# Getting Started with GenomeRing

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## 1   General Usage of GenomeRing

### 1.1   Mouse interaction

Besides the operations available through GenomeRing's menu bar, the following mouse interactions are possible directly on the visualization:

- **Rotation**
  Use the mouse wheel to rotate the ring.

- **Zooming**
  Hold the CTRL key and turn the mouse wheel.

- **Show/hide block labels**
  Double-click on the plot background to show/hide the block names.

- **Adjust path width**
  Hold the SHIFT key and turn the mouse wheel to increase/decrease the width of the genomes' paths.

- **Adjust inter-block gap size**
  Hold the ALT key and turn the mouse wheel to increase/decrease the angular width of the inter-block gaps.

- **Adjust the radial distance between jump connections**
  Hold the ALTGR key and turn the mouse wheel to increase/decrease the distance between jump connection arcs.

- **Activate path animation**
  Right-click anywhere on the plot to start path animation. The animation will stop after about 20 seconds.

- **Get position information**
  Click on any position within a block to show a tool tip with information about the precise base position, block number, etc.

- **Scroll a linked genome browser view**
  Double-click on any position within a block to scroll a linked genome browser view to the respective coordinate.

## 1.2   Linking Genome Browser views with GenomeRing

1. In the MAYDAY main window, select a probe list of interest from the dataset corresponding to one of the organisms shown in GenomeRing (refer to the main MAYDAY documentation for details on using MAYDAY's core features) and open a genome browser visualization via the menu *ProbeList→Visualization→Genome Browser*.  This will open a new genome browser window and create a new visualizer.

2. Add tracks that you want to display. You can always add further tracks later.

3. Select the GenomeRing window, and choose *SuperGenome→Connect Genomes to Visualizers...*

4. Pick the genome corresponding to the dataset and, from the drop-down list, choose the visualizer you just created (check the number in angle brackets in the genome browsers window title, if you are unsure).

5. Click OK in the dialog window.

6. If you want to link further visualizations, use the toolbar of the genome browser window, or select one from the menu *Visualizer→Add window*, also from the genome browser window. Refer to the main MAYDAY documentation for details on the visualization model).

# 2   The *Campylobacter jejuni* example

## 2.1   Loading the *Campylobacter jejuni* SuperGenome blocks

To open the SuperGenome blocks of the *Campylobacter jejuni* alignment as shown in the paper please procede as follows.  For this example we set the minimal block size to 10000.  Files for minimal block sizes of 5000 or 7500 are also provided on our website.

- Please download the file `Campylobacter_jejuni_10000.blocks` from our website.

- After starting MAYDAY open Genome Ring by clicking on *GenomeRing preview* in the *Mayday* menu.

- In the *File* menu click on *Load SuperGenome....*

- Select the downloaded file `Campylobacter_jejuni_10000.blocks`.

## 2.2   Linking GenomeRing to Mayday's genome browser

To load genome annotations for one of the aligned strains into MAYDAY's Genome Browser and connect it to GenomeRing please procede as follows. The example is for NC_003912 but the procedure is analogous for the other three genomes.

- Please download the file `Campylobacter_jejuni.maydayz` from our website.

**In Mayday's main window**

- Open the file in MAYDAY by clicking *Open...* in MAYDAY's *File* menu and selecting the downloaded file.

- In MAYDAY's *DataSets* list (upper panel on the left side) select *NC_003912*.

- In MAYDAY's *Probe List* menu click on *Visualization → Genome Browser*.

**In the Genome Browser**

- Initially, the Genome Browser displays information on how to zoom in, etc. Read it, then close the help panel by clicking on the red cross (upper left corner).

- Open the genome annotations by right-clicking in the white area and selecting *add track... → Locus Information*.

- In the appearing *Track Settings* dialog make sure that *NC_003912* is selected in the *Locus mapping drop-down list* and click *OK*.

- In the Genome Browser you can zoom-in (e.g., by holding the CTRL key and turning the mouse wheel, or by dragging the mouse over the ruler displayed at the top).

**In the GenomeRing window**

- Start GenomeRing and load the *Campylobacter jejuni* example as described above.

- For linking the GenomeBrowser to GenomeRing click on *SuperGenome → Connect Genomes to Visualizers...* in the menu bar of GenomeRing.

- In the *NC_003912* drop-down list select *NC_003912, Visualizer* and click *OK*.

- In GenomeRing double-click somewhere on *NC_003912*'s lane to jump to this position in the connected Genome Browser.

**In the Genome Browser**

- In the Genome Browser you can get further information on a specific gene by selecting it. Then click on the *info* icon (*i*) in the icon bar. In the tables menu bar click *View → Jump to selection*. Gene names and functional annotations are shown in the table.