

# GeneSpring-First step

- Install Genome
- Import data- affymetrix format

# What is genome in GeneSpring?

- A genome contains information about all the genes in your chip or microarray setup.
- A GeneSpring genome does not correspond exactly to the biological definition of a genome. A genome in GeneSpring is composed of discrete genes as opposed to the full nucleotide sequence.

# Where is genome folder located?

- GeneSpring saves information about each genome in the data subdirectory of the GeneSpring folder. For example, on a Windows system, this might be

*C:\Program Files*

*\SiliconGenetics*

*\GeneSpring*

*\data\*

- This directory contains a folder for each genome contained in GeneSpring.

# Remove/Restore genome

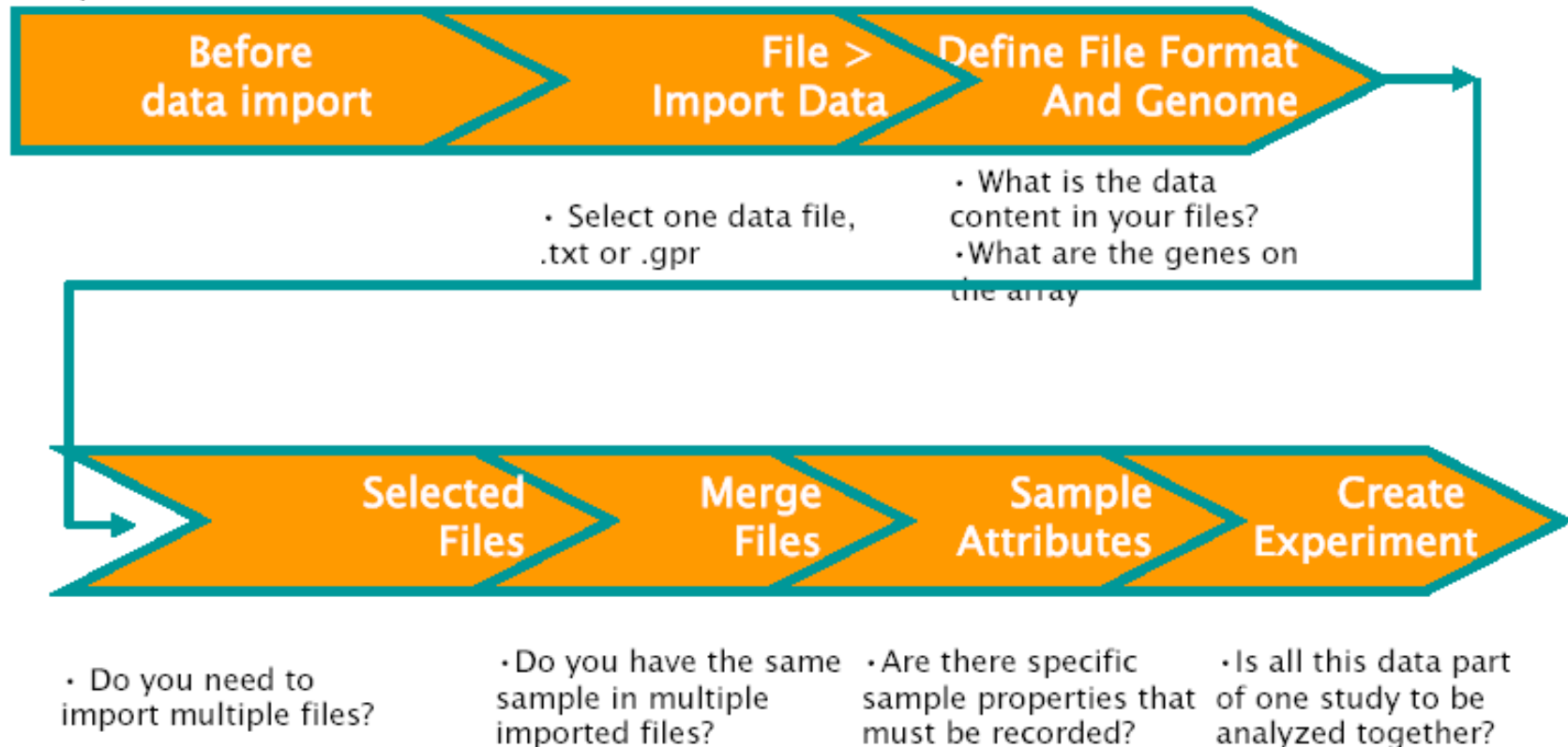
- You can remove a genome from GeneSpring without deleting its data by moving its folder to another location outside the GeneSpring data directory, such as a temporary directory or your own user directory. The genome will not appear the next time you start GeneSpring.
- To restore a genome removed in this way, replace its folder in the GeneSpring data directory. The genome reappears the next time you start GeneSpring.

# Import data

- Importing raw data files
  - File | Import Data
- Accessing experiment and sample data and annotation
  - Gene Inspector
  - Sample Inspector
- Incorporating and retrieving updated annotation
  - Annotations | GeneSpider
  - File | New Genome Installation Wizard

# The Data Import Process

- Are the raw data files correctly formatted for import?



# Formatting Raw Data Files

- Acceptable file types
  - Tab-delimited text (.txt)  
**OR**
  - GenePix data (.gpr)
- Required column content of files
  - Key gene identifiers
  - Numerical expression intensities
- Files can also contain
  - Header information
  - Header rows
  - Extra data column fields
  - Multiple samples' data

1-color data

A	8345
B	35
C	356
D	257

2-color data

cat1	46	688
dog8	757	670
bat35	168	32
rat13	690	249

# Import Data-continue

- An experiment can be created after data import or from previously imported data
  - Create New Experiment
    - Displays all previously imported sample data
    - Filters to refine sample search
- Review/enter details relevant to sample
  - Sample Inspector
    - Attributes/correlations/associated files
    - Access through Sample Manager or “All Samples” interpretation

# Summary

- Data files are saved as .txt or .gpr files and imported into GeneSpring to create an experiment
- Sample data can be viewed at the experiment or individual sample level
- A genome must exist or be created for an array type to define the genes
- Gene annotation, can be incorporated in various ways, relates gene function to experimental behavior