

What Is A Polygenic Trait

Genotype contributes to phenotype, the observable traits and characteristics in an individual or organism. The degree to which genotype affects phenotype depends on the trait. For example, the petal color in a pea plant is exclusively determined by genotype. The petals can be purple or white depending on the alleles present in the pea plant. However, other traits are only partially influenced by genotype. These traits are often called complex traits because they are influenced by additional factors, such as environmental and epigenetic factors. Not all...
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Linkage disequilibrium score regression The approach involves using regression analysis to examine the relationship between linkage disequilibrium scores and the test statistics of the single-nucleotide polymorphisms (SNPs) from the GWAS. Here, the "linkage disequilibrium score" for a SNP "is the sum of LD r^2 measured with all other SNPs".
disequilibrium score regression (LDSR or LDSC) is a technique that aims to quantify the separate contributions of polygenic effects and various confounding factors In statistical genetics, linkage disequilibrium score regression (LDSR or LDSC) is a technique that aims to quantify the separate contributions of polygenic effects and various confounding factors, such as population

stratification, based on summary statistics from genome-wide association studies (GWASs) bbe3130e2d

Biological pleiotropy, where a genetic variant directly affects... bbe3130e2d == Overview == bbe3130e2d Natural selection is known to be one of the most important biological processes behind evolution . There are many variations of traits, and some cause greater or lesser reproductive success of the individual. The effect of selection is to promote certain alleles, traits, and individuals that have a higher chance to survive and reproduce in their specific environment. Since the environment has a carrying capacity, nature acts on this mode of selection on individuals to let only the most fit offspring survive and reproduce to their full potential. The more advantageous the trait is the more common it will become in the population. Disruptive selection is a specific type of natural selection that actively selects against the intermediate in a population, favoring both extremes... bbe3130e2d Historically, many traits were thought to be governed by a single causative gene (in what is deemed monogenic inheritance), however work in genetics revealed that these traits are comparatively rare, and in most cases so-called monogenic traits are predominantly influenced by one gene, but can be mediated by other genes of small effect. bbe3130e2d Recent progress in genetics has developed polygenic predictors of complex human traits, including risk for many important complex diseases that are typically affected by many genetic variants, each of which confers a small effect on overall

risk. In a polygenic risk predictor, the lifetime (or age-range) risk for the disease is a numerical function captured by the score which depends on the states of thousands of individual genetic variants (i.e., single-nucleotide polymorphisms, or SNPs). bbe3130e2d A formal alternative would be to look at the products of evolution as the result of neutral evolution, in terms of structural constraints, or in terms of a mixture of factors including (but not limited to) natural selection. bbe3130e2d The most obvious justification for an adaptationist perspective is the belief that traits are, in fact, always adaptations built by natural selection for their functional role. This position is called "empirical adaptationism" by Godfrey-Smith. However, Godfrey-Smith also identifies "methodological" and "explanatory" flavors of adaptationism, and argues that all three are found in the evolutionary literature (see for explanation). bbe3130e2d Pleiotropy can result from several distinct but potentially overlapping mechanisms, including gene pleiotropy, developmental pleiotropy, and selectional pleiotropy. Gene pleiotropy occurs when a gene product interacts with multiple proteins or catalyzes different reactions. Developmental pleiotropy refers to mutations that produce several phenotypic effects during development. Selectional pleiotropy occurs when a single phenotype influences evolutionary fitness in multiple ways (depending on factors such as age and sex). bbe3130e2d == History == bbe3130e2d

Oligogenic inheritance Oligogenic inheritance represents an intermediate between monogenic inheritance in which a

trait is determined by a single causative gene, and polygenic inheritance, in which a trait is influenced by many genes and often environmental factors. monogenic inheritance in which a trait is determined by a single causative gene, and polygenic inheritance, in which a trait is influenced by many genes and Oligogenic inheritance (Greek ὀλίγος - ὀλιγος = few, a little) describes a trait that is influenced by a few genes bbe3130e2d

== Extensions == bbe3130e2d Moreover... bbe3130e2d

Adaptationism Many traits are polygenic, for example human height. To drastically change a polygenic trait is likely to require multiple changes Adaptationism is a scientific perspective on evolution that focuses on accounting for the products of evolution as collections of adaptive traits, each a product of natural selection with some adaptive rationale. of separate genes bbe3130e2d

== Definition == bbe3130e2d

Polygenic score Recent progress in genetics has developed polygenic predictors of In genetics, a polygenic score (PGS) is a number that summarizes the estimated effect of many genetic variants on an individual's phenotype. The PGS is also called the polygenic index (PGI) or genome-wide score; in the context of disease risk, it is called a polygenic risk score (PRS or PR score) or genetic risk score. account; and it is typically calculated as a weighted sum of trait-associated alleles. The score reflects an individual's estimated genetic predisposition for a given trait and can

be used as a predictor for that trait. It gives an estimate of how likely an individual is to have a given trait based only on genetics, without taking environmental factors into account; and it is typically calculated as a weighted sum of trait-associated alleles bbe3130e2d

The proposed Omnigenic Model is type of non-mendellian inheritance that builds off of previous research regarding the Polygenic Model and Fisher's Infinitesimal Model. Under the Polygenic Model, for traits, like height, to be continuous in a population there must be many genes that code for the trait. Otherwise, the expression of the trait is limited by the number of possible combinations of alleles. The many genes which code for the continuous trait... bbe3130e2d

Omnigenic model In addition, the model states that the peripheral genes, ones that do not have a direct impact on expression, explain more heritability of traits than core genes, ones that have a direct impact on expression. Boyle, Yang I. regarding the Polygenic Model and Fisher's Infinitesimal Model. The process that the authors propose that facilitates this effect is called "network pleiotropy", in which peripheral genes can affect core genes, not by having a direct effect, but rather by virtue of being mediated within the same cell. Li, and Jonathan K. Pritchard, describes a hypothesis regarding the heritability of complex traits. Expanding beyond polygenes, the authors propose that all genes expressed within a cell affect the expression of a given trait. Under the Polygenic Model, for traits, like height, to be continuous in a

population there The Omnigenic Model, first proposed by Evan A

History LDSC can also be applied across traits to estimate genetic correlations. This extension of... The recognition of...

Concordance (genetics) The pair of individuals are concordant if both present the trait and discordant if only one presents it. Important clinical examples include the chance of offspring having a certain disease if the mother has it, if the father has it, or if both parents have it. Concordance can be measured with concordance rates, reflecting the odds of one person having the trait if the other does. In genetics, concordance is the probability that a pair of individuals will both have a certain characteristic (phenotypic trait) given that one of the pair has the characteristic.

Disruptive selection In this case, the variance of the trait increases and the population is divided into two distinct groups. In this case, the variance of the trait increases and the population is divided into two. In evolutionary biology, disruptive selection, also called diversifying selection, describes changes in population genetics in which extreme values for a trait are favored over intermediate values. In this more individuals acquire peripheral character value at

both ends of the distribution curve. extreme values for a trait are favored over intermediate values

Pleiotropy Mutations in pleiotropic genes can affect several traits simultaneously, often because the gene product is used in various cells and affects different biological targets through shared signaling pathways. The goal of GWAS was to identify how strongly a specific genetic variant, typically a single-nucleotide polymorphism (SNP), is associated with a trait. **Pleiotropy** (from Ancient Greek πλείων (pleíōn) 'more' and τρόπος (trópos) 'turn, way, manner, style') is a condition in which a single gene or genetic variant influences multiple phenotypic traits. A gene that has such multiple effects is referred to as a pleiotropic gene. SNP-based polygenic predictors for complex human traits

Concordance among siblings is similarly of interest: what are the odds of a subsequent offspring having the disease if an older child does? In research, concordance is often discussed in the context of both members of a pair of twins. Twins are concordant when both have or both lack a given trait. The ideal example of concordance is that of identical twins, because the genome is the same, an equivalence that helps in discovering causation via deconfounding, regarding genetic effects versus epigenetic and environmental effects (nature versus nurture). In contrast, discordance occurs when a similar trait is not shared by the persons...

Quantitative trait locus This is often an early step in

identifying the actual genes that cause the trait variation. e. region of DNA which is associated with a particular phenotypic trait, which varies in degree and which can be attributed to polygenic effects, i. QTLs are mapped by identifying which molecular markers (such as SNPs or AFLPs) correlate with an observed trait. , the A quantitative trait locus (QTL) is a locus (section of DNA) that correlates with variation of a quantitative trait in the phenotype of a population of organisms bbe3130e2d

Although adaptationism has always existed— the view that the features of organisms are wonderfully adapted predates evolutionary thinking— and was sometimes criticized for its "Panglossian" excesses (e.g., by Bateson or Haldane), concerns about the role of adaptationism in scientific research did not become a major issue... bbe3130e2d There are also three main types of genetic pleiotropic effects when a variant or gene is associated with more than one trait: bbe3130e2d Polygenic scores are widely... bbe3130e2d A quantitative trait locus (QTL) is a region of DNA which is associated with a particular phenotypic trait, which varies in degree and which can be attributed to polygenic effects, i.e., the product of two or more genes, and their environment. These QTLs are often found on different chromosomes. The number of QTLs which explain variation in the phenotypic trait indicates the genetic architecture of a trait. It may indicate that plant height is controlled by many genes of small effect, or by a few genes of large effect. bbe3130e2d LDSC can be used to produce SNP-based heritability estimates, to partition

this heritability into separate categories, and to calculate genetic correlations between separate phenotypes. Because the LDSC approach relies only on summary statistics from an entire GWAS, it can be used efficiently even with very large sample sizes. In LDSC, genetic correlations are calculated based on the deviation between chi-square statistics and what would be expected assuming the null hypothesis. bbe3130e2d Typically, QTLs underlie continuous traits (those traits which vary continuously, e.g. height) as opposed to discrete traits (traits that have two or several character values, e.g. red hair in humans, a recessive trait, or smooth vs. wrinkled peas used by Mendel in his experiments). bbe3130e2d Around the 1930s/40s, evidence that multiple genes could affect the risk of disease that showed discrete inheritance patterns, due to differences in the age of onset of disease for siblings. The age of onset for sibling pairs was very similar, but between pairs of siblings could be quite different, and would in some cases cluster into several age brackets. This suggested a major gene that controlled the risk for a disease, and other genes that impacted age of onset. bbe3130e2d

Genotype If the alleles are different, the genotype is referred to as heterozygous. the individual has a bb genotype, then the person is bald which masks the A gene entirely. A polygenic trait is one whose phenotype is dependent on the The genotype of an organism is its complete set of genetic material. Genotype can also be used to refer to the alleles or variants an individual carries

in a particular gene or genetic location. In diploid species like humans, two full sets of chromosomes are present, meaning each individual has two alleles for any given gene. If both alleles are the same, the genotype is referred to as homozygous. The number of alleles an individual can have of a specific gene depends on the number of copies of each chromosome found in that species, also referred to as ploidy bbe3130e2d

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