

Batch correction of microarray data substantially improves the identification of genes differentially expressed in rheumatoid arthritis and osteoarthritis.

Kupfer P, Guthke R, Pohlers D, Huber R, Koczan D, Kinne RW (2012) Batch correction of microarray data substantially improves the identification of genes differentially expressed in rheumatoid arthritis and osteoarthritis. *BMC Med Genomics* 5, 23.

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Abstract

Batch effects due to sample preparation or array variation (type, charge, and/or platform) may influence the results of microarray experiments and thus mask and/or confound true biological differences. Of the published approaches for batch correction, the algorithm

Involved units

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