breast and lung cancer subtype analysis. Bioinformatics. 25(22):2906-12.

Bayesian Cell Mixture Model (CMM)

This is a zip file containing R code to implement CMM for analyzing tissue microarray data.
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Reference: Shen, Taylor, and Ghosh (2008) Reconstructing tumor-wise protein expression in tissue microarray studies using a Bayesian cell mixture model. Bioinformatics. 24(24):2880-6.

Eigengene-based Linear Discriminant Analysis (ELDA)

This is a zip file containing R code to implement ELDA for tumor classification problems using gene expression microarray data. The README file describes how to use the code.
Download zip file

Reference: Shen et al. (2006) Eigengene-based linear discriminant model for tumor classification using gene expression microarray data.Bioinformatics. 22(21):2635-42.

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