**10 Probability**

Script

1. Origins 101— Probability
2. In the presentation about the origin of information in the cell, we talked about the probability of a protein forming by chance, but we didn’t go into much detail about how the probability was calculated.
3. In this presentation, we will define probability, review how to calculate it, and look at the kinds of probability calculations common in discussions about origins.
4. Probability is the likelihood or chance of something happening. / It is expressed as a fraction. / The bottom of the fraction is the number of possible outcomes that exist. / The top of the fraction is the number of outcomes that fit a certain criterion
5. For example, look at this die. It has six sides, each containing a different number between 1 and 6. Because of this, rolling the die could produce 6 possible outcomes—a 1, 2, 3, 4, 5, or 6. / Because 6 different outcomes are possible, the bottom number of our fraction would always be a 6. / Because each number appears on only one face of the die, the top number of our fraction would have to be a 1. The probability of rolling a 4 would be 1/6. And so would the probability of rolling a 5, a 3, or a 1.
6. Since this spinner contains only four possible outcomes (yellow, green, red, and blue), the probability of the spinner landing on any one of them-say red, for example—/ is ¼. / The 4 on the bottom means there are 4 possible outcomes. The 1 on top means there is only one outcome that is red. The probability would the same for yellow, green, and blue, as well.
7. Now let’s say we are going to draw a marble from a dish that contains 34 red marbles, / 33 blue marbles, / and 1 green one. / Since there are 68 marbles total in the jar, / there are 68 possible outcomes, / so 68 is the bottom number in our fraction. / If we want to calculate the probability of drawing a red marble, the number of red marbles would be the top number. The probability of drawing a red marble would be 34 over 68, or 34 out of 68.
8. When we state probabilities, we always reduce the fraction, so we would reduce 34 over 68 to one half.
9. The probability of drawing a blue marble would be 33 over 68
10. And the probability of drawing the green marble would be only 1 out of 68.
11. The probability of drawing a purple marble is zero, because there are no purple marbles in the jar.
12. We can also calculate the probability of multiple events happening or the same event happening multiple times in a row. We do this by multiplying the individual probabilities. / Since the probability of rolling a 6 is 1/6, / the probability of rolling a 6 two times in a row would be 1/6 times 1/6, or 1/36.
13. The probability of rolling a 6 three times in a row is 1/6 times 1/6 times 1/6, or one over 216.
14. To calculate the probability of drawing a green, / then a blue, / and then a red (assuming you put the marble back in the dish each time) / you would multiply the individual probabilities: (You can see how the bottom number increases rapidly.)
15. The probability of drawing the only green marble three times in a row is very small.
16. It’s pretty easy to understand when the number of options are small, / like four colors on the spinner, / six sides on the die, / or 68 marbles in the jar. But the numbers can become hard to imagine pretty quickly when there are lots more possible outcomes.
17. Take this combination lock, for example. / If we wanted to calculate the probability of finding a certain combination on this lock, we would need to know how many possible combinations there are. / To do that, we need to know two things: / the number of possible digits on each of the dials and how many dials there are.
18. Each dial has 10 possible digits (0-9) so we start with the number 10
19. We use the number of dials as the exponent. / Remember that ten to the fourth power is the same thing as 10 times itself four times, / or 10,000. Notice that the number of zeroes on the 10,000 is the same as the exponent. This means there are 10,000 different combinations possible on this lock, so the denominator of a fraction about the probability of opening this lock would be 10,000.
20. Let’s do the same thing with a different kind of combination lock. Instead of ten digits from zero to nine on each dial, / this lock has the letters of the alphabet on each dial. / Since there are 26 letters in the alphabet, there are 26 possibilities for each dial.
21. Then, since there are five dials, we would use five as the exponent. 26 to the fifth power means we multiply 26 by itself five times.
22. Which means there are nearly 12 million possible combinations on this lock.
23. Let’s think about an amino acid chain that has 150 amino acids. / How many possible ways can those 150 amino acids be combined? / Think back to this combination lock./ We started with the number of letters on each dial, which was 26. / Then we used the number of dials—in this case 5—as the exponent. / Since there are 20 different kinds of amino acids—kind of like an alphabet with only 20 letters instead of 26—we start with the number 20. / because the chain contains 150 amino acids—kind of like having 150 dials on a combination lock—we use 150 as the exponent.
24. Another way to express the same number is one times ten to the one hundred ninety-fifth power—or a one with 195 zeros after it, (which is how we got this figure in the previous presentation.)
25. Now that we know how many possible combinations there are, we can think about the probability of finding any one of them.
26. The number we just calculated is the number of possible combinations, / so that would be the bottom of the fraction.
27. …which would look like this if we wrote out all 195 zeros!
28. Out of all those options, only *one* would have that specific amino acid sequence, / so the top of the fraction would be a 1.
29. Therefore, the probability of forming any one, specific sequence of 150 amino acids by chance is 1 in 10to the one hundred ninety-fifth power. The probability is way too low to be realistic.
30. But what if we allowed for *any* potentially useful protein, regardless of its amino acid sequence? / Remember that an amino acid chain has to be able to fold before it can be a useful protein. To accurately calculate the probability of forming a useful proteins by chance, then, we will only consider the number of amino acid sequences that are capable of folding.
31. Douglas Axe performed some experiments / and concluded that only about 1 in 10 to the 74th amino acid sequences is able to fold into a useful protein, so we’ll use that number instead of the 1 x 10 to the one hundred ninety-fifth.
32. But we also need to consider two additional factors that affect probability— / chirality / and chemical bonding—which make the problem much worse.
33. Amino acids occur in two forms— called right handed and left handed. Chirality refers to their right- or left-handedness. / Only left-handed ones are used in living cells.
34. The probability of choosing a single, left-handed amino acid should be about 1 in 2
35. Using this figure, the probability of choosing 150 left-handed amino acids in a row is one half multiplied by itself 150 times, or one in ten to the 45th power.
36. Chemical bonding also affects the probability of forming proteins. Amino acids bond in different ways, but proteins only use a certain kind of bond, called a peptide bond, to link their amino acids.
37. The probability of two amino acids joining by a peptide bond should also be about 1 in 2.
38. Since a chain of 150 amino acids has 149 chemical bonds linking them, we calculate the probability by multiplying one half by itself 149 times. This makes the probability of getting 149 peptide bonds in a row about 2 in 10 to the 45th power.
39. With all that background, we are ready to calculate the probability of getting just one functional protein by chance.
40. We do it the same way that we calculated the probability of picking a certain sequence of marbles from the jar—by multiplying the probabilities of the individual events.
41. To calculate the probability of getting one small protein that is just 150 amino acids long by chance, we need to multiply three separate probabilities: The probability of getting a specific sequence of amino acids that is capable of folding…
42. by the probability of getting 150 left-handed amino acids in a row
43. By the probability of them being joined with peptide bonds.
44. When we multiply these individual probabilities, we add their exponents—which is where the 164 comes from.
45. This means that the probability of getting even one folded protein capable of performing a function / is no better than about two in ten to the 164th power.

(46) These figures are estimates, not measurements, so we have to make some allowance for variation in the final answer. But it doesn’t matter. The probabilities are far beyond anything reasonable, whether they are slightly too high or too low.

1. These calculations do not reflect the problem of contamination. / In the real world, other chemicals are present that would interfere with protein formation. This would effectively reduce the probability to zero.
2. Suppose we ignore the problem of contamination, / and suppose we ignore the problem of where the amino acids would come from, / and suppose we ignore the problem of finding the right conditions for the amino acids to react together. / Is it reasonable to think that a protein might form by chance?
3. One way to evaluate this is by thinking about how many opportunities there have been for that event to happen.
4. We could do this by comparing the probability of a protein forming by chance, with the number of events that scientists say have occurred in the history of the universe. / But how would we know how many events have happened?
5. William Dembski has attempted to figure this out. First, he estimated the number of elementary particles in universe.
6. And multiplied that by the number of possible interactions with each other per second
7. Finally, he multiplied that by the number of seconds since the beginning of time, based on current scientific theory. We don’t know for sure how old the universe is, but scientists estimate it is about 13 billion years old, which is about 1016 seconds.
8. By multiplying these three estimates, he calculates the total events in the entire history of the universe to be 1 x 10 to the 139. That is a one with 139 zeroes after it.
9. Now compare these two numbers. / Notice that the number of events in the history of the universe / is smaller than the number necessary to allow for the formation of a protein by chance. In fact, it is a trillion trillion times smaller. In other words, getting a functional protein by chance requires more probabilistic resources than have been available in the history of the universe. Add to this the fact that most proteins are much longer than 150 amino acids. Most have several hundred or even several thousand amino acids. And we can see that making a functional protein by chance is mathematically impossible.
10. The probability is so low that it has been compared to the probability of a tornado blowing through a junkyard and producing a Boeing 747 airplane.
11. From our study of probabilities, we can conclude that even if the universe were made entirely of amino acids, it is unrealistic to expect a protein to form by chance. / Living organisms require hundreds or thousands of proteins in order to live. / Creation is the best explanation for the origin of living organisms.