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Finding out where and when a gene is expressed is often the first approach to discovering its physiological function. To help researchers follow expression patterns, the Cancer Genome Anatomy Project has established [SAGEmap](#), a database of expression data from serial analysis of gene expression (SAGE) studies. In the Early Edition of the [Proceedings of the National Academy of Sciences](#), Boon *et al.* report the creation of [SAGE Genie](#), a set of [bioinformatics tools](#) that allow the user to navigate the mountains of gene expression-data. Boon *et al.* began with 6.8 million experimentally observed SAGE tags, which they processed into 105 databases according to different features. They also assessed the quality and reliability of each tag sequence, and created a list of 'confidence SAGE tags'. The 'SAGE Anatomic Viewer' offers a simple interface, showing the graphical representation of tissue-specific gene-expression patterns. Such web-based tools will be critical to future attempts to link gene-expression data to human diseases.

References

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