

## 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.