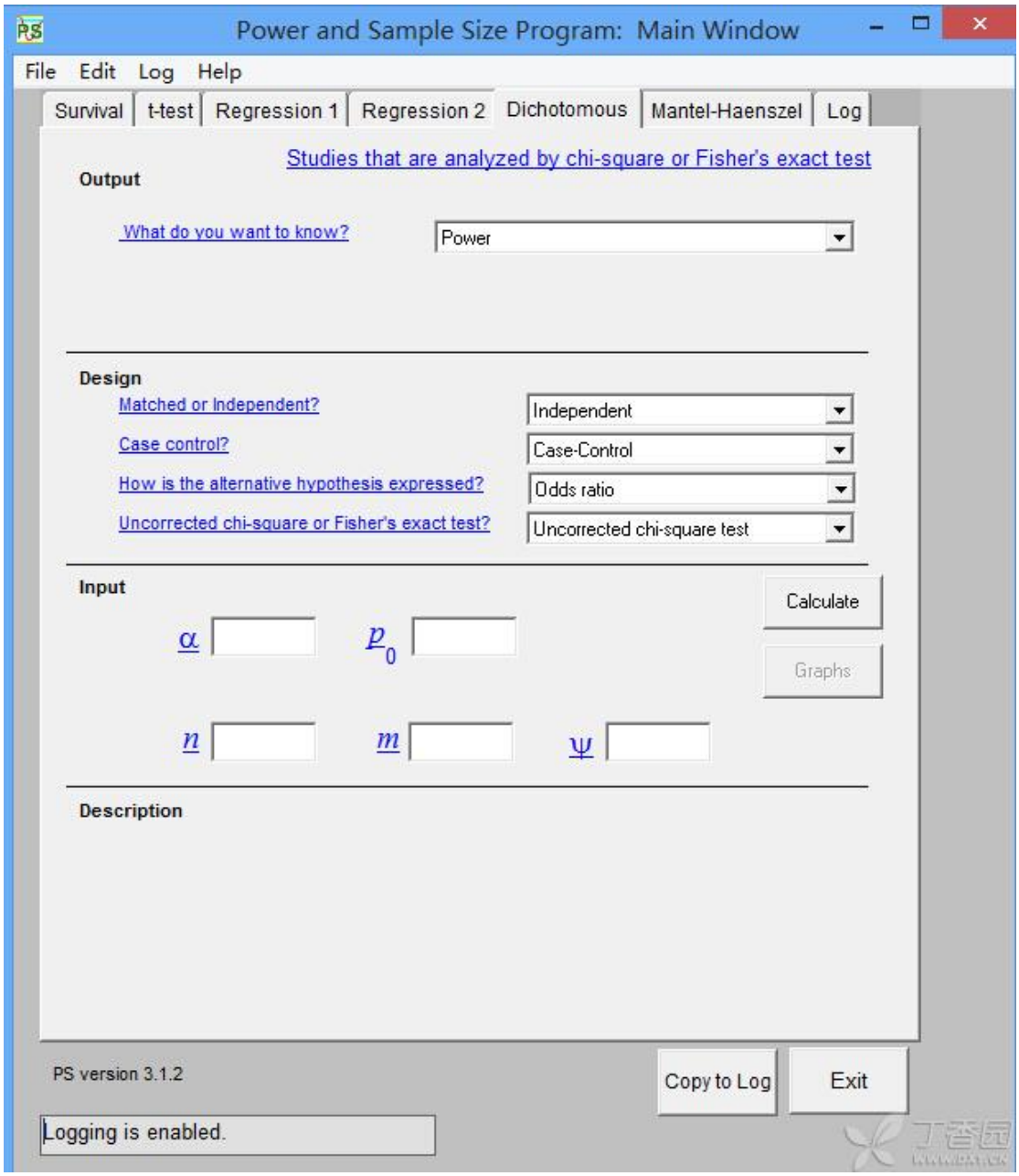
候选 SNP 位点 power 计算流程

使用 Power and Sample Size Program。SNP 方面的内容应该是二分类数据，下图是给出的相关文章的数据及相关软件的操作界面。

Table 2
Logistic regression analysis of associations between *STAT4* rs7574865 G/T polymorphisms and risk of rheumatoid arthritis and ankylosing spondylitis.

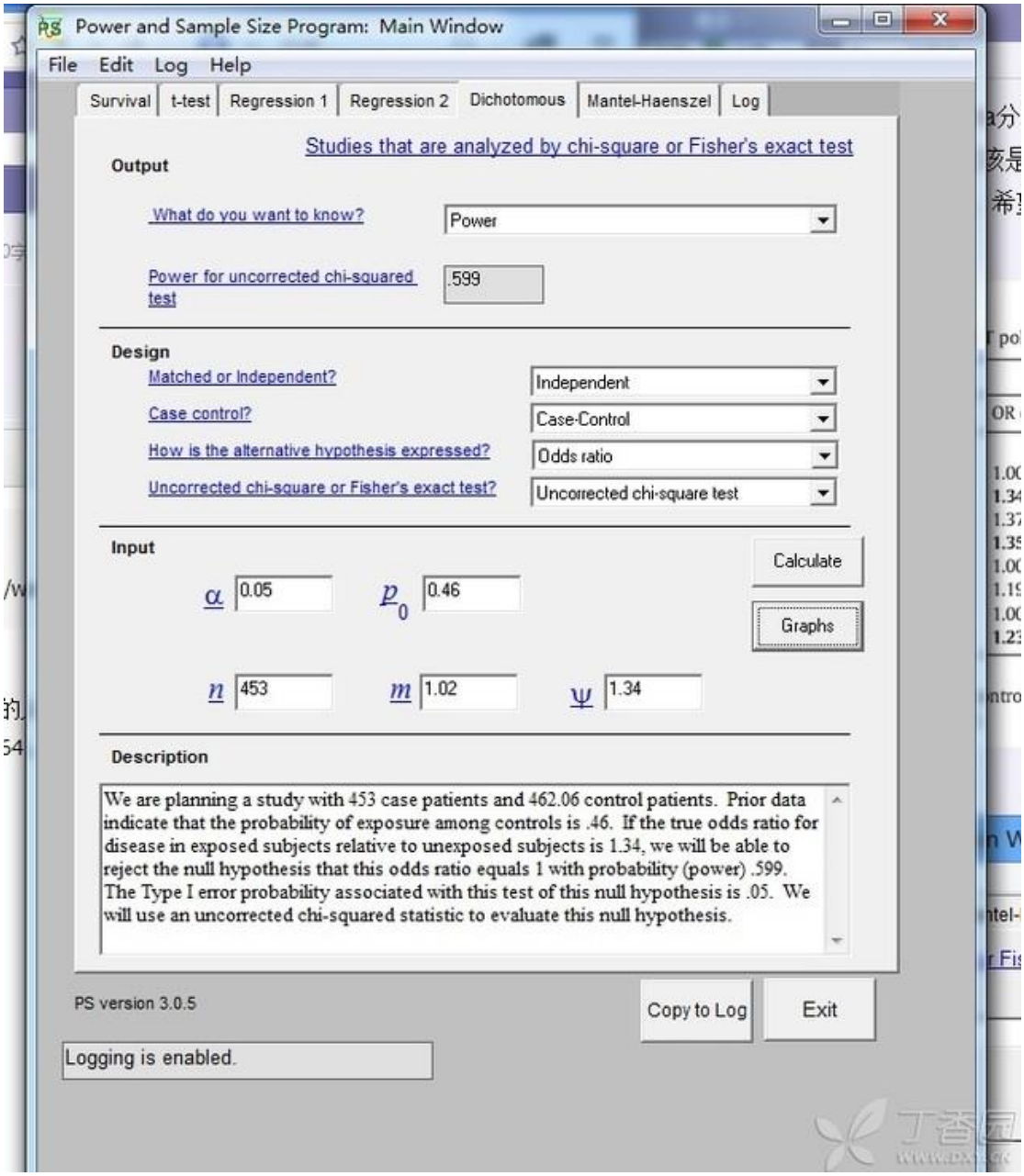
Genotype	Controls (n = 520)	RA[a] (n = 520)			AS (n = 100)		
	No. (%)	No. (%)	OR (95% CI)	*P*	No. (%)	Adjusted OR[b] (95% CI)	*P*
STAT4: rs7574865 G/T							
GG	252 (48.5)	213 (41.1)	1.00		42 (42.0)	1.00	
GT	212 (40.8)	240 (46.3)	**1.34 (1.03–1.74)**	**0.027**	46 (46.0)	1.31 (0.79–2.20)	0.299
TT	56 (10.8)	65 (12.5)	1.37 (0.92–2.05)	0.121	12 (12.0)	1.24 (0.56–2.72)	0.598
GT + TT	268 (51.5)	305 (58.9)	**1.35 (1.05–1.72)**	**0.018**	58 (58.0)	1.30 (0.80–2.11)	0.296
GG + GT	464 (89.2)	453 (87.5)	1.00		88 (88.0)	1.00	
TT	56 (10.8)	65 (12.5)	1.19 (0.81–1.74)	0.373	12 (12.0)	1.08 (0.51–2.27)	0.838
G allele	716 (68.8)	666 (64.3)	1.00		130 (65.0)	1.00	
T allele	324 (31.2)	370 (35.7)	**1.23 (1.02–1.47)**	**0.028**	70 (35.0)	1.19 (0.87–1.64)	0.285

Bold values are statistically significant ($P < 0.05$).
[a] Genotyping was successful in 518 RA cases, 100 AS cases and 520 controls for *STAT4* rs7574865 G/T.
[b] Adjusted for age and sex (not adjusted in allele comparison model).



这里面的α是检验水准即是 0.05，P0 是对照组的暴露比例，n 是病例组的人数，m 是对照组与病例组的比值，那个特殊符号即是 OR 值，对你提供的资料：比如 GT vs GG 这两行对照组人数是 464，病例组是 n，453，Po 是危险基因的频率 212/464，m 即是 464/453, OR

OR 值是 1.34，代入计算 po



wer 是 0.559,其他以此类推。