

Abstract

Many research hypotheses being explored following modern biological developments require collaborations that may include biological, computational, mathematical and statistical scientists. As a consequence, today we have a proliferation of bioinformatic techniques and they range from the very ad hoc to very highly parameterised procedures. A major stumbling block continues to be that, in general, we do not understand the "information" in the biology and the output produced by much current biological technology as well as we would like in order to be able to develop truly relevant and robust approaches. In this talk, examples will be given mainly drawn from genomics (including microarrays) of useful statistical methods we have been developing to gain insight into biological mechanisms.