

Session 1: Case-Control Association Testing

Analysis of LHON Data with R

Before you begin:

- Make sure that R is installed on your computer: <http://cran.r-project.org/mirrors.html>
- Go to the course website and locate the `LHON.txt` dataset that we will be using.

1. Load the `LHON.txt` data file into your R session. You can read the file directly from the web (if you are connected to the web) using the following command:

```
LHON=read.table("http://faculty.washington.edu/tathorn  
t/sisg/LHON.txt",header=TRUE)
```

Alternatively, save the file to your computer and read it into R from the directory where the file is:

```
LHON=read.table("LHON.txt",header=TRUE)
```

2. The `LHON.txt` dataset is from the LHON case-control study discussed in session 4. Data includes both phenotype data and genotype data for a candidate gene.
 - a. Perform the logistic regression analysis from session 4 for this data with CC as the reference genotype.
 - b. Obtain odds ratios and confidence intervals for the CT and TT genotypes.
3. Now redo the logistic regression analysis from question 2, but with TT as the reference genotype. How do the results change? Explain the results. (Hint: Use a plot to gain some insight.)