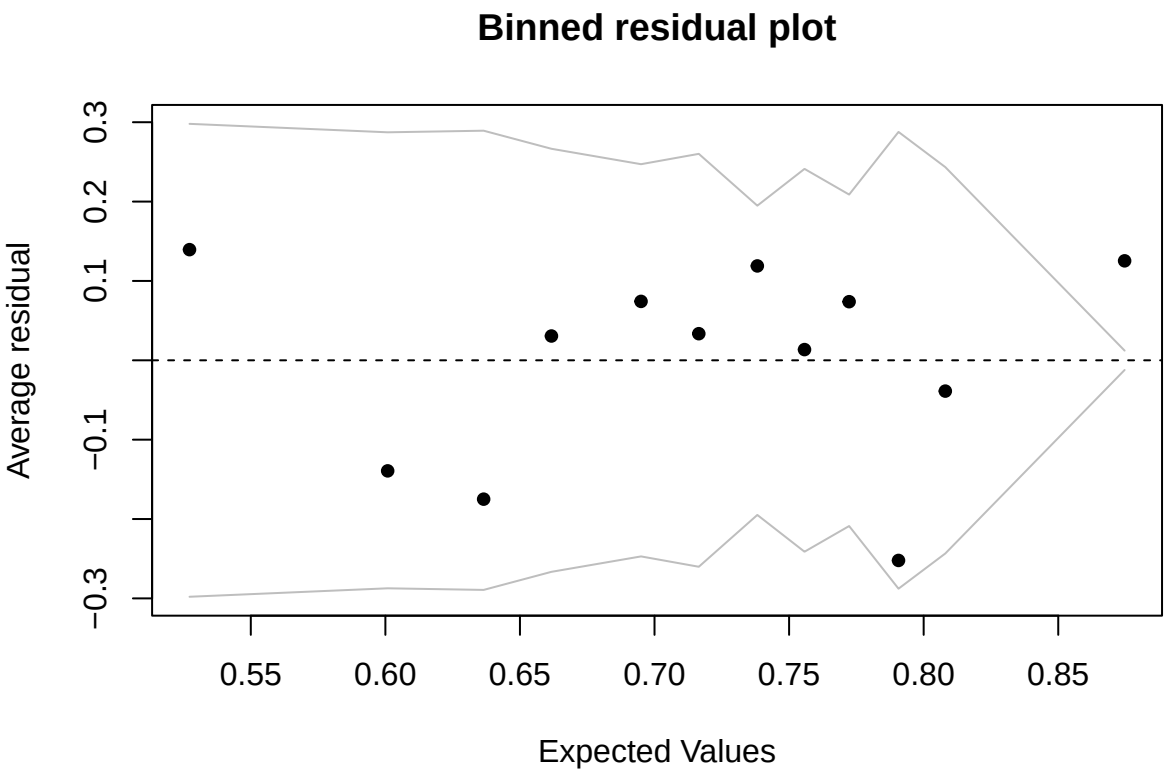


Figure 4: Binned residual plot for full model

Appendix

Model without Cancer Stage

```
model2 <- glm(`Genetics Referrals` ~   `ECOG at Initial (#0-4)`
              + `Age at Dx (#)` +
                `Ethnicity/ Ancestry` +
                `Sex Assigned
at Birth (m/f)` ,
family = "binomial", data = dat_1)
summary(model2)
```

```
##
## Call:
## glm(formula = `Genetics Referrals` ~ `ECOG at Initial (#0-4)` +
##     `Age at Dx (#)` + `Ethnicity/ Ancestry` + `Sex Assigned\nat Birth (m/f)`,
##     family = "binomial", data = dat_1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8419  -1.3603   0.7124   0.8382   1.2384
##
## Coefficients:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                          2.29660    1.39086   1.651   0.0987 .
## `ECOG at Initial (#0-4)`            -0.04970    0.19004  -0.262   0.7937
## `Age at Dx (#)`                     -0.02543    0.01943  -1.309   0.1907
## `Ethnicity/ Ancestry`white           0.19515    0.44769   0.436   0.6629
## `Sex Assigned\\nat Birth (m/f)`male  0.52785    0.36674   1.439   0.1501
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 184.94  on 154  degrees of freedom
## Residual deviance: 179.46  on 150  degrees of freedom
## AIC: 189.46
##
## Number of Fisher Scoring iterations: 4
```

Model without ECOG level

```
model3 <- glm(`Genetics Referrals` ~  `Stage at Dx (#0-4)` +
                `Age at Dx (#)` +
                `Ethnicity/ Ancestry` +
                `Sex Assigned
at Birth (m/f)` , family = "binomial", data = dat_1)
summary(model3)
```

```
##
## Call:
## glm(formula = `Genetics Referrals` ~ `Stage at Dx (#0-4)` + `Age at Dx (#)` +
##     `Ethnicity/ Ancestry` + `Sex Assigned\nat Birth (m/f)`, family = "binomial",
##     data = dat_1)
##
## Deviance Residuals:
```

```
##     Min       1Q   Median       3Q      Max
## -1.8613  -1.3438   0.7106   0.8357   1.2903
##
## Coefficients:
##                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)                        3.48520    1.75846   1.982   0.0475 *
## `Stage at Dx (#0-4)`              -0.29780    0.27537  -1.081   0.2795
## `Age at Dx (#)`                   -0.02778    0.01862  -1.492   0.1357
## `Ethnicity/ Ancestry`white         0.22809    0.44797   0.509   0.6106
## `Sex Assigned\\nat Birth (m/f)`male  0.50323    0.36703   1.371   0.1703
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 184.94  on 154  degrees of freedom
## Residual deviance: 178.24  on 150  degrees of freedom
## AIC: 188.24
##
## Number of Fisher Scoring iterations: 4
```