GeneSpring GX®

QuickStart Guide

To analyze your data in GeneSpring GX, follow the steps listed below. If you don't have sample data to load, follow our Tutorial (accessed from the Help menu) instead to learn how to use key GeneSpring GX features with preloaded data.

Step 1. Load Genome Information

1. Select *File* > *Import Genome***.**
2. If you are using a standard commercial chip, select "Download a standard genome" and browse through the available chips; ensure you have an active internet connection at the time.
3. Alternatively, if you are using a custom chip, select "Create a Custom Genome" and pick a custom setting according to the type of file that you have.

Step 2. Load Experimental Data

1. Select *File* > *Import Data.*
2. Browse and select one of your raw data files (tab-delimited text format).
3. In the *Define File Format and Genome* window, GeneSpring will identify standard formats. If you have a custom format, specify "custom" for the "File Format" setting.
4. Check that the chip or genome highlighted under "Select Genome" matches the chip your data was generated from.

More details
LOADING AFFYMETRIX DATA

Step 3. Specify Data Set-up

1. Select *Experiments* > *Experiment Normalizations*. Check the default normalization settings and change as desired.
2. Select *Experiments* > *Change Experiment Parameters*. Add new parameters and parameter values as required (i.e. time, dose, etc).

3. Select *Experiments* > *Change Experiment Interpretation*. Set data mode (ratio or log of ratio), define replicate groups and specify data display.

More details
SETTING PARAMETERS AND INTERPRETATIONS

Step 4. Analyze Data

Go to the Filtering menu or select *Tools* > *Statistical Analysis* and filter genes by your desired quantitative criteria.

More details
QC:FILTERING ON CONTROL SIGNAL
QC FILTERING BY FLAG
FILTERING ON FOLD CHANGE
ONE-WAY ANOVA