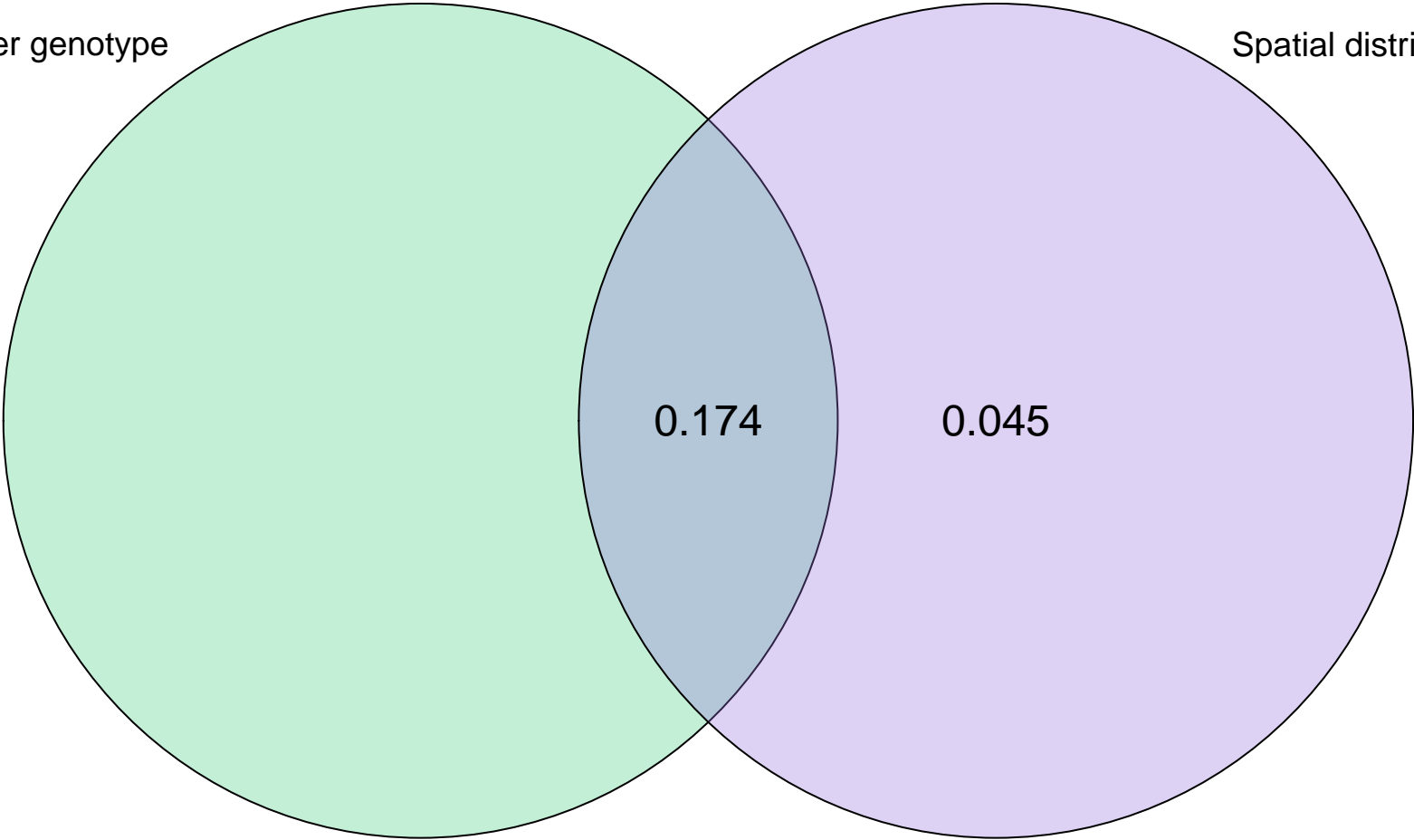


We find that -0.3% of the variance is explained by clover genotype

sig:  
[a+b] Clover genotype without controlling for spatial distribution p=0.001  
[b+c] Spatial distribution without controlling for clover genotype p=0.002  
  
not sig:  
[a] Clover genotype alone p = 0.095  
[c] Spatial distribution alone p = 0.066

lover genotype

Spatial distributi



Residuals = 0.785

Values <0 not shown