

In 2014, a high-quality sequence was announced for the genome of *Homo neanderthalensis* (Neanderthals), an extinct species closely related to present-day humans. These genomes are of great interest in their own right, but they also provide important insights into evolution as well as other biological processes. Broadening the human-chimpanzee comparison to the genomes of other primates and more distantly related animals should reveal the sets of genes that control group-defining characteristics. Beyond that, comparisons with the genomes of bacteria, archaea, fungi, protists, and plants should enlighten us about the long evolutionary history of the ancient genes we all share.

With the genomes of many species fully sequenced, scientists can study whole sets of genes and their interactions, an approach called **genomics**. The sequencing efforts that feed this approach have generated, and continue to generate, enormous volumes of data. The need to deal with this ever-increasing flood of information has spawned the field of **bioinformatics**, the application of computational methods to store and analyze biological data.

We will begin this chapter by discussing two approaches to genome sequencing and some of the advances in bioinformatics and its applications. We will then summarize what has been learned from the genomes that have been sequenced thus far. Next, we will describe the composition of the human genome as a representative genome of a complex multicellular eukaryote. Finally, we will explore current ideas about how genomes evolve and about how the evolution of developmental mechanisms could have generated the great diversity of life on Earth today.

CONCEPT 21.1

The Human Genome Project fostered development of faster, less expensive sequencing techniques

Sequencing of the human genome, an ambitious undertaking, officially began as the **Human Genome Project** in 1990. Organized by an international, publicly funded consortium of scientists at universities and research institutes, the project involved 20 large sequencing centres in six countries plus a host of other labs working on smaller parts of the project.

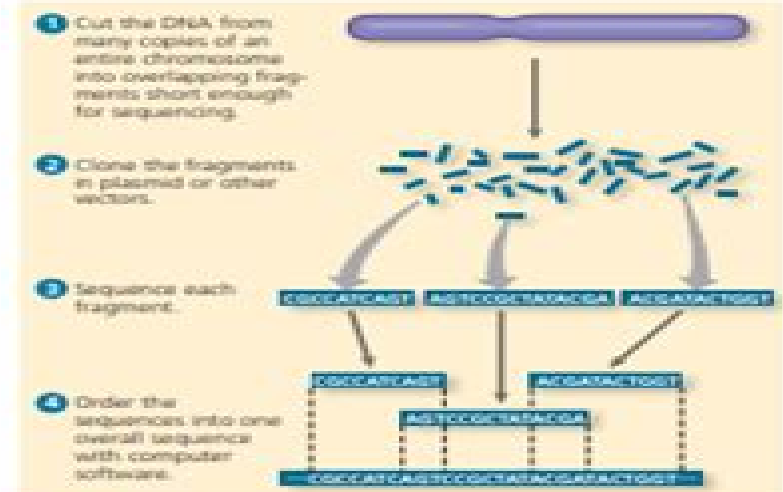
After the human genome sequence was largely completed in 2003, the sequence of each chromosome was analyzed and described in a series of papers, the last of which covered chromosome 1 and was published in 2006. At this point, the sequencing was declared “virtually complete.”

The ultimate goal in mapping any genome is to determine the complete nucleotide sequence of each chromosome. For the human genome, this was accomplished by sequencing machines, using the dideoxy chain termination method mentioned in Concept 20.1. Even with automation, though, the sequencing of all 3 billion base pairs in a haploid set of human chromosomes presented a formidable challenge. In fact, a major thrust of the Human Genome Project was the development of

technology for faster sequencing. Improvements over the years chipped away at each time-consuming step, enabling the rate of sequencing to accelerate impressively: Whereas a productive lab could typically sequence 1000 base pairs a day in the 1980s, by the year 2000 each research centre working on the Human Genome Project was sequencing 1000 base pairs per second. As of 2016, the most widely used automated machines can sequence nearly 25 million base pairs per second, while developers of some newer techniques claim they can achieve a rate of 66 billion base pairs per second. Methods that can analyze biological materials very rapidly and produce enormous volumes of data are said to be “high-throughput.” Sequencing machines are an example of high-throughput devices.

Two approaches complemented each other in obtaining the complete sequence. The initial approach was a methodical one that built on an earlier storehouse of human genetic information. In 1998, however, molecular biologist J. Craig Venter set up a company (Celera Genomics) and declared his intention to sequence the entire human genome using an alternative strategy. The **whole-genome shotgun approach** starts with the cloning and sequencing of DNA fragments from randomly cut DNA. Powerful computer programs then assemble the resulting very large number of overlapping short sequences into a single continuous sequence (**Figure 21.2**).

Y Figure 21.2 Whole-genome shotgun approach to sequencing. In this approach, developed by Craig Venter and colleagues at Celera Genomics, random DNA fragments are cloned, sequenced and then ordered relative to each other.



VISUAL SKILLS ▶ The fragments in step 2 of this figure are depicted as scattered, rather than being in an ordered array. How does this depiction reflect the approach?



HHMI Animation: Shotgun Sequencing



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leadership and drug discovery from both industry academic and charity perspectives they provide unparalleled insight into the field in a single invaluable volume **Cystic Fibrosis, Third Edition** Margaret Hodson,Andrew Bush,Duncan Geddes,2012-12-11 This international and authoritative work which brings together current knowledge in the field of cystic fibrosis has become established in previous editions as a leading reference in the field The third edition continues to provide everything that the clinician or allied health professional treating patients with cystic fibrosis will need in a single manageable volume Thoroughly revised and updated throughout it reflects the significant advances that have been made in the field since the second edition published in 2000 Cystic Fibrosis evaluates in detail the basic science that underlies the disease and its progression putting it into a clinical context Diagnostic and clinical aspects are covered in depth as are monitoring the condition and the importance of multi disciplinary care reflected in the sections into which the new edition has been sub divided to improve accessibility Future developments including novel therapies are covered in a concluding section The clinical areas have been much expanded with the introduction of separate chapters covering sleep lung mechanics and the work of breathing upper airway disease insulin deficiency and diabetes bone disease and sexual and reproductive issues A new section on monitoring discusses the use of databases to improve patient care and covers monitoring in different age groups exercise testing and the outcomes of clinical trials in these areas Separate chapters are devoted to paramedical issues including nursing physiotherapy psychology and palliative and spiritual care Throughout the emphasis is on providing an up to date and balanced review of both the clinical and basic sciences aspects of the subject and to reflect the multi disciplinary nature of the cystic fibrosis care team Drawing on the expertise of a team of international specialists from a variety of backgrounds the third edition of Cystic Fibrosis will continue to find a broad readership among respiratory physicians paediatricians specialist nurses and other health professionals working with patients with cystic fibrosis *Elsevier Comprehensive Guide PGME With Companion Website - Volume 3* Exam,2009 Biology Neil A. Campbell,Jane B. Reece,2005 The Art Notebook contains all the line art from the text without labels so students can take notes in class without having to draw the diagrams **Fetal and Neonatal Physiology for the Advanced Practice Nurse** Amy Jnah,Amy J. Jnah,Andrea Nicole Trembath,2019-01-08 Written for neonatal and pediatric nurse practitioner students Fetal and Neonatal Physiology for the Advanced Practice Nurse explores the developmental physiology of premature and term infants and presents common diseases that affect this specialized population This unique text offers an innovative and engaging approach to learning normal and abnormal physiology to prepare students for their roles as resourceful and informed problem solvers caregivers and health promoters Part One introduces core concepts including fetal origins of disease genetic inheritance patterns and placental physiology Part Two investigates each major human body system Finally Part Three offers an exploration into the transition to extrauterine life and common challenges for perinatal and neonatal clinicians With a multitude of student learning resources and tools Fetal and Neonatal Physiology for the Advanced Practice

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