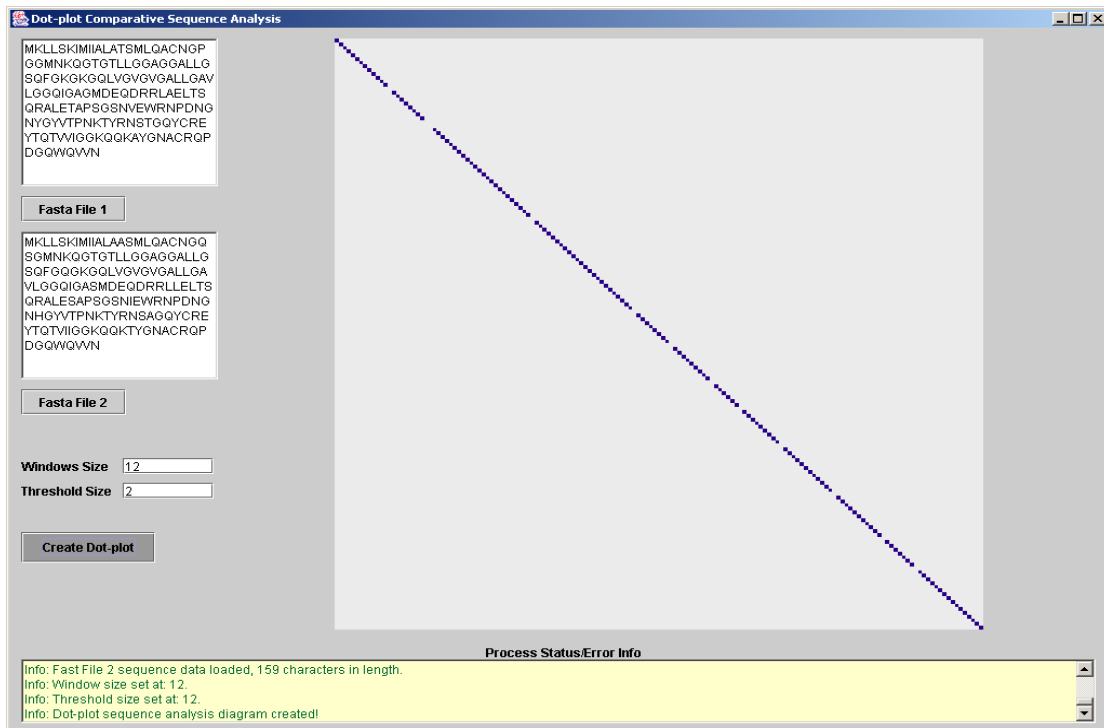


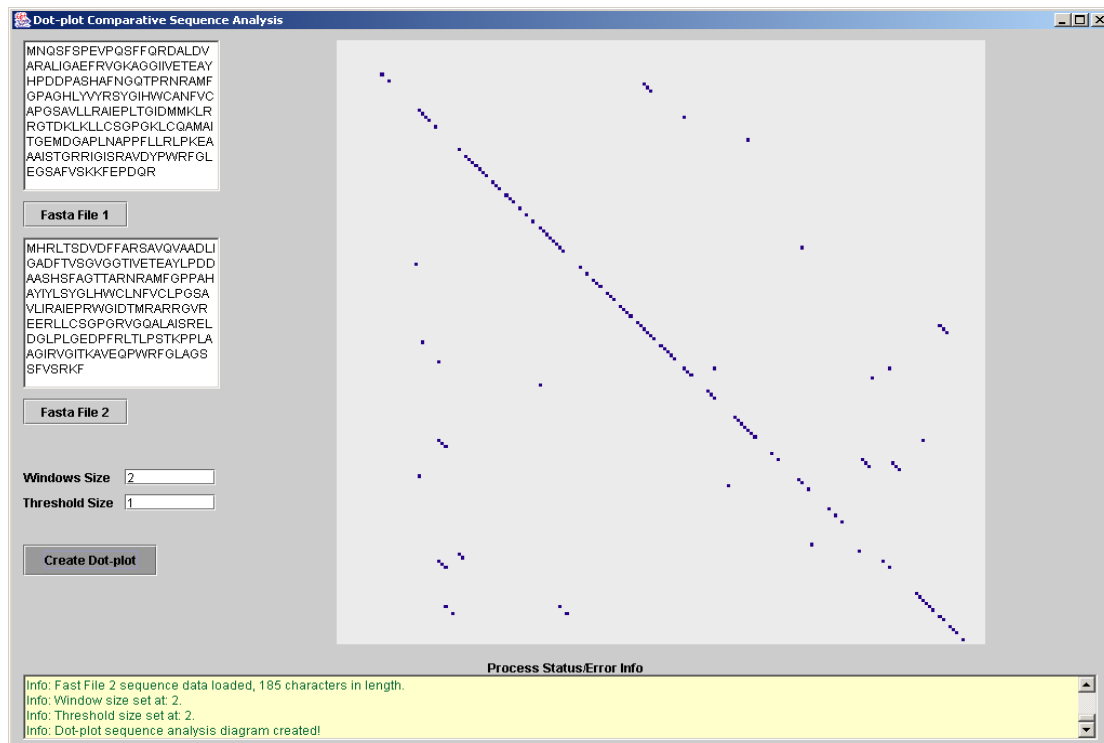
### Comparison of the Rickettsia Prowazekii Genome to the Rickettsia Conorii

Here the threshold is set 1 and the window size to 0. The dot-plot is quite “liberal” in its match rate but a definite pattern is clearly visible between the two genomic sequences.



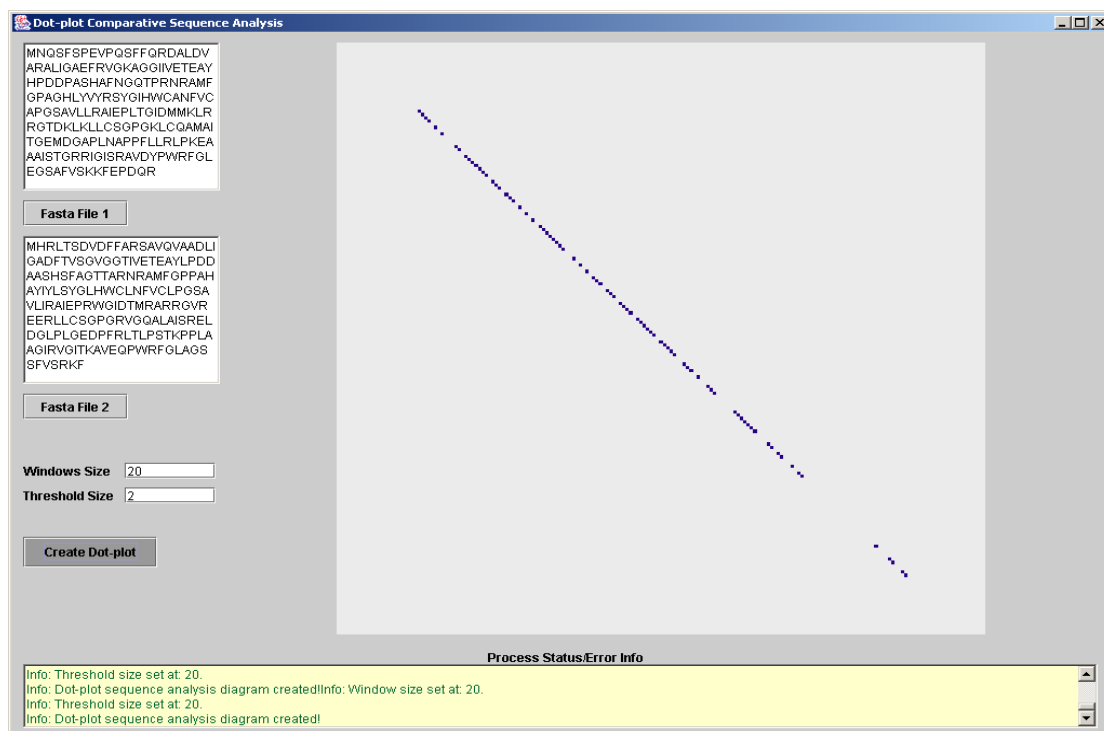
### Comparison of the Rickettsia Prowazekii Genome to the Rickettsia Conorii

Here as we increase the window size to 12 and only incrementing the threshold by 1, we see that the dot-plot parameter filters out accidental matches and focuses on the real relationship between the bacterial genome sequences.



### Comparison of Sinorhizobium Meliloti Genome to Agrobacterium Tumefaciens

Here the threshold is 1 and the window size is 2. Again we can see there is a definite relationship, particularly in the central regions. With the high threshold-window ratio there is also a lot of noise or accidental matches present in the plot.



### Comparison of Sinorhizobium Meliloti Genome to Agrobacterium Tumefaciens

Here we have increased the window to 20 and only raised the threshold by one. This gives us a strongly defined dot-plot showing there is a definite relationship or similarity between the genomes. The similarity trails off towards the remaining sequences.