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The cover image shows a direct interaction network of genes that are potentially important in mediating the effects of tobacco smoke in human oral mucosa. The color red reflects a higher level of gene expression and green reflects a lower level of gene expression in smokers versus in never smokers; the increasing intensities of color signify the magnitude of the expression change. Genes with no significant expression change (white) are shown because they potentially contribute to the effects of smoking and are involved in signaling pathways perturbed in the oral mucosa of smokers. Network analysis identified specific molecular interactions, hubs, and key transcription regulators. Computational biology, including molecular network mapping as represented on this cover, is a strategy to identify potential targets for chemopreventive agents. See articles by Boyle, Gümüş, et al. (beginning on page 266) and Spira (beginning on page 255) for more information.