

*A decomposition model to track gene expression signatures: preview on
observer-independent classification of ovarian cancer
Martoglio, Miskin, Smith, and MacKay (2002) Bioinformatics*

Gene signatures revealed by independent component analysis (ICA) of ovarian cDNA array data: Learning run.

Hybridization signal profiles for fifteen ovarian samples were analyzed by independent component analysis (ICA). Tissues 1, 3, 4, and 5 correspond to normal ovary; tissues 6-10 to serous papillary adenocarcinoma (spa); tissues 11, 12, and 14 to poorly differentiated serous papillary adenocarcinoma (pd-spa); tissue 15 to benign serous cystadenoma; and tissues 16 and 17 correspond to samples of ovarian benign mucinous cystadenoma. A number of hidden gene expression profiles (gene signatures) were unveiled by the initial ICA run and are represented at each row. Gene signature 3 (blue circle), 7 (green circle), and 12 (red circle) are seen to be distinctively prominent in bmc, bsc, and pd-spa samples, respectively.

