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Sommario/riassunto	As has been well-discussed, the explosion of interest in Bayesian methods over the last 10 to 20 years has been the result of the convergence of modern computing power and eficient Markov chain Monte Carlo (MCMC) algo- rithms for sampling from and summarizing posterior distributions. Prac- titioners trained in traditional, frequentist statistical methods appear to have been drawn to Bayesian approaches for three reasons. One is that Bayesian approaches implemented with the majority of their informative content coming from the current data, and not any external prior informa- tion, typically have good frequentist properties (e.g., low mean squared er- ror in repeated use). Second, these methods as now readily implemented in WinBUGS and other MCMC-driven software packages now over the simplest approach to hierarchical (random erects) modeling, as routinely needed in longitudinal, frailty, spatial, time series, and a wide variety of other settings featuring interdependent data. Third, practitioners are

attracted by the greater flexibility and adaptivity of the Bayesian approach, which permits stopping for efacacy, toxicity, and futility, as well as facilitates a straightforward solution to a great many other specialized problems such as dose-nding, adaptive randomization, equivalence testing, and others we shall describe. This book presents the Bayesian adaptive approach to the design and analysis of clinical trials--Provided by publisher.