Prostate cancer is one of the most common cancers in the world, with approximately 12.9% of men being diagnosed with it at some point in their lives. Prostate cancer begins when the cells of the prostate begin to divide uncontrollably. Most prostate cancers are adenocarcinomas, as they begin from gland cells. However other types of cancers can also occur in the prostate like sarcomas and carcinomas. Ras Associated Domain Family 1A (*RASSF1A*) is a tumour suppressor gene located on chromosome 3 [1]. Ordinarily the RASSF1A protein acts in many cell growth control pathways and can help induce apoptosis or cell cycle arrest [2]. *RASSF1A* has been implicated in many cancers, including prostate cancer. In prostate cancer, the gene undergoes epigenetic alterations which affects its expression and its promoter region can be found to be hypermethylated [1, 3]. In the USA, black males have a higher incidence of prostate cancer than white and Asian males. The cause of this is unknown, it is also *unknown if the levels of methylation in black males is higher than in white or Asian males.*

My **primary goa**l is to determine if black males undergo more epigenetic changes in the *RASSF1A* gene promoter region than white or Asian males.

My **hypothesis** is that black men do have higher levels of DNA methylation in the promoter region of the RASSF1A gene.

My **long term goal** is to identify why race affects epigenetic status’ differently.

[1] Ge, YZ., Xu, LW., Jia, RP. et al. 2014. The association between RASSF1A promoter methylation and prostate cancer: evidence from 19 published studies. *Tumour Biol*. **35**: 3881
[2] Donninger, H. Vos, M.D. & Clark, G.J. 2007. The RASSF1A tumour suppressor. *Journal of Cell Science*. **120**: 3163-3172.
[3] Yegnasubramanian, S., Kowalski, J., Gonzalgo, M.L. et al. 2004. Hypermethylation of GpG islands in primary and metastatic human prostate cancer. *Cancer Research*. **64**(6): 1975-1986.