DOWNLOAD PDF THE DNA STORY: GERMS, GENES, AND GENOMICS

Chapter 1 : DNA and Genomics | Q?rius, Smithsonian National Museum of Natural History

Chapter 4: The DNA Story: Germs, Genes, and Genomics 1: In Griffith's experiment, the transforming factor that changed a harmless strain of pneumococci into a pathogenic strain was: toxin.

These 10 facts about space will blow your mind A genome is defined as all the deoxyribonucleic acid DNA that is inside a cell. This includes the DNA in the mitochondria and the chromosomes inside the nucleus of the cell. The DNA transmits instructions to build and maintain the cells that comprise each person. The complete set of instructions is called the genome. Many people wonder about the purpose of the genome. The chromosomes give the instruction that allow a single cell develop from an embryo to an adult with over trillion cells. The DNA also instructs cells how to respond to various stimuli throughout the life of the person, such as how to respond to germs, pollutants, and foods. The DNA forms a twisted double- helix that is comprised of about 3 billion pairs of nucleotides - adenosine, cytosine, thymine, and guanine. In addition, the way the nucleotides are strung together makes specific genes and tells the cell how to make certain proteins. Thousands and thousands of proteins are required to build a human and each genome contains approximately 20, genes. Ad The Human Genome Project was an international research project. The goal was to sequence and map out all the genes in the human body. It was completed in and gave researchers the chance to look at the complete map for what it takes to build a human being, from a genetic standpoint. There are a few small gaps; however, until researchers can invent newer technologies, those gaps will remain blank. New research projects are constantly in the works regarding the genome. Scientists are now excited over comparative genomics. Comparative genomics compared the genome sequences of several different organisms, such as humans, mice, yeast , and monkeys. By comparing the human genome with genomes from other species, researchers home to identify both differences and similarities. The goal is to help researchers learn more about how human genes work and thereby fight human diseases. As with many scientific research projects, the study of the genome can cause raise some moral questions. As researchers learn more about evolution from the study of the human, it may affect views of gender and race. It also may lend to new factors to consider regarding identity and what it means to be human and raise social, moral, psychological, and ethical question for both present and future generations.

Chapter 2 : Is Elizabeth Warrenâ€™s genetic test conclusive? Itâ€™s complicated - The Boston Globe

Chapter 4: The DNA Story: Germs, Genes, and Genomics. Â«Back to All Flashcards To use these Flashcards, you must have Macromedia Flash Player installed on your computer (a free download).

You might be wondering how we can identify the precise order of nucleotides of a DNA molecule. This is where DNA sequencing comes into action. What is DNA Sequencing? Sequencing is the operation of determining the precise order of nucleotides of a given DNA molecule. DNA sequencing is used to determine the sequence of individual genes, full chromosomes or entire genomes of an organism. In , Sanger had completed the sequence of all the amino acids in insulin. His work provided evidence that proteins consisted of chemical entities with a specific pattern, rather than a mixture of substances. Frederick Sanger Image Source: It was the most widely used sequencing method for approximately 40 years. Gene sequences are typically thousands of bases long. The largest known gene is the one associated with Duchenne muscular dystrophy. It is approximately 2. In order to study one whole gene, scientists use a simple strategy known as shotgun sequencing. The long DNA sequence is assembled from a series of shorter overlapping sequences. Shotgun Sequencing Shotgun Sequencing Special machines, known as sequencing machines are used to extract short random DNA sequences from a particular genome we wish to determine target genome. Current DNA sequencing technologies cannot read one whole genome at once. It reads small pieces of between 20 and bases, depending on the technology used. These short pieces are called reads. Special software are used to assemble these reads according to how they overlap, in order to generate continuous strings called contigs. These contigs can be the whole target genome itself, or parts of the genome as shown in the above figure. The process of aligning and merging fragments from a longer DNA sequence, in order to reconstruct the original sequence is known as Sequence Assembly. In order to obtain the whole genome sequence, we may need to generate more and more random reads, until the contigs match to the target genome. Given a set of sequences, find the minimal length string containing all members of the set as substrings. The sequence assembly problem can be compared to a real life scenario as follows. Assume that you take many copies of a book, pass each of them through a shredder with a different cutter, and then you try to make the text of the book back together just by gluing together the shredded pieces. It is obvious that this task is pretty difficult. Furthermore, there are some extra practical issues as well. The original copy may have many repeated paragraphs, and some shreds may be modified during shredding to have typos. Parts from another book may have also been added in, and some shreds may be completely unrecognizable. It sounds very confusing and quite impossible to be carried out. This problem is known to be NP Complete. NP complete problems are problems whose status is unknown. No polynomial time algorithm has yet been discovered for any NP complete problem, nor has anybody yet been able to prove that no polynomial-time algorithm exists for any of them. However, there are greedy algorithms to solve the sequence assembly problem, where experiments have proven to perform fairly well in practice. A common method used to solve the sequence assembly problem and perform sequence data analysis is sequence alignment. The similarity being identified, may be a result of functional, structural, or evolutionary relationships between the sequences. If we compare two sequences, it is known as pairwise sequence alignment. If we compare more than two sequences, it is known as multiple sequence alignment. Next-Generation Sequencing Next-generation sequencing NGS , also known as high-throughput sequencing, is the collective term used to describe many different modern sequencing technologies such as,.

Chapter 3 : Genome: Unlocking Life's Code | Timeline

The DNA Story (Germs, Genes & Genomes) Chapter 4. STUDY. PLAY. Chapter 4 Multiple Choice Questions 1. The base sequence of a messenger RNA molecule which is.

By Razib Khan September 11, For example, imagine the phylogeny and population genetic characteristics of organisms which are endemic to the islands of Hawaii. Because the Hawaiian islands are an isolated archipelago the expectation is that lineages native to the region are going to be less shaped by the parameter of migration, or gene flow between distinct populations, than might otherwise be the case. The various characteristics, or states, which we see in the present in an individual, population, or set of populations, are the outcome of a long historical process, a sequence of precise events. To understand evolution properly it behooves us to attempt to infer the nature and magnitude of these distinct dynamic parameters which have shaped the tree of life. Verisimilus For many the image of evolutionary processes brings to mind something on a macro scale. But one can also reduce the phenomenon to a finer-grain on a concrete level, as in specific DNA molecules. Or, transform it into a more abstract rendering manipulable by algebra, such as trajectories of allele frequencies over generations. Both of these reductions emphasize the genetic aspect of natural history. Johnuniq Obviously evolutionary processes are not just fundamentally the flux of genetic elements, but genes are crucial to the phenomena in a biological sense. It therefore stands to reason that if we look at patterns of variation within the genome we will be able to infer in some deep fashion the manner in which life on earth has evolved, and conclude something more general about the nature of biological evolution. These are not trivial affairs; it is not surprising that philosophy-of-biology is often caricatured as philosophy-of-evolution. Fisher But shifting from such near-metaphysical generalities to more in-the-trenches science as it is done, we are faced today with the swell of sequence data due to the genomic revolution. What does this matter for our understanding of evolution? Many of the original arguments of evolutionary geneticists such as R. Fisher and Sewall Wright were predicated on inferences from the inheritance patterns of a few genes which were easily identifiable by their phenotypic markers. But a more likely frame for the dispute was one where the inferences were purely theoretical , deduction with a minimal level of empirical messiness intervening. These new data, first and foremost from humans due to the funding priorities of biomedical science , have stimulated a renaissance of method development to take advantage of the richness of the genetic variation now being uncovered. Consider PSMC , which allows one to make demographic inferences of population history from one genome by surveying patterns of heterozygosity within a single individual. Last week I reviewed a preprint which illustrated the power of extensive data analysis in shading and refining previous results which seemed straightforward on the face of it. The authors compared variation at different categories of bases synonymous vs. Looking at diferences between synonymous vs. These allow for the inference of correlated patterns of markers across adjacent genomic segments. This trend toward haplotype methods naturally triggered their antithesis, and the resulting synthesis to some extent can be seen in two papers, both Grossman et al. These are improvements upon earlier work in the aughts, a reassessment which had already started to occur in the literature after the excesses of genomic methods in their detection of ubiquitous selection in human populations. More specifically, the newer techniques focused on recent selective events which leave long blocks of the genome within populations homogenized. As causal markers rapidly increase in frequency due to positive selection, they drag along flanking region in sweep events. For many generations after the initial selection event these flanking regions will produce regions of linkage disequilibrium , as recombination only slowly breaks apart apart the associations across loci. But a key drawback with these methods is that selection is not the only dynamic which results in long haplotypes and linkage disequilibrium. More specifically demographic stochasticity, colloquially the vicissitudes of population history, can also generate long homogeneous blocks of markers. The initial candidate regions yielded by a statistic like iHS were saturated by the effects of population specific history. CMS , debuted in Grossman et al. Natural selection within the genome leaves more evidence behind in regards to its operation than just long halotype blocks and linkage disequilibrium. Selected alleles often exhibit greater between population difference than the average

region of the genome i. By combining tests which survey patterns of variation across loci i. This does not necessarily allow for simple follow up when you have dozens of genes and millions of bases which are potential candidates. The second paper, Grossman et al. No matter the genuine issue of false positives it does seem that recent human evolution and frankly, evolution more generally has a fixation on these traits, no pun intended. I do wonder sometimes if this is just an feature of the fact that we humans notice exterior phenotypes, as well as disease related markers e. One of the major concerns in the second paper is that a selection signature without a phenotype is often without utility, but perhaps the phenotypes are lacking in utility because humans are blind in terms of what traits are of interest. I am still skeptical of explanations for what exactly the target of selection around the EDAR locus in East Asians is. Two alleles of SLC24A5, citation: One of the more intriguing results from CMS in Grossman et al. This locus has an allele within it that is almost disjoint in frequency between Europeans and Sub-Saharan Africans. By this, I mean that almost all Africans carry one base, while nearly all Europeans care the other. It is a gene which is famously correlated with lighter skin in humans and zebrafish. And yet there remains the mystery that it is present at very high frequencies rather far south, and it is certainly not a necessary condition for light skin. East Asians are nearly fixed for the ancestral variant which is common in Sub-Saharan Africa. A possible explanation is that these sorts of salient phenotypic loci have been reshaped due to very strong bouts of selection targeting particular diseases in the recent past. If this is correct, the phenotypic characteristics which we find salient in human beings may simply be pleiotropic side effects of selective sweeps anchored around disease resistance. I am not proposing here that genomics can solve and explain evolution. The heirs of G. Simpson may have something to say about that. Rather, I am suggesting that the genetic piece of the puzzle will not be lacking in data to any extent within our lifetimes. My hunch is that many evolutionary genetic questions will be soluble when we have thousands of complete genomes of high quality on thousands of organisms. There is no likely windfall of fossils in the near future, so palentology will have to continue to operate in a relatively data constrained environment. For those who work in the domain of evolutionary genetics and genomics the onus is on human ingenuity, and analytic skill and savvy. Thinking hard and deep about difficult problems, rather than putting in long hours on the bench to glean more data.

Chapter 4 : Lungs, Germs, and Metabolites: A Cystic Fibrosis Story

History through a genetic lens: Genes, genomes, geneticists and the human past. If the media are to be believed, there is a new kind of history out there, one written and embedded in the human body itself, and just waiting to be read by genetic and genomic scientists.

Researchers stitched together the movie at Harvard University in Cambridge, Mass. Those are the codes that direct a cell to make the proteins that do its work. The new editing tool is a molecular technology that lets scientists cut apart DNA and paste it back together â€" usually in a new way. This changes the code in those genes, and therefore what they do. Last year, Seth Shipman and his colleagues at Harvard recorded bits of information. Now, this team is taking things a step further. It encoded images in bacterial DNA of a human hand, as well as of a short movie. That movie was a GIF of a galloping horse. Its five frames were images by famous turn-of-the-century photographer Eadweard Muybridge, who took pictures of animals and people in motion. The researchers stored the moving images as nucleotides. The movie has five bypixel frames. When the researchers decoded the images from later generations of bacteria, the movie looked almost as good. Original image, left; image reconstructed from bacteria, right. Strings of three nucleotides stood for 21 different shades, ranging from black to white. The scientists grew the bacteria for several generations. Then they peered into the DNA of the newest bacteria. About 90 percent of the encoded information had survived. Shipman and his colleagues shared their results July 12 in Nature. The study is part of a larger effort to use DNA to store data â€" from audio recordings and poetry to entire books. Maybe it could even store a recipe for some popcorn to go with that movie. These dwell nearly everywhere on Earth, from the bottom of the sea to inside animals. It has a value of either 0 or 1. They are copied from the genetic material of viruses that infect bacteria. The RNA then guides an enzyme, called Cas9, to cut up the virus and make it harmless. These lab-made RNAs guide the enzyme to cut specific genes in other organisms. Scientists use them, like a genetic scissors, to edit â€" or alter â€" specific genes so that they can then study how the gene works, repair damage to broken genes, insert new genes or disable harmful ones. For digital information the type stored by computers , those data typically are numbers stored in a binary code, portrayed as strings of zeros and ones. It is built on a backbone of phosphorus, oxygen, and carbon atoms. In all living things, from plants and animals to microbes, these instructions tell cells which molecules to make. Offspring inherit genes from their parents. Genes influence how an organism looks and behaves. The field of science dealing with these biological instructions is known as genetics. People who work in this field are geneticists. An animated GIF file is one that can move on the internet, such as a swirling flag or jumping frog. Molecules can be made of single types of atoms or of different types. For example, the oxygen in the air is made of two oxygen atoms O2 , but water is made of two hydrogen atoms and one oxygen atom H2O. A adenine , T thymine , C cytosine and G guanine. In RNA, uracil takes the place of thymine. A tiny area of illumination on a computer screen, or a dot on a printed page, usually placed in an array to form a digital image. Photographs are made of thousands of pixels, each of different brightness and color, and each too small to be seen unless the image is magnified.

Chapter 5 : Hybrid Vigour? Genes, Genomics, and History

The DNA Story: Germs, Genes, and Genomics Chapter Outline Introduction: Microbes as sources for discoveries about DNA A. The Roots of DNA Research Mendel and Morgan.

Facts Methods and Technology Timeline: History of genomics A timeline depicting the key events in the history of genomics and genetic research alongside those in popular culture. First international rugby union match played between England and Scotland. He finds that concentrations of thymine and adenine, and cytosine and guanine, are always found in equal amounts in samples of DNA. This suggested that A always pairs with T and C always pairs with G. Mother Theresa opens a home for the dying and destitute in Calcutta. Each codon specifies an amino acid which is added to the protein during synthesis. Kennedy becomes President of the USA. American civil rights activist Martin Luther King Jr. American rock singer Elvis Presley dies. British singer and songwriter John Lennon is shot dead in New York. Seatbelt use for drivers and front seat passengers becomes compulsory in the UK. The project aims to sequence all 3 billion letters of a human genome in 15 years. Nelson Mandela is released from prison in South Africa. Euro Disney opens near Paris in France. The film Jurassic Park is a box office hit across the world. Tom Hanks wins the Oscar for best actor for the film Forrest Gump. Rapper Tupac Shakur is shot dead in Las Vegas. Louis publish the genome of the nematode worm, C. Search engine Google is founded. Ensembl genome browser launched. The Euro is introduced as a currency in Europe. The Summer Olympics are held in Sydney, Australia. The genome of the parasite Plasmodium falciparum, which causes malaria in humans, is completed. Queen Elizabeth, the Queen Mother, dies aged years. The human genome is sequenced to Saddam Hussein, former President of Iraq, is captured by American troops in a small town km northwest of Baghdad. The genome is smaller than the human genome but larger than the mouse genome. The first same-sex marriage in the USA is performed in Massachusetts. The chimpanzee genome is completed. Apple introduces the iPhone. Next-generation sequencing platforms result in dramatic drop in sequencing costs. Barack Obama is elected as first black president of the USA. Neanderthal genome published in Nature. A magnitude 7 earthquake hits Haiti and devastates the country. Supreme Court rules that naturally occurring DNA cannot be patented. The Zebrafish genome is completed.

Chapter 6 : What is a Genome? (with pictures)

Timeline: History of genomics A timeline depicting the key events in the history of genomics and genetic research alongside those in popular culture. From the discovery of DNA, and the election of Roosevelt, right through to whole genome sequencing and Andy Murray winning Wimbledon for the first time.

Chapter 7 : The end of genomics, the beginning of analysis - Gene Expression

Genetics is the study of genes; genomics is the study of genomes. Genes are pieces of DNA that carry - among other things - the blueprints for particular traits. Those genetic recipes tell the cell how to make the proteins that form the body's structure and control vital functions.

Chapter 8 : Baltimore Sun - We are currently unavailable in your region

In the alphabet of our genes there are four letters: A, C, G and T. Just like the letters in a book make words to tell a story, so do the letters in our genomes. Genomics is the study of the sequence of these letters in your DNA and how each string of letters passes information to help each cell in your body work properly.

Chapter 9 : Microbes and Society, Third Edition

Synthetic Genomics was founded in by genomics pioneers Craig Venter, Ph.D., and Nobel Laureate Hamilton Smith, M.D., shortly after the completion of the Human Genome Project, which for the first time mapped the DNA sequence of the human genome.