different from the hits you got in Discovery Question 5 (with default value of 1), and why? Find the numerical evidence of the change you made at the bottom of the BLAST report.

Most of the hits are to the same sequences, and have the same alignments. However, the raw scores, bit scores, and E-values are different because of the modified reward for a match. The parameters lambda and K change to adjust for the change in the match score.

Math Minute 2.4  Can You Estimate the Number of Inversions in a Dot Plot?

1. Go to the GRIMM site and enter the mouse gene order from the top line of Table MM2.6 into the “Source genome” box. You can leave the “Destination genome” box empty, because the program assumes the default target order of positive numbers 1 through 11. Select “multichromosomal or undirected” and “signed” options before hitting the “run” button. Does the program sort by reversals in the same number of steps as in Table MM2.6? Explain the differences in the reversal steps between the GRIMM site and Table MM2.6. How do these differences affect how you interpret the results of sorting by reversals?

Yes, the program sorts by reversals in the same number of steps (7) as in the table. However, the steps are different. In the GRIMM program, the first two reversals are of single genes (6 and then 9), whereas the first two steps in the table are reversals of 7 and 6 genes, respectively. The single gene reversals occur in steps 3 and 4 in the table. It is important to realize that the number of reversals may be minimized by more than one reversal process. In other words, the predicted inversion history is not unique.

2. At the GRIMM site, select “Human Mouse (123 genes)” from the “choose sample data” drop-down menu. Scroll down to see the results. What operations other than reversals have been performed? Why are these additional operations needed?

Fusions and translocations are also included in the history. These are needed because multiple chromosomes are being compared between mouse and human, and each mouse chromosome contains genes from multiple human chromosomes, and vice versa. To achieve the human ordering from the mouse ordering, genes must be moved across chromosomes as well as inverted on an individual chromosome.

Math Minute 2.5  How Do You Fit a Line to Data?

1. One possible explanation for the choice of line (1) over lines (2) and (3) is that the regression line was constrained to go through the origin. Why would it make sense for the line to pass through the origin?

If a chromosome truly had 0 CpG islands per Mb, it is a very simple chromosome. Because you would expect at least one CpG island to appear just by chance on a sequence as long as a chromosome, the case where there are 0 CpG islands could be thought of as a “zero” or “empty” chromosome. An “empty” chromosome, one without enough sequence complexity to have even one CpG island, might also be expected to have zero genes on it.

2. Redraw lines (1), (2), and (3) with the additional restriction that each line must go through the origin. Under this restriction, do you agree with the investigators that line (1) is the best fit?

The line of best fit of type (1) under the restriction that the line must go through the origin would look something like the solid line in the figure below. The line of type (2) through the origin would look something like the dotted line, and the line of type (3) through the origin would look something like the dashed line. Lines (1) and (2) are both reasonable explanations. Line (3) misses so much of the cluster