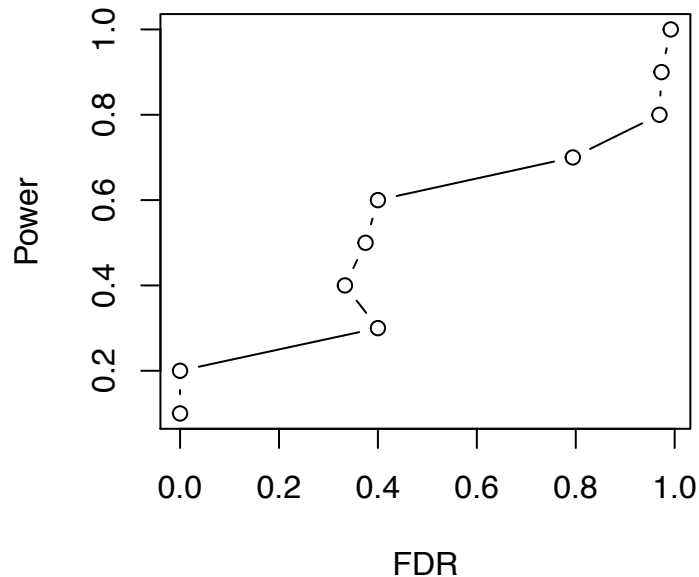


GAPIT.FDR.TypeI()

One question we didn't figure out is to use the GAPIT.FDR.TYPEI function correctly. Here is how to use it: First, imagining that we have already loaded the materials (package and data), and conducted a GWAS by GAPIT package. In this case, the GAPIT output is saved as 'gapit.glm'. The following shows how to use GAPIT.FDR.TypeI:

The key is the organize GWAS output to fit the GAPIT.FDR.TypeI function (see the GWAS=cbind(myGM, gapit.glm\$P)line in the function)

```
glm.power=GAPIT.FDR.TypeI(  
  WS=1e5, # WS = window size  
  GM=myGM, # dataset  
  seqQTN=mySim$QTN.position, # QTN position  
  GWAS=cbind(myGM, gapit.glm$P)  
)  
  
# Then if you would like to generate a FDR-POWER plot:  
plot(Power~FDR, data=glm.power, type="b")
```



Meanwhile, remember HW3? In question 3 and 4 of HW3 we counted the number of false positives and false negatives. That is the intuitive idea of power analysis. You may apply same method in this homework to analyze power and false discover rate. Since the input are the same (gene map, QTN locations, p values), you should only need non or minor modifications of HW3 code to get desire result for this homework.

PLINK

We are asked to run PLINK in question 3. Similar to BLINK, PLINK is also a stand alone program run by command line. Information about PLINK could be found at <http://zzz.bwh.harvard.edu/plink/>.

To download PLINK, navigate to the **stable download** tab in the PLINK website. **Windows users** please download the "MS-DOS" version; and **Mac users** please download the "Apple Mac (Intel)" version. I encourage you to try it with the PLINK user's manual. Meanwhile, I am also working on PLINK right now, feel free to ask question, share progress and/or discuss.