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offers a comprehensive introduction to using Mathematica and the Wolfram Language for Bioinformatics. The chapters build gradually from basic concepts and the introduction of the Wolfram Language and coding paradigms in Mathematica, to detailed worked examples derived from typical research applications using Wolfram Language code. The coding examples range from basic sequence analysis, accessing genomic databases, differential gene expression, and machine learning implementations to time series analysis of longitudinal omics experiments, multi-omics integration and building dynamic interactive bioinformatics tools using the Wolfram Language. The topics address the daily bioinformatics needs of a broad audience: experimental users looking to understand and visualize their data, beginner bioinformaticians acquiring coding expertise in providing biological research solutions, and practicing expert bioinformaticians working on omics who wish to expand their toolset to include the Wolfram Language.

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Kansas' Forest Resources, 2005 W. Keith Moser 2007 The USDA Forest Service, Northern Research Station, Forest Inventory and Analysis (NRS-FIA) program is changing to a Web-based, dynamically linked reporting system. As part of the process, this year NRS-FIA is producing this abbreviated summary of 2005 data. This resource bulletin reports on area, volume, and biomass using data from 2001 through 2005. Estimates from this inventory showed a total of 2.1 million acres of forest land in the State, with almost all of it, 2.0 million acres, classified as timberland. The estimate of total net volume of live trees on forest land was 2.7 billion cubic feet. Kansas net growing-stock volume on timberland was 1.5 billion cubic feet. Aboveground live-tree biomass on timberland was estimated at 70.1 million dry tons.

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