Ploygenic traits and the central limit theorem

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Darwin was once also frustrated with math...

*Mathematics ... was repugnant to me ... [but] I have deeply regretted that I did not proceed far enough at least to understand something of the great leading principles of mathematics; for men thus endowed seem to have an extra sense.* -Charles Darwin (Autobiography)

But this quote shows he **came to understand why math was important, even for him.**

Have you heard of Darwin Finches from the Galapagos Islands and how they are used to illustrate the interaction between evolution and ecology (beak length variation)?

Have you heard explanations of evolutionary changes that go all the way to the effect of multiple genes? Well, Ricklefs, my undergrad ecology class book author brings genes into the explanation of evolutionary phenomena
An example: polygenic traits

Why (to the first sentence of the caption)? What does the book author means here???
From the effect of one gene to the effect of many genes

- The beak size of Darwin’s finches is known to be controlled by many genes.
From the effect of one gene to the effect of many genes

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• Suppose that the contribution of a single gene to the total beak size of a polygenic trait can be either Small, Medium or Large (say 1, 2 or 3 cms. of width respectively) depending on the physiology, other genes present, etc...
From the effect of one gene to the effect of many genes

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- Suppose that the contribution of a single gene to the total beak size of a polygenic trait can be either Small, Medium or Large (say 1, 2 or 3 cms. of width respectively) depending on the physiology, other genes present, etc...
- Then, suppose that for a single gene involved in the beak size, the probability that the conditions are such that its effect is small is 0.6, medium 0.3, large 0.1.
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- This probabilistic model for the trait effect is what in probability is known as a “discrete probability distribution.”
The probability distribution of the effect of a single gene

10000 draws from the gene effect prob. distribution

Gene effect size

<table>
<thead>
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<th>Frequency</th>
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<tbody>
<tr>
<td>0</td>
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<tr>
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• Calculation and definition of the mean effect size and the variance in the effect size for a single gene.
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• Calculation and definition of the mean effect size and the variance in the effect size for a single gene.

• What would the distribution of the sum of two identical genes look like? And three?
The probability distribution of the effect of 2 genes

100000 draws adding the effect of two genes

Frequency

Two genes effect size

0 10000 20000 30000
The probability distribution of the effect of 3 genes

100,000 draws adding the effect of three genes

Frequency

Three genes effect size

0 5000 15000 25000

0 5000 15000 25000
The probability distribution of the effect of 4 genes

100000 draws adding the effect of four genes

<table>
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<tr>
<td>6</td>
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<td>8</td>
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<td>12</td>
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</tr>
</tbody>
</table>
The probability distribution of the effect of 5 genes

100000 draws adding the effect of five genes

Five genes effect size
Frequency
6 8 10 12 14
0 5000 10000 15000 20000 25000
The probability distribution of the effect of many genes

100000 draws adding the effect of 30 genes

30 genes effect size
Frequency
35 40 45 50 55 60
0 5000 10000 15000 20000
Suppose one starts with a single random variable (like the distribution of one gene’s effect on the overall size of the beak), with a given mean (say $m$) and variance (say $v$). Then, the Central Limit Theorem (CLT) that you learn in your most basic stats class tells us that if we add the outcome of a large number (say $n$) of random variables that each have the same distribution and are independent from each other, then the resulting sum will be normally distributed. The mean of that normal distribution will be $nm$ and its variance will be $nv$. 
Now, in a dry year, mostly finches with larger beaks survive, and the population distribution shifts to the right. Did that shift (evolution) really happen?

We saw that the frequency distribution of the effect of 30 genes affecting beak size can be well described with a Normal distribution with mean \( \mu = 45 \) and variance \( \sigma^2 = 13.5 \) (standard deviation \( = \sqrt{(\sigma^2)} \approx 3.674235 \)).

Suppose that to gather evidence regarding whether evolution happened after drought we capture \( n = 30 \) birds and measure the beak, obtaining a sample mean of \( \bar{x} = 46.5 \). Is that evidence to show that evolution occurred?

Amazingly, the very same piece of math (the Central Limit Theorem) that allows us to describe a polygenic trait with a normal distribution, allows us to answer this scientific question
The central limit theorem and the sample mean

- If we want to answer our biological question of interest (did evolution occurred after a dry year), we’ll need the following result.

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- Now, before answering the question of interest, we need to learn about sampling distributions, and the distribution of the sample mean!