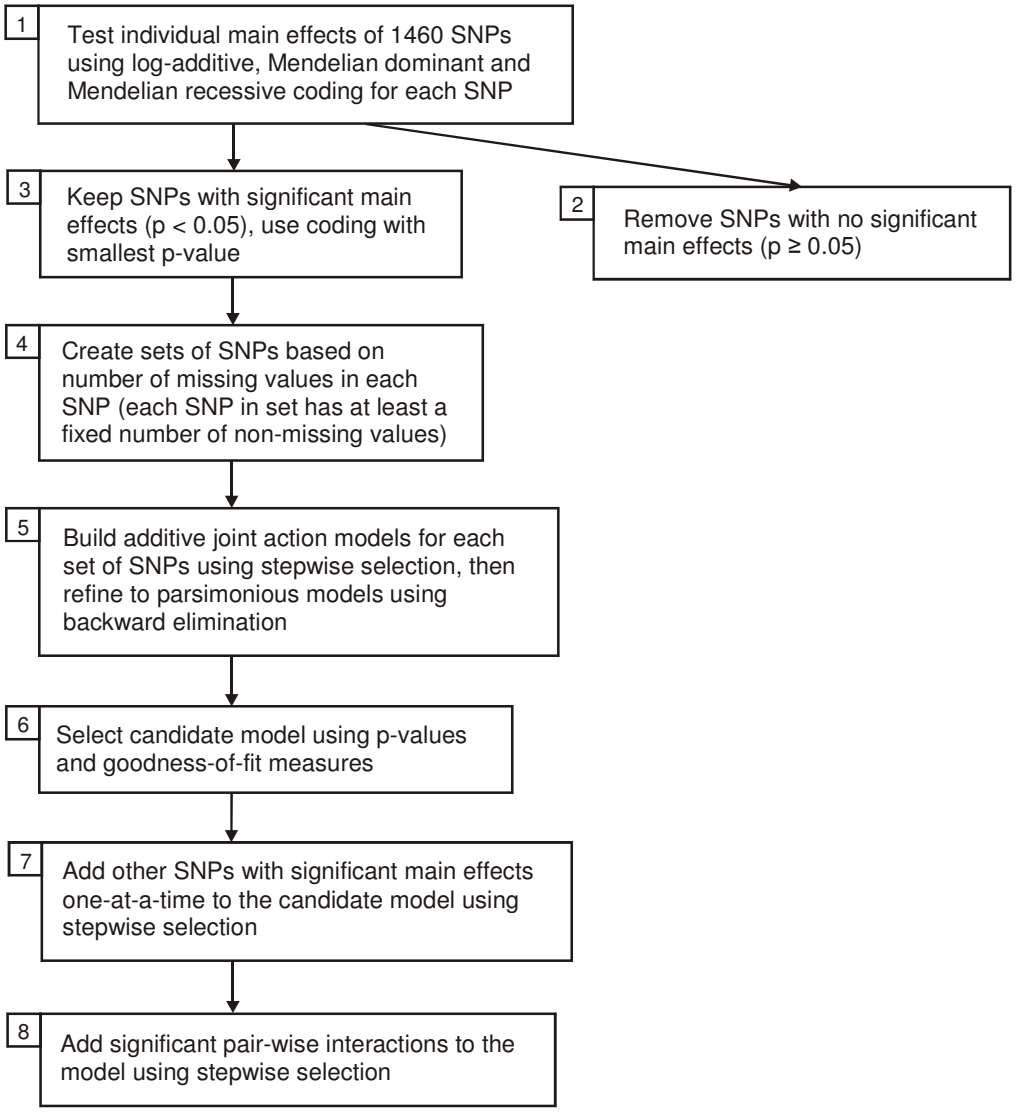
1
Test individual main effects of 1460 SNPs using log-additive, Mendelian dominant and Mendelian recessive coding for each SNP
2
Remove SNPs with no significant main effects (p ≥ 0.05)
3
Keep SNPs with significant main effects (p < 0.05), use coding with smallest p-value
4
Create sets of SNPs based on number of missing values in each SNP (each SNP in set has at least a fixed number of non-missing values)
5
Build additive joint action models for each set of SNPs using stepwise selection, then refine to parsimonious models using backward elimination
6
Select candidate model using p-values and goodness-of-fit measures
7
Add other SNPs with significant main effects one-at-a-time to the candidate model using stepwise selection
8
Add significant pair-wise interactions to the model using stepwise selection