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The Role and Importance of Genome Sequencing in Prediction of Cancer Risk

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Abstract : The role and relative importance of intrinsic and extrinsic factors in the development of complex diseases such as cancer still remains a controversial issue. Determining the amount of variation explained by these factors needs experimental data and statistical models. These models are nevertheless based on the occurrence and accumulation of random mutational events during stem cell division, thus rendering cancer development a stochastic outcome. We demonstrate that not only individual genome sequencing is uninformative in determining cancer risk, but also assigning a unique genome sequence to any given individual (healthy or affected) is not meaningful. Current whole-genome sequencing approaches are therefore unlikely to realize the promise of personalized medicine. In conclusion, since genome sequence differs from cell to cell and changes over time, it seems that determining the risk factor of complex diseases based on genome sequence is somewhat unrealistic, and therefore, the resulting data are likely to be inherently uninformative.

Keywords : cancer risk, extrinsic factors, genome sequencing, intrinsic factors
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