

Graphic Lasso: Data analysis

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1 Gtex with top variance-variance genes

Table 1 is the result for Gtex data with top variance-variance genes with $r = 3, \rho = 1500$.

$A_0 : u_{kl} = 0$	Brain - Amygdala
$A_{11} : u_{k1} > 0$	Brain - Hippocampus, Brain - Hypothalamus Brain - Spinal cord (cervical c-1)
$A_{12} : u_{k1} < 0$	Brain - Cortex Brain - Anterior cingulate cortex (BA24) Brain - Frontal Cortex (BA9)
$A_{21} : u_{k2} > 0$	Brain - Cerebellum Brain - Cerebellar Hemisphere
$A_{21} : u_{k2} < 0$	Brain - Caudate (basal ganglia) Brain - Nucleus accumbens (basal ganglia) Brain - Putamen (basal ganglia)
$A_3 : u_{k3} \neq 0$	Brain - Substantia nigra

Table 1: Membership result for 13 brain tissues with $r = 3, \rho = 1500$ of Gtex data with var-var genes.

Similar results are given under the setting $r = 3, \rho = 2000$ and $r = 2, \rho = 1500, 2000$. But the clustering results do not hold when ρ is small, such as $\rho = 1000, \rho = 500$.

2 Gtex with top mean-variance genes

The Gtex data with top mean-variance genes does not work as good as variance-variance data. See Table 2.

$A_0 : u_{kl} = 0$	Brain - Putamen (basal ganglia) Brain - Amygdala Brain - Cerebellar Hemisphere
$A_{11} : u_{k1} > 0$	Brain - Cortex Brain - Cerebellum Brain - Cortex Brain - Anterior cingulate cortex (BA24)
$A_{12} : u_{k1} < 0$	Brain - Hippocampus Brain - Hypothalamus Brain - Spinal cord (cervical c-1)
$A_2 : u_{k2} \neq 0$	Brain - Substantia nigra
$A_3 : u_{k3} \neq 0$	Brain - Caudate (basal ganglia) Brain - Nucleus accumbens (basal ganglia)

Table 2: Membership result for 13 brain tissues with $r = 3, \rho = 1500$ of Gtex data with mean-var genes.

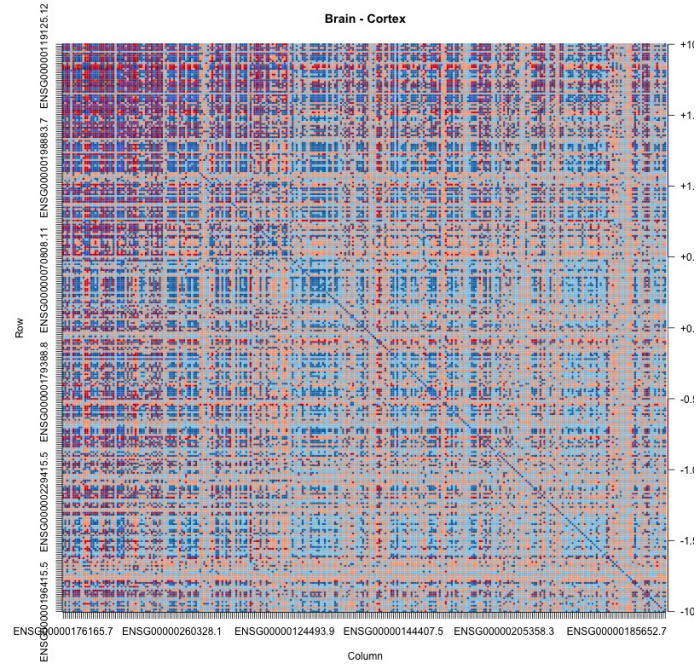


Figure 1: Cortex covariance matrix with mean-var genes.

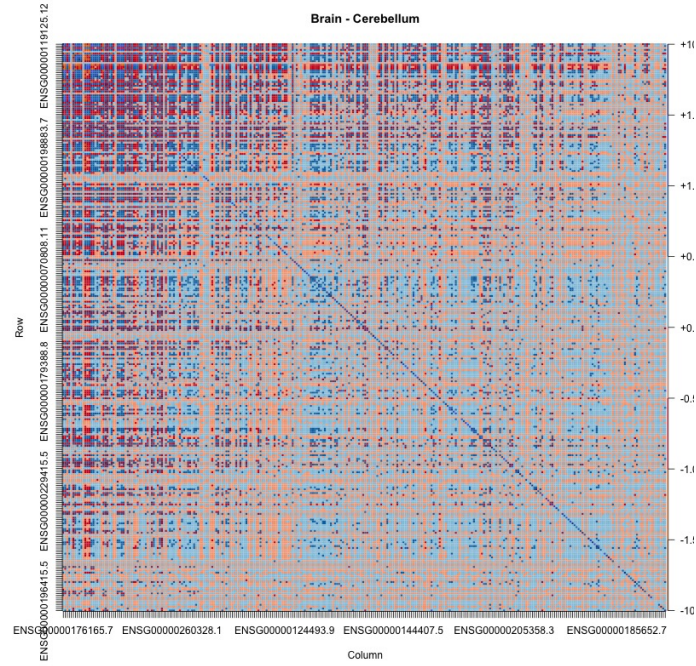


Figure 2: Cerebellum covariance matrix with mean-var genes.

Graphical checks reveal some problems.