Talk on 2011-10-21

1. Finish the type I error for our method (both the epi test and the One Gene Test). In detail, for the Epi test, we need to consider 3 different cases: 1). $G_1=0$, $G_2=0$, $G_{12}=0$; 2). $G_1 \neq 0, G_2 = 0, G_{12} = 0$; 3). $G_1 \neq 0, G_2 \neq 0, G_{12} = 0$. The same to the One Gene Test: 2 different cases are needed to add: 1). $G_1 = 0, G_2 = 0$; 2). $G_1 = 0, G_2 \neq 0$

2. For the Warfarin data, we need to add the result from PCA and PLS. (Hope they are not as good as our method).

3. About the Average similarity matrix, Jung-Ying shown me another way to prove that S$_{\text{average}}$ is positive definite: Suppose we need to compare the similarity between person i and person j on the l-allelic marker. According to my idea, just look at the $l \times l$ matrix to get the similarity score of for i and j on the marker. But Jung-Ying's idea is that transfer the person i's genotype into and $1 \times l$ vector g_i and the score would $s_{ij} = g_i^T \times g_j$. From this view, the S$_{\text{average}}$ matrix should always be positive definite. I think the easiest way to check that is to calculate all the possible s_{ij} then compare to S$_{\text{average}}$ to see the difference.

4. For the simulation, rewrite the result part, and pay more attention to how to explain the result. Try to figure out the way. (Jung-Ying told me I should be passionate about my project, not working as her secretory)