

Method	Pros	Cons
Combining P-values [1]		• Over non-conservative
Fisher-Z [2]	• Increased power • Mean effect size • Heterogeneity estimate	• Globally defined effect size • Assume correlations are comparable across different systems • REM has less assumptions but with dramatically reduced power
Order statistics [3]	• Assumption free • Effect size is gene context specific	• Less power • Lack of the concept of a mean effect size • No heterogeneity measurement

References:

1. Hong F, Breitling R (2008) A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. *Bioinformatics* 24: 374-382.
2. Hu P, Greenwood CM, Beyene J (2005) Integrative analysis of multiple gene expression profiles with quality-adjusted effect size models. *BMC Bioinformatics* 6: 128.
3. Stuart JM, Segal E, Koller D, Kim SK (2003) A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. *Science* 302: 249-255.