

GeneMapper approximate instructions

1. After opening program, you will see an empty table in “Samples” view.
2. If you are running a new microsatellite:
 - under “Tools”, choose “Panel Manager”.
 - in Panel Manager, highlight “Panel Manager” in box under toolbar
 - in “File” menu, click on “New Kit”.
 - enter name for kit
 - highlight kit name in box.
 - click on blue “New Panel” symbol on toolbar, to create panel (your collection of markers)
 - highlight panel name in box.
 - click on red and blue “New Marker” symbol on toolbar, to create definition for one microsat
 - highlight panel name again; fill out columns to describe marker
 - click on “OK”
3. If you have used Genemapper previously, or already have a Panel including your marker:
 - under “File”, choose “Add Samples to Project”.
 - find your marker data files, highlight runs, and click “Add to list”.
 - when all desired files in list on right, click “Add”.
 - you should see your data listed under the “Samples” view.
 - in the “Analysis Method” column, choose “Microsatellite Default”.
 - in the “Panel” column, choose the panel name for your marker.
 - in the “Size Standard” column, choose “GS500-3730 LIZ”.
 - click green arrow button above sample list to analyze, choose a name to save file as.
 - when analysis complete, change tab to “Genotypes”.
 - highlight group of samples, click on multicolored peak symbol on toolbar to view peaks.
 - Note: can also view peaks under “Samples” tab by highlighting sample, and choosing “Display Plots” under “Analysis” menu; can view ladder here.
 - if all of your desired peaks are not labeled, left click on desired peak, right click and then click on “Add allele call”. Leave comment field blank, and hit “OK”.
4. When you are finished, save project, and close program.