GENETICS

BIGGER IS BETTER

12.08.2006

John Todd has always been advocating that we should use larger sample sizes in our genetic association studies. I agree, it is also true that larger sample sizes will lead to smaller p--values. In his recent nature genetics comment he now suggest a p of less than 10 up minus 8 to be relevant. Yes, all of his 6 examples show that significance level but only 1 provides functional evidence (the SLE study). All other studies including Todd`s own studies are number-crunchers. I fear that in the absence of functional data 10-8 may not even be sufficient. Think of 500,000 SNPs, 20 possible traits, 5 genetic models and 20 competing groups – this multiplies to 10-9. Interestingly, the SLE study, showed a p of 10-16! Having good functional evidence I would be even willing to accept 10-2. May I point you to an excellent study describing a new rSNP by means of CHIP and expression analysis of de Gobbi – using just a couple of families. Yea, yea.