

Double clicking mapsview icon will open a window as shown in Fig.1. Fig.2 shows the window after opening several files, and Fig.3 shows the name of each part in the window.

To use mapsview, first open genome fasta file, by clicking on “Open genome fasta” button and then read the Genbank file by clicking on “Open GenBank” button. This will display positions of genes on both Genome overview and Genome area view. Also, the genome area view will display color bars reflecting the kind of base at each position.

To display plots in plot views, open .peb files output from pmapsr or pair\_map. There are 12 plotviews as shown in Fig. 3. Height of each view can be adjusted by dragging boundary. **Before opening plot files, choose the plot type and plot view for the file from the menu below.** Then press “Open files” button to select the files to be opened. For example, in Fig. 2, “peb intensity” file is displayed in plot view 1 and “peb edge” file is displayed in plot view 2, and plot view 3~12 are hidden. In the edge view, left edges of the region are shown in orange and right edges are shown in blue. **Height of each plot can be scaled by using scroll wheel in each plot view.**

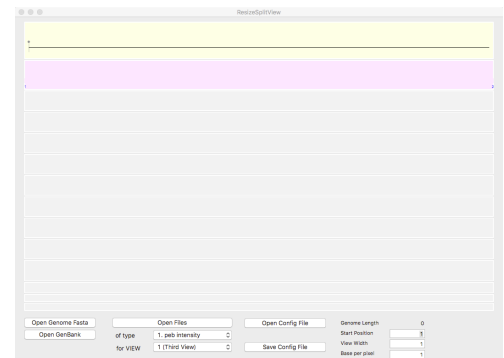


Figure 1. Start up window of mapsview

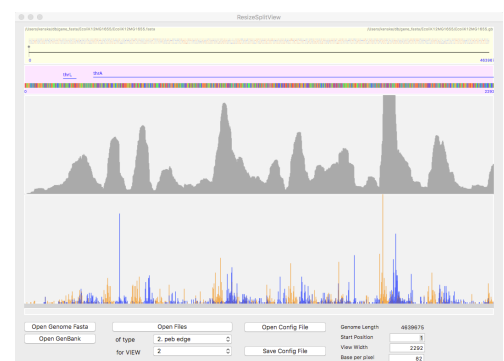


Figure 2. Example display of mapsview

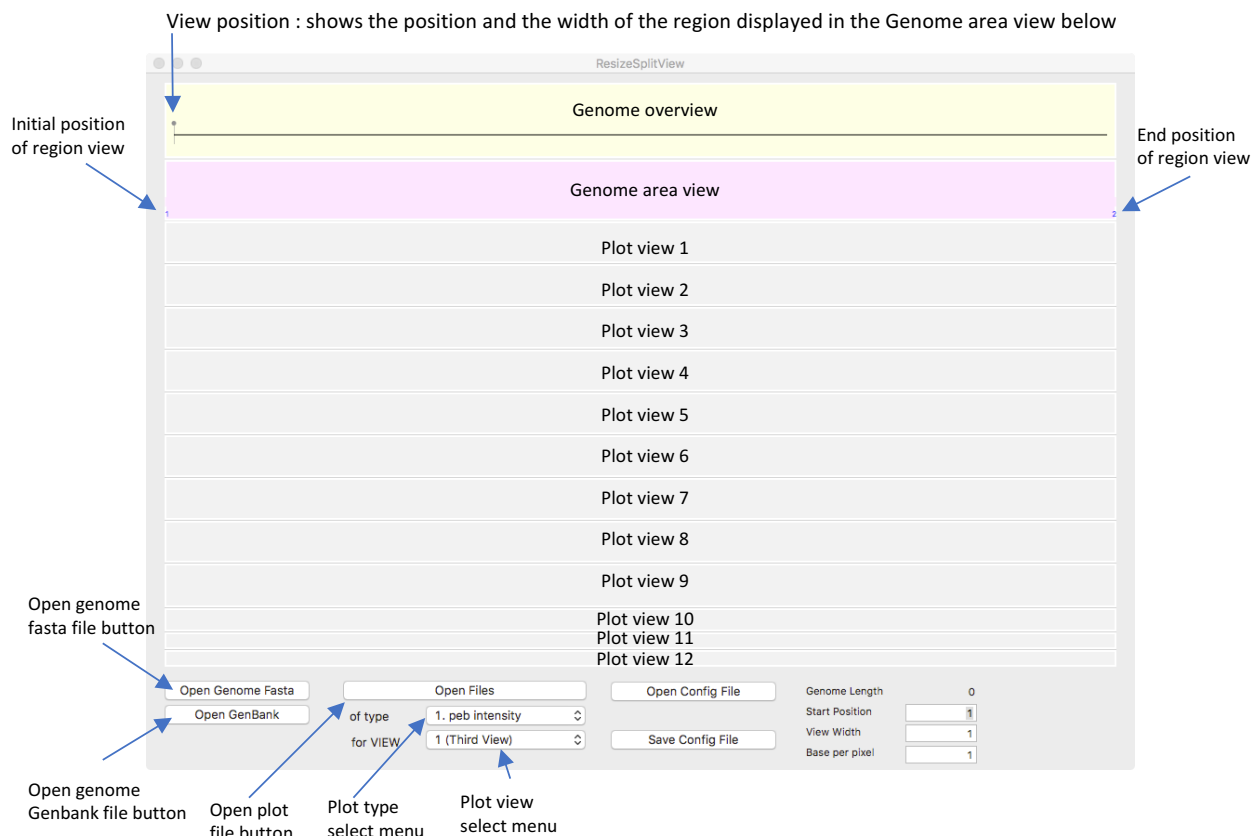


Figure 3. mapsview window parts

Fig. 4 and 5 shows the magnified view of the Genome overview and the Genome area view. The black horizontal line in Genome overview represents the entire genome. Fig.5 shows the size of this genome (E. coli K12 MG1655) is about 4,639,675 bp. Right most base in the Genome area view is 2,292. By default, the Genome area view displays a base in a pixel. In the Genome over view, the thin vertical line with a gray circle on the top at 0, shows the position and width of the region displayed in the Genome area view. The blue horizontal lines in the Genome area view are the positions of genes with captions as their names (thrL, thrA etc.). The gene positions are also displayed in Genome overviews as very small color dots.

The width of the Genome area view can be altered by rotating the scroll wheel in the Genome overview. Position of the genome area view can be scrolled by dragging cursor in horizontal direction, in the Genome overview (coarse) or in the Genome area view (fine). Fig.6 shows a display with broader Genome area view. Fig. 7 shows a Genome area view with a base resolution.



Figure 4. Left end of Genome overview and Genome area view



Figure 5. Right end of Genome overview and Genome area view

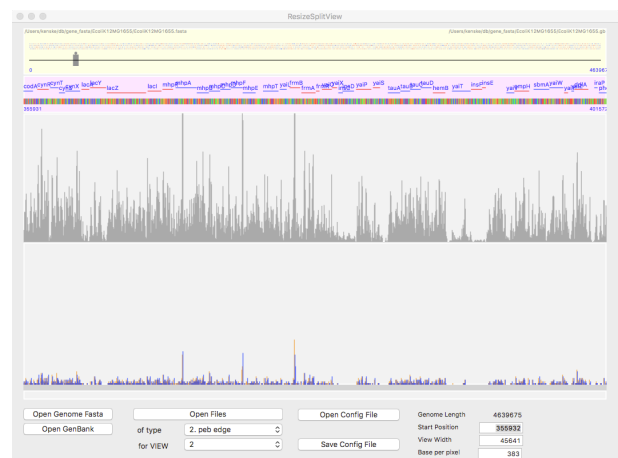


Figure 6. Expanding the Genome area view

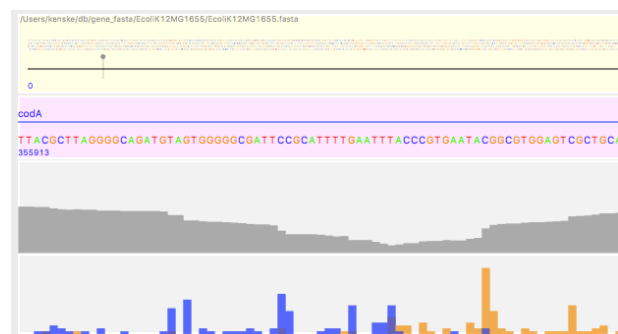


Figure 7. Magnifying the Genome area view to a base display