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About the Author. Jotun Hein
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natural selection, and no gene flow or population structure, meaning that each variant is equally likely to have been passed from one generation to the next. The model looks backward in time, merging alleles into a

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"An introduction to
coalescent theory, which
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genetics and genomics.

Coalescent theory is the conceptual framework for studies of DNA sequence variation within species, and is the source of essential tools for making inferences about mutation,

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recombination, population
structure and natural
selection from DNA sequence
data"--Provided by
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Annotation In 1950, Stebbins
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Evolution and Evolution in
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synthetic theory of
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2000 on the 50th anniversary of the publication of Stebbins' classic. Following a Stebbins appreciation talk (originally slotted for his own words), papers branch into sections on: early evolution and the origin of

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Evolution, virus and bacterial
models, protocist models
(having to do with RNA
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"What underlying forces are responsible for the observed patterns of variability, given a collection of DNA sequences?" In approaching this question a number of

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probability models are
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analyzed. Throughout the
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Conceptual and empirical
richness of the field, and
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also the sense of genuine
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phylogeographic perspectives
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anthropology, evolutionary biology, medical sciences and psychology. The chapters are organized around four broad themes, with sections devoted to phenotypic and genetic variation within and between human populations,

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Molecular understanding of
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progression is at the
forefront of many research
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modern molecular techniques produce a wealth of molecular data about the structure, and function of cells, tissues, and organisms. Correctly analyzed and interpreted these data hold the promise

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of bringing new markers for prognostic and diagnostic use, for new treatment schemes, and of gaining new biological insight into the evolution of cancer and its molecular, pathological, and clinical consequences. Aimed

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at graduates and
researchers, this book
discusses novel advances in
informatics and statistics
in molecular cancer
research. Through eight
chapters from carefully
chosen experts it brings the

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reader up to date with
specific topics in cancer
research, how the topics
give rise to development of
new informatics and
statistics tools, and how
the tools can be applied.
The focus of the book is to

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understanding of key

concepts and tools, rather

than focusing on technical

issues. A main theme is the

extensive use of array

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expression and exon arrays, SNP and copy number arrays, and methylation arrays - to derive quantitative and qualitative statements about cancer, its progression and aetiology, and to understand how these technologies on

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one hand allow us learn
about cancer tissue as a
complex system and on the
other hand allow us to
pinpoint key genes and
events as crucial for the
development of the disease.

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"The present book is intended as a progress report on [the] synthetic approach to evolution as it applies to the plant kingdom." With this simple statement, G. Ledyard Stebbins formulated the

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natural selection within the
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At the time, Variation and
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significantly extended the

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plants. Plants, with their
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