

# GeneSpring<sup>®</sup>

## QuickStart Guide

To analyze your data in GeneSpring, follow the steps listed below. If you don't have sample data to load, follow our [tutorial](#) instead to learn how to use key GeneSpring features with preloaded data.

If you have downloaded GeneSpring from the web, you may still need to obtain the GeneSpring User Manual. Select *Help menu | Update GeneSpring*, check the box to agree to the End User License Agreement, and click the *Update Documentation* button.

### Step 1. Load Gene Array Information

*(Optional but recommended)*

If you are using commercial chips, [email us](#) for standard genomes (Affymetrix, Clontech, etc.) Alternatively, start loading custom chip gene information by selecting *File > New Genome Installation* and providing the information requested.

*More details*

[LOADING A CUSTOM GENOME](#)

### 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 CUSTOM CHIP DATA](#)

[LOADING AFFYMETRIX DATA](#)

[LOADING GENEPIX 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*

[FILTERING ON FOLD CHANGE](#)

[QC FILTERING BY FLAG](#)

[ONE-WAY ANOVA](#)