

Genetics and Bioinformatics

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Genome-wide Association Studies

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1 Setting the pace

1.a What can your spit tell you about your DNA?

The use of saliva

- People spit for a variety of reasons. We've all employed the technique to remove a hair or some other distasteful object from our mouths. People who chew tobacco do it for obvious reasons. Ball players do it because they're nervous, bored or looking to showcase their masculinity. And people in many different cultures spit on their enemies to show disdain.
- Thanks to a phenomenon known as **direct-to-consumer genetic testing** or **at-home genetic testing**, people are spitting today for a much more productive (and perhaps more sophisticated) reason -- to get a glimpse of their own DNA.

(science.howstuffworks.com)



All from home. No blood. No needles. Just a small saliva sample.

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- ## 1 Order

Your saliva collection kit typically arrives within 3 to 5 days. Express shipping is available.
- ## 2 Spit

Follow kit instructions to spit in the tube provided – all from home. Register your saliva collection tube using the barcode so we know it belongs to you, and mail it back to our lab in the pre-paid package.
- ## 3 Discover

In approximately 6-8 weeks, we will send you an email to let you know your reports are ready in your online account. Log in and start discovering what your DNA says about you.



From saliva to DNA

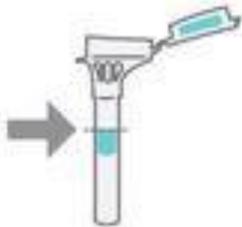
- Your saliva contains a veritable mother load of biological material from which your genetic blueprint can be determined.
- For example, a mouthful of spit contains hundreds of complex protein molecules – enzymes -- that aid in the digestion of food.
- Swirling around with those enzymes are cells sloughed off from the inside of your cheek.
- Inside each of those cells lies a nucleus, and inside each nucleus, chromosomes, which themselves are made up of DNA



Example: 23andMe



Do not eat, drink, smoke, chew gum, brush your teeth, or use mouthwash for at least 30 minutes prior to providing your sample.



Collect the recommended volume of saliva. The recommended volume of saliva to provide is 2 mL, or about $\frac{1}{2}$ teaspoon. Your saliva sample should be just above the fill line.



Provide your sample and add the stabilization buffer within 30 minutes. The full saliva sample should be collected within 30 minutes and the funnel contents should be released into the tube immediately. Waiting longer than 30 minutes may decrease the yield and quality of your DNA.



Cap securely before shipping. Remember to remove and discard the funnel lid and place the tube cap on securely before mailing your sample to our laboratory.

Your estimated lifetime risk

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Condition name



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Service Provider:	23andMe	deCODEme	Navigenics
Arthritis	✱	✱	✱
Asthma	✱	✱	
Bipolar/Depression	✱		
Cardiovascular Disease	✱	✱	✱
Multiple Sclerosis	✱	✱	✱
Osteoporosis	✱		
Parkinson's Disease			
Schizophrenia	✱		
Thrombosis	✱	✱	
Type 1/2 Diabetes	✱	✱	✱



NewStatesman



SCIENCE & TECH 15 JANUARY 2015

23andMe: Why bother with predictions about yourself when you are almost certainly average?

Want to understand your genes? Call your parents.

ETHNIC AND RACIAL STUDIES, 2016
VOL. 39, NO. 2, 142–161
<http://dx.doi.org/10.1080/01419870.2016.1105990>



In the blood: the myth and reality of genetic markers of identity

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ABSTRACT

The differences between copies of the human genome are very small, but tend to cluster in different populations. So, despite the fact that low inter-population differentiation does not support a biological definition of races statistical methods are nonetheless claimed to be able to predict successfully the population of origin of a DNA sample. Such methods are employed in commercial genetic ancestry tests, and particular genetic signatures, often in the male-specific Y-chromosome or maternally-inherited mitochondrial DNA, have become widely identified with particular ancestral or existing groups, such as Vikings, Jews, or Zulus. Here, we provide a primer on genetics, and describe how genetic markers have become associated with particular groups. We describe the conflict between population genetics and individual-based genetics and the pitfalls of over-simplistic genetic interpretations, arguing that although the tests themselves are reliable, the interpretations are unreliable and strongly influenced by cultural and other social forces.



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How many types of genetic tests exist?

- There are >2000 genetic tests available to physicians to aid in the diagnosis and therapy for >1000 different diseases. Genetic testing is performed for the following reasons:
 - conformational diagnosis of a symptomatic individual
 - presymptomatic testing for estimating risk developing disease
 - presymptomatic testing for predicting disease
 - **prenatal screening**
 - newborn screening
 - preimplantation genetic diagnosis
 - carrier screening
 - **forensic testing**
 - **paternal testing**

How is genetic testing used clinically?

- **Diagnostic medicine:** identify whether an individual has a certain genetic disease. This type of test commonly detects a specific gene alteration but is often not able to determine disease severity or age of onset. It is estimated that there are >4000 diseases caused by a mutation in a single gene. Examples of diseases that can be diagnosed by genetic testing includes cystic fibrosis and Huntington's disease.
- **Predictive medicine:** determine whether an individual has an increased risk for a particular disease. Results from this type of test are usually expressed in terms of probability and are therefore less definitive since disease susceptibility may also be influenced by other genetic and non-genetic (e.g. environmental, lifestyle) factors. Examples of diseases that use genetic testing to identify individuals with increased risk include certain forms of breast cancer (BRCA) and colorectal cancer.

How is genetic testing used clinically?

- **Pharmacogenomics:** classifies subtle variations in an individual's genetic makeup to determine whether a drug is suitable for a particular patient, and if so, what would be the safest and most effective dose. Learn more about pharmacogenomics. → DNA passports ... are no science fiction!
- **Whole-genome and whole-exome sequencing:** examines the entire genome or exome to discover genetic alterations that may be the cause of disease. Currently, this type of test is most often used in complex diagnostic cases, but it is being explored for use in asymptomatic individuals to predict future disease. See also, supporting doc on the course website: “The promise and challenges of next-generation genome sequencing for clinical care” (JAMA Intern Med. 2014)

The basics of SNP-based genetic tests

- As we will see, we can measure (genetic) **variation between individuals** at several positions on the genome, using so-called **molecular markers** such as **Single Nucleotide Polymorphisms (SNPs)**
- To run a SNP test, scientists can embed a subject's DNA into for instance a small silicon chip containing reference DNA from both healthy individuals and individuals with certain diseases.
- By analyzing how the SNPs from the subject's DNA match up with SNPs from the **reference DNA**, the scientists can determine if the subject might be predisposed to certain diseases or disorders.

Reference genome

- A reference genome (also known as a reference assembly) is a digital nucleic acid sequence database, assembled by scientists as a representative example of a species' set of genes.
- As they are often assembled from the sequencing of DNA from a number of donors, reference genomes do not accurately represent the set of genes of any single person. Instead a reference provides a haploid mosaic of different DNA sequences from each donor.
- For example GRCh37, the Genome Reference Consortium human

genome (build 37) is derived from thirteen anonymous volunteers from Buffalo, New York



"Wellcome genome bookcase" by Russ London at en.wikipedia.
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https://commons.wikimedia.org/wiki/File:Wellcome_genome_bookcase.png#/media/File:Wellcome_genome_bookcase.png

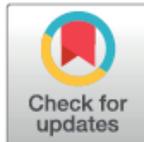
Reference genome



RESEARCH ARTICLE

Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study

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OPEN ACCESS

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1.b Speaking the language

Types of molecular markers (Schlötterer 2004)

OPINION

The evolution of molecular markers — just a matter of fashion?

Christian Schlötterer

In less than half a century, molecular markers have totally changed our view of nature, and in the process they have evolved themselves. However, all of the molecular methods developed over the years to detect variation do so in one of only three conceptually different classes of marker: protein variants (allozymes), DNA sequence polymorphism and DNA repeat variation. The latest techniques promise to provide cheap, high-throughput methods for genotyping existing markers, but might other traditional approaches offer better value for some applications?

Being able to distinguish between genotypes that are relevant to a trait of interest is a key goal in genetics. Often, this distinction is not based directly on the trait of interest, but on informative marker systems. A genetic marker provides information about allelic variation at a given locus. The first genetic map of *Drosophila melanogaster* was built by Sturtevant using phenotypic markers¹. How-

continuous improvement in the way in which we assay genetic variation; that is, the latest marker systems are the most informative ones. Nevertheless, in reviewing the history of molecular markers and their pros and cons, I argue that there are only a few conceptually different classes of marker and that recently developed high-throughput methods might not be unconditionally superior to more traditional approaches.

Allozymes

The first true molecular markers to be established were allozymes (a term that originates from a contraction of the phrase 'allelic variants of enzymes'). The principle of allozyme markers is that protein variants in enzymes can be distinguished by native gel electrophoresis according to differences in size and charge caused by amino-acid substitutions. To visualize the allozyme bands, the electrophoretic gels are treated with enzyme-specific stains that contain substrate for the enzyme, cofactors and an oxidized salt (for example, nitro-blue tetra-

sample sizes are typically studied in allozyme surveys. Nevertheless, the number of informative marker loci is too small to use allozymes for mapping and ASSOCIATION STUDIES⁸. Furthermore, surveys of natural variation based on allozymes were often challenged by non-neutral evolution of some of the markers used (see, for example, REFS 9–11).

The arrival of DNA-based markers

One of the criticisms levelled at allozyme markers is that they are an indirect and insensitive method of detecting variation in DNA. A more direct molecular marker would survey DNA variation itself, rather than rely on variations in the electrophoretic mobility of proteins that the DNA encodes. Another important advantage that DNA-based markers have over allozymes is that they allow the number of mutations between different alleles to be quantified. Given these unambiguous advantages, the arrival of DNA manipulation techniques promoted a shift from enzyme-based to DNA-based markers.

“...the arrival of DNA manipulation techniques promoted a shift from enzyme-based to DNA-based markers.”

Types of molecular markers

- Enzyme based:
 - Enzymes are biological molecules (proteins) that act as catalysts and help complex reactions occur everywhere in life.
- DNA sequence-based:
 - Nowadays, **genetic markers** represent sequences of DNA which have been traced to specific locations on the chromosomes and associated with particular traits (i.e., coded phenotype = coded subject's/object's characteristic).
 - They demonstrate **polymorphism**, which means that the genetic markers in different organisms of the same species are different.

Marker	Advantages	Disadvantages
SNPs	<ul style="list-style-type: none"> • Low mutation rate • High abundance • Easy to type • New analytical approaches are being developed at present • Cross-study comparisons are easy; data repositories already exist 	<ul style="list-style-type: none"> • Substantial rate heterogeneity among sites • Expensive to isolate • Ascertainment bias • Low information content of a single SNP
Microsatellites	<ul style="list-style-type: none"> • Highly informative (large number of alleles, high heterozygosity) • Low ascertainment bias • Easy to isolate 	<ul style="list-style-type: none"> • High mutation rate • Complex mutation behaviour • Not abundant enough • Difficult to automate • Cross-study comparisons require special preparation
Allozymes	<ul style="list-style-type: none"> • Cheap • Universal protocols 	<ul style="list-style-type: none"> • Requirement for fresh or frozen material • Some loci show protein instability • Limited number of available markers • Potentially direct target of selection
RAPDs and derivatives	<ul style="list-style-type: none"> • Cheap • Produces a large number of bands, which can then be further characterized individually (for example, converted into single locus markers) 	<ul style="list-style-type: none"> • Low reproducibility • Mainly dominant • Difficult to analyse • Difficult to automate • Cross-study comparisons are difficult
DNA sequencing	<ul style="list-style-type: none"> • Highest level of resolution possible • Not biased • Cross-study comparisons are easy; data repositories 	<ul style="list-style-type: none"> • Still significantly more expensive than the other techniques

Be critical

(date of publication = 2004)

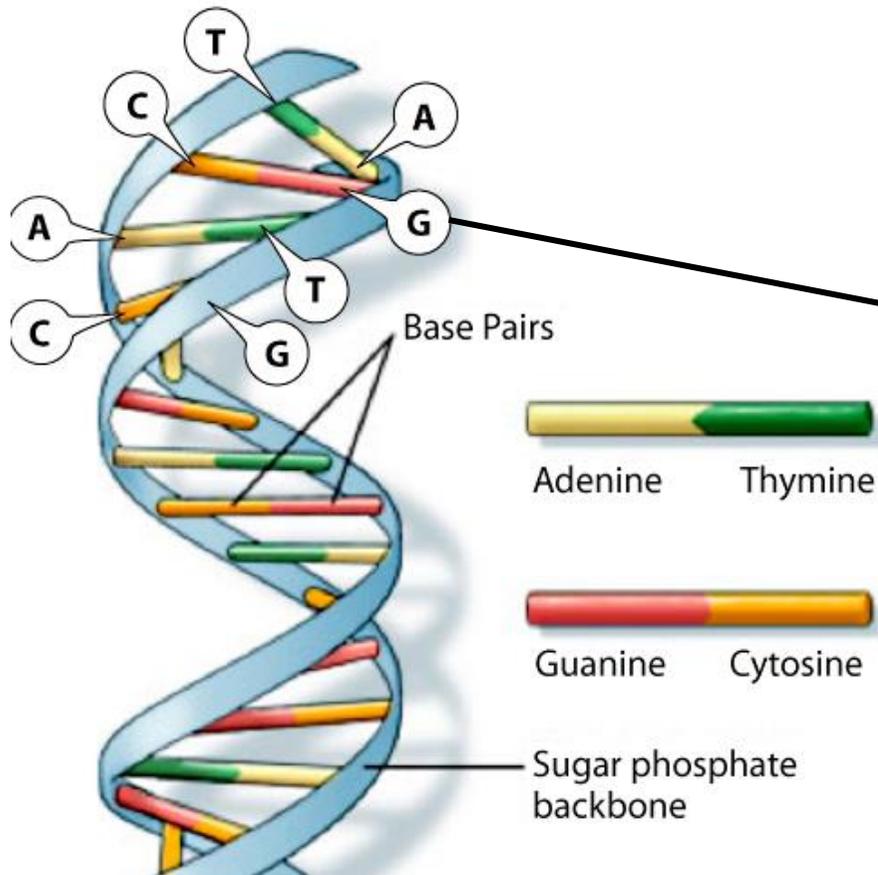
Hence, it is important to keep the historical time lines and achievements in mind

Types of genetic markers: single nucleotide polymorphisms or SNPs

- Variations in single base, i.e., one base substituted by another base
- In theory: four different nucleotides possible at base
- In practice: generally only two different nucleotides observed
- Definition strict and loose:
 - Strict: minor allele frequency $\geq 1\%$
 - Loose: ≥ 2 nucleotides observed in two individuals at position
- Nomenclature:
 - ss-number (submitted SNP number)
 - rs-number: searchable in dbSNP, mapped to external resources, unique
 - rs-numbers do not provide information about possible function of SNP
 - Alternative: nomenclature of Human Genome Variation Society

(Ziegler and Van Steen, Brazil 2010)

Types of genetic markers: single nucleotide polymorphisms



Single Nucleotide Polymorphisms (SNPs)	Frequency in general population
G	95%
A	5% > 1%

Types of genetic markers: single nucleotide polymorphisms

*Submissions received after reclustering of current build will appear as new rs# clusters in the next build.

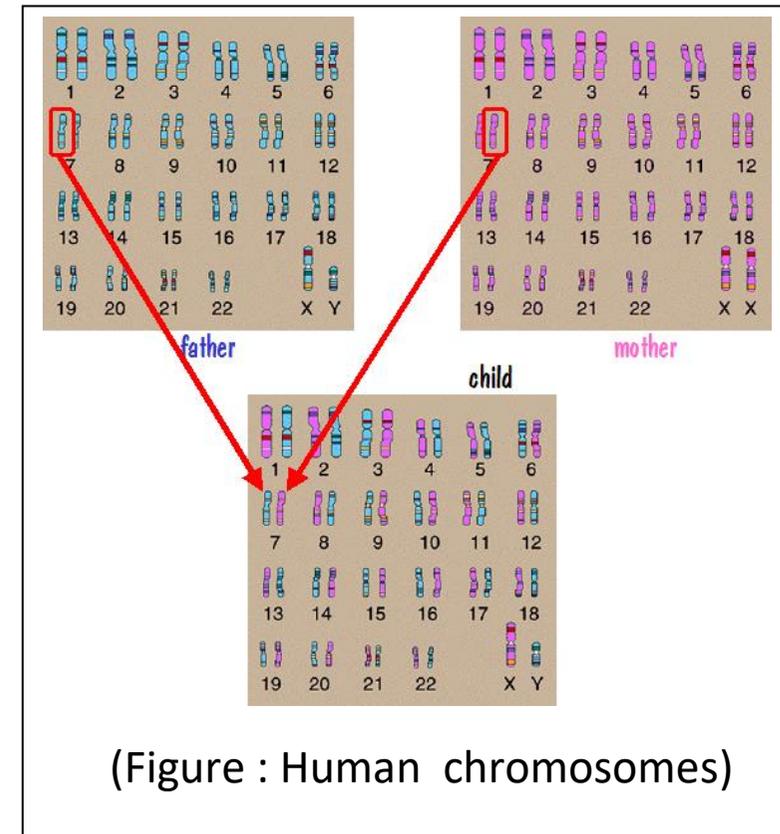
BUILD STATISTICS:

Organism	dbSNP Build	Genome Build	Number of Submissions (ss#'s)	Number of RefSNP Clusters (rs#'s) (# validated)	Number of (rs#'s) in gene	Number of (ss#'s) with genotype	Number of (ss#'s) with frequency	Number of weight 1 SNPs	Number of weight 2+ SNPs
Homo sapiens	150	38.3	907,237,763	325,658,303 (135,967,291)	191,585,061	73,917,935	129,875,536		
Bos taurus	150	7.2	332,061,559	104,286,568 (12,102,319)	46,308,631	10,202	968		
Mus musculus	150	38.5	189,214,027	84,152,707 (6,466,270)	40,278,667	24,843,897	77	DIV:9911312 MNV:452 Named:6779 SNV:67883617	DIV:180165 MNV:2259 SNV:1647286
Sus scrofa	150	5.1	195,656,177	67,116,509 (8,107,358)	36,126,981	52	184		
Ovis aries	150	2.1	147,584,937	63,745,118 (3,570,277)	30,029,327	65	173		
Macaca mulatta	150	2.1	95,808,453	53,929,680 (2,760,325)	23,087,008	29	8,072	DIV:9 SNV:32798877	SNV:38416
Zea mays	150	1.1	86,608,237	58,915,360 (14,672,946)	13,436,128	90			
Gallus gallus	150	4.1	73,244,003	24,277,657 (15,305,602)	14,926,051	3,624,831	203		
Bos indicus	150	1.1	30,533,959	17,758,946 (621)	5,131,669		223		
Arabidopsis thaliana	150	9.2	15,307,574	13,412,809 (5,947)	9,174,636	299		DIV:4 MNV:5 SNV:1069121	MNV:1 SNV:338

Genes

- The **gene** is the basic physical unit of inheritance.
- Genes are passed from parents to offspring and contain the information needed to specify traits.
- They are arranged, one after another, on structures called chromosomes.
- A chromosome contains a single, long DNA molecule, only a portion

of which corresponds to a single gene.



Gene Annotation

- An annotation (irrespective of the context) is a note added by way of explanation or commentary.
- **Genome annotation** is the process of identifying the locations of genes and all of the coding regions in a genome and determining what those genes do.
- Once a genome is sequenced, it needs to be annotated to make sense of it

→ links to giving an “interpretation”

Alleles

- Allele: one of several alternative forms of DNA sequence at specific chromosomal location
- Polymorphism: often used to indicate the existence of at least 2 alleles at a single “locus”
- **Homozygosity** (homozygous): both alleles identical at locus
- **Heterozygosity** (heterozygous): different alleles at locus
- Genetic marker: polymorphic DNA sequence at single locus
[Mutations ~polymorphisms (see later)]

Hunting for genes to answer relevant questions

- Developing new and better tools to make gene hunts faster, cheaper and practical for any scientist was a primary goal of the **Human Genome Project** (HGP).
- One of these tools is **genetic mapping**, the first step in isolating a gene. Genetic mapping – in the early days - can offer firm evidence that a disease transmitted from parent to child is **linked** to one or more genes. It also provides “clues” about where the gene lies.
- Genetic maps have been used successfully to find the single gene responsible for relatively rare inherited disorders, like cystic fibrosis, but have also been useful as a guide to identify the possible many genes underlying more common disorders, like asthma.

How to generate a genetic map?

- To produce a genetic map, researchers collect blood or tissue samples from **family members** where a certain disease or trait is prevalent.
- Using various laboratory techniques, the scientists isolate DNA from these samples and examine it for the unique patterns of bases seen only in family members who have the disease or trait. These characteristic molecular patterns are referred to as polymorphisms, or markers.
- Before researchers identify the gene responsible for the disease or trait, DNA markers can tell them roughly where the gene is on the chromosome.

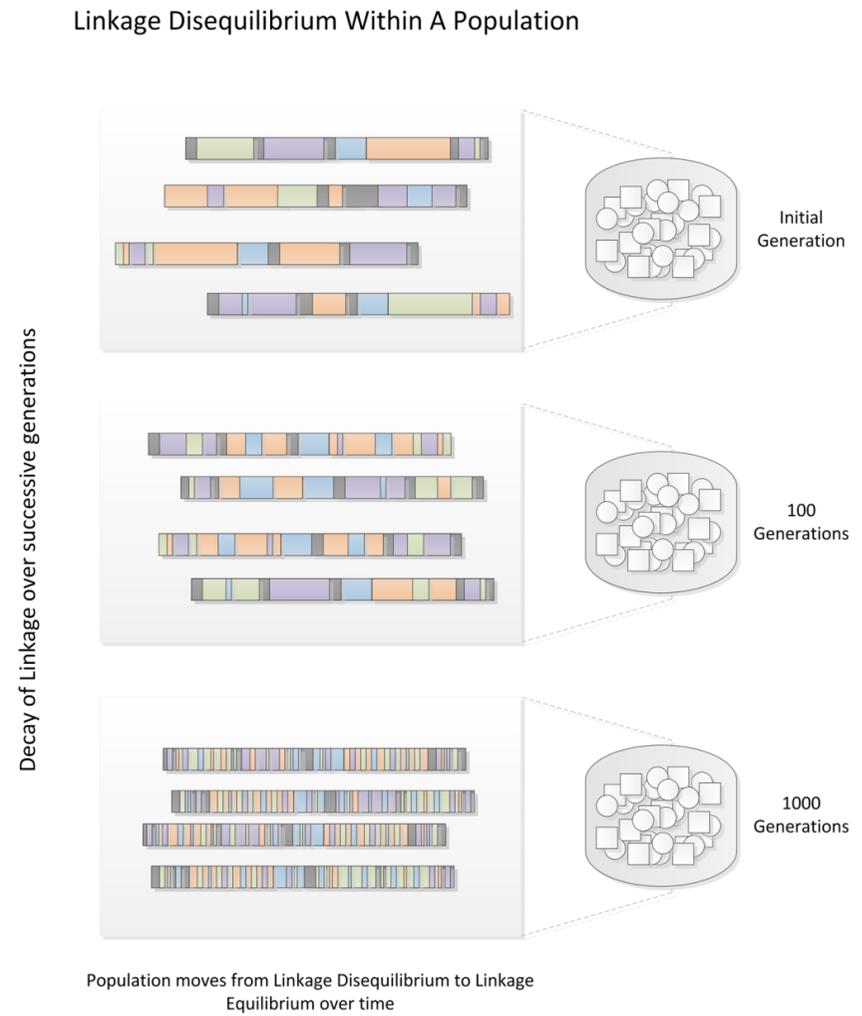
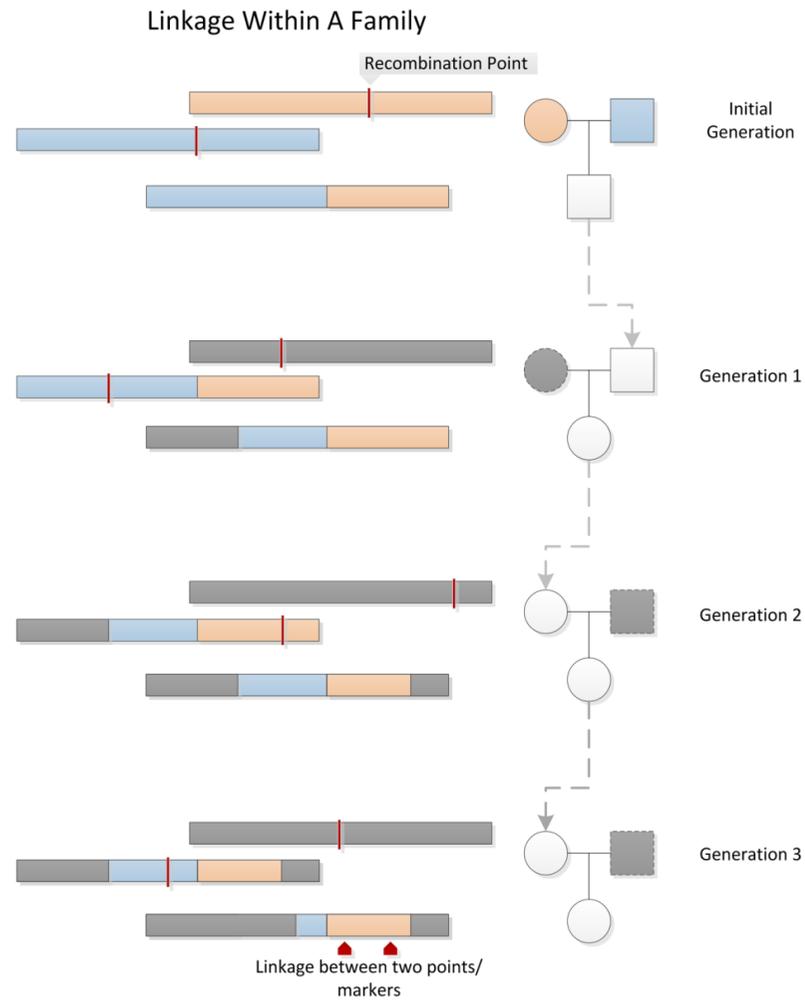
How is this possible?

How to generate a genetic map? (continued)

- This is possible because of a genetic process known as recombination.

As eggs or sperm develop within a person's body, the 23 pairs of chromosomes within those cells exchange - or recombine - genetic material. If a particular gene is close to a DNA marker, the gene and marker will likely stay together during the recombination process, and be passed on together from parent to child. So, if each family member with a particular disease or trait also inherits a particular DNA marker, chances are high that the gene responsible for the disease lies near that marker.

How to generate a genetic map? (continued)



(Bush et al. 2012)

How to generate a genetic map? (continued)

- The more DNA markers there are on a genetic map, the more likely it is that one will be closely linked to a disease gene - and the easier it will be for researchers to zero-in on that gene.
- One of the **first major achievements of the HGP was to develop dense maps of markers spaced evenly across the entire collection of human DNA.**

(<http://www.genome.gov/10000715#a1-3>)

1.c “The Human Genome Project”

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All About The Human Genome Project (HGP)



The Human Genome Project (HGP) was one of the great feats of exploration in history - an inward voyage of discovery rather than an outward exploration of the planet or the cosmos; an international research effort to sequence and map all of the genes - together known as the genome - of members of our species, *Homo sapiens*. Completed in April 2003, the HGP gave us the ability, for the first time, to read nature's complete genetic blueprint for building a human being.

In this section, you will find access to a wealth of information on the history of the HGP, its progress, cast of characters and future.

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See Also:

[YouTube White House Announcement](#)
 June 26, 2000

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 Access to the full human sequence

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Educational Resources

- [An Interactive Timeline of the Human Genome](#) [unlockinglifescode.org]
 An interactive, hyper-linked timeline of genetics that takes the reader from Mendel (1865) to the completion of the mapping of the human genome (2003).
- [The Human Genome: A Decade of Discovery, Creating a Healthy Future](#)
 A workshop for science reporters about the 10th anniversary of the completion of the draft sequence of the human genome and to look at the future of genomic research.
- [Understanding the Human Genome Project](#)
 NHGRI's Online Education Kit
- [An Overview of the Human Genome Project](#)
 A brief overview of the HGP.
- [50 Years of DNA: From Double Helix to Health](#)
 Information about the celebration of the completion of the HGP and the 50th anniversary of the discovery of the

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Historical overview

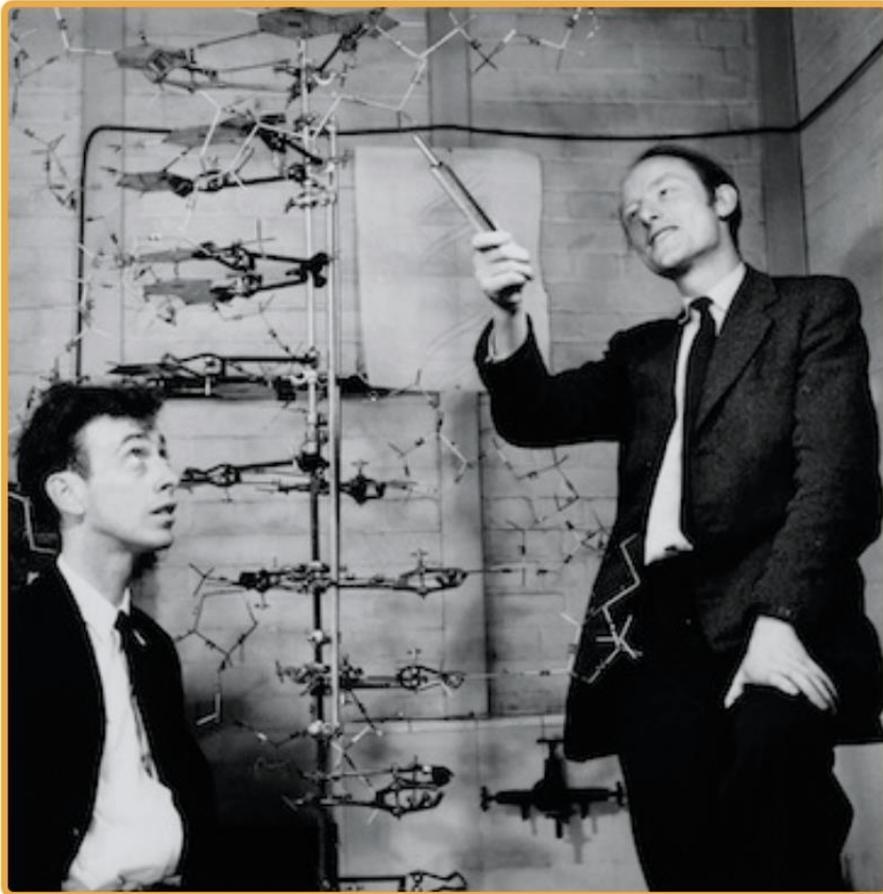


Gregor Mendel, the father of modern genetics, presents his research on experiments in plant hybridization ✕

Gregor Mendel, a 19th century Augustinian monk, is called the father of modern genetics. He used a monastery garden for crossing pea plant varieties having different heights, colors, pod shapes, seed shapes, and flower positions. Mendel's experiments, between 1856 and 1863, revealed how traits are passed down from parents. For example, when he crossed yellow peas with green peas, all the offspring peas were yellow. But when these offspring reproduced, the next generation was $\frac{3}{4}$ yellow and $\frac{1}{4}$ green. Mendel's work, which was presented in 1865, showed that what we now call "genes" determine traits in predictable ways.

1865

Historical overview

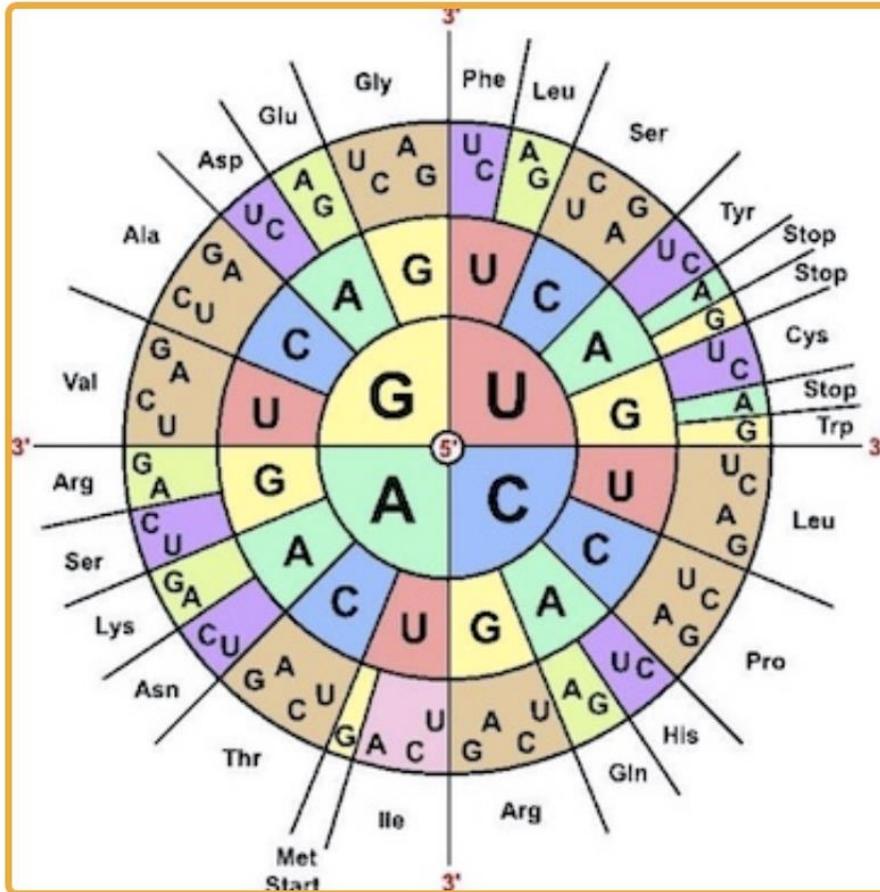


James Watson and Francis Crick discover the double helix structure of DNA

When Francis Crick and James Watson modeled the structure of DNA, they used paper cutouts of the bases (A, C, G, T) and metal scraps from a machine shop. Their model represented DNA as a double helix, with sugars and phosphates forming the outer strands of the helix and the bases pointing into the center. Hydrogen bonds connect the bases, pairing A–T and C–G; and the two strands of the helix are parallel but oriented in opposite directions. Their 1953 paper notes that the model “immediately suggests a possible copying mechanism for the genetic material.”

1953

Historical overview

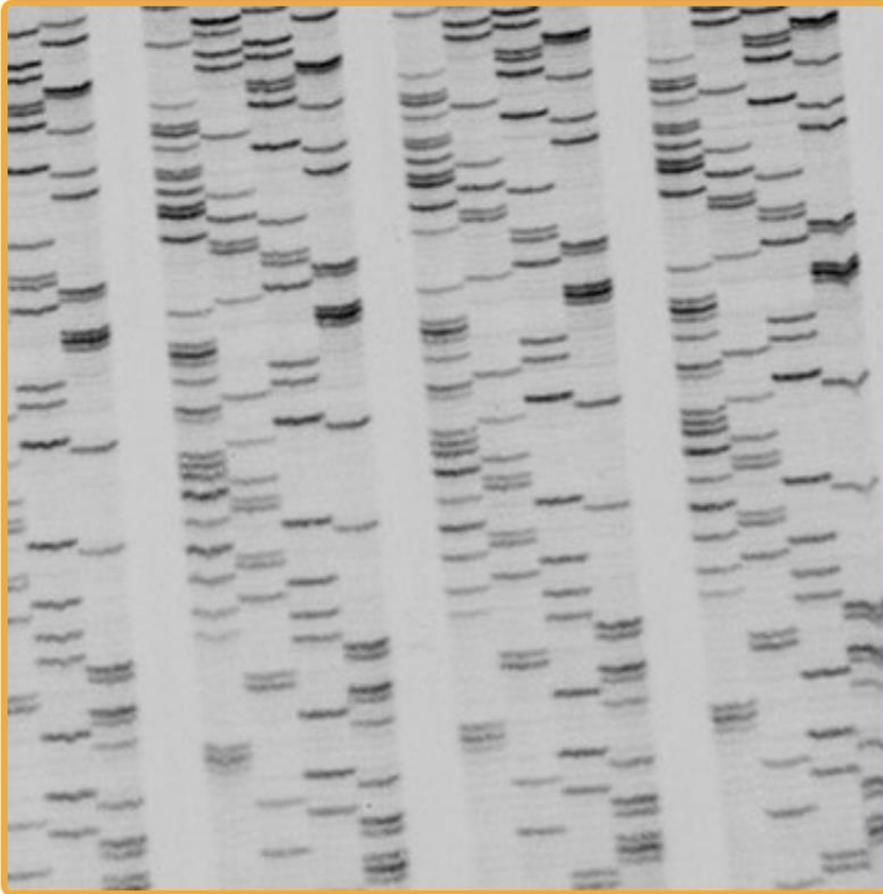


Marshall Nirenberg cracks the genetic code for protein synthesis

In the early 1960s, Marshall Nirenberg and National Institutes of Health colleagues focused on how DNA directs protein synthesis and the role of RNA in these processes. Their 1961 experiment, using a synthetic messenger RNA (mRNA) strand that contained only uracils (U), yielded a protein that contained only phenylalanines. Identifying UUU (three uracil bases in a row) as the RNA code for phenylalanine was their first breakthrough. Within a few years, Nirenberg's team had cracked the 60 mRNA codons for all 20 amino acids. In 1968, Nirenberg shared the Nobel Prize in Physiology or Medicine for his contributions to breaking the genetic code and understanding protein synthesis.

1961

Historical overview

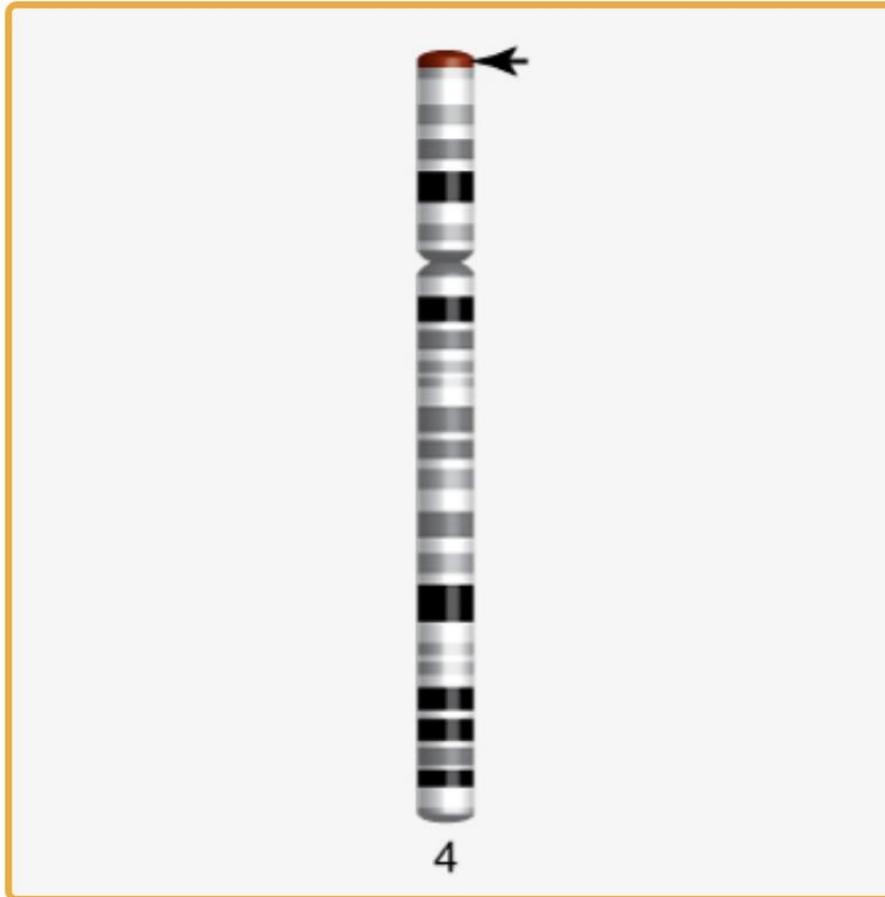


Frederick Sanger develops rapid DNA sequencing technique ✕

In 1977, Frederick Sanger developed the classical “rapid DNA sequencing” technique, now known as the Sanger method, to determine the order of bases in a strand of DNA. Special enzymes are used to synthesize short pieces of DNA, which end when a selected “terminating” base is added to the stretch of DNA being synthesized. Typically, each of these terminating bases is tagged with a radioactive marker, so it can be identified. Then the DNA fragments, of varying lengths, are separated by how rapidly they move through a gel matrix when an electric field is applied – a technique called electrophoresis. Frederick Sanger shared the 1980 Nobel Prize in Chemistry for his contributions to DNA-sequencing methods.

1977

Historical overview

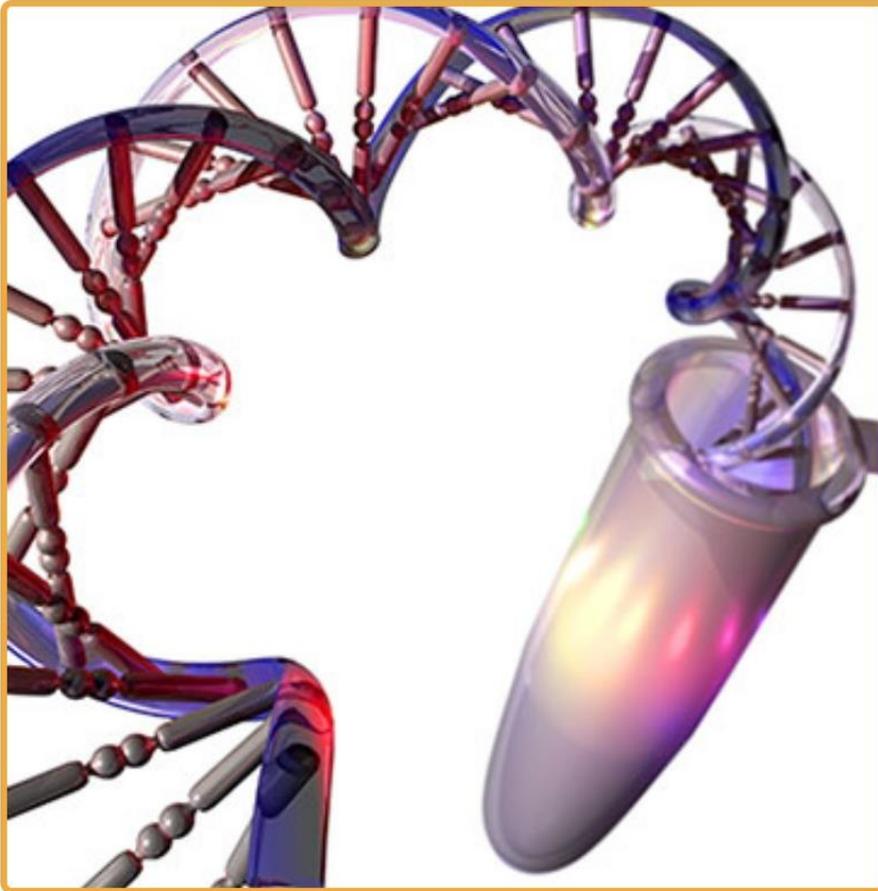


First genetic disease mapped, [✕] Huntington's Disease

Huntington's disease (HD) causes the death of specific neurons in the brain, leading to jerky movements, physical rigidity, and dementia. Symptoms usually appear in midlife and worsen progressively. The location of the HD gene, whose mutation causes Huntington's disease, was mapped to chromosome 4 in 1983, making HD the first disease gene to be mapped using DNA polymorphisms – variants in the DNA sequence. The mutation consists of increasing repetitions of "CAG" in the DNA that codes for the protein huntingtin. The number of CAG repeats may increase when passed from parent to child, leading to earlier HD onset in each generation. The gene was finally isolated in 1993.

1983

Historical overview

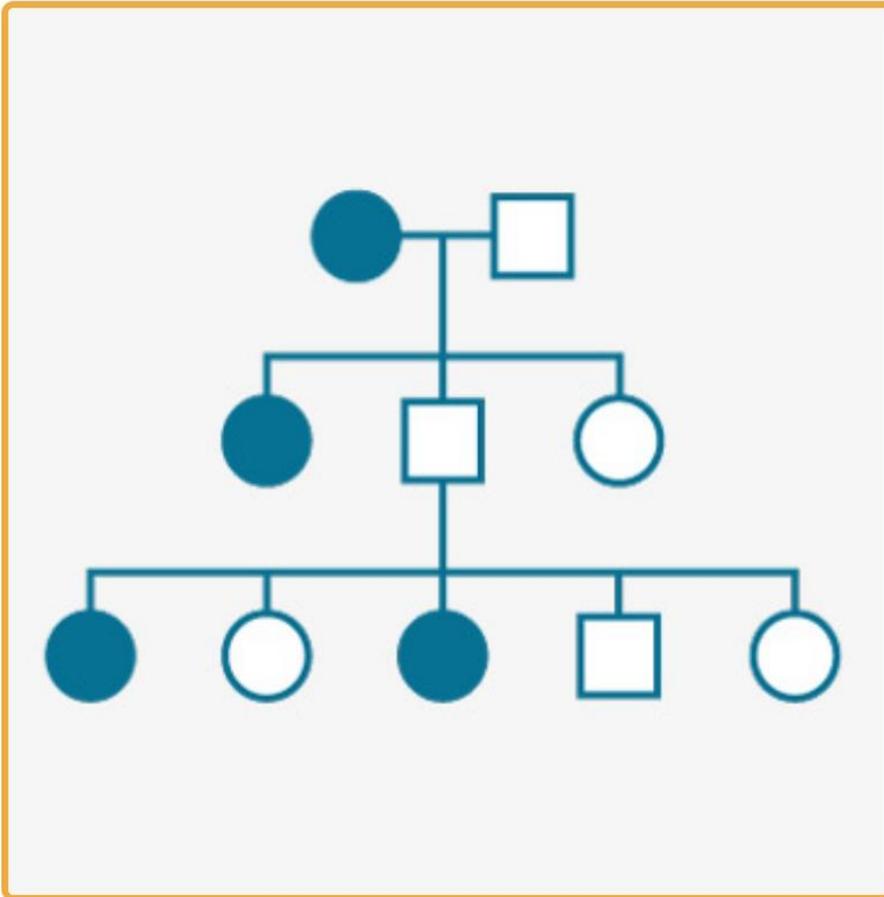


Invention of polymerase chain reaction (PCR) technology for amplifying DNA

Conceived in 1983 by Kary Mullis, the Polymerase Chain Reaction (PCR) is a relatively simple and inexpensive technology used to amplify or make billions of copies of a segment of DNA. One of the most important scientific advances in molecular biology, PCR amplification is used every day to diagnose diseases, identify bacteria and viruses, and match criminals to crime scenes. PCR revolutionized the study of DNA to such an extent that Dr. Mullis was awarded the Nobel Prize in Chemistry in 1993.

1983

Historical overview



First evidence provided for the existence of the BRCA1 gene

BRCA1 (BReast CAncer gene 1) is a “tumor suppressor gene,” which normally produces a protein that prevents cells from growing and dividing out of control. However, certain variations of BRCA1 can disrupt its normal function, leading to increased hereditary risk for cancer. The first evidence for existence of the BRCA1 gene was provided in 1990 by the King laboratory at University of California Berkeley. After a heated international race, the gene was finally isolated in 1994. Today, researchers have identified more than 1,000 mutations of the BRCA1 gene, many of them associated with increased risk of cancer, particularly breast and ovarian cancers in women.

1990

Historical overview



The Human Genome Project ✕ begins

Beginning in 1984, the U.S. Department of Energy (DOE), National Institutes of Health (NIH), and international groups held meetings about studying the human genome. In 1988, the National Research Council recommended starting a program to map the human genome. Finally, in 1990, NIH and DOE published a plan for the first five years of an expected 15-year project. The project would develop technology for analyzing DNA; map and sequence human and other genomes – including fruit flies and mice; and study related ethical, legal, and social issues.

1990

Historical overview

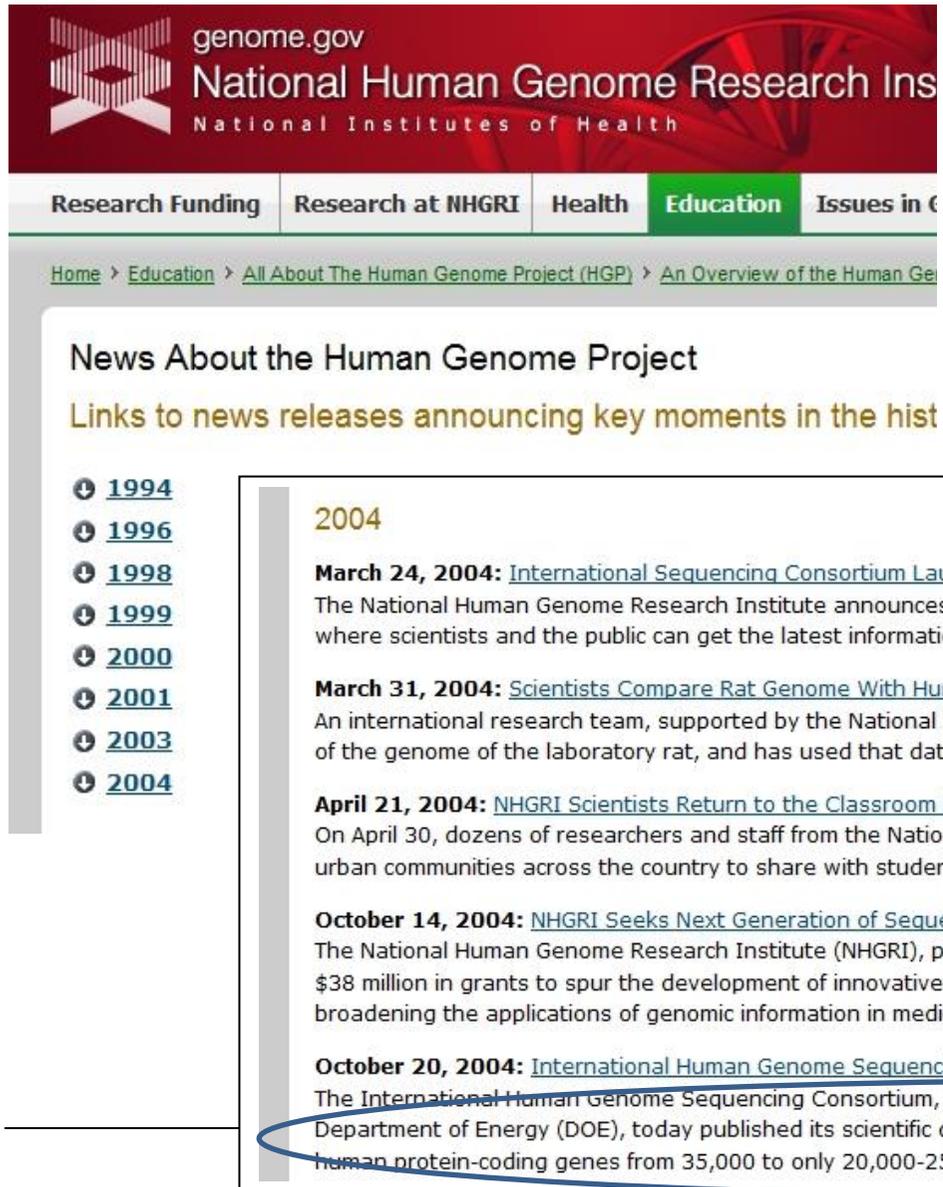
THE HUMAN GENOME

The Sequence of the Human Genome

J. Craig Venter,^{1*} Mark D. Adams,¹ Eugene W. Myers,¹ Peter W. Li,¹ Richard J. Mural,¹ Granger G. Sutton,¹ Hamilton O. Smith,¹ Mark Yandell,¹ Cheryl A. Brans,¹ Robert A. Holt,¹ Jeannine D. Goczyns,¹ Peter Amanatides,¹ Richard M. Ballaw,¹ Daniel H. Huson,¹ Jennifer Russo Wortman,¹ Qing Zhang,¹ Chinnappa D. Kodira,¹ Xiangqun H. Zheng,¹ Lin Chen,¹ Marian Skupski,¹ Gangadharan Subramanian,¹ Paul D. Thomas,¹ Jinghui Zhang,¹ George L. Gabor Miklos,² Catherine Nelson,² Samuel Broder,¹ Andrew G. Clark,⁴ Joe Nadeau,⁵ Victor A. McKusick,⁶ Norton Zinder,⁷ Arnold J. Levine,⁷ Richard J. Roberts,⁸ Mal Simon,⁹ Carolyn Slayman,¹⁰ Michael Hunkapiller,¹¹ Randall Bolanos,¹ Arthur Delcher,¹ Ian Dew,¹ Daniel Fasulo,¹ Michael Flanagan,¹ Liliana Flores,¹ Aaron Halpern,¹ Sridhar Hannenhalli,¹ Saul Kravitz,¹ Samuel Levy,¹ Clark Mobarry,¹ Knut Rainart,¹ Karin Remington,¹ Jane Abu-Threideh,¹ Ellen Beasley,¹ Kandra Biddick,¹ Vivian Bonazzi,¹ Rhonda Brandon,¹ Michele Cargill,¹ Ishwar Chandramouliwaran,¹ Rosana Charlab,¹ Kabir Chaturvedi,¹ Zuoming Deng,¹ Valentina Di Francesco,¹ Patrick Dunn,¹ Karen Elbeck,¹ Carlos Brangulista,¹ Andrei E. Gabrielian,¹ Weiniu Gan,¹ Wangmao Ge,¹ Fangchang Gong,¹ Zhiping Gu,¹ Ping Guan,¹ Thomas J. Heiman,¹ Maureen E. Higgins,¹ Rui-Ru Ji,¹ Zhaoxi Ke,¹ Karen A. Kutchum,¹ Zhongwu Li,¹ Yiding Lei,¹ Zhanya Li,¹ Jiyin Li,¹ Yong Liang,¹ Xiaoying Lin,¹ Fu Lu,¹ Gennady V. Markulov,¹ Natalia Milshina,¹ Helen M. Moore,¹ Ashwinkumar K Nalk,¹ Vaibhav A. Narayan,¹ Beena Neelam,¹ Daborah Nusskarn,¹ Douglas B. Rusch,¹ Steven Saltzberg,¹² Wai Shao,¹ Bkiong Shua,¹ Jingtao Sun,¹ Zhen Yuan Wang,¹ Aihui Wang,¹ Xin Wang,¹ Jian Wang,¹ Ming-Hui Wai,¹ Ron Wides,¹² Chunlin Xie,¹ Chunxun Yan,¹ Allison Yao,¹ Jane Ye,¹ Ming Zhan,¹ Weiqing Zhang,¹ Hongyu Zhang,¹ Qi Zhao,¹ Liansheng Zhang,¹ Fei Zhong,¹ Wanyan Zhong,¹ Shaoqing C. Zhu,¹ Shaying Zhao,¹² Dennis Gilbert,¹ Suzanne Baumhueter,¹ Gene Spier,¹ Christine Carter,¹ Anibal Cravchik,¹ Trevor Woodage,¹ Farooz Ali,¹ Huljin An,¹ Aderonke Awo,¹ Danita Baldwin,¹ Holly Baden,¹ Mary Barnstead,¹ Ian Barrow,¹ Karen Beeson,¹ Dana Busam,¹ Amy Carver,¹ Angela Carter,¹ Ming Lai Cheng,¹ Liz Curry,¹ Steve Danaher,¹ Lionel Davanport,¹ Raymond Desillets,¹ Susanne Dietz,¹ Kristina Dodson,¹ Lisa Doup,¹ Steven Ferriera,¹ Naha Garg,¹ Andreas Gluecksmann,¹ Brit Hart,¹ Jason Haynes,¹ Charles Haynes,¹ Cheryl Halner,¹ Suzanne Hladin,¹ Damon Hostin,¹ Jarratt Houck,¹ Timothy Howland,¹ Chinyere Ibegwam,¹ Jeffery Johnson,¹ Francis Kalush,¹ Lesley Kline,¹ Shashi Koduru,¹ Amy Love,¹ Falecia Mann,¹ David May,¹ Steven McCawley,¹ Tina McIntosh,¹ Ivy McHullen,¹ Moe Moy,¹ Linda Moy,¹ Brian Murphy,¹ Keith Nelson,¹ Cynthia Pfannkoch,¹ Eric Pratts,¹ Vinita Puri,¹ Hina Qureshi,¹ Matthew Reardon,¹ Robert Rodriguez,¹ Yu-Hui Rogers,¹ Deanna Romblad,¹ Bob Ruftal,¹ Richard Scott,¹ Cynthia Sitter,¹ Michelle Smallwood,¹ Erin Stewart,¹ Renee Strong,¹ Ellen Suh,¹ Reginald Thomas,¹ Ni Ni Tint,¹ Sukyae Tsa,¹ Claire Vech,¹ Gary Wang,¹ Jeremy Watter,¹ Sherita Williams,¹ Monica Williams,¹ Sandra Windsor,¹ Emily Winn-Daen,¹ Kerillien Wolfe,¹ Jayshree Zaveri,¹ Karana Zaveri,¹ Josep F. Abril,¹⁴ Roderic Guigo,¹⁴ Michael J. Campbell,¹ Kimman V. Sjolander,¹ Brian Karlak,¹ Anish Kajarwal,¹ Hualyu Mi,¹ Betty Lazarova,¹ Thomas Hatton,¹ Apurva Narechania,¹ Karan Diemer,¹ Anushya Muruganujan,¹ Nan Guo,¹ Shinji Sato,¹ Vinodt Bafna,¹ Sorin Istrail,¹ Ross Lippert,¹ Russell Schwartz,¹ Brian Walenz,¹ Shibu Yooseph,¹ David Allen,¹ Anand Basti,¹ James Baxendale,¹ Louis Blick,¹ Marcelo Caminha,¹ John Carnes-Stino,¹ Parris Caulk,¹ Yen-Hui Chiang,¹ My Coyne,¹ Carl Dahlke,¹ Anne Deslattes Mays,¹ Maria Dombroski,¹ Michael Donnelly,¹ Dale Ely,¹ Shiva Esparham,¹ Carl Foster,¹ Harold Gire,¹ Stephen Glanowski,¹ Kenneth Glasser,¹ Anna Glodak,¹ Mark Gorokhov,¹ Ken Graham,¹ Barry Gropman,¹ Michael Harris,¹ Jeremy Hall,¹ Scott Henderson,¹ Jeffrey Hoover,¹ Donald Jennings,¹ Catherine Jordan,¹ James Jordan,¹ John Kasha,¹ Leonid Kagan,¹ Cheryl Kraft,¹ Alexander Lavitsky,¹ Mark Lewis,¹ Xiangjun Liu,¹ John Lopez,¹ Daniel Ma,¹ William Majoros,¹ Joe McDaniel,¹ Sean Murphy,¹ Matthew Newman,¹ Trung Nguyen,¹ Ngoc Nguyen,¹ Marc Nodell,¹ Sue Pan,¹ Jim Pock,¹ Marshall Peterson,¹ William Rowe,¹ Robert Sanders,¹ John Scott,¹ Michael Simpson,¹ Thomas Smith,¹ Arlan Sprague,¹ Timothy Stockwell,¹ Russell Turner,¹ Eli Venter,¹ Mei Wang,¹ Melyuan Wen,¹ David Wu,¹ Mitchell Wu,¹ Ashley Xia,¹ Ali Zandieh,¹ Xiaohong Zhu¹

- In June 2000 came the announcement that the majority of the human genome had in fact been sequenced, which was followed by the publication of **90 percent of the sequence of the genome's three billion base-pairs** in the journal *Nature*, in February 2001
- Surprises accompanying the sequence publication included:
 - the relatively small **number of human genes**, perhaps as few as **30,000-35,000**;
Note: 100,000 → 30000-35000 → 24000 → 19000-20000
 - the complex architecture of human proteins compared to their homologs - similar genes with the same functions - in, for example, roundworms and fruit flies;
 - the lessons to be taught by repeat sequences of DNA.

Historical overview



genome.gov
National Human Genome Research Institute
National Institutes of Health

Research Funding | Research at NHGRI | Health | **Education** | Issues in C

Home > Education > All About The Human Genome Project (HGP) > An Overview of the Human Genome Project

News About the Human Genome Project

Links to news releases announcing key moments in the history of the Human Genome Project

- 1994
- 1996
- 1998
- 1999
- 2000
- 2001
- 2003
- 2004

2004

March 24, 2004: [International Sequencing Consortium Launches Online Resource](#)
The National Human Genome Research Institute announces that the International Sequencing Consortium (ISC) has launched a free, online resource where scientists and the public can get the latest information on the status of sequencing projects for animal, plant and other eukaryotic genomes.

March 31, 2004: [Scientists Compare Rat Genome With Human, Mouse](#)
An international research team, supported by the National Institutes of Health (NIH), today announced it has completed a high-quality, draft sequence of the genome of the laboratory rat, and has used that data to explore how the rat's genetic blueprint stacks up against those of mice and humans.

April 21, 2004: [NHGRI Scientists Return to the Classroom For Second Annual National DNA Day](#)
On April 30, dozens of researchers and staff from the National Human Genome Research Institute (NHGRI) will head back to high schools in rural and urban communities across the country to share with students some of the exciting research taking place at the National Institutes of Health (NIH).

October 14, 2004: [NHGRI Seeks Next Generation of Sequencing Technologies](#)
The National Human Genome Research Institute (NHGRI), part of the National Institutes of Health (NIH), today announced it has awarded more than \$38 million in grants to spur the development of innovative technologies designed to dramatically reduce the cost of DNA sequencing, a move aimed at broadening the applications of genomic information in medical research and health care.

October 20, 2004: [International Human Genome Sequencing Consortium Describes Finished Human Genome Sequence](#)
The International Human Genome Sequencing Consortium, led in the United States by the National Human Genome Research Institute (NHGRI) and the Department of Energy (DOE), today published its scientific description of the finished human genome sequence, reducing the estimated number of human protein-coding genes from 35,000 to only 20,000-25,000, a surprisingly low number for our species.

Historical overview


National Human Genome Research Institute
National Institutes of Health

Research Funding
Research at NHGRI
Health
Education
Issues in Genetics
Newsroom
Careers & Training
About
For You

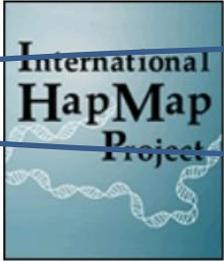



Home > [Education](#) > [Understanding the Human Genome Project](#) > [Dynamic Timeline](#) > [2004-The Future](#) > **2005b: HapMap Project Completed**

Online Education Kit: 2004–The Future

- 2004a: Rat and Chicken Genomes Sequenced
- 2004b: FDA Approves First Microarray
- 2004c: Refined Analysis of Complete Human Genome Sequence
- 2004d: Surgeon General Stresses Importance of Family History
- 2005a: Chimpanzee Genomes Sequenced
- 2005b: HapMap Project Completed
- 2005c: Trypanosomatid Genomes Sequenced
- 2005d: Dog Genomes Sequenced
- 2006a: The Cancer Genome Atlas (TCGA) Project Started
- 2006b: Second Non-human Primate Genome is Sequenced
- 2006c: Initiatives to Establish the Genetic and Environmental Causes of Common Diseases Launched
- The Future

2005: HapMap Project Completed



The International HapMap Consortium published a catalog of human genetic variation that is expected to help speed the identification of genes associated with common diseases such as asthma, cancer, diabetes, and heart disease. While the Human Genome Project focused on the DNA sequence from a single individual, the HapMap project focused on variation in the genome and on human populations. The \$138 million project was a three-year collaboration between more than 200 researchers from Canada, China, Japan, Nigeria and the United States. The new paper described the completion of a Phase I HapMap that contains more than 1 million markers of genetic variation. At the time of the publication, the consortium was nearing completion of a Phase II HapMap that would contain more than 3 million genetic markers.

 Share
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See Also:

[2005 Release: International Consortium Completes Map](#)

[International HapMap Project](#)

On Other Sites:

[International HapMap Project](#)
Web page for the International HapMap Consortium

More Information

References:

The International HapMap Consortium. Integrating ethics and science in the International HapMap Project. *Nature Genetics*, 5: 467-475. 2004. [[Full Text](#)] 

International HapMap Consortium. A haplotype map of the human genome. *Nature*, 437: 1229-1320. 2005. [[Full Text](#)] 

Klein, R.J., Zeiss, C., Chew, E.Y., Tsai, J.Y., et al. Complement factor H polymorphism in age-related macular degeneration. *Science*, 308: 385-389. 2005. [[PubMed](#)]

To view the PDFs on this page, you will need Adobe Reader.



Historical overview

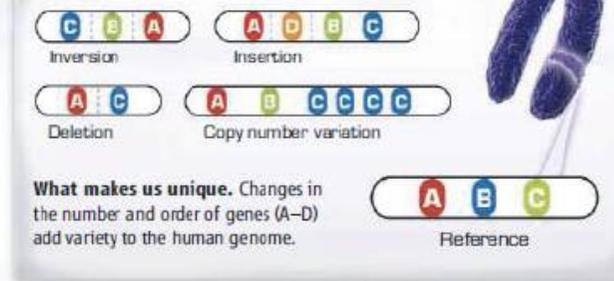
BREAKTHROUGH OF THE YEAR

Human Genetic Variation

Equipped with faster, cheaper technologies for sequencing DNA and assessing variation in genomes on scales ranging from one to millions of bases, researchers are finding out how truly different we are from one another

THE UNVEILING OF THE HUMAN GENOME ALMOST 7 YEARS AGO cast the first faint light on our complete genetic makeup. Since then, each new genome sequenced and each new individual studied has illuminated our genomic landscape in ever more detail. In 2007, researchers came to appreciate the extent to which our genomes differ from person to person and the implications of this variation for deciphering the genetics of complex diseases and personal traits.

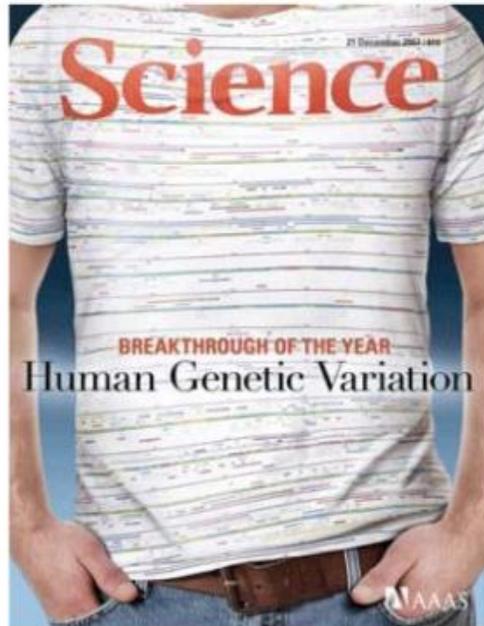
Less than a year ago, the big news was triangulating variation between us and our primate cousins to get a better handle on genetic changes along the evolutionary tree that led to humans. Now, we have moved from asking what in our DNA makes us human to striving to know what in my DNA makes me me.



Pennisi 2007 Science 318:1842-3

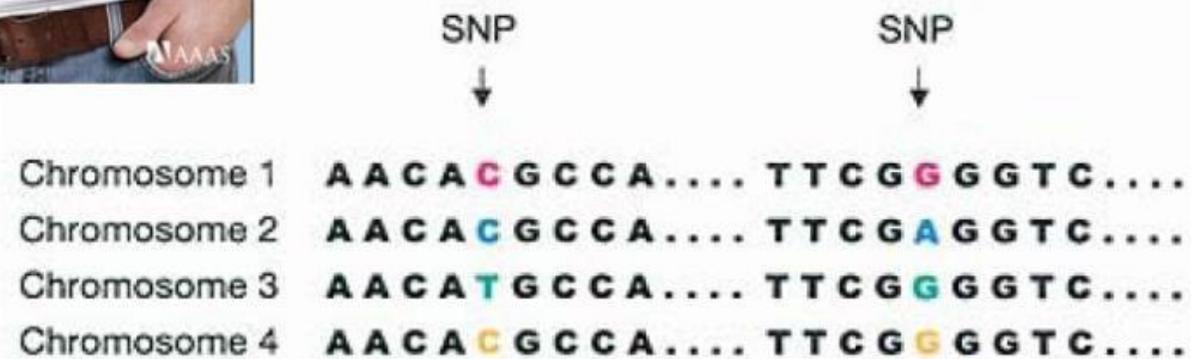
2007 SCIENTIFIC BREAKTHROUGH OF THE YEAR

Science Magazine, December 21, 2007



“It’s all about me!”

Single Nucleotide Polymorphisms (SNPs)



Historical overview: associating genetic variation to disease outcomes



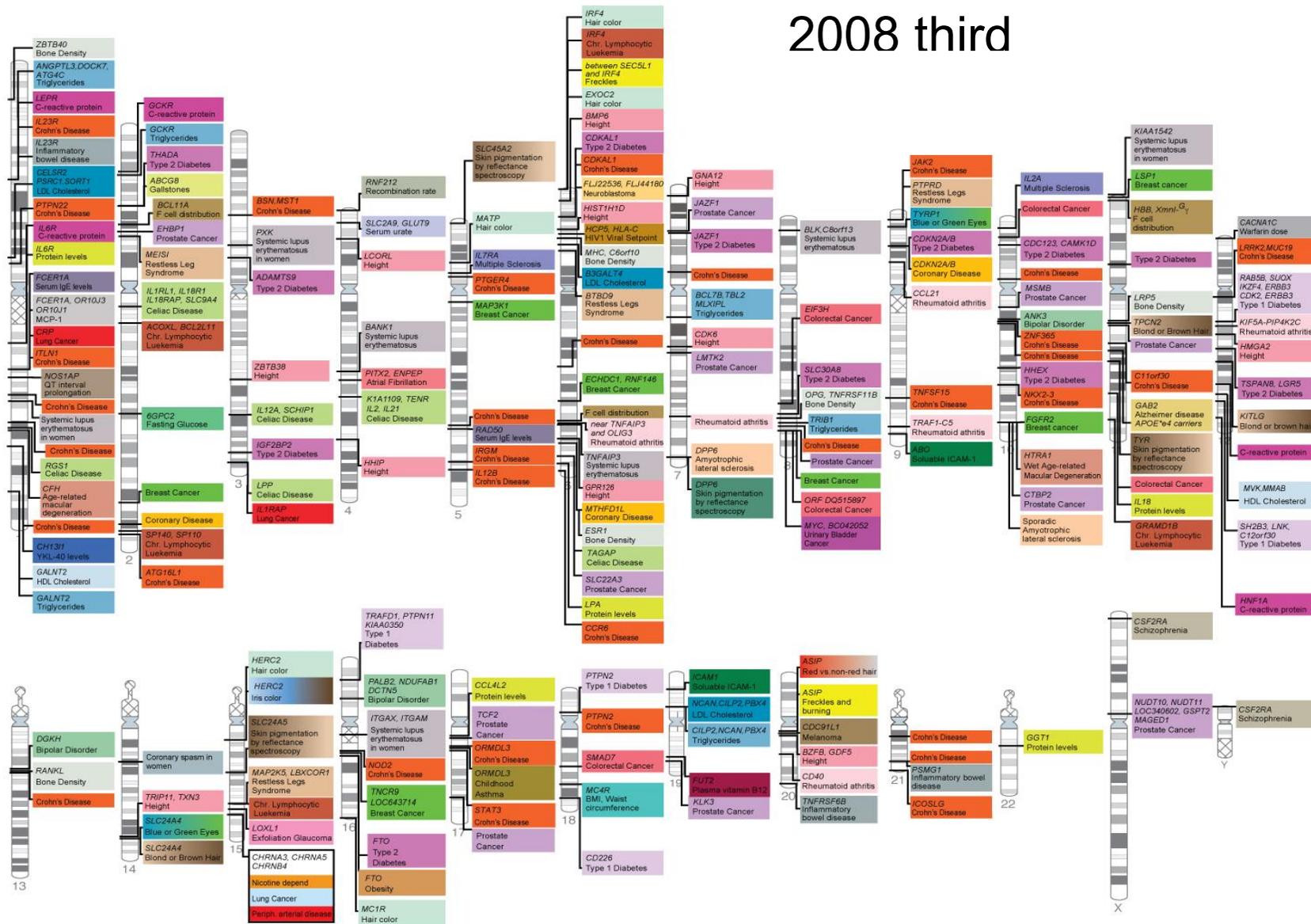
BREAKTHROUGH OF THE YEAR: The Runners-Up

Science 314, 1850a (2006);
DOI: 10.1126/science.314.5807.1850a

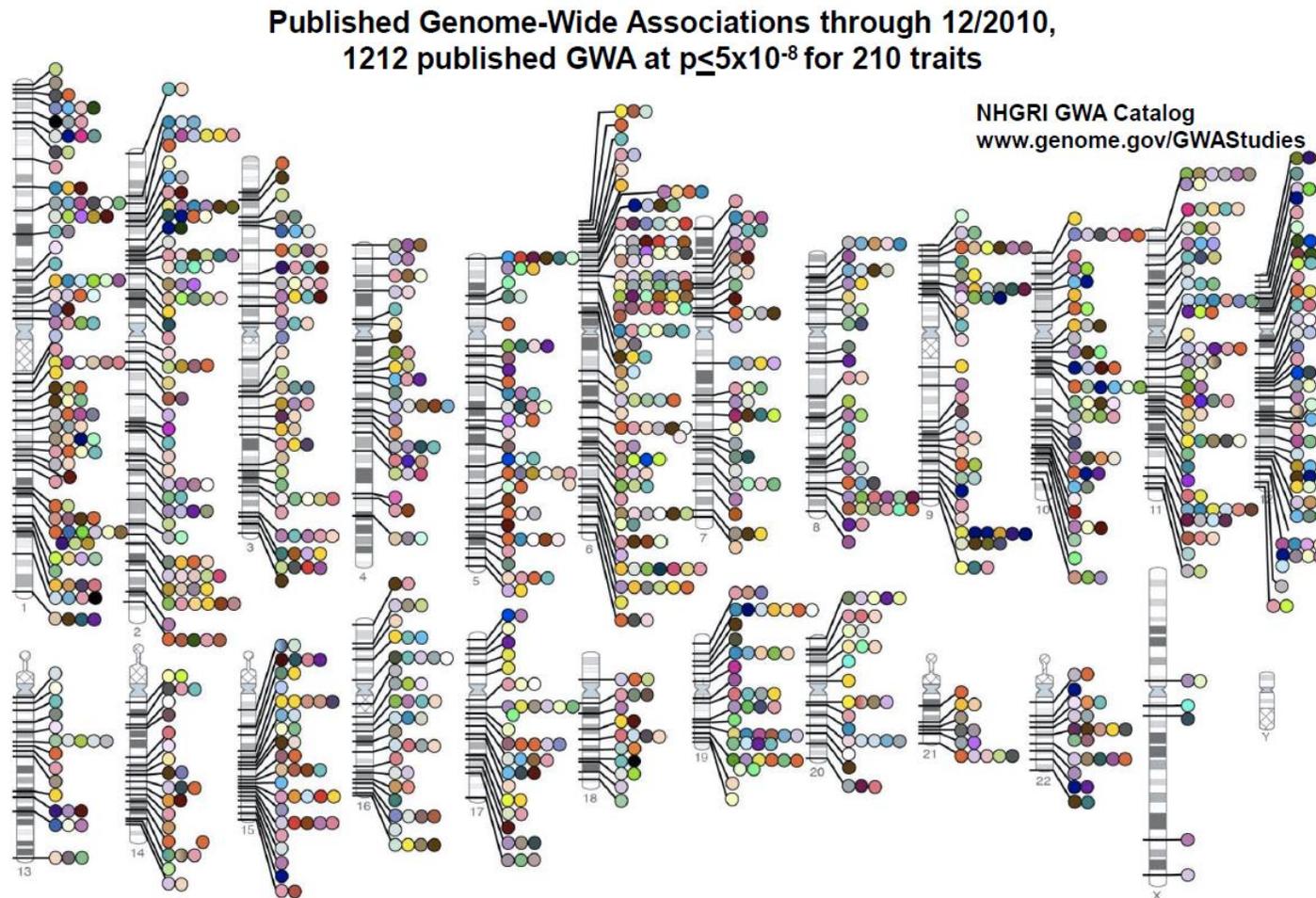
Areas to Watch in 2007

Whole-genome association studies. The trickle of studies comparing the genomes of healthy people to those of the sick is fast becoming a flood. Already, scientists have applied this strategy to macular degeneration, memory, and inflammatory bowel disease, and new projects on schizophrenia, psoriasis, diabetes, and more are heating up. But will the wave of data and new gene possibilities offer real insight into how diseases germinate? And will the genetic associations hold up better than those found the old-fashioned way?

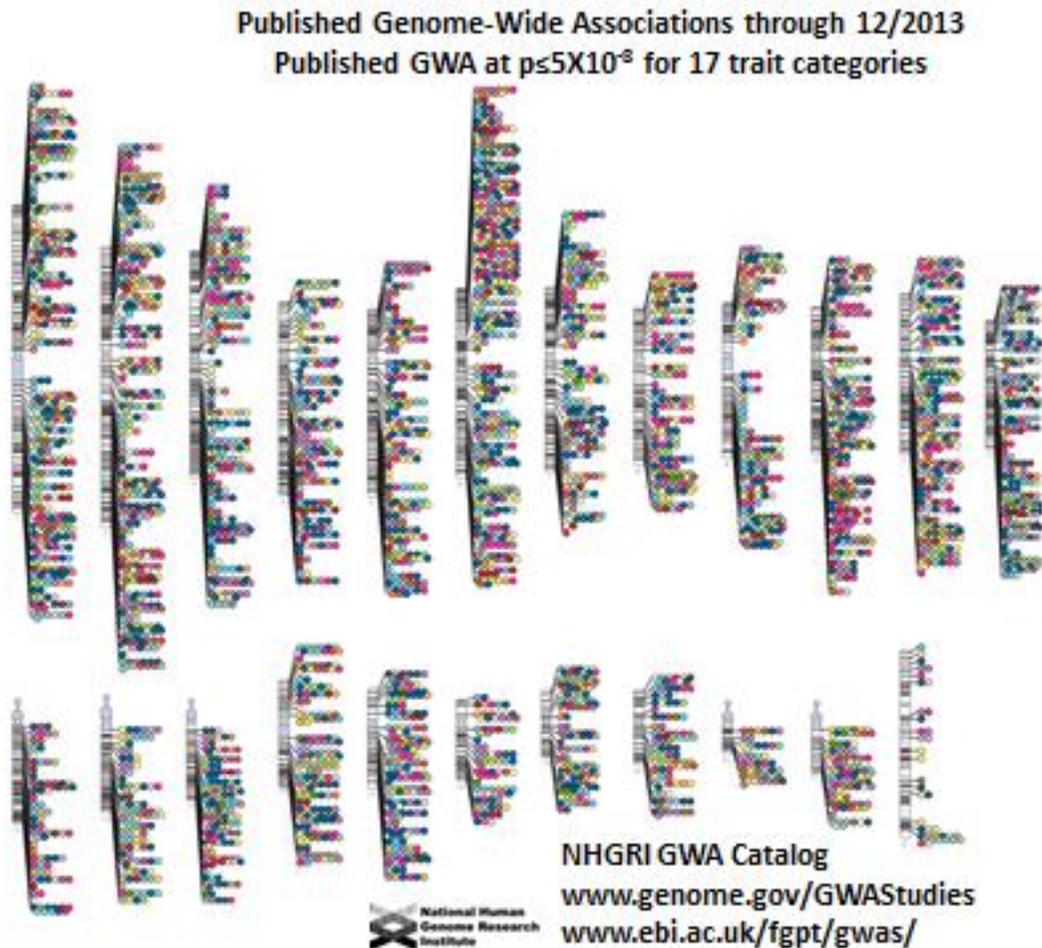
Historical overview: GWAs as a tool to “map” diseases



Historical overview: 210 traits – multiple loci (sites, locations)



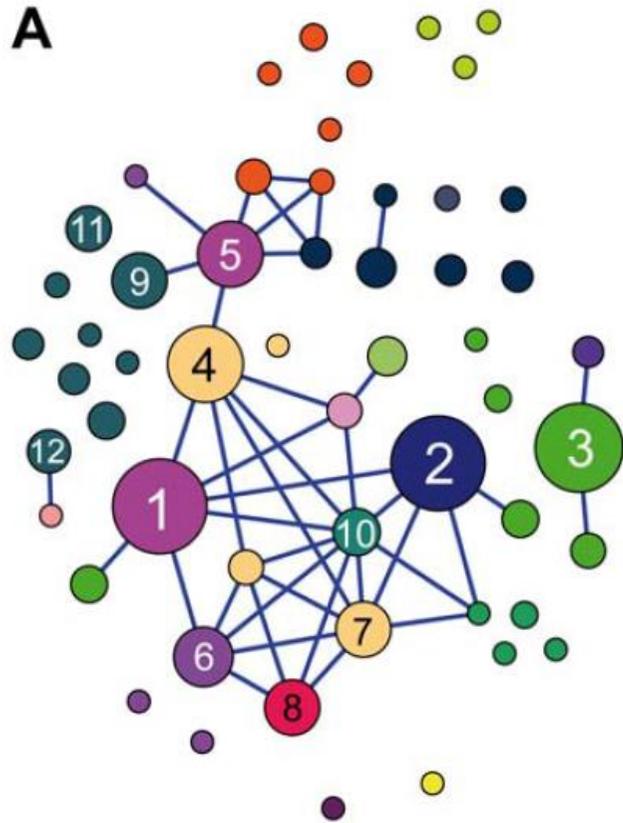
Historical overview: trait categories



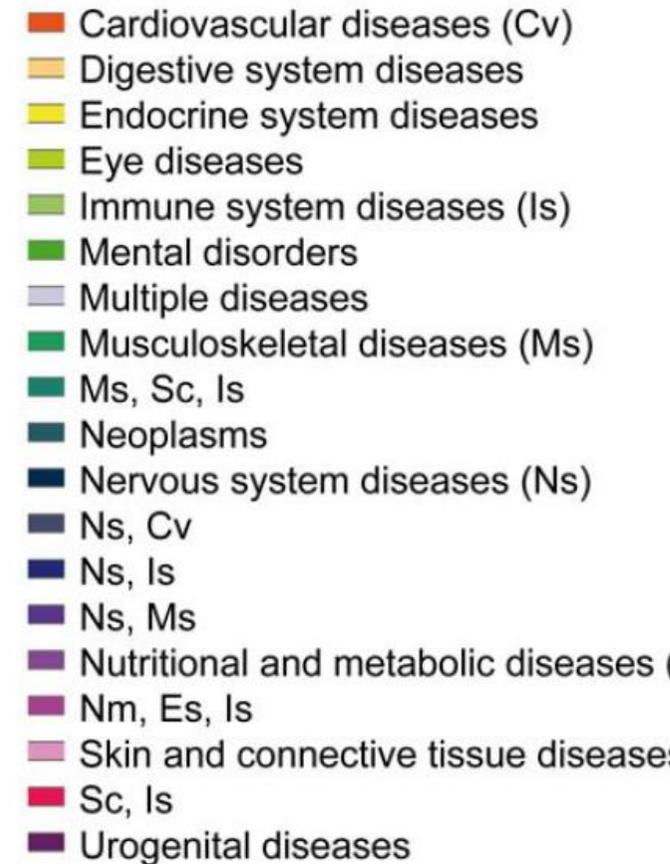
- Digestive system disease
- Cardiovascular disease
- Metabolic disease
- Immune system disease
- Nervous system disease
- Liver enzyme measurement
- Lipid or lipoprotein measurement
- Inflammatory marker measurement
- Hematological measurement
- Body measurement
- Cardiovascular measurement
- Other measurement
- Response to drug
- Biological process
- Cancer
- Other disease
- Other trait

Historical overview: inter-relationships (networks)

A

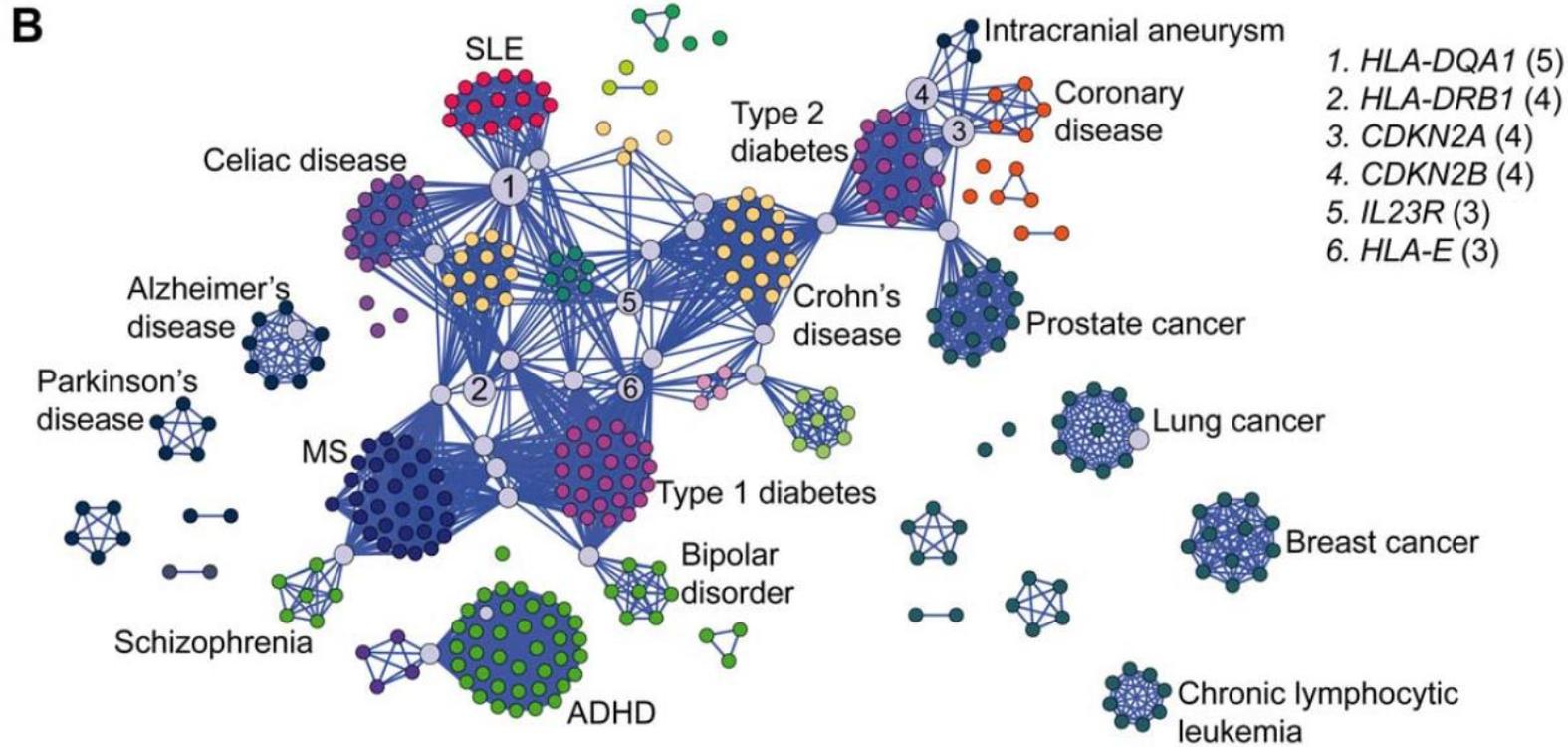


1. Type 1 diabetes (36)
2. Multiple sclerosis (36)
3. ADHD and conduct disorder (33)
4. Crohn's disease (27)
5. Type 2 diabetes (22)
6. Celiac disease (19)
7. Ulcerative colitis (17)
8. Systemic lupus erythematosus (17)
9. Prostate cancer (17)
10. Rheumatoid arthritis (13)
11. Breast cancer (12)
12. Lung cancer (11)



(Barrenas et al 2009: complex disease network – nodes are diseases)

Historical overview: inter-relationships (networks)



(Barrenas et al 2009: complex disease GENE network – nodes are genes)

Historical overview: monitoring the progress

NCBI Resources How To Sign in to NCBI

OMIM OMIM Search

Limits Advanced Help



OMIM

OMIM is a comprehensive, authoritative compendium of human genes and genetic phenotypes that is freely available and updated daily. OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh. Its official home is omim.org.

Using OMIM

- [Getting Started](#)
- [FAQ](#)

OMIM tools

- [OMIM API](#)

Related Resources

- [ClinVar](#)
- [Gene](#)
- [GTR](#)
- [MedGen](#)

Last updated on: 05 Oct 2014

OMIM: molecular dissection of human disease

- Online Mendelian Inheritance in Man (OMIM[®]) is a continuously updated **catalog of human genes and genetic disorders and traits** (i.e. coded phenotypes, where phenotype is any characteristic of the organism), with particular focus on the molecular relationship between genetic variation and phenotypic expression.
- It can be considered to be a phenotypic companion to the Human Genome Project. OMIM is a continuation of Dr. Victor A. McKusick's Mendelian Inheritance in Man, which was published through 12 editions, the last in 1998.
- OMIM is currently biocurated at the McKusick-Nathans Institute of Genetic Medicine, The Johns Hopkins University School of Medicine.
- Frequently asked questions: <http://www.omim.org/help/faq>

Accessing OMIM

The screenshot shows the NCBI website interface. At the top, there is a search bar and navigation icons. The main navigation menu on the left is expanded to show 'All Databases', which includes a list of various biological databases. 'OMIM' is highlighted in the list. Below the navigation menu, the main content area features several sections: 'Welcome to NCBI', 'Submit', 'Download', 'Learn', 'Develop', 'Analyze', and 'Research'. On the right side, there are sections for 'Popular Resources' (including PubMed, Bookshelf, etc.) and 'NCBI News & Blog'.

Navigation Menu (Left):

- NCBI Home
- Resource List (A-Z)
- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
- Variation

All Databases (Dropdown):

- Genome
- GEO DataSets
- GEO Profiles
- GSS
- GTR
- HomoloGene
- Identical Protein Groups
- MedGen
- MeSH
- NCBI Web Site
- NLM Catalog
- Nucleotide
- OMIM
- PMC
- PopSet
- Probe
- Protein
- Protein Clusters
- PubChem BioAssay
- PubChem Compound

Main Content Area:

- Welcome to NCBI:** Center for Biotechnology Information advances science and health by providing access to genomic information.
- Submit:** Submit data or manuscripts to our databases.
- Download:** Transfer NCBI data to your computer.
- Learn:** Find help documents, attend a class or watch a tutorial.
- Develop:** Build APIs and code to build applications.
- Analyze:** Identify an NCBI tool for your data analysis task.
- Research:** Explore NCBI research and collaborative projects.

Popular Resources (Right):

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI News & Blog (Right):

- PubMed Labs is now part of NCBI Labs (03 Oct 2017)
- About two years ago, NCBI launched PubMed Labs, a gathering place for discovering and experimenting with new...
- October 11 NCBI Minute: Introducing the New RefSeq Functional Elements Project

Historical overview: exome sequencing, full genome sequencing

NCBI Resources How To Sign in to NCBI

1000 Genomes Browser Homo sapiens: GRCh37.p13 (GCF_000001405.25) Chr 1 (NC_000001.10): 1 - 249.3M

Reset All Share this page FAQ Help Version 3.3

Ideogram View

Exon Navigator

There are too many genes in the region (3570). Please narrow the region to enable exon navigation.

NC_000001.10: 1..249M (249Mbp)

Segmental Duplications on GRCh37

1000 Genomes Phase 1 Strict Accessibility Mask

Genes, NCBI Homo sapiens Annotation Release 105

ClinVar Short Variations based on dbSNP 141 (Homo sapiens Annotation Release 105)

dbSNP 141 (Homo sapiens Annotation Release 105) HapMap Recombination Rate

dbSNP 141 (Homo sapiens Annotation Release 105) all data

Data not in 1000 Genomes Phase 1, dbSNP 141 (Homo sapiens Annotation Release 105)

Zoom to see data! Download data for this region

Genotypes

Go to Selection	Scroll Region	114,057,996	114,058,146	114,058,215	114,058,280	114,058,349	114,058,466	114,058,537	114,058,563	114,058,640	114,058,739	114,058,746	114,058,853	114,059,189	114,059,335	114,059,373	114,059,380	114,059,727	114,059,954	114,059,998	114,060,051	114,0
		rs6685909	rs114841421	rs183004883	rs4838988	rs4839323	rs187330676	rs78691846	rs113381680	rs191384074	rs114985670	rs141799806	rs145542737	rs147746490	rs141083549	rs150301358	rs183913552	rs79656665	rs141847716	rs115616102	rs149798012	rs116
Populations / Samples		G=0.2039	C=0.9927	A=0.9995	C=0.7332	T=0.6809	G=0.9995	C=0.9986	G=0.9991	G=0.9986	C=0.9968	G=0.9940	G=0.9991	G=0.9995	C=0.9995	G=0.9995	G=0.9995	G=0.9927	TA=0.9853	G=0.9982	GA=0.9862	T=0
Show: Allele frequencies		A=0.7961	T=0.0073	T=0.0005	T=0.2668	C=0.3191	T=0.0005	A=0.0014	T=0.0009	A=0.0014	T=0.0032	A=0.0060	A=0.0009	A=0.0005	A=0.0005	A=0.0005	A=0.0005	A=0.0073	T=0.0147	A=0.0018	G=0.0138	G=0
ASW Americans of African...		G=0.0656	C=0.9754	A=1.0000	C=0.9590	T=0.8279	G=1.0000	C=1.0000	G=1.0000	G=1.0000	C=0.9836	G=1.0000	G=1.0000	G=1.0000	C=1.0000	G=1.0000	G=1.0000	G=0.9508	TA=0.9590	G=0.9918	GA=0.9426	T=0
		A=0.9344	T=0.0246	T=0.0000	T=0.0410	C=0.1721	T=0.0000	A=0.0000	T=0.0000	A=0.0000	T=0.0164	A=0.0000	A=0.0000	A=0.0000	A=0.0000	A=0.0000	A=0.0000	A=0.0492	T=0.0410	A=0.0082	G=0.0574	G=0

2 The rise of GWAs



(slide Doug Brutlag 2010)

What are GWAs?

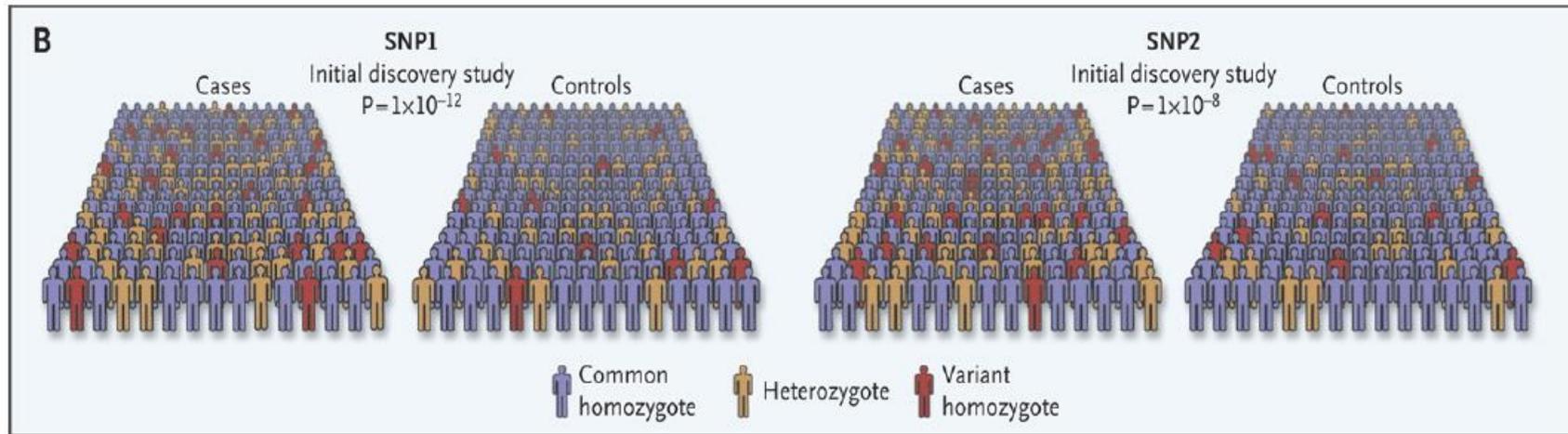
- A **genome-wide association study** is an approach that involves rapidly scanning markers across the complete sets of DNA, or genomes, of many people to find genetic variations associated with a particular trait.
- **Recall:** a **trait** can be defined as a coded phenotype, a particular characteristic such as hair color, BMI, disease, gene expression intensity level, ...

Genome-wide association studies: basic principles

The genome-wide association study is typically (but not solely!!!) based on a case-control design in which single-nucleotide polymorphisms (SNPs) across the human genome are genotyped ... (Panel A: small fragment)



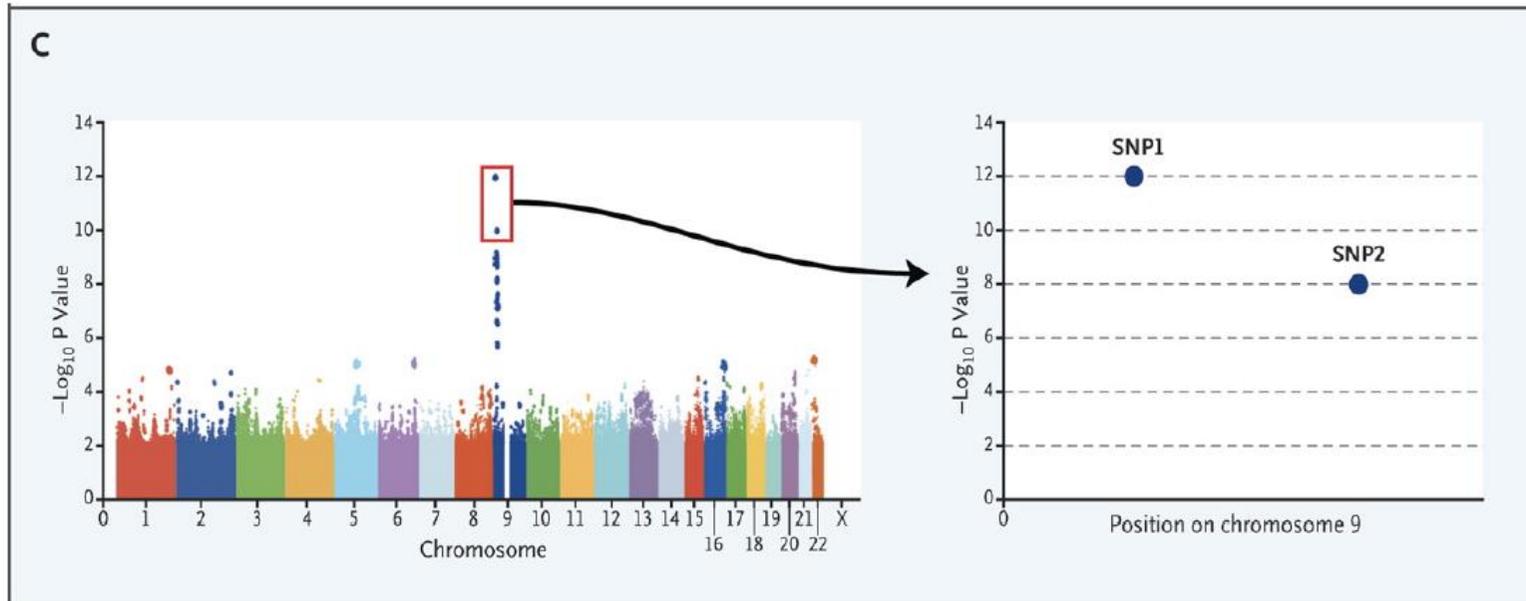
Genome-wide association studies: basic principles



- Panel B, the strength of association between each SNP and disease is calculated on the basis of the prevalence of each SNP in cases and controls. In this example, SNPs 1 and 2 on chromosome 9 are associated with disease, with P values of 10^{-12} and 10^{-8} , respectively

(Manolio 2010)

Genome-wide association studies: basic principles



- The plot in Panel C shows the P values for all genotyped SNPs that have survived a quality-control screen (each chromosome, a different color).
- The results implicate a locus on chromosome 9, marked by SNPs 1 and 2, which are adjacent to each other (graph at right), and other neighboring SNPs.

(Manolio 2010)

How can we use genome-wide association studies results?

- Once new genetic associations are identified, researchers can use the information to develop better strategies to detect, treat and prevent the disease.

The screenshot shows the NIH Office of Extramural Research website. The header includes the U.S. Department of Health & Human Services logo and the URL www.hhs.gov. The main navigation menu includes Home, About Grants, Funding, Forms & Deadlines, Grants Policy, News & Events, About OER, and NIH Home. The 'Funding' menu is selected, and the 'Genome-Wide Association Studies (GWAS)' page is displayed.

Genome-Wide Association Studies (GWAS)

The NIH is interested in advancing genome-wide association studies (GWAS) to identify common genetic factors that influence health and disease. For the purposes of this policy, a genome-wide association study is defined as any study of genetic variation across the entire human genome that is designed to identify genetic associations with observable traits (such as blood pressure or weight), or the presence or absence of a disease or condition. Whole genome information, when combined with clinical and other phenotype data, offers the potential for increased understanding of basic biological processes affecting human health, improvement in the prediction of disease and patient care, and ultimately the realization of the promise of personalized medicine. In addition, rapid advances in understanding the patterns of human genetic variation and maturing high-throughput, cost-effective methods for genotyping are providing powerful research tools for identifying genetic variants that contribute to health and disease. The purpose of this Website is to support the implementation of the GWAS Policy.

The NIH will continue to release additional guidance information on this site. Please e-mail GWAS@mail.nih.gov with any questions.

Recent News

- [NIH Background Fact Sheet on GWAS Policy Update](#) - (08/28/2008) (PDF - 40 KB)
- [NIH Modifications to Genome-Wide Association Studies \(GWAS\) Data Access](#) - (08/28/2008) (PDF - 43 KB)

Data Access Information

- [Senior Oversight Committee \(SOC\) Charge and Roster](#) - (07/10/2008) (PDF - 103 KB)
- [Data Access Committees \(DACs\) Charge and Roster](#) - (07/10/2008) (PDF - 50 KB)

Left Sidebar Navigation:

- Funding Opportunities**
 - Funding Opportunities (RFAs, PAs) & Notices
 - Unsolicited Applications (Parent Announcements)
 - Research Training & Career Development
 - Small Business (SBIR/STTR)
 - Contract Opportunities
- NIH-Wide Initiatives**
 - Stem Cell Information
 - New and Early Stage Investigators
 - Genome-Wide Association Studies (GWAS)
 - NIH Roadmap for Medical Research
- Global OER Resources**
 - Glossary & Acronyms

View the GWAs catalogue (<http://www.genome.gov/gwastudies/>)

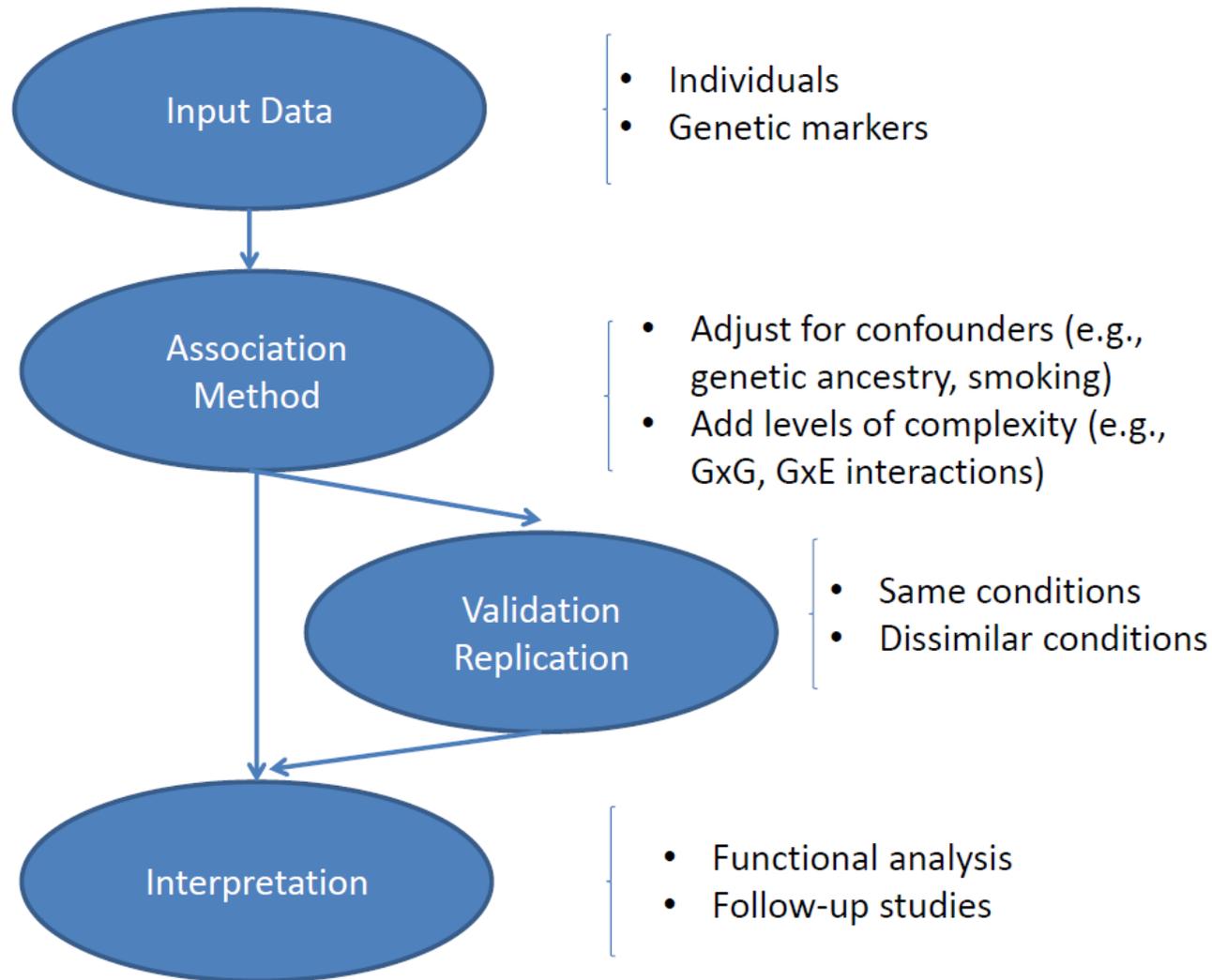
2317 studies (6/10/2014)

(Entries 1-50 of 2317)

Page 1 of 47 [Next >](#) [Last >>](#)

Date Added to Catalog (since 11/25/08)	First Author/Date/Journal/Study	Disease/Trait	Initial Sample Description	Replication Sample Description	Region	Reported Gene(s)	Mapped Gene(s)	Strongest SNP-Risk Allele	Context	Risk Allele Frequency in Controls	P-value	OR or beta-coefficient and [95% CI]	Platform [SNPs passing QC]	CNV
04/16/14	Chung CM March 03, 2014 <i>Diabetes Metab Res Rev</i> Common quantitative trait locus downstream of RETN gene identified by genome-wide association study is associated with risk of type 2 diabetes mellitus in Han Chinese: a Mendelian randomization effect.	Resistin levels	382 Han Chinese ancestry individuals	559 Han Chinese ancestry individuals	19p13.2	RETN	RETN - C19orf59	rs1423096-G		0.78	1×10^{-7}	.322 [0.25-0.40] ug/mL increase	Illumina [NR]	N
10/03/14	Zhang B January 21, 2014 <i>Int J Cancer</i> Genome-wide association study identifies a new SMAD7 risk variant associated with colorectal cancer risk in East Asians.	Colorectal cancer	1,773 East Asian ancestry cases, 2,642 East Asian ancestry controls	6,902 East Asian ancestry cases, 7,862 East Asian ancestry controls	18q21.1	SMAD7	SMAD7	rs7229639-A	intron	0.145	3×10^{-11}	1.22 [1.15-1.29]	Affymetrix & Illumina [1,695,815] (imputed)	N
10/06/14	Xie T January 17, 2014 <i>Neurobiol Aging</i> A genome-wide association study combining pathway analysis for typical sporadic	Amyotrophic lateral sclerosis (sporadic)	250 Han Chinese ancestry cases, 250 Han Chinese ancestry controls	NA	View full set of 175 SNPs								Illumina [859,311] (pooled)	N
					NA	RAB9P1	NA	kgp22272527-?		NR	8×10^{-11}	NR		
					NA	MYO18B	NA	kgp8087771-?		0.2	2×10^{-10}	3.0327 [2.212039-4.157817]		
					12q24.33	GPR133	GPR133	rs11061269-?	intron	0.08	8×10^{-10}	3.7761 [2.49-5.74]		
					21q22.3	TMPRSS2	TMPRSS2 -	rs9977018-?		0.05	2×10^{-9}	NR		

Genome-wide association studies: key components



Genome-wide association studies: key components

- To carry out a GWAs, several tools are needed, which include those that deal with data generation and data handling:
 - Computerized data bases with reference human genome sequence
 - Map of human genetic variation
 - Technologies that can quickly and accurately analyze (whole genome) samples for genetic variations that contribute to disease

(<http://www.genome.gov/pfv.cfm?pageID=20019523>)

Rise of bioinformatics determines rise of GWAs (1)

BIOINFORMATICS APPLICATIONS NOTE Vol. 23 no. 10 2007, pages 1294–1296
doi:10.1093/bioinformatics/btm108

Genetics and population analysis

GenABEL: an R library for genome-wide association analysis

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Advance Access publication March 23, 2007

Associate Editor: Martin Bishop

ABSTRACT

Here we describe an R library for genome-wide association (GWA) analysis. It implements effective storage and handling of GWA data, fast procedures for genetic data quality control, testing of association of single nucleotide polymorphisms with binary or quantitative traits, visualization of results and also provides easy interfaces to standard statistical and graphical procedures implemented in base R and special R libraries for genetic analysis. We evaluated GenABEL using one simulated and two real data sets. We conclude that GenABEL enables the analysis of GWA data on desktop computers.

Availability: <http://cran.r-project.org>

Contact: i.aoultchenko@erasmusmc.nl

With these objectives in mind, we developed the GenABEL software, implemented as an R library. R is a free, open source language and environment for statistical analysis (<http://www.r-project.org/>). Building upon existing statistical analysis facilities allowed for rapid development of the package.

2 IMPLEMENTATION

2.1 Objective (1)

GWA data storage using standard R data types is ineffective. A SNP genotype for a single person may take four values (AA, AB, BB and missing). Two bits, therefore, are required to store these data. However, the standard R data types occupy 32 bits, leading to an overhead of 1500%, compared to the theoretical optimum. Use of the raw R data format, occupying

Rise of bioinformatics determines rise of GWAs (2)

BIOINFORMATICS

Vol. 26 ISMB 2010, pages i208–i216
doi:10.1093/bioinformatics/btq191

Multi-population GWA mapping via multi-task regularized regression

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ABSTRACT

Motivation: Population heterogeneity through admixing of different founder populations can produce spurious associations in genome-wide association studies that are linked to the population structure rather than the phenotype. Since samples from the same population generally co-evolve, different populations may or may not share the same genetic underpinnings for the seemingly common phenotype. Our goal is to develop a unified framework for detecting causal genetic markers through a joint association analysis of multiple populations.

Results: Based on a multi-task regression principle, we present a multi-population group lasso algorithm using L_1/L_2 -regularized regression for joint association analysis of multiple populations that are stratified either via population survey or computational estimation. Our algorithm combines information from genetic markers across populations, to identify causal markers. It also implicitly accounts for correlations between the genetic markers, thus enabling better control over false positive rates. Joint analysis across populations enables the detection of weak associations common to all populations with greater power than in a separate analysis of each population. At the same time, the regression-based framework allows causal alleles that are unique to a subset of the populations to be correctly identified. We demonstrate the effectiveness of our method on HapMap-simulated and lactase persistence datasets, where we significantly outperform state of the art methods, with greater power for detecting weak associations and reduced spurious associations.

Availability: Software will be available at <http://www.sailing.cs.cmu.edu/>

the geographical distribution of the individuals. For example, it has been shown that such heterogeneity is present in the HapMap data (The International HapMap Consortium, 2005) across European, Asian and African populations; and heterogeneity at a finer scale within European ancestry has been found in many genomic regions in the UK samples of Wellcome trust case control consortium (WTCCC) dataset (Wellcome Trust Case Control Consortium, 2007). Although the standard assumption in existing approaches for association mapping is that the effects of causal mutations are likely to be common across multiple populations, the individuals in the same population or geographical region tend to co-evolve, and are likely to possess a population-specific causal allele for the same phenotype. For example, Tishkoff *et al.* (2006) reported that the lactase-persistence phenotype is caused by different mutations in Africans and Europeans. In addition, the same genetic variation has been observed to be correlated with gene-expression levels with different association strengths across different HapMap populations. Our goal is to be able to leverage information across multiple populations, to find causal markers in a multi-population association study.

1.1 Highlights of this article

We propose a novel multi-task-regression-based technique that performs a joint GWA mapping on individuals from multiple populations, rather than separate analysis of each population, to detect associated genome variations. The joint inference is achieved by using a multi-population group lasso (MPGL), with an L_1/L_2

Rise of bioinformatics determines rise of GWAs (3)

BIOINFORMATICS APPLICATIONS NOTE Vol. 24 no. 1 2008, pages 140–142
doi:10.1093/bioinformatics/btm549

Genetics and population analysis

GWAsimulator: a rapid whole-genome simulation program

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Advance Access publication November 15, 2007

Associate Editor: Martin Bishop

ABSTRACT

Summary: GWAsimulator implements a rapid moving-window algorithm to simulate genotype data for case-control or population samples from genomic SNP chips. For case-control data, the program generates cases and controls according to a user-specified multi-locus disease model, and can simulate specific regions if desired. The program uses phased genotype data as input and has the flexibility of simulating genotypes for different populations and different genomic SNP chips. When the HapMap phased data are used, the simulated data have similar local LD patterns as the HapMap data. As genome-wide association (GWA) studies become increasingly popular and new GWA data analysis methods are being developed, we anticipate that GWAsimulator will be an important tool for evaluating performance of new GWA analysis methods.

Availability: The C++ source code, executables for Linux, Windows and MacOS, manual, example data sets and analysis program are available at <http://biostat.mc.vanderbilt.edu/GWAsimulator>

Contact: chun.li@vanderbilt.edu

Supplementary information: Supplementary data are available at *Bioinformatics* online.

2 METHODS

The program can generate unrelated case-control (sampled retrospectively conditional on affection status) or population (sampled randomly) data of genome-wide SNP genotypes with patterns of LD similar to the input data.

2.1 Phased input data and control file

The program requires phased data as input. If the HapMap data are used, the number of phased autosomes and X chromosomes are 120 and 90 for both CEU and YRI, 90 and 68 for CHB, and 90 and 67 for JPT. Additional parameters needed by the program should be provided in a control file, including disease model (see Section 2.2), window size (see Section 2.3), whether to output the simulated data (see Section 2.4), and the number of subjects to be simulated.

2.2 Determination of disease model

For simulations of case-control data, a disease model is needed. The program allows the user to specify disease model parameters, including disease prevalence, the number of disease loci, and for each disease locus, its location, risk allele and genotypic relative risk. If the user wants to simulate specific regions, the start and end positions need

Rise of bioinformatics determines rise of GWAs (4)

BIOINFORMATICS APPLICATIONS NOTE

Vol. 25 no. 5 2009, pages 662–663
doi:10.1093/bioinformatics/btp017

Genome analysis

AssociationViewer: a scalable and integrated software tool for visualization of large-scale variation data in genomic context

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Associate Editor: John Quackenbush

ABSTRACT

Summary: We present a tool designed for visualization of large-scale genetic and genomic data exemplified by results from genome-wide association studies. This software provides an integrated framework to facilitate the interpretation of SNP association studies in genomic context. Gene annotations can be retrieved from Ensembl, linkage disequilibrium data downloaded from HapMap and custom data imported in BED or WIG format. AssociationViewer integrates functionalities that enable the aggregation or intersection of data tracks. It implements an efficient cache system and allows the display of several, very large-scale genomic datasets.

Availability: The Java code for AssociationViewer is distributed under the GNU General Public Licence and has been tested on Microsoft Windows XP, MacOSX and GNU/Linux operating systems. It is available from the SourceForge repository. This also includes Java webstart, documentation and example datafiles.

Contact: brian.stevenson@licr.org

Supplementary information: Supplementary data are available at <http://sourceforge.net/projects/associationview/> online.

represented in BED or WIG format and implements aggregation (union) or intersection of data tracks.

2 PROGRAM OVERVIEW

2.1 Cache and memory management

With increasing data volumes, efficient resource management is essential. One approach is to store the data in a cache with fast indexing mechanisms to retrieve the data, and to keep in memory only the information that is visualized. We implemented such a system in AssociationViewer. For comparison, loading a single dataset with 500 K SNPs in WGAViewer needs about 224 MB of RAM, whereas loading 10 different datasets (a total of 10 M data points) and displaying all genes on chromosome 1 needs only 50 MB in AssociationViewer.

2.2 Data import and export

A typical GWA dataset consists of a list of SNPs with *P*-values derived from an association analysis. In AssociationViewer, such

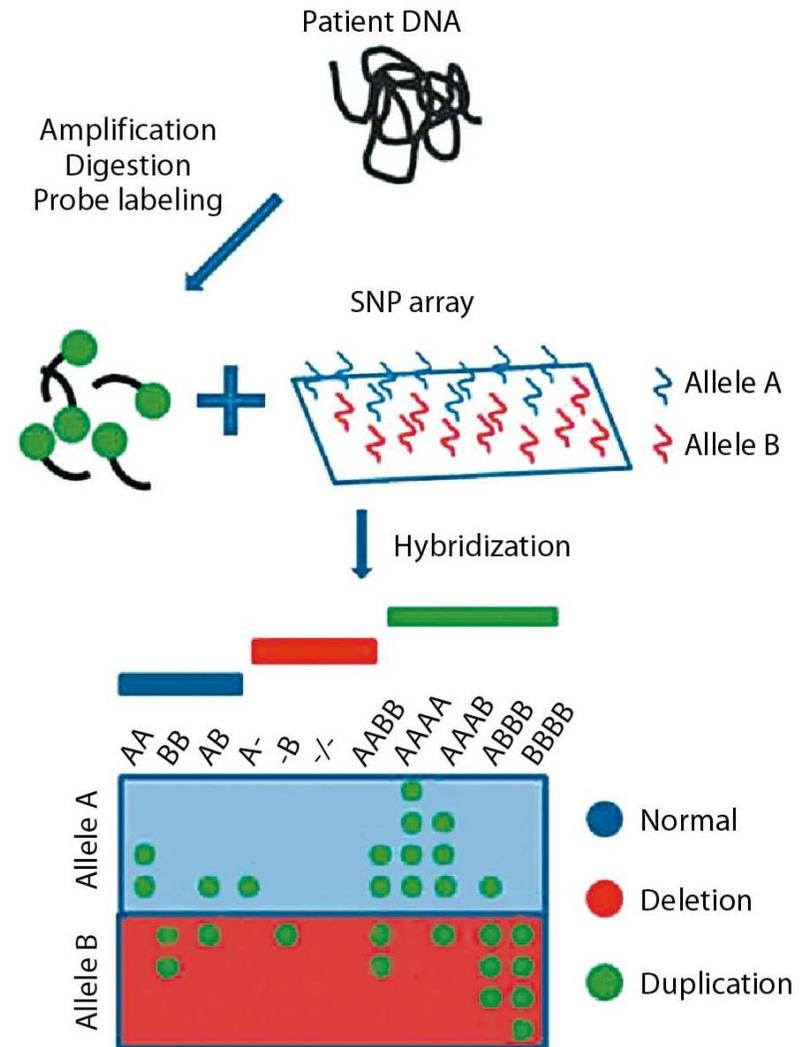
3 Study Design

Components of a study design for GWA studies

- The design of a genetic association study may refer to
 - study scale:
 - Genetic (e.g., hypothesis-drive, panel of candidate genes)
 - Genomic (e.g., hypothesis-free, genome-wide)
 - marker design:
 - Which markers are most informative in GWAs? Common variants-SNPs and/or Rare Variants (MAF<1%)
 - Which platform is the most promising? Least error-prone? Marker-distribution over the genome?
 - subject design

3.a Marker Level

- Costs may play a role, but a balance is needed between costs and chip/sequencing platform performance
- Coverage also plays a role (e.g., exomes only or a uniform spread).
- When choosing **Next Generation Sequencing platforms**, also rare **variants** can be included in the analysis, in contrast to the older **SNP-arrays** (see right panel).



From common variants towards including rare variants

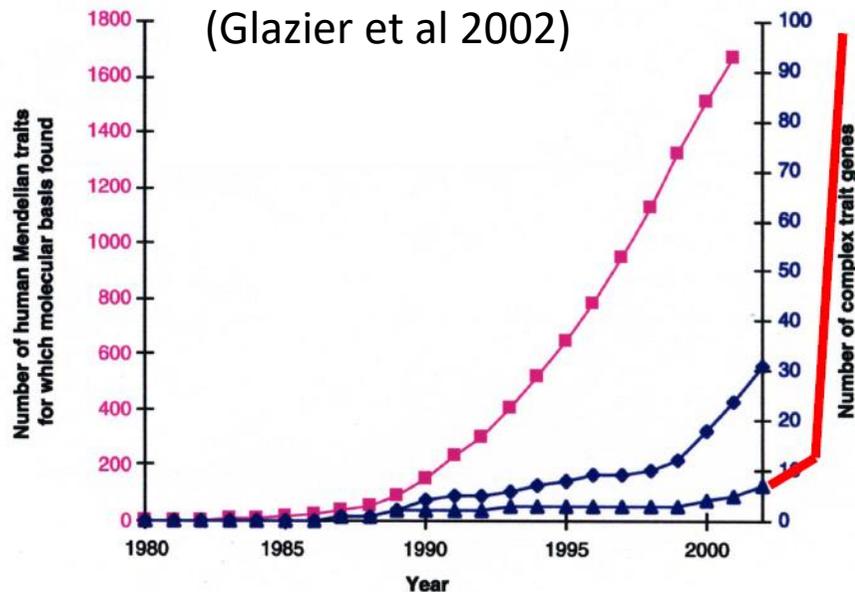
- Hypothesis 1 for GWAs: Common Disease – Common Variant (CDCV):
 - This hypothesis argues that **genetic variations with appreciable frequency** in the population at large, but **relatively low penetrance** (i.e. the probability that a carrier of the relevant variants will express the disease), are the major contributors to genetic susceptibility to common diseases (Lander, 1996; Chakravarti, 1999; Weiss & Clark, 2002; Becker, 2004).
 - The hypothesis speculates that the gene variation underlying susceptibility to common heritable diseases existed within the **founding population of contemporary humans** → explains the success of GWAs?

From common variants towards including rare variants

- Hypothesis 2 for GWAs: Common Disease – Rare Variant (CDRV):
 - This hypothesis argues that **rare DNA sequence variations**, each with **relatively high penetrance**, are the major contributors to genetic susceptibility to common diseases.
 - Some argumentations behind this hypothesis include that by reaching an appreciable frequency for common variations, these variations are not as likely to have been subjected to negative selection. Rare variations, on the other hand, may be **rare because they are being selected against due to their deleterious nature**.

There is room for both hypothesis in current research !
(Schork et al. 2009)

Identified # of traits for which a molecular basis exists: **importance of SNPs**



PINK : Human Mendelian traits

BLUE middle line : All complex traits

BLUE bottom line + red extension:

Human complex traits

Complex disease (definition):

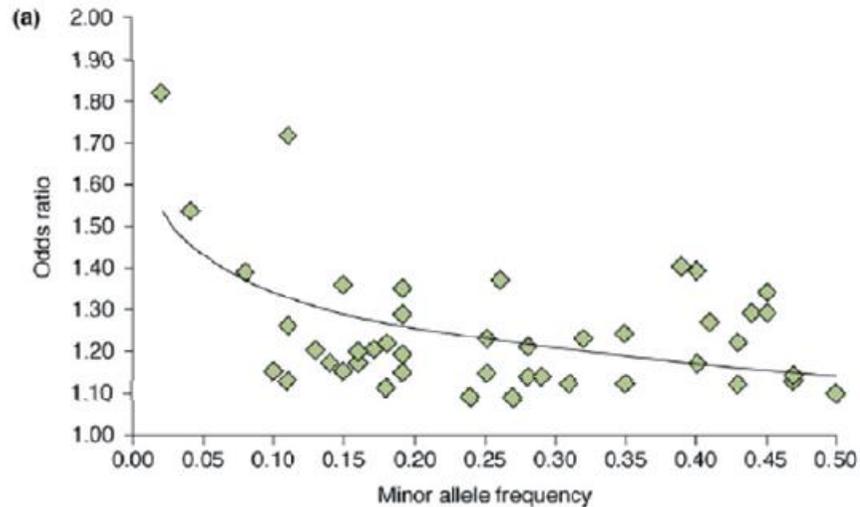
The term complex trait/disease refers to any phenotype that

does NOT exhibit classic Mendelian inheritance attributable to a single gene;

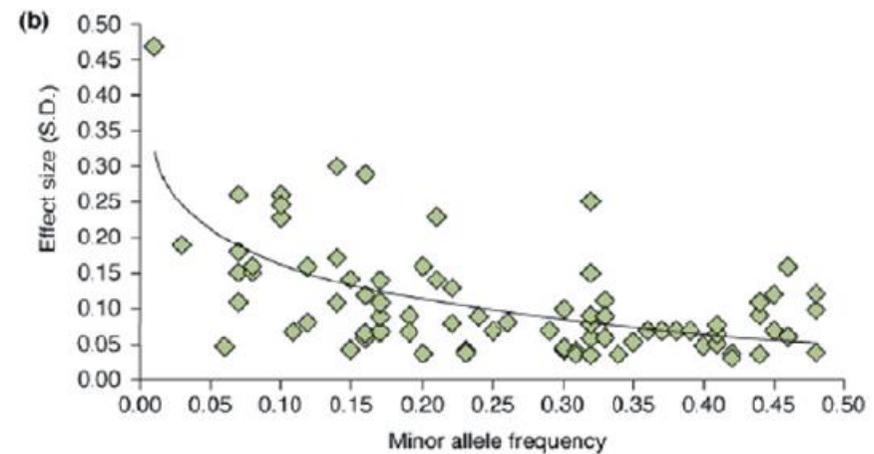
although they may exhibit familial tendencies (familial clustering, concordance among relatives).

Distribution of SNP “effects”

Dichotomous Traits



Quantitative Traits



Arking & Chakravarti 2009 Trends Genet

Food for thought:

- The higher the MAF, the lower the effect size
- Rare variants analysis is in its infancy in 2009

3.b Subject Level

Aim	Selection scheme
Increased effect size	Extreme sampling: Severely affected cases vs. extremely normal controls
Genes causing early onset	Affected, early onset vs. normal, elderly
Genes with large / moderate effect size	Cases with positive family history vs. controls with negative family history
Specific GxE interaction	Affected vs. normal subjects with heavy environmental exposure
Longevity genes	Elderly survivors serve as cases vs. young serve as controls
Control for covariates with strong effect	Affected with favorable covariates vs. normal with unfavorable covariate

Morton & Collins 1998 Proc Natl Acad Sci USA 95:11389

Popular design 1: cases and controls

Avoiding bias – checking assumptions:

1. Cases and controls drawn from same population
2. Cases representative for all cases in the population
3. All data collected similarly in cases and controls

Advantages:

1. Simple
2. Cheap
3. Large number of cases and controls available
4. Optimal for studying rare diseases

Disadvantages:

1. Population stratification
2. Prone to batch effects and other biases
3. Case definition / severity
4. Overestimation of risk for common diseases

Popular design 2: family-based

Avoiding bias – checking assumptions:

1. Families representative for population of interest
2. Same genetic background in both parents

Advantages:

1. Controls immune to population stratification (no association without linkage, no “spurious” (false positive) association)
2. Checks for Mendelian inheritance possible (fewer genotyping errors)
3. Parental phenotyping not required (late onset diseases)

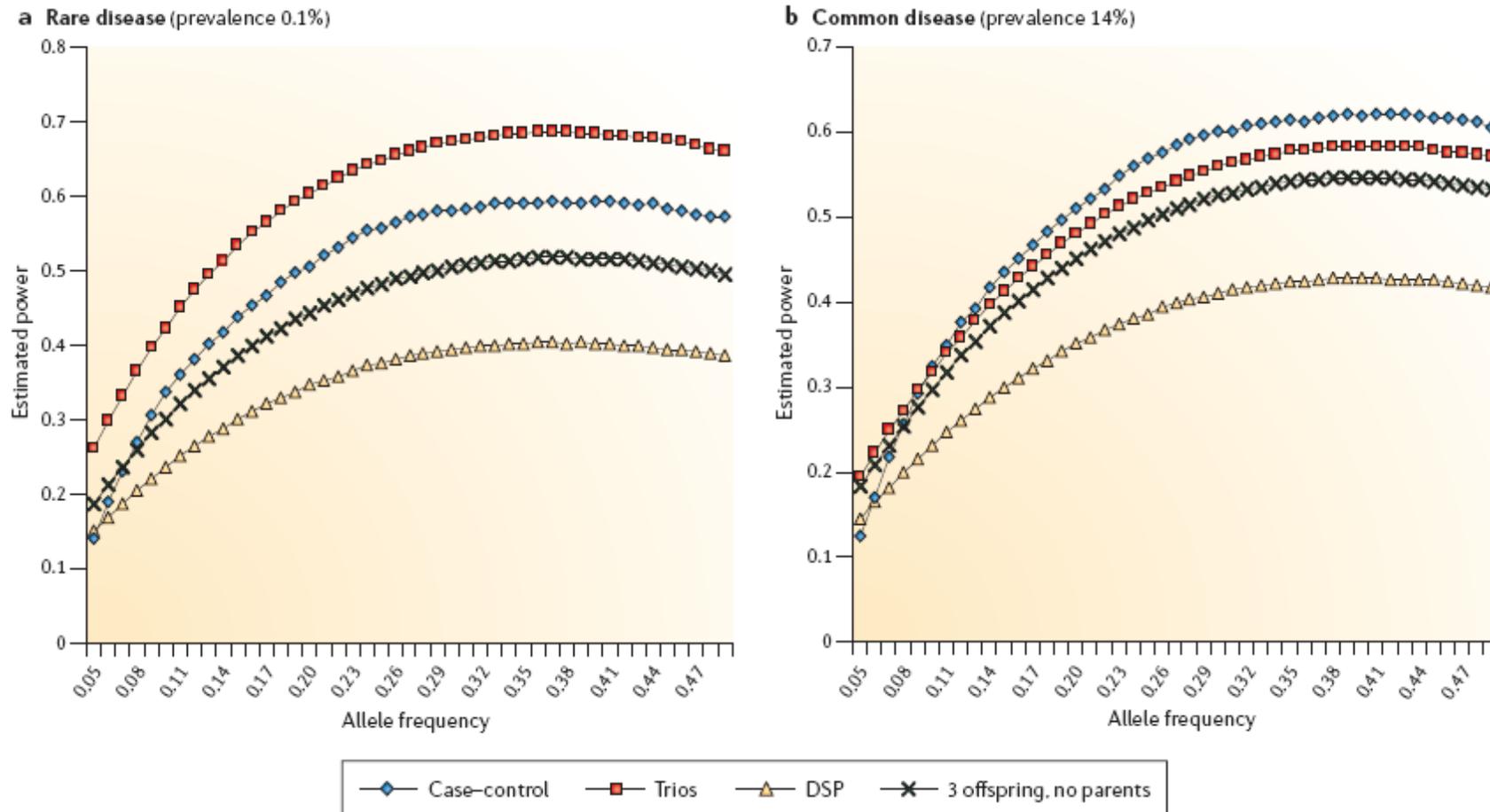
4. Simple logistics for diseases in children
5. Allows investigating imprinting (“bad allele” from father or mother?)

Disadvantages

1. Cost inefficient
2. Sensitive to genotyping errors
3. Lower power when compared with case-control studies

Some more power considerations

- Rare versus common diseases (Lange and Laird 2006)



4 Pre-analysis steps

4.a Quality control

Standard file format for GWA studies

Standard data format: tped = transposed ped format file

FamID	PID	FID	MID	SEX	AFF	SNP1 ₁	SNP1 ₂	SNP2 ₁	SNP2 ₂
1	1	0	0	1	1	A	A	G	T
2	1	0	0	1	1	A	C	T	G
3	1	0	0	1	1	C	C	G	G
4	1	0	0	1	2	A	C	T	T
5	1	0	0	1	2	C	C	G	T
6	1	0	0	1	2	C	C	T	T

ped file

Chr	SNP name	Genetic distance	Chromosomal position
1	SNP1	0	123456
1	SNP2	0	123654

map file

Standard file format for GWA studies (continued)

Chr	SNP	Gen. dist.	Pos	PID 1	PID 2	PID 3	PID 4	PID 5	PID 6						
1	SNP1	0	123456	A	A	A	C	C	C	A	C	C	C	C	C
1	SNP2	0	123654	G	T	G	T	G	G	T	T	G	T	T	T

tfam file: First 6 columns of standard ped file

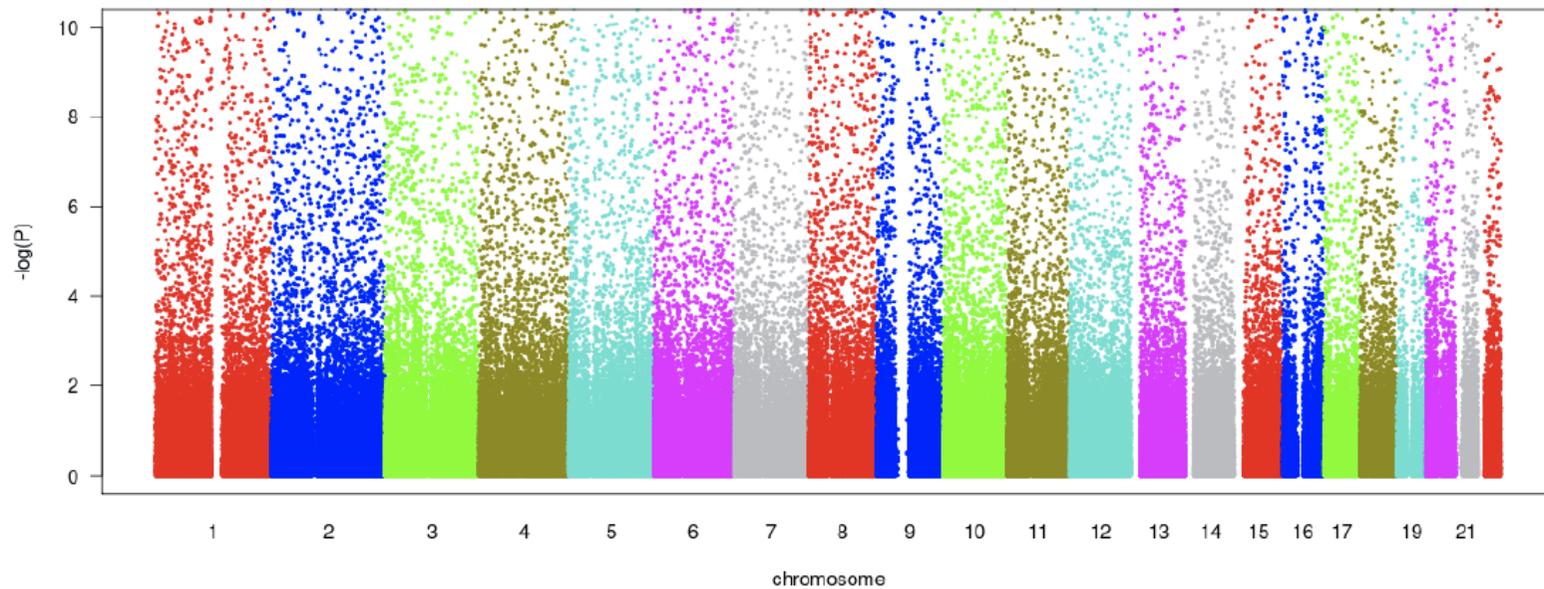
tped file

FamID	PID	FID	MID	SEX	AFF
1	1	0	0	1	1
2	1	0	0	1	1
3	1	0	0	1	1
4	1	0	0	1	2
5	1	0	0	1	2
6	1	0	0	1	2

tfam file

Why is quality control (QC) important?

BEFORE QC → true signals are lost in false positive signals

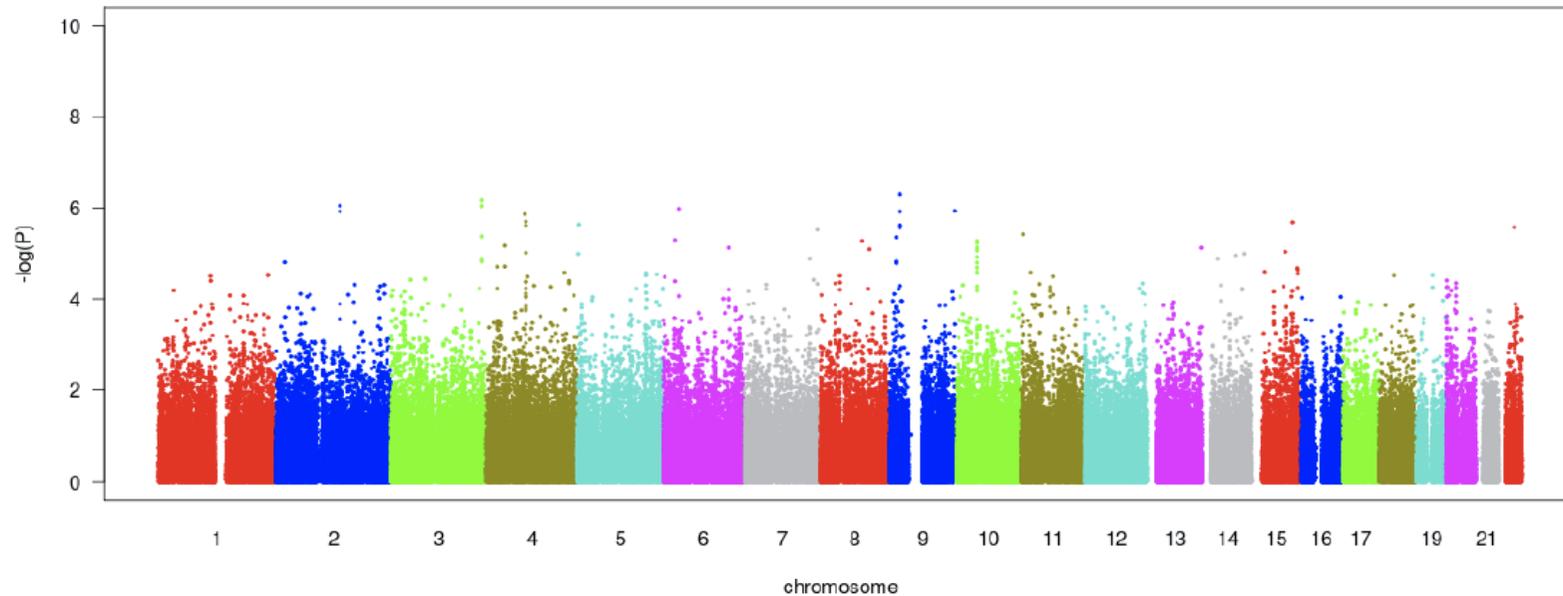


Ger MI FS I, Affymetrix 500k array set, SNPs on chip: 493,840

(Ziegler and Van Steen 2010)

Why is quality control important?

AFTER QC → skyline of Manhattan (→ name of plot: Manhattan plot):



Ger MI FS I, Affymetrix 500k array set, SNPs on chip: 493,840

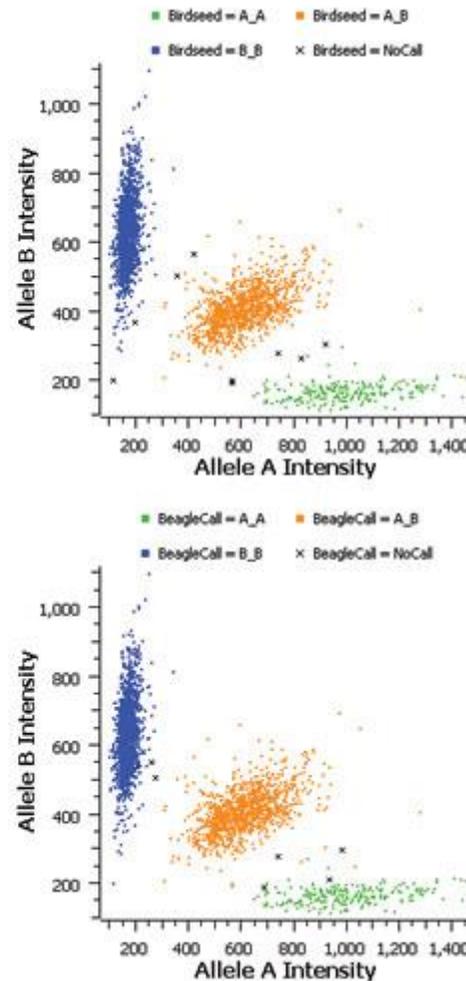
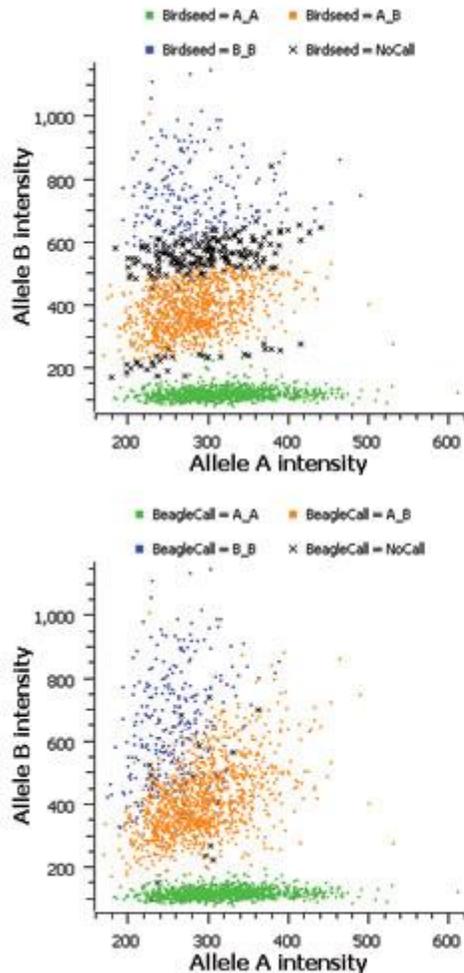
SNPs passing standard quality control: 270,701

(Ziegler and Van Steen 2010)

What is the standard quality control?

- Quality control can be performed on different levels:
 - Subject or sample level
 - Marker level (in this course: SNP level)
 - X-chromosomal SNP level (in this course not considered)
- Consensus on how to best QC data has led to the so-called “Travemünde criteria” (obtained in the town Travemünde) – see later

Marker level QC thresholds may be genotype calling algorithm dependent



Allele signal intensity genotype calling cluster plots for two different SNPs from the same study population.

Upper panels: Birdseed genotypes

Lower panels: BEAGLECALL genotypes.

The plots on the left show a SNP with poor resolution of A_B and B_B genotype clusters and the increased clarity of genotype calls that comes from using BEAGLECALL (Golden Helix Blog)

Quality control at the marker level

- **Minor allele frequency (MAF):**

- Genotype calling algorithms perform poorly for SNPs with low MAF
- Power is low for detecting associations to genetic markers with low MAF (with standard large-sample statistics)

- **Missing frequency (MiF)**

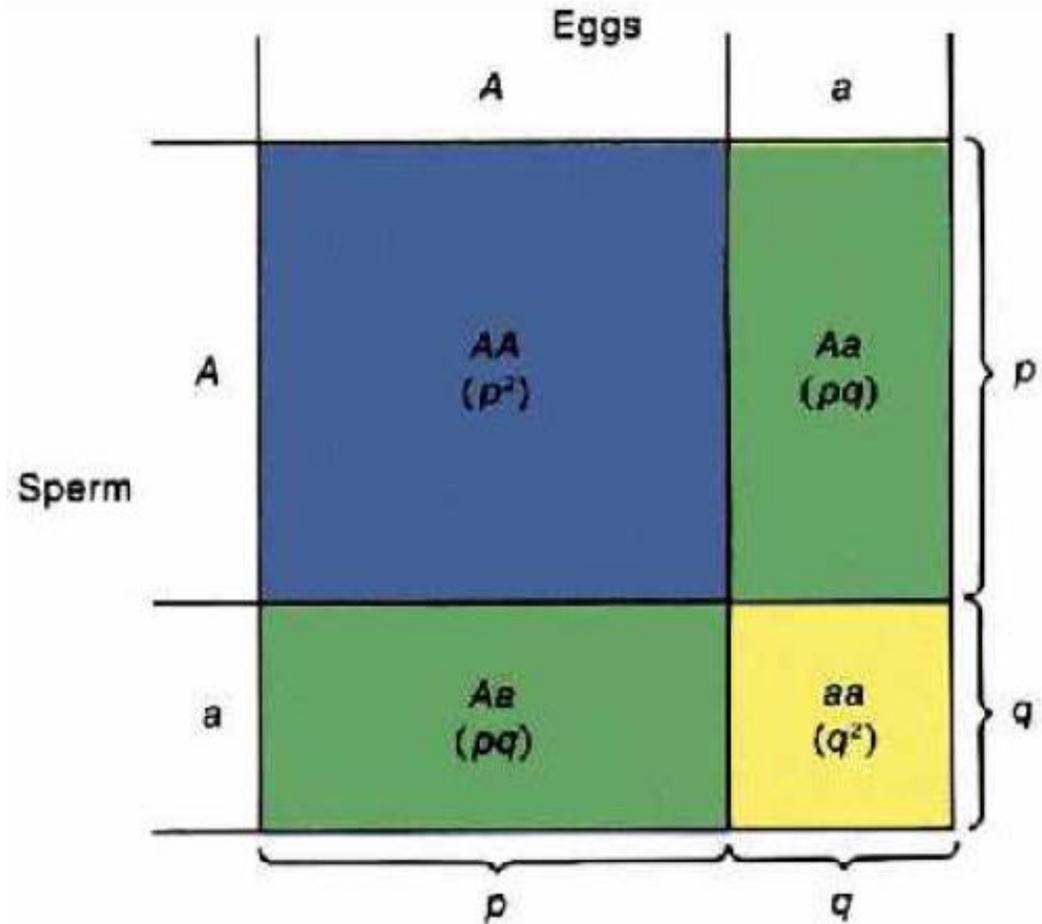
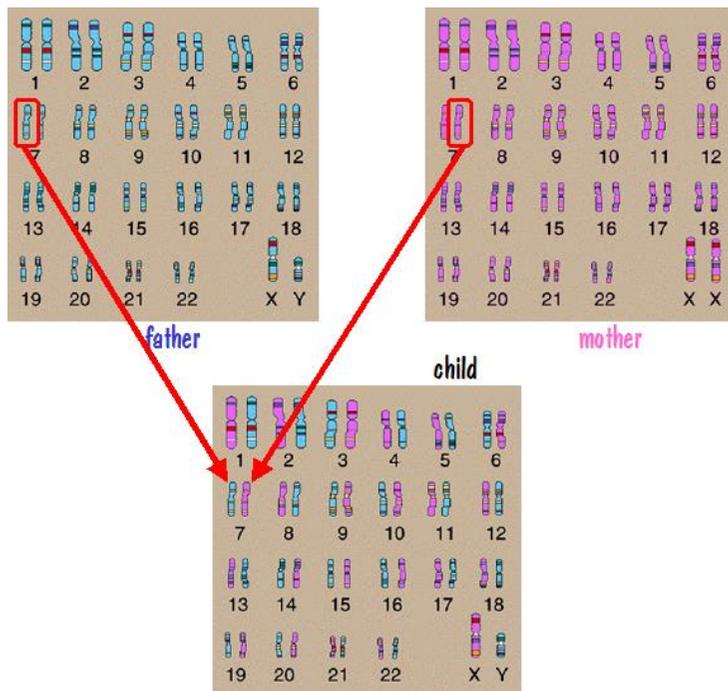
- 1 minus call rate
- MiF needs to be investigated separately in cases and controls because differential missingness may bias association results

- **Hardy-Weinberg equilibrium (HWE)**

- SNPs excluded if substantially more or fewer subjects heterozygous at a SNP than expected (excess heterozygosity or heterozygote deficiency)

What is Hardy-Weinberg Equilibrium (HWE)?

Consider diallelic SNP with alleles A and a



What is Hardy-Weinberg Equilibrium (HWE)?

Consider diallelic SNP with alleles A_1 and A_2

- Genotype frequencies

$$P(A_1A_1) = p_{11}, P(A_1A_2) = p_{12}, P(A_2A_2) = p_{22}$$

- Allele frequencies $P(A_1) = p = p_{11} + \frac{1}{2}p_{12}$, $P(A_2) = q = p_{22} + \frac{1}{2}p_{12}$

If

- $P(A_1A_1) = p_{11} = p^2$
- $P(A_1A_2) = p_{12} = 2pq$
- $P(A_2A_2) = p_{22} = q^2$

the population is said to be in HWE at the SNP

(Ziegler and Van Steen 2010)

Distorting factors to HWE causing evolution to occur

1. Non-random mating

2. Mutation - by definition mutations change allele frequencies causing evolution

3. Migration - if new alleles are brought in by immigrants or old alleles are taken out by emigrants then the frequencies of alleles will change causing evolution

4. Genetic drift - random events due to small population size (bottleneck caused by storm and leading to reduced variation, migration events leading to founder effects)

5. Natural selection – some genotypes give higher reproductive success
(Darwin)

The Travemünde criteria

Level	Filter criterion	Standard value for filter
Sample level	Call fraction	$\geq 97\%$
	Cryptic relatedness	Study specific
	Ethnic origin	Study specific; visual inspection of principal components
	Heterozygosity	Mean \pm 3 std.dev. over all samples
	Heterozygosity by gender	Mean \pm 3 std.dev. within gender group
SNP level	MAF	$\geq 1\%$
	MiF	$\leq 2\%$ in any study group, e.g., in both cases and controls
	MiF by gender	$\leq 2\%$ in any gender
	HWE	$p < 10^{-4}$

(Ziegler 2009)

The Travemünde criteria

Level	Filter criterion	Standard value for filter
SNP level	Difference between control groups	$p > 10^{-4}$ in trend test
	Gender differences among controls	$p > 10^{-4}$ in trend test
X-Chr SNPs	Missingness by gender	No standards available
	Proportion of male heterozygote calls	No standards available
	Absolute difference in call fractions for males and females	No standards available
	Gender-specific heterozygosity	No standard value available

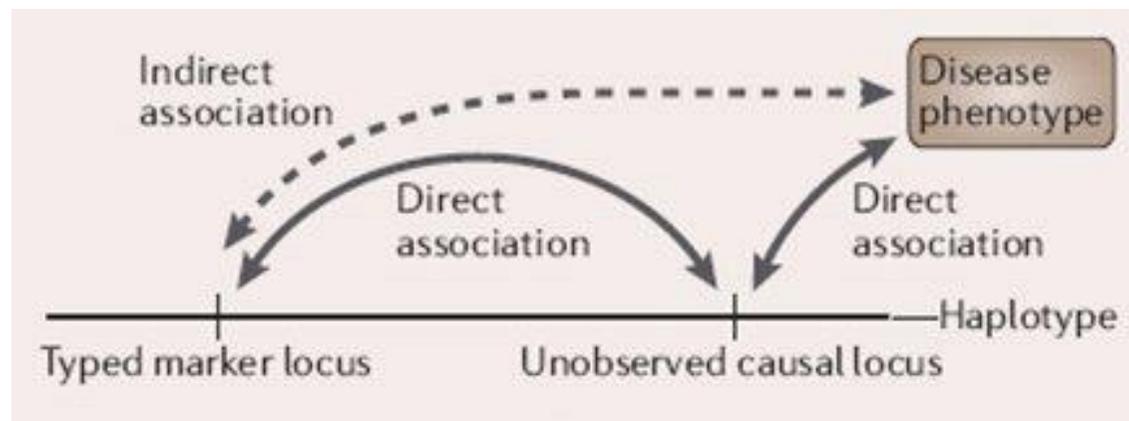
(Ziegler 2009)

4.b Linkage disequilibrium

- **Linkage Disequilibrium (LD)** is a measure of co-segregation of alleles in a population – linkage + allelic association

Two alleles at different loci that occur together on the same chromosome (or gamete) more often than would be predicted by random chance.

- It is a very important concept for GWAs, since it gives the rationale for performing genetic association studies



4.c Confounding by shared genetic ancestry – “population stratification”

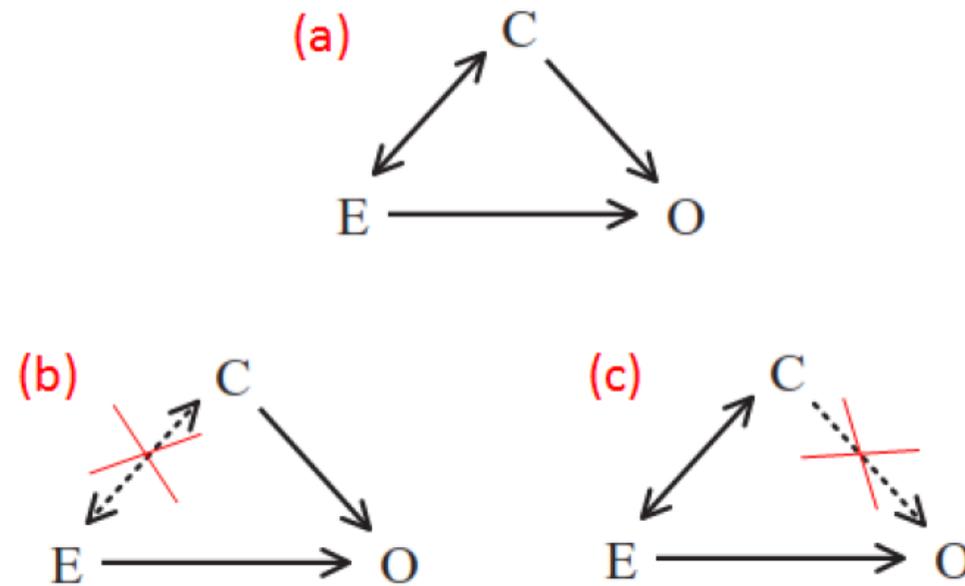


Figure 1: Schematic illustration of confounding control. Arrows represent causal effects, double arrows associations of any nature.
E = exposure, C = confounder, O = outcome.

(Cois 2014)

5 Analysis Steps

5.a Testing for Associations

The role of regression analysis

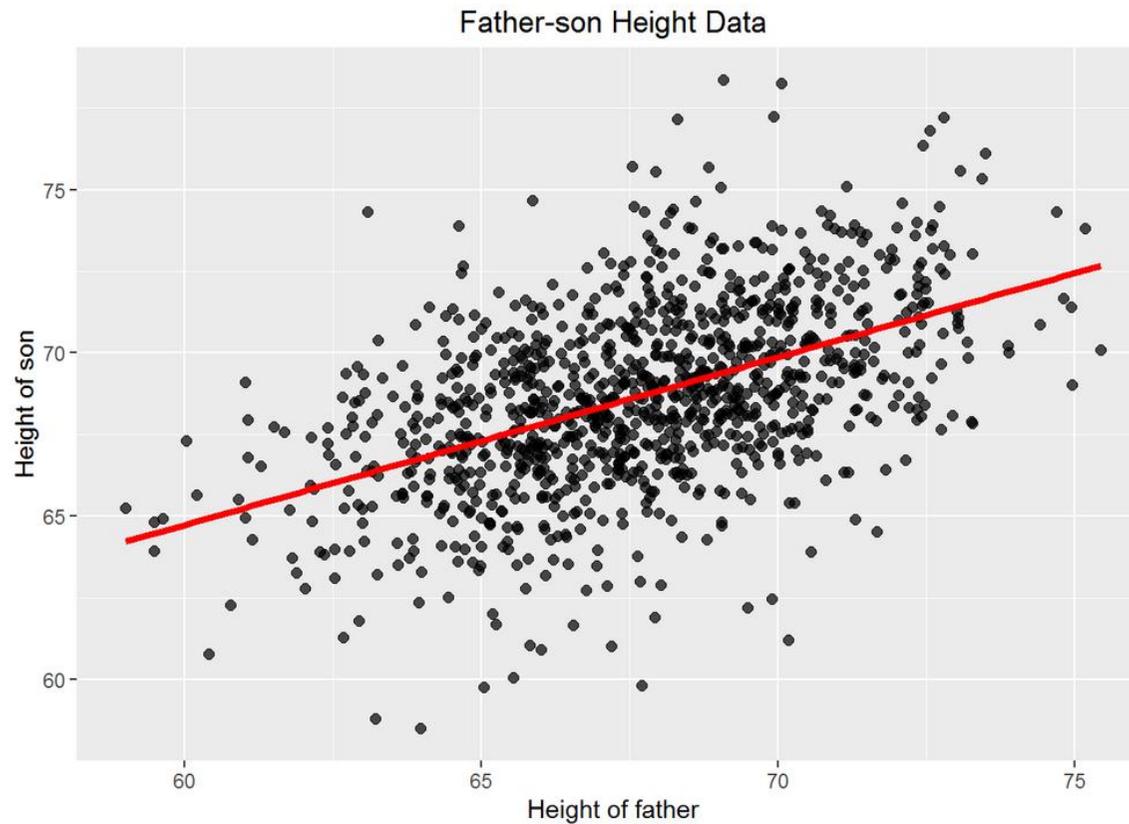
- Galton used the following equation to explain the phenomenon that sons of tall fathers tend to be tall but not as tall as their fathers while sons of short fathers tend to be short but not as short as their fathers:

$$\frac{y - \bar{y}}{SD_y} = r \frac{(x - \bar{x})}{SD_x}$$

This effect is called the **regression effect**.

The use of regression analysis

- **regression line** goes through (mean Y, mean X)



(https://rstudio-pubs-static.s3.amazonaws.com/204984_dd2112475db84af2a03260c4a4f830ac.html)

The use of regression analysis

- **Regression analysis** is used for explaining or modeling the relationship between a single variable Y , called the response, output or dependent variable, and one or more predictor, input, independent or explanatory variables, X_1, \dots, X_p .
- When $p=1$ it is called simple regression but when $p > 1$ it is called multiple regression or sometimes multivariate regression.
- When there is more than one Y , then it is called multivariate multiple regression
- Regression analyses have several possible objectives including
 - Prediction of future observations.
 - Assessment of the effect of, or relationship between, explanatory variables on the response.
 - A general description of data structure

The linear regression model

$$y = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \epsilon$$

- y : response variable.
- x_1, \dots, x_k : regressor variables, independent variables.
- $\beta_0, \beta_1, \dots, \beta_k$: regression coefficients.
- ϵ : model error.
 - ▶ Uncorrelated: $\text{cov}(\epsilon_i, \epsilon_j) = 0, i \neq j$.
 - ▶ Mean zero, Same variance: $\text{var}(\epsilon_i) = \sigma^2$. (homoscedasticity)
 - ▶ Normally distributed.

Linear vs non-linear

Linear Models Examples:

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + \epsilon$$

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 + \epsilon$$

$$y = \beta_0 + \beta_1 \log x_1 + \beta_2 \log x_2 + \epsilon$$

$$\log y = \beta_0 + \beta_1 \left(\frac{1}{x_1} \right) + \beta_2 \left(\frac{1}{x_2} \right) + \epsilon$$

Nonlinear Models Examples:

$$y = \beta_0 + \beta_1 x_1^{\gamma_1} + \beta_2 x_2^{\gamma_2} + \epsilon$$

$$y = \frac{\beta_0}{1 + e^{\beta_1 x_1}} + \epsilon$$

Regression inference

$$y = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \epsilon$$

- Least square estimation of the regression coefficients.
 $b = (X^T X)^{-1} X^T y.$
- Variance estimation for σ^2 (see later)
- Coefficient of Determination. R^2 .
- Partial F test or t-test for $H_0 : \beta_j = 0$.

What is R-squared?

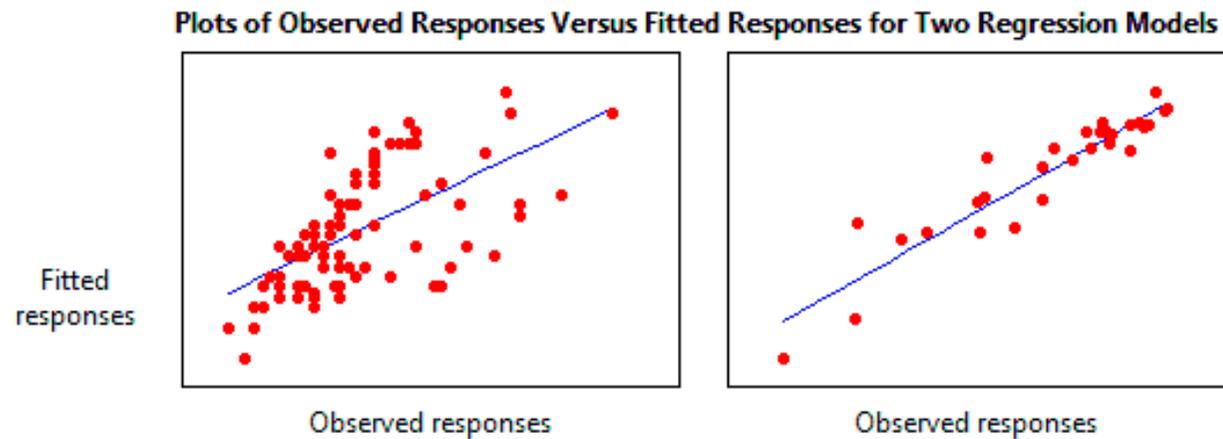
- R-squared is a statistical measure of how close the data are to the fitted regression line. It is also known as the **coefficient of determination, or the coefficient of multiple determination for multiple regression.**
- The definition of R-squared is fairly straight-forward; it is the percentage of the response variable variation that is explained by a linear model:

$$\text{R-squared} = \text{Explained variation} / \text{Total variation}$$

- R-squared is always between 0 and 100%:
 - 0% indicates that the model explains none of the variability of the response data around its mean.
 - 100% indicates that the model explains all the variability of the response data around its mean.

Graphical representation of R-squared

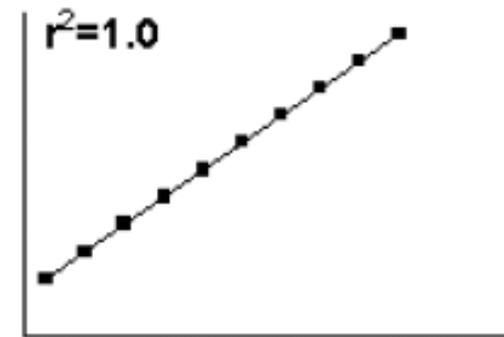
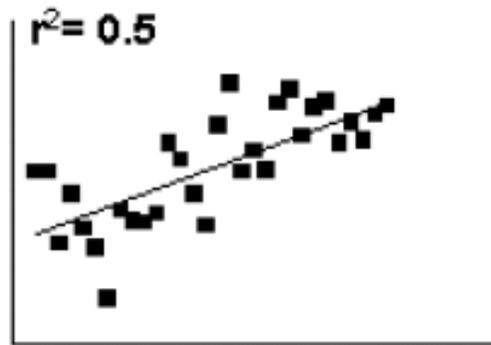
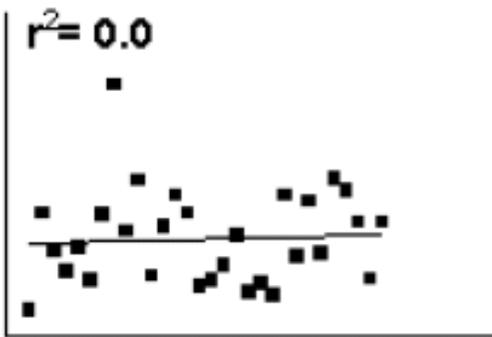
- Plotting fitted values by observed values graphically illustrates different R-squared values for regression models.



- The regression model on the left accounts for 38.0% of the variance while the one on the right accounts for 87.4%. The more variance that is accounted for by the regression model the closer the data points will fall to the fitted regression line.

Coefficient of determination \sim squared correlation coefficient r^2

- An R^2 value of 0.0 means that knowing X does not help you predict Y. There is no linear relationship between X and Y, and the best-fit line is a horizontal line going through the mean of all Y values.
- When R^2 equals 1.0, all points lie exactly on a straight line with no scatter. Knowing X lets you predict Y perfectly.



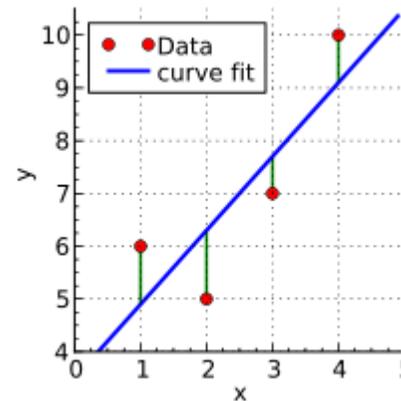
General linear test approach

- The full model (continuous response, say “BMI”):

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \varepsilon$$

- Fit the model by f.i. the method of least squares (this leads to estimations b for the beta parameters in the model)
- It will also lead to the **error sums of squares** (SSE): the sum of the squared deviations of each observation Y around its estimated expected value
- The error sums of squares of the full model SSE(F):

$$\begin{aligned} \sum [Y - b_0 - b_1 X_1 - b_2 X_2]^2 \\ = \sum (Y - \hat{Y})^2 \end{aligned}$$



General linear test approach

- Next we consider a null hypothesis H_0 of interest:

$$H_0: \beta_1 = 0$$

$$H_1: \beta_1 \neq 0$$

- The model when H_0 holds is called **the reduced or restricted model**. When $\beta_1 = 0$, then the regression model reduces to

$$Y = \beta_0 + \beta_2 X_2 + \varepsilon$$

- Again we can fit this model with f.i. the least squares method and obtain an error sums of squares, now for the reduced model: $SSE(R)$
- Question: which error sums of squares will be smaller? $SSE(F)$ or $SSE(R)$

General linear test approach

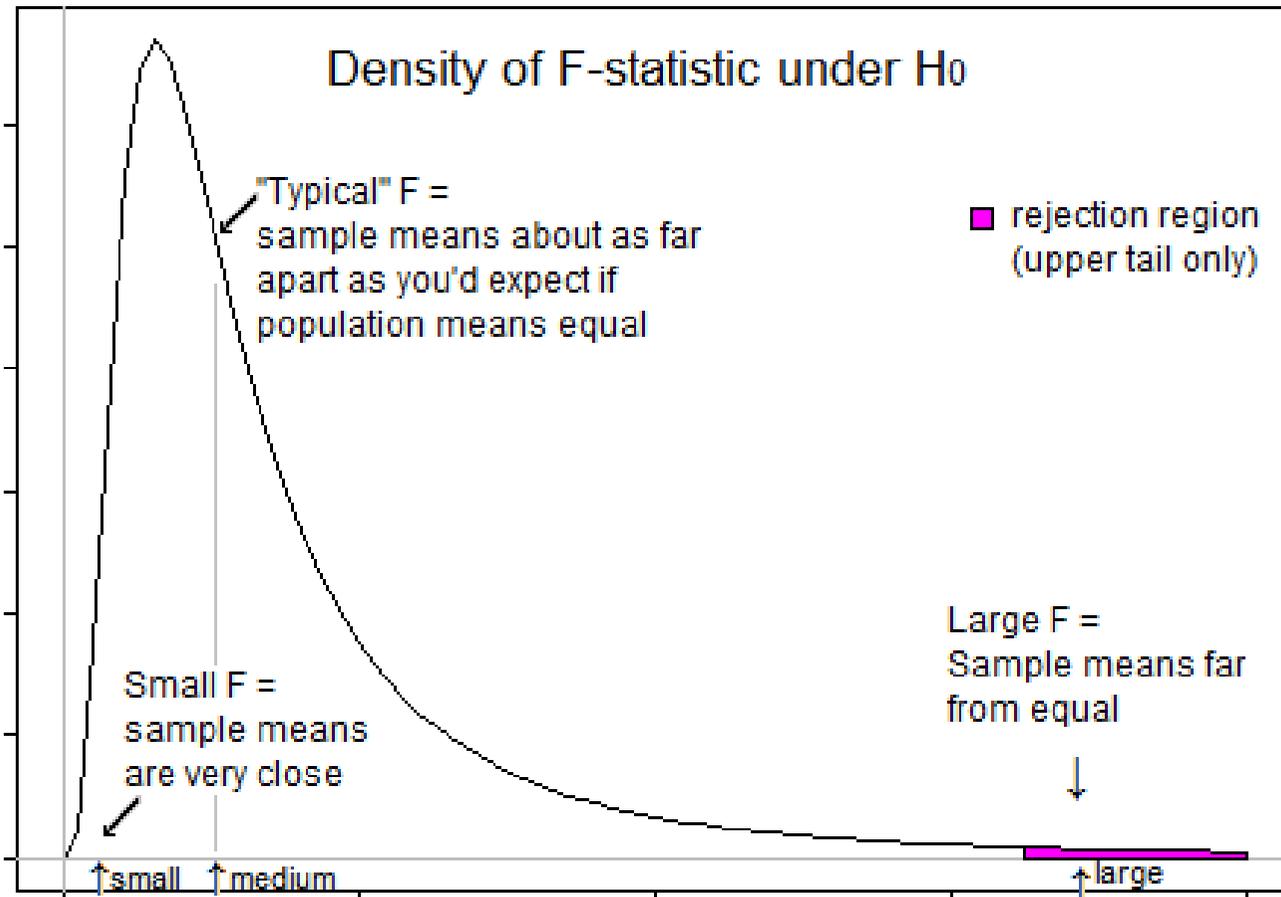
- The logic now is to compare both SSEs. The actual test statistic is a function of $SSE(R)$ - $SSE(F)$:

$$F^* = \frac{SSE(R) - SSE(F)}{df_R - df_F} : \frac{SSE(F)}{df_F}$$

which follows an F distribution when H_0 holds

- The decision rule (for a given alpha level of significance) is:
If $F^* \leq F(1 - \alpha; df_R - df_F, df_F)$, you cannot reject H_0
If $F^* > F(1 - \alpha; df_R - df_F, df_F)$, conclude H_1

Recall: rejection and non-rejection regions



Tests in GWAS using the regression framework

- **Example 1:**

$$Y = \beta_0 + \beta_1 SNP + \varepsilon$$

- $H_0: \beta_1 = 0$
- $H_1: \beta_1 \neq 0$
- $df_F = n - 2$ (this links to df in variance estimation)
- $df_R = n - 1$ (this links to df in variance estimation)

It can be shown that for testing $\beta_1 = 0$ versus $\beta_1 \neq 0$

$$- F^* = \frac{SSE(R) - SSE(F)}{df_R - df_F} : \frac{SSE(F)}{df_F} = \frac{b_1^2}{s^2(b_1)} = (t^*)^2$$

Why is the t-test more flexible?

Tests in GWAS using the regression framework

- **Example 2:**

$$Y = \beta_0 + \beta_1 SNP + \beta_2 PC_1 + \beta_3 PC_2 + \varepsilon$$

- $H_0: \beta_1 = 0$
- $H_1: \beta_1 \neq 0$
- $df_F = n - 4$
- $df_R = n - 3$

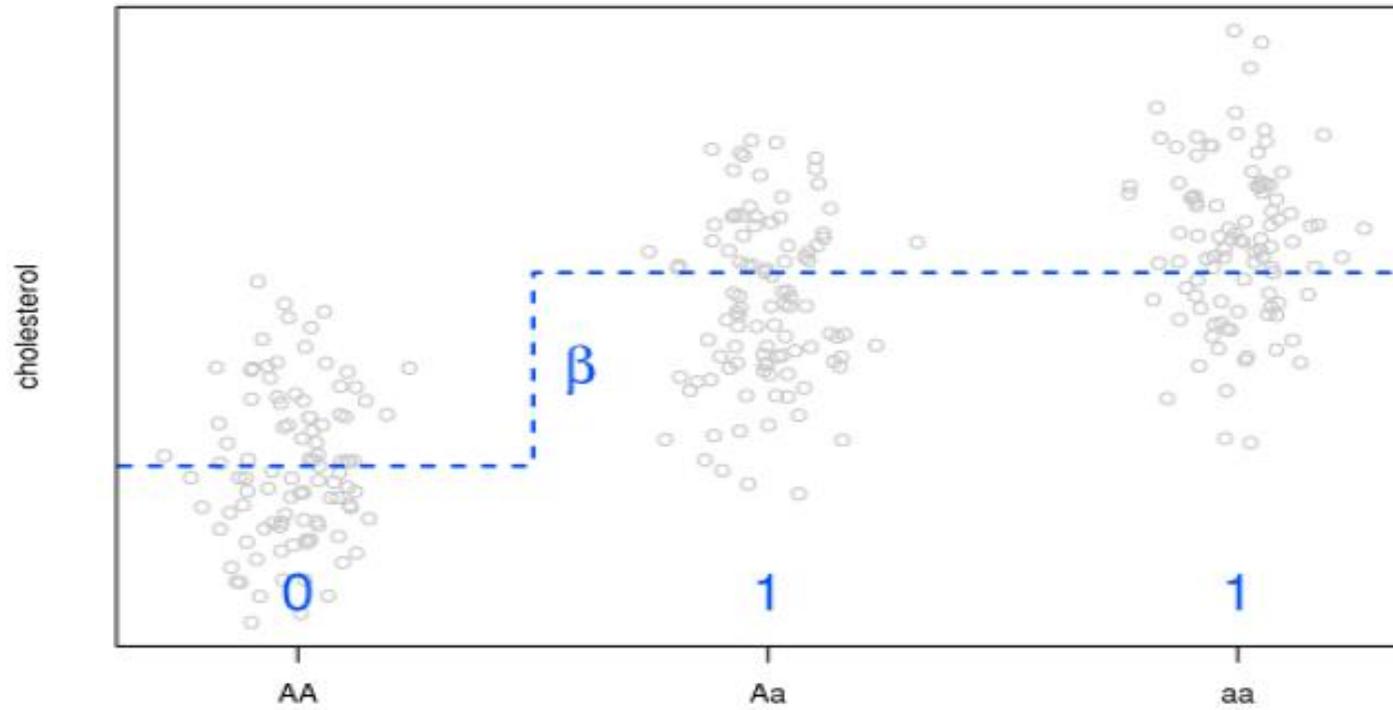
How many dfs would the corresponding F-test have?

How many dfs would a corresponding $t^{(2)}$ test have?

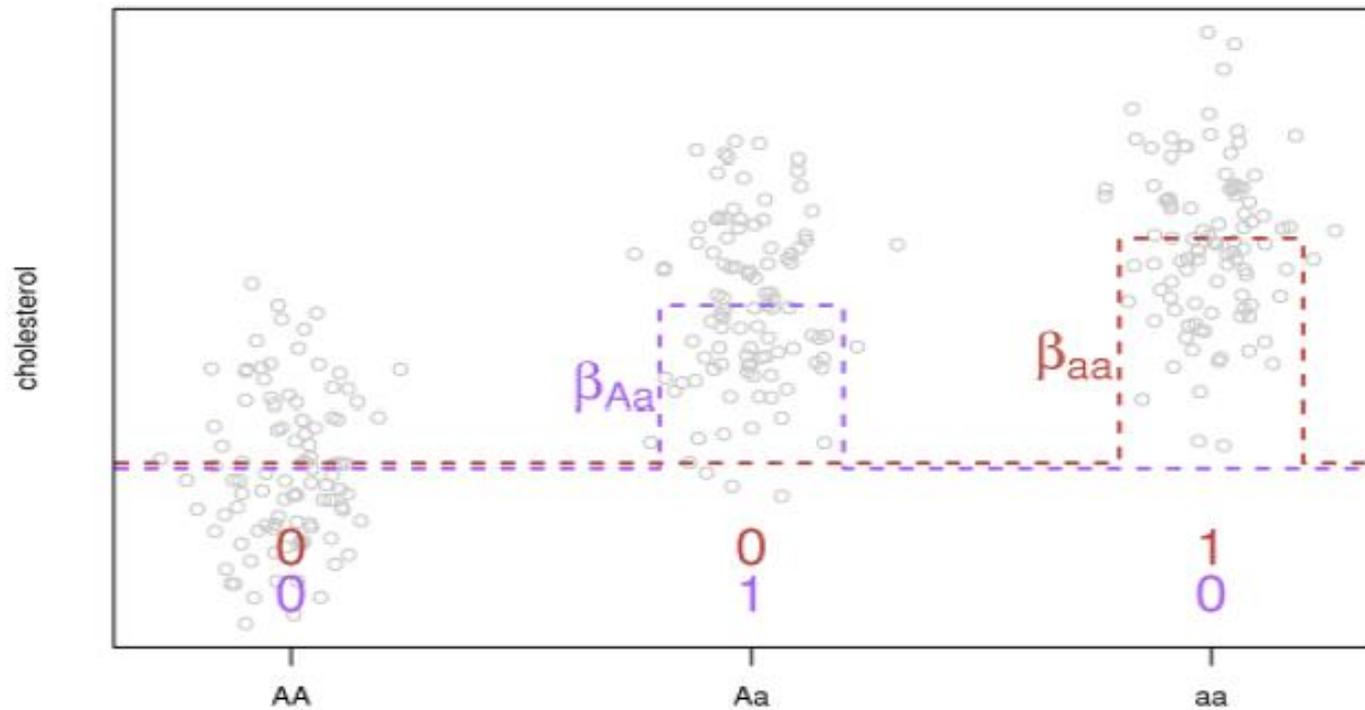
The impact of different encoding schemes for SNPs

	Coding scheme for statistical modeling/testing					
Indiv. genotype	X1	X1	X2	X1	X1	X1
	Additive coding	Genotype coding (general mode of inheritance)		Dominant coding (for a)	Recessive coding (for a)	Advantage Heterozygous
AA	0	0	0	0	0	0
Aa	1	1	0	1	0	1
aa	2	0	1	1	1	0

Which encoding scheme provides a good fit to the data?

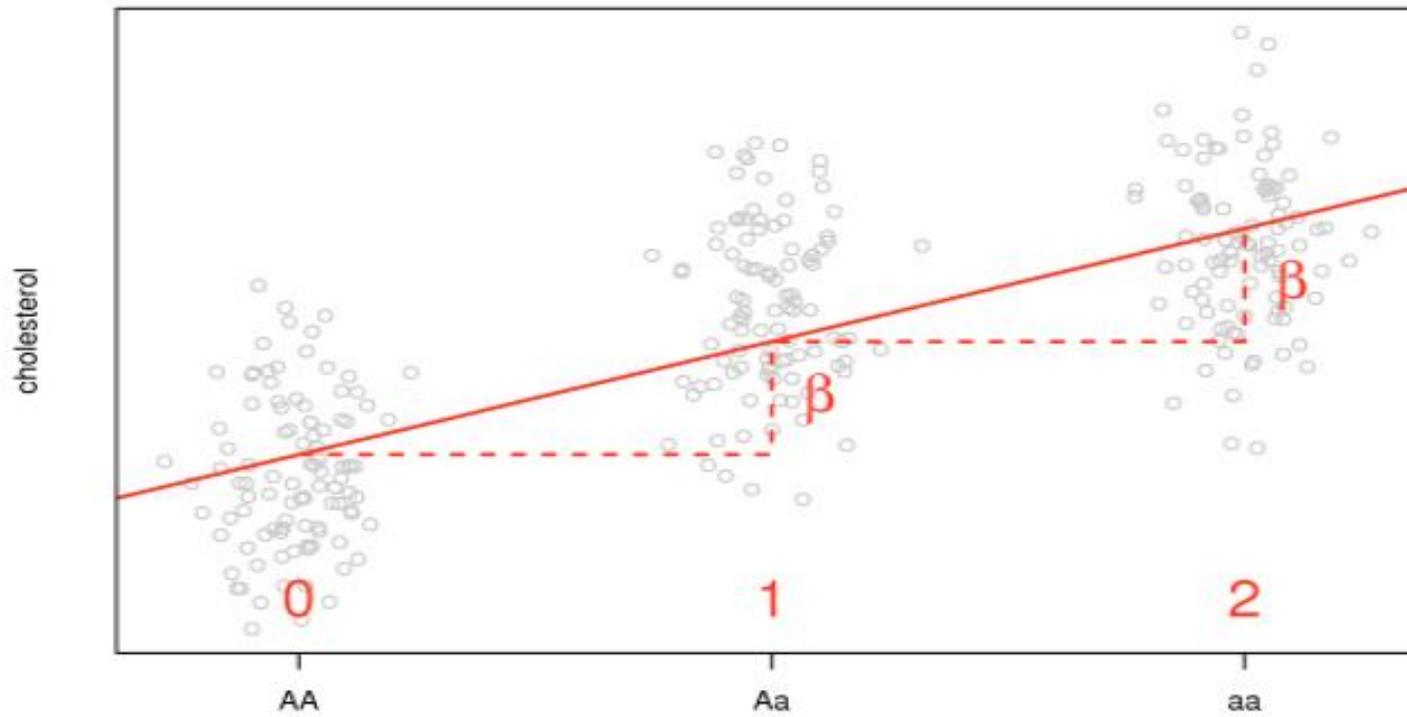


Which encoding scheme provides a good fit to the data?



Robust vs overkill ?

Which encoding scheme provides a good fit to the data?



Most commonly used

Regression analysis in R

- Main functions
 - The basic syntax for doing regression in R is **lm()** to fit linear models
 - The R function **glm()** can be used to fit generalized linear models (i.e., when the response is not normally distributed)
- General syntax rules in R model fitting are given on the next slide.

Regression analysis in R

Syntax	Model	Comments
$Y \sim A$	$Y = \beta_0 + \beta_1 A$	Straight-line with an implicit y-intercept
$Y \sim -1 + A$	$Y = \beta_1 A$	Straight-line with no y-intercept; that is, a fit forced through (0,0)
$Y \sim A + I(A^2)$	$Y = \beta_0 + \beta_1 A + \beta_2 A^2$	Polynomial model; note that the identity function $I()$ allows terms in the model to include normal mathematical symbols.
$Y \sim A + B$	$Y = \beta_0 + \beta_1 A + \beta_2 B$	A first-order model in A and B without interaction terms.
$Y \sim A:B$	$Y = \beta_0 + \beta_1 AB$	A model containing only first-order interactions between A and B.
$Y \sim A*B$	$Y = \beta_0 + \beta_1 A + \beta_2 B + \beta_3 AB$	A full first-order model with a term; an equivalent code is $Y \sim A + B + A:B$.
$Y \sim (A + B + C)^2$	$Y = \beta_0 + \beta_1 A + \beta_2 B + \beta_3 C + \beta_4 AB + \beta_5 AC + \beta_6 BC$	A model including all first-order effects and interactions up to the n^{th} order, where n is given by $()^n$. An equivalent code in this case is $Y \sim A*B*C - A:B:C$.

Model diagnostics are model-dependent ...

- There are 4 principal assumptions which justify the use of **linear regression** models for purposes of prediction:
 - **linearity** of the relationship between dependent and independent variables
 - independence of the errors (no serial correlation)
 - homoscedasticity (constant variance) of the errors
 - versus time (when time matters)
 - versus the predictions (or versus any independent variable)
 - normality of the error distribution. (<http://www.duke.edu/~rnau/testing.htm>)
- To check **model assumptions**: go to **quick-R** and regression diagnostics (<http://www.statmethods.net/stats/rdiagnostics.html>)

QQ plots for model diagnostics – Q for Quantile

- Quantiles are points in your data below which a certain proportion of your data fall.

What is the 0.5 quantile for normally distributed data?

- Here we generate a random sample of size 200 from a normal distribution and find the quantiles for 0.01 to 0.99 using the quantile function:

```
quantile(rnorm(200),probs = seq(0.01,0.99,0.01))
```

- Q-Q plots take your sample data, sort it in ascending order, and then plot them versus quantiles calculated from a theoretical distribution.

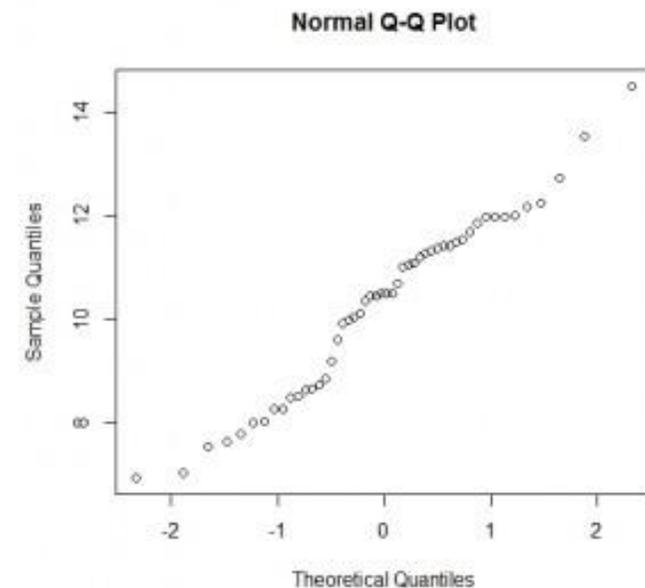
The number of quantiles is selected to match the size of your sample data.

The quantile function in R offers 9 different quantile algorithms!

See `help(quantile)`

QQ plots for model diagnostics – Q for Quantile

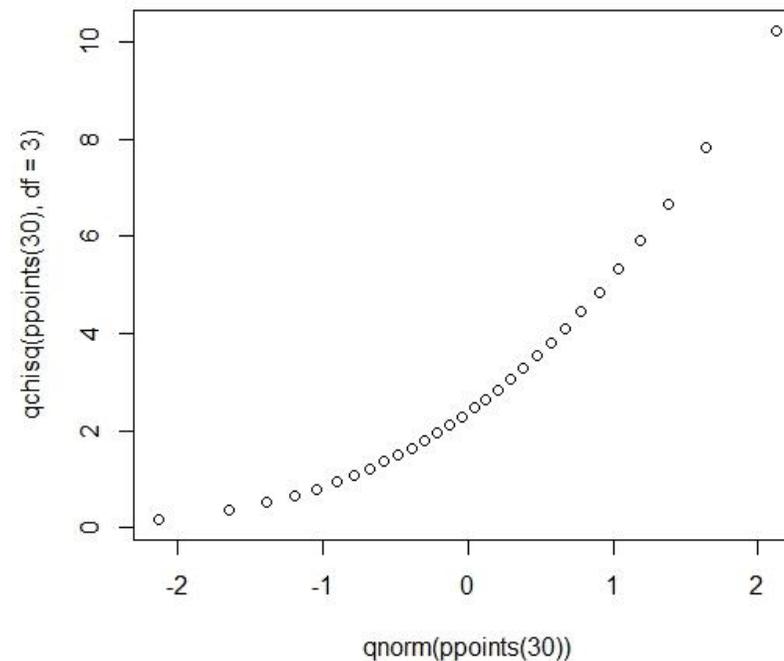
- A Q-Q plot is a scatterplot created by plotting **two sets of quantiles** against one another.
- If both sets of quantiles come from the same distribution, we should see the points forming a line that's roughly straight.
- Here's an example of a Normal Q-Q plot when both sets of quantiles truly come from Normal distributions.



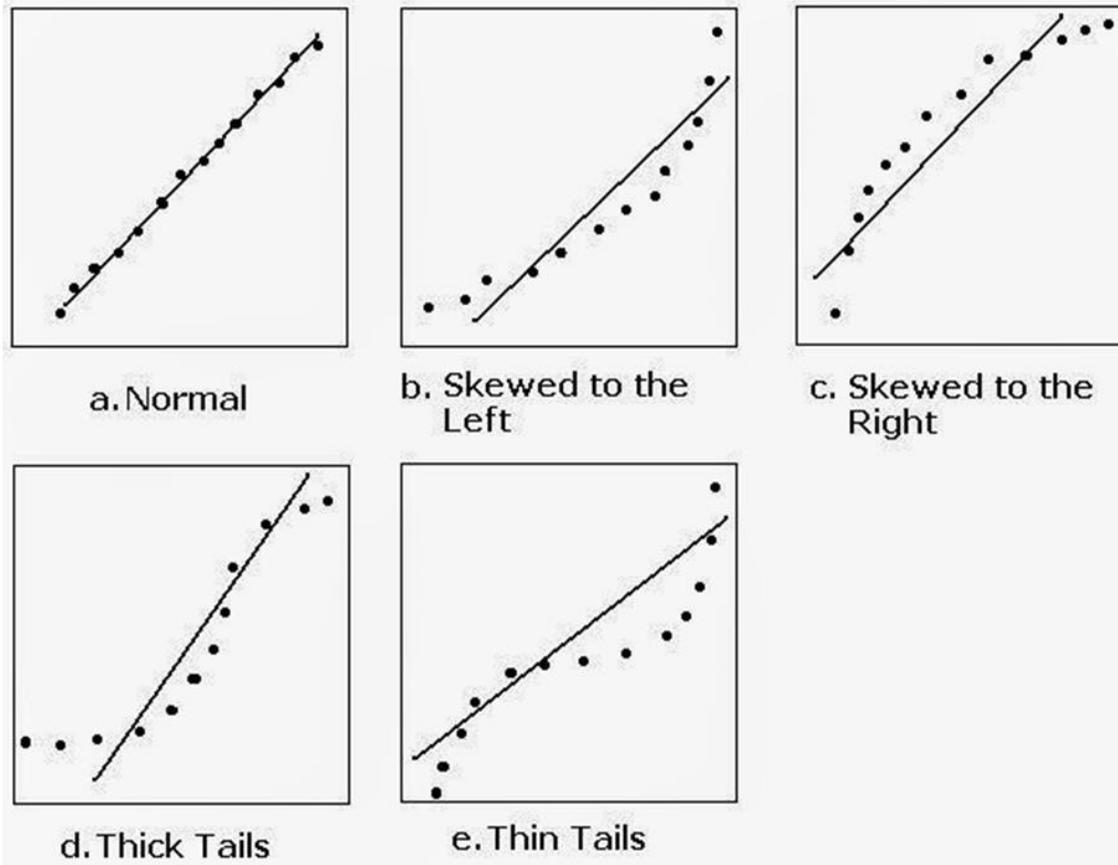
Examples of QQ plots: no straight line

- QQ plot of a distribution that's skewed right; a Chi-square distribution with 3 degrees of freedom against a Normal distribution

```
qqplot(qnorm(ppoints(30)), qchisq(ppoints(30),df=3))
```



Examples of QQ plots: some frequent scenarios



Testing for association between case/control status and a SNP

- Fill in the table below and perform a chi-squared test for independence between rows and columns → **genotype test** → **2 df**

	AA	Aa	aa
Cases			
Controls			

Sum of entries =
cases+controls

- Fill in the table below and perform a chi-squared test for independence between rows and columns → **allelic test (ONLY valid under HWE)** → **1df**

	A	a
Cases		
Controls		

Sum of entries is
2 x (cases + controls)

Testing for association between case/control status and a SNP

- The **genotype test involves a 2df test** (note that two variables X1 and X2 were needed for genotype coding).
- It has been shown that usually, the additive coding gives adequate power, even when the true underlying mode of inheritance is NOT additive (note that the **additive coding can be achieved by only using 1 variable (X1)**).
- For large sample sizes, a “test for trend” (risk for disease, or average trait increases/decreases with increasing number of “a” copies) theoretically follows a chi-squared distribution with **1df**.

Instead of

$$Y = \beta_0 + \beta_1 SNP + \varepsilon; Y \text{ continuous}$$

and modelling

$$E[Y|SNP] = \beta_0 + \beta_1 SNP \text{ (without error term!)}$$

consider

$\beta_0 + \beta_1 SNP = \boldsymbol{\eta}$ representing the linear combination as it can never be equal to a binary variable (0/1 response; control/case status)

and model

$$\boldsymbol{g}(E[Y|SNP]) = \beta_0 + \beta_1 SNP = \boldsymbol{\eta}$$

where $\boldsymbol{g}()$ is called a **link function**

and thus

$$E[Y|SNP] = \boldsymbol{g_inv}(\boldsymbol{\eta})$$

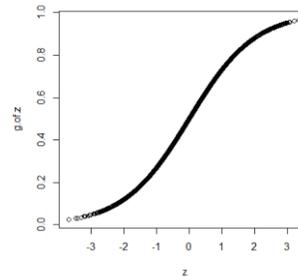
For a binary trait Y:

$$E[Y|SNP] = Prob(Y = 1|SNP)$$
$$= \frac{\exp(\eta)}{(1 + \exp(\eta))} = \frac{1}{(1 + \exp(-\eta))} = g_inv(\eta)$$

where

g_inv is the **logistic function (sigmoid function)**
(squashing the linear predictor to an acceptable range)

```
> Z <- rnorm(10000)
> g.of.Z <- (1/(1+exp(-Z)))
> plot(Z,g.of.Z)
```



Since

$$Prob(Y = 1|SNP) = \frac{\exp(\eta)}{(1+\exp(\eta))}$$

we have

$$\frac{Prob(Y = 1|SNP)}{1 - Prob(Y = 1|SNP)} = \exp(\eta)$$

and thus

$$\mathbf{g}(E[Y|SNP]) = \beta_0 + \beta_1 SNP = \log\left(\frac{Prob(Y = 1|SNP)}{1 - Prob(Y = 1|SNP)}\right) = \boldsymbol{\eta}$$

(g is called **the logit function**)

Estimation of β_0 and β_1 in logistic regression

- In **standard linear models** we estimate the parameters by minimizing the sum of the squared residuals
- This is equivalent to finding parameters that **maximize the likelihood**
- In a **logistic regression** we can also fit parameters by maximizing the likelihood
- The **deviance** is 2 times the log-likelihood ratio of the full model compared to the reduced model (in logistic regression models this has a similar role to comparison of SSEs in linear regression models with a continuous outcome Y)
- Estimation is equivalent to finding parameter values that **minimize** a minus 2 log likelihood (in the literature also sometimes confusingly be called deviance)

5.b Causation

“Association does not imply causation”

- Meaning:

In all observational epidemiologic studies, findings of an association between a substance or exposure and a health effect do not necessarily imply causation.

For example, a study might show that the habit of carrying matches is associated with an increased likelihood of later developing lung cancer.

"Correlation (as a measure of association) is not causation"

- Meaning:

Just because two things correlate does not necessarily mean that one causes the other.

As a seasonal example, just because people in Belgium tend to spend more in the shops when it's cold and less when it's hot doesn't mean cold weather causes high street spending.

Establishing causation: randomized controlled trials

- Randomized trials are studies in which human volunteers are randomly assigned to receive either the agent being studied or an inactive placebo, usually under double-blind conditions (where neither the participants nor the investigators know which substance each individual is receiving), and their health is then monitored for a period of time.
- This type of study can provide strong evidence for a causal effect, especially if its findings are replicated by other studies.

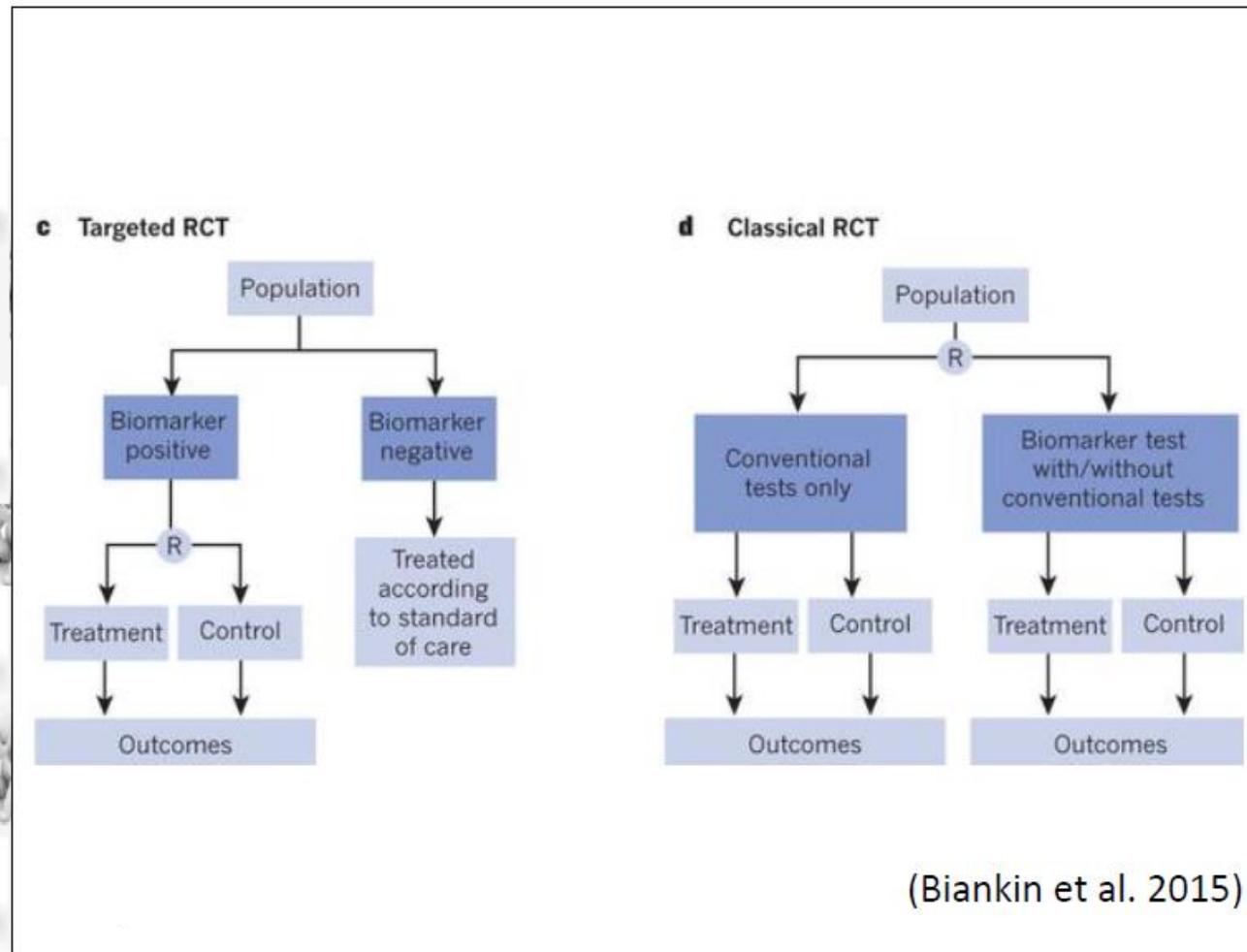
(<https://www.acsh.org>)

What are randomised controlled trials good for?

Nancy Cartwright

Abstract Randomized controlled trials (RCTs) are widely taken as the gold standard for establishing causal conclusions. Ideally conducted they ensure that the treatment ‘causes’ the outcome—in the experiment. But where else? This is the venerable question of external validity. I point out that the question comes in two importantly different forms: Is the specific causal conclusion warranted by the experiment true in a target situation? What will be the result of implementing the treatment there? ~~This paper explains how the probabilistic theory of causality implies that RCTs can establish causal conclusions and thereby provides an account of what exactly that causal conclusion is. Clarifying the exact form of the conclusion shows just what is necessary for it to hold in a new setting and also how much more is needed to see what the actual outcome would be there were the treatment implemented.~~

Designing RCTs for testing precision-medicine strategies is an evolving field!



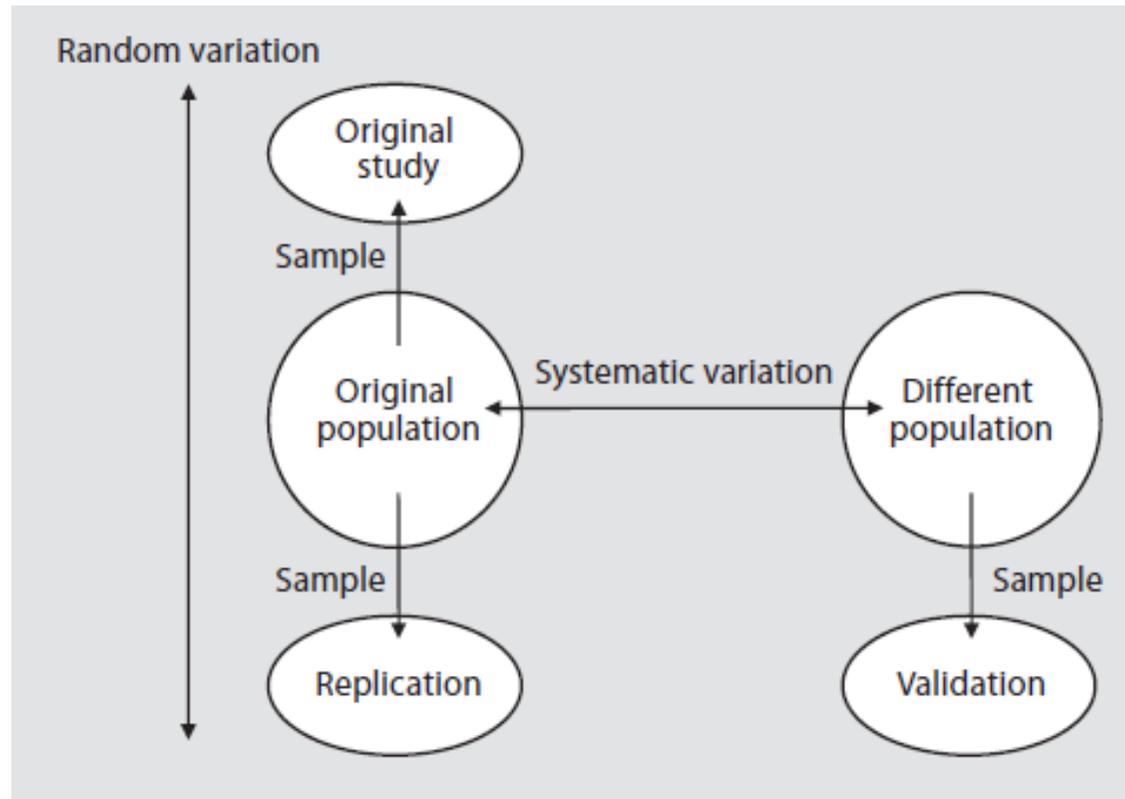
Establishing causation: causal variants for human complex traits

- Wet lab efforts
 - Gene knock-out experiments
 - The findings of animal experiments may not be directly applicable to the human situation because of genetic, anatomic, and physiologic differences
- Dry lab efforts
 - As opposed to association studies that benefit from LD, the main challenge in identifying causal variants at associated loci analytically lies in distinguishing among the many closely correlated variants due to LD.
 - Also here, corrections for population structure are needed to remove potential spurious associations.

6 Post-analysis Steps

6.a Replication and Validation

The difference



(Igl et al. 2009)

Guidelines for replication studies

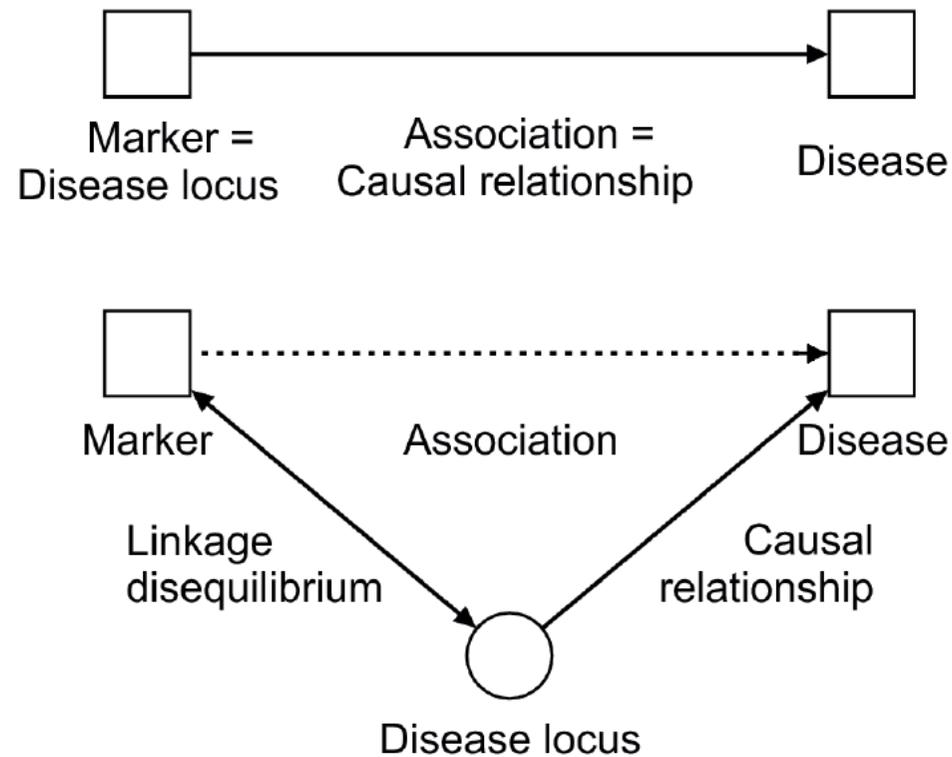
- Replication studies should be of sufficient size to demonstrate the effect
- Replication studies should be conducted in independent datasets
- Replication should involve the same phenotype
- Replication should be conducted in a similar population
- The same SNP should be tested
- The replicated signal should be in the same direction
- Joint analysis should lead to a lower p -value than the original report
- Well-designed negative studies are valuable

Note that SNPs are most likely to replicate when they

- show modest to strong statistical significance,
- have common minor allele frequency,
- exhibit modest to strong **genetic effect size** (~strength of association)

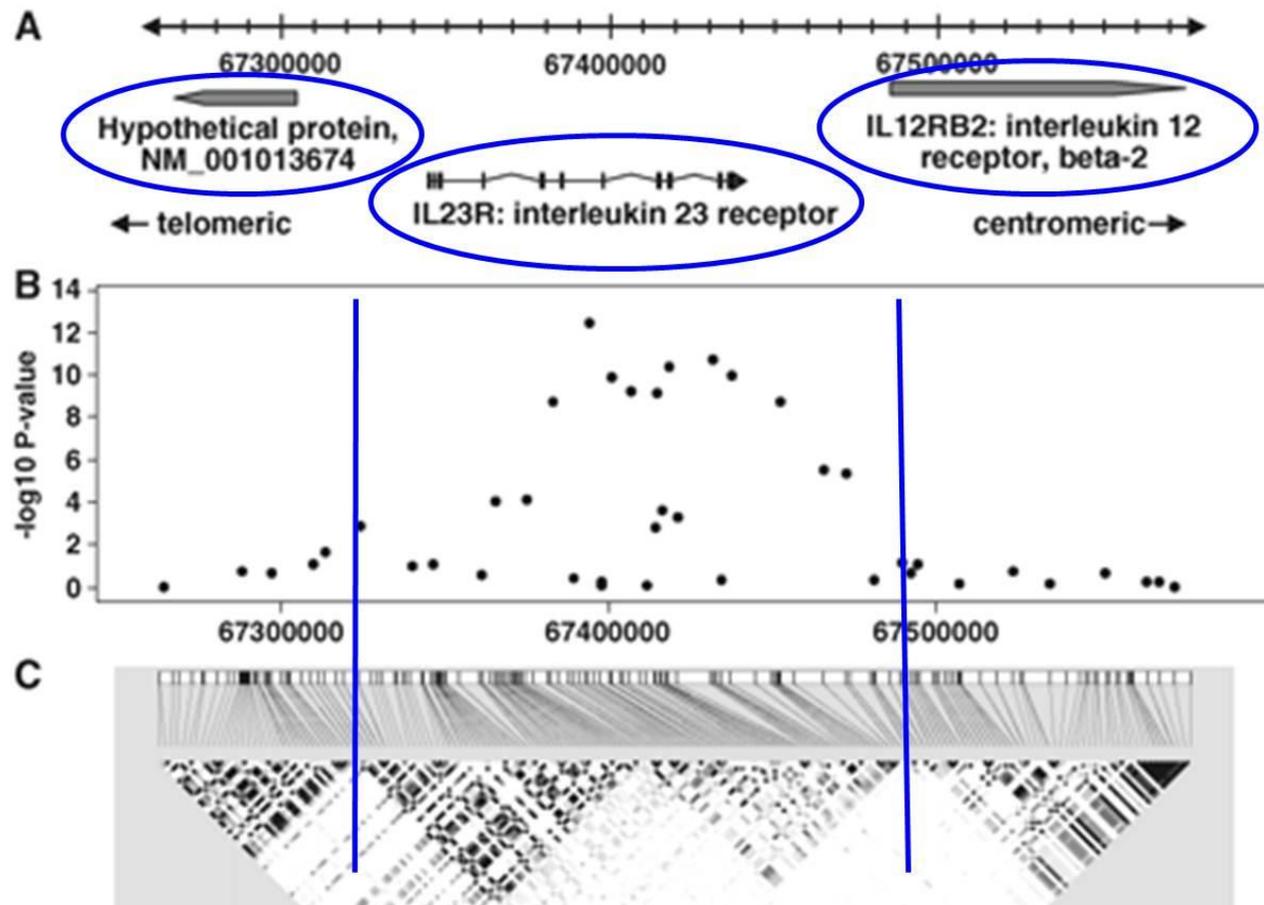
6.b GWA Interpretation and follow-up

Entering the field of functional genomics



(Ziegler and Van Steen, Brazil 2010)

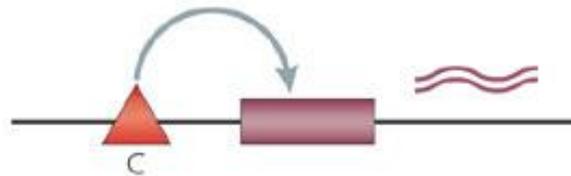
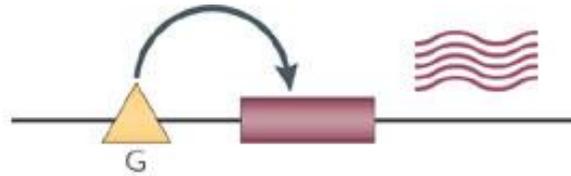
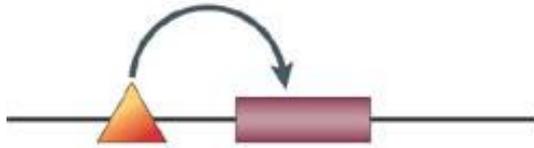
Finding the “relevant” loci



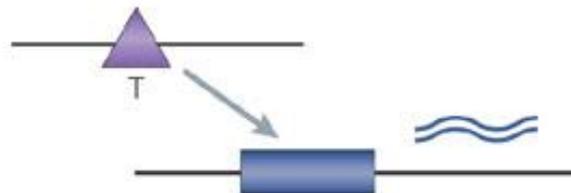
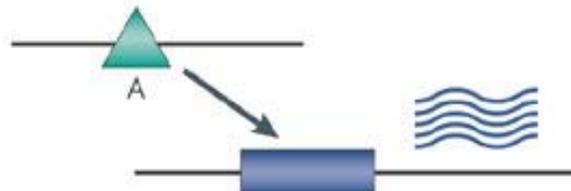
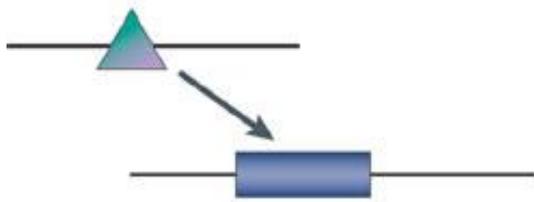
(Duerr et al 2006)

Finding the “relevant” loci

a *Cis* (local)



b *Trans* (distal)



- Cis-acting variants are found close to the target genes and trans-acting variants are located far from the target genes, often on another chromosome.
- Different allelic forms of the cis- and trans-acting variants have different influence on gene expression.

(Cheung and Spielman 2009)

Nature Reviews | Genetics

Finding the “relevant” loci: finding “genes” and “eQTLs” in whole blood



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"DEPICT" your association study

DEPICT is an integrative tool that based on predicted gene functions systematically prioritizes the most likely causal genes at associated loci, highlights enriched pathways, and identifies tissues/cell types where genes from associated loci are highly expressed

Download DEPICT (2.9 GB) today

(<https://data.broadinstitute.org/mpg/depict/>)

From SNPs to genes as units of (follow-up) analysis

- Evaluating the functional properties of gene sets is commonly used both to verify that the genes implicated in a biological experiment are **functionally relevant** and to **discover unexpected shared functions** between those genes.
- DEPICT can test the null hypotheses:
 - “Genes in associated loci do not enrich for the reconstituted gene set”
 - “Genes in associated are not highly expressed in the given tissue or cell type”
- Many **functional annotation databases** have been developed in order to classify genes according their various roles in the cell (e.g., Gene Ontology (GO) repository, widely consulted by many functional enrichment tools).

(Glass and Girvan 2014)

Functional annotation in R



Search:

Home Install Help Developers About

Home » BiocViews

All Packages

Bioconductor version 2.14 (Release)

Autocomplete biocViews search:

Packages found under **FunctionalAnnotation**:
 Show entries Search table:

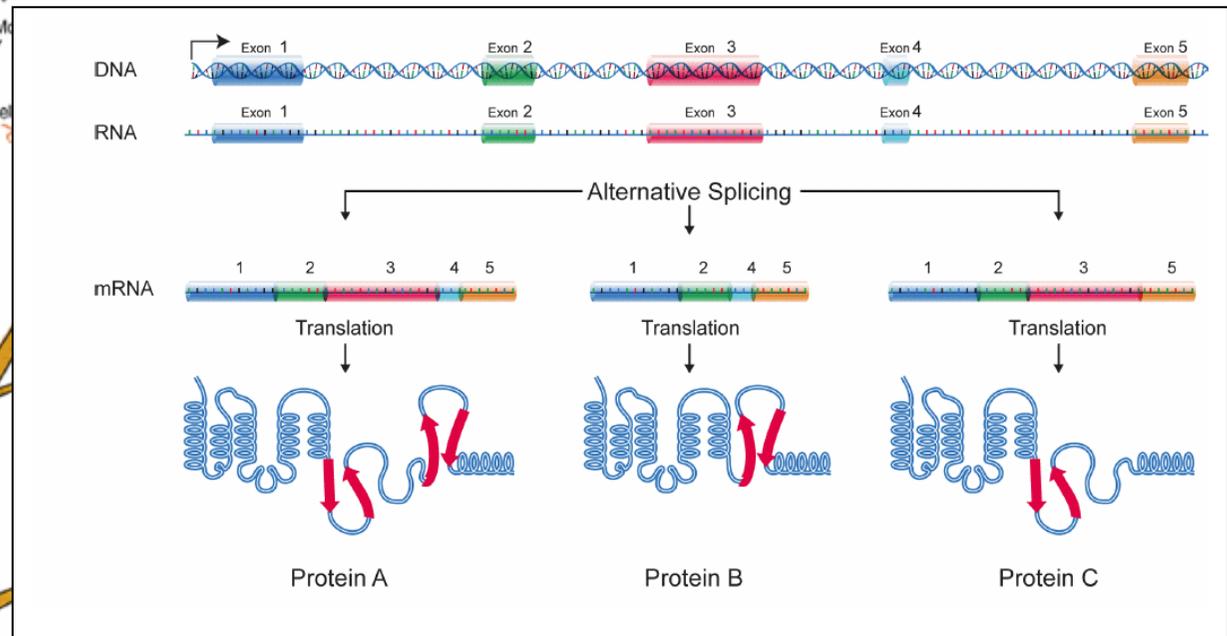
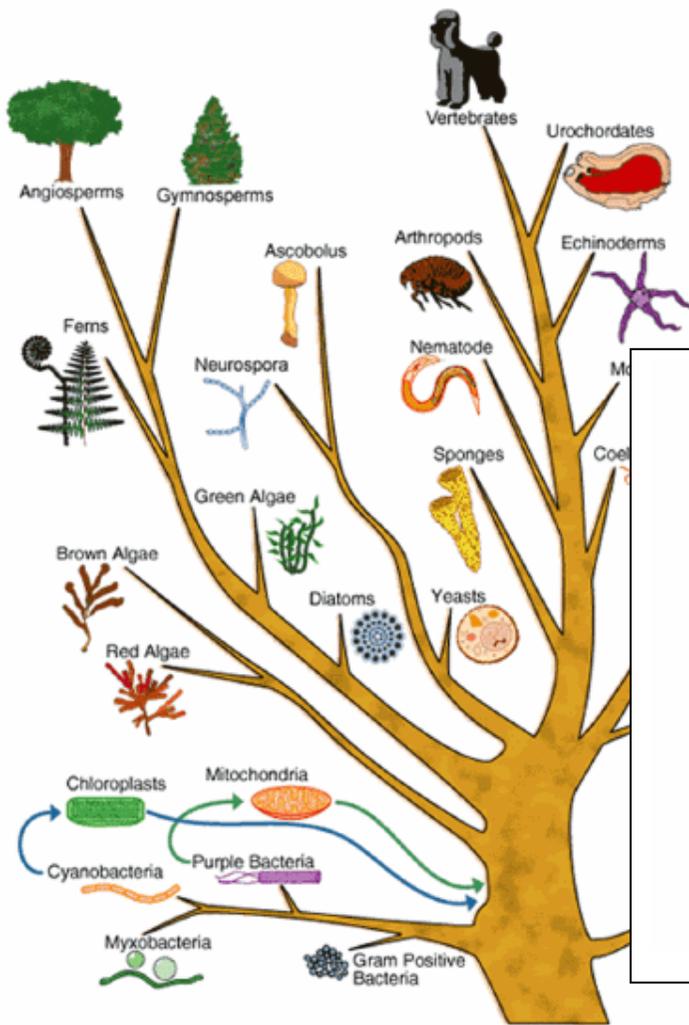
Package	Maintainer	Title
DO.db	Jiang Li	A set of annotation maps describing the entire Disease Ontology
GO.db	Bioconductor Package Maintainer	A set of annotation maps describing the entire Gene Ontology
humanCHRLOC	Biocore Data Team	A data package containing annotation data for humanCHRLOC
KEGG.db	Bioconductor Package Maintainer	A set of annotation maps for KEGG
MeSH.AOR.db	Koki Tsuyuzaki	A set of annotation maps describing the entire MeSH
MeSH.db	Koki Tsuyuzaki	A set of annotation maps describing the entire MeSH
MeSH.PCR.db	Koki Tsuyuzaki	A set of annotation maps describing the entire MeSH
mirbase.db	James F. Reid	miRBase: the microRNA database
mouseCHRLOC	Biocore Data Team	A data package containing annotation data for mouseCHRLOC
ratCHRLOC	Biocore Data Team	A data package containing annotation data for ratCHRLOC

- ▶ Software (824)
- ▼ AnnotationData (867)
 - ▶ ChipManufacturer (370)
 - ▶ ChipName (195)
 - ▶ CustomArray (2)
 - ▶ CustomCDF (16)
 - ▶ CustomDBSchema (10)
 - ▶ **FunctionalAnnotation (13)**
 - ▶ Organism (529)
 - ▶ PackageType (638)
 - ▶ SequenceAnnotation (2)
 - ▶ ExperimentData (202)

Gene expression as an extra source of information

Q: "How can something as complicated as a human have only 25 percent more genes than the tiny roundworm *C. elegans*?"

Part of the answer seems to involve **alternative splicing**:



Model organisms as an extra source of information

- Suppose that we have an unknown human DNA sequence that is associated with the disease cystic fibrosis.
- A bioinformatic analysis finds a similar sequence from mouse that is associated with a gene that codes for a membrane protein that regulates salt balance.
- A good bet may be that the human sequence also is part of a gene that codes for a membrane protein that regulates salt balance.

More about sequence analyses in the subsequent classes

*“The more we find, the more we see, the more we come to learn.
The more that we explore, the more we shall return.”*

Sir Tim Rice, *Aida*, 2000

Main supporting doc to this class (complementing course slides)



OPEN ACCESS Freely available online



Education

Chapter 11: Genome-Wide Association Studies

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A tutorial on statistical methods for population association studies

David J. Balding

Abstract | Although genetic association studies have been with us for many years, even for the simplest analyses there is little consensus on the most appropriate statistical procedures. Here I give an overview of statistical approaches to population association studies, including preliminary analyses (Hardy–Weinberg equilibrium testing, inference of phase and missing data, and SNP tagging), and single-SNP and multipoint tests for association. My goal is to outline the key methods with a brief discussion of problems (population structure and multiple testing), avenues for solutions and some ongoing developments.

Nature reviews Genetics 2006; 5:63-70 – for those interested in technical (statistical) details

Questions?

Homework assignment (papers)

Check out the document

“Critical evaluation of a paper/report”