Lu.Getz.Miska.Nature.June.2005.clustering.ep.miRNA

Module name: Lu.Getz.Miska.Nature.June.2005.clustering.ep.miRNA
Description: Hierarchical clustering of 89 epithelial samples in miRNA space.
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Summary
Hierarchical clustering of 89 epithelial samples (for which there are both mRNA and miRNA data) in the space of miRNAs shows that samples from the gastrointestinal tract are clustered together.

Hierarchical clustering of 89 epithelial samples in miRNA space

Clustering 89 epithelial samples (of the 218 miGCM samples) for which there are both mRNA and miRNA data identify a cluster which groups together samples from the gastrointestinal tract (colon, liver, pancreas and stomach), reflecting their common derivation from tissues of embryonic endoderm. In contrast, when clustering the same samples in mRNA space the coherence of gut-derived samples was not recovered.

Hierarchical clustering was performed with average linkage, unweighted average distance (UPGMA), using (1-Pearson correlation) as the distance measure. Before clustering, data were filtered to eliminate genes with expression lower than 7.25 (on a log2 scale) in all samples. Next, all features (miRNAs) were centered and normalized to a mean of 0 and a standard deviation of 1. Clustering was performed on both the samples and genes axes.

References:

- Lu, Getz, Miska, et al. “MicroRNA Expression Profiles Classify Human Cancers,” Nature 435, 834-838 (9 June 2005)
- Jain, A. K. & Dubes, R. C. Algorithms for clustering data. Prentice-Hall Inc., Upper Saddle River (1988).