

C121

A new (Bayesian) classification of Human breast cancer

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For node-negative breast cancer great uncertainty still exists in identifying those women who require adjuvant chemotherapy and those who could safely avoid such aggressive treatment. A 70 gene expression signature has recently been used to define poor and good prognosis breast cancers, and it is now proposed that this two group classification should be used to guide the use of adjuvant chemotherapy (van de Vijver et al., 2002, N Engl J Med 347:1999-2009). Here we use Bayesian methods to reanalyse this 70 gene expression profile from 295 breast cancer patients. Our analyses support the originally proposed two group division but shows that it is a sub-optimal interpretation of the data. Instead patients should be assigned to a minimum of four processes or groups: two distinct high risk groups, a low risk group and one group with no risk of death from disease. Use of Bayesian methods on further independent breast cancer microarray datasets also classified cancers into four main processes, and provided additional evidence for the existence of a separate novel category of breast cancer associated with little or no risk of death from disease.