Algorithm for identifying ASD genes and networks

A Create supernodes

B

HMRF model clusters genes according to risk:

\[ P(I = \eta) \propto \exp(b^T \eta + c\eta^T \Sigma \eta) \]

C

D clustered

unclustered

E closeup

Network genes (nASD) -> probable risk genes (rASD)

F z’s distributed as a mixture of null and risk genes

G

rASD