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Training microarrays

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   Translating data from microarray gene profiling experiments into reliable diagnostic tools for cancer is a formidable challenge. In the June issue of Nature Medicine, Khan *et al.* describe a method to train computers to perform cancer classification (*Nature Medicine* 2001, **7:**673-679). They chose to tackle pediatric small round blue-cell tumours (SRBCTs), as they are heterogeneous and difficult to diagnose. They used artificial neural networks (ANNs), computer algorithms that are modelled on human brain function and can be trained to 'learn' complex pattern recognition. Data from cDNA microarrays containing over 6500 genes were used to train ANN models with 63 SRBCT samples (23 tumours and 40 cell lines). The patterns of 96 gene transcripts could distinguish between four distinct tumour subtypes. The ANN models were 100% efficient in diagnosing and classifying subsequent tumours samples. The set of SRBCT-expressed genes includes a large number not previously associated with the disease.

References

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