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Session : Classification

Progress and open challenges in extremely high-dimensional medical outcome prediction

par **Kevin Bleakley**

Using biological data for medical decisions requires "extremely high" prediction accuracy; mistakes can lead to death. Very few current statistical methods are good enough to be used in life-threatening clinical decisions, e.g. choice of low vs high chemotherapy dose for breast cancer patients. Difficulties include (1) the above moral reason, (2) high-dimensionality of data ($p \gg n$) and (3) the possibility that data does not contain enough information to construct a near-perfect classification rule. I will review the current state-of-the-art in high-dimensional biological decision-making, showing what statistical methods are being used, their success (or lack of), and suggest possible future research directions. In particular, I will describe Next Generation Sequencing approaches, their faster-than-exponential drop in cost, and implications for the next five years at the statistics/biology interface.

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