

## Assessing Risk in Families with Cancer

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### Abstract

Identifying individuals at high risk of cancer because of inherited genetic susceptibility is complex and important. Probabilistic prediction algorithms that exploit domain knowledge of Mendelian inheritance and other biological characteristics of susceptibility genes successfully contribute to improved cancer screening, prevention, and genetic testing, and to the design and analysis of cancer studies. I will first briefly present the principles behind four Mendelian models: BRCAPRO for the BRCA genes, MMRpro for HNPCC, PancPRO for pancreatic cancer, and MelaPRO for melanoma. I will focusing on recent progress including incorporation on molecular markers. I will then discuss issues in software for dissemination of familial risk algorithms, and present some of the challenges that remain to be addressed.

*Keywords:* Risk prediction; Genetics; Mendelian models; Molecular markers.

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