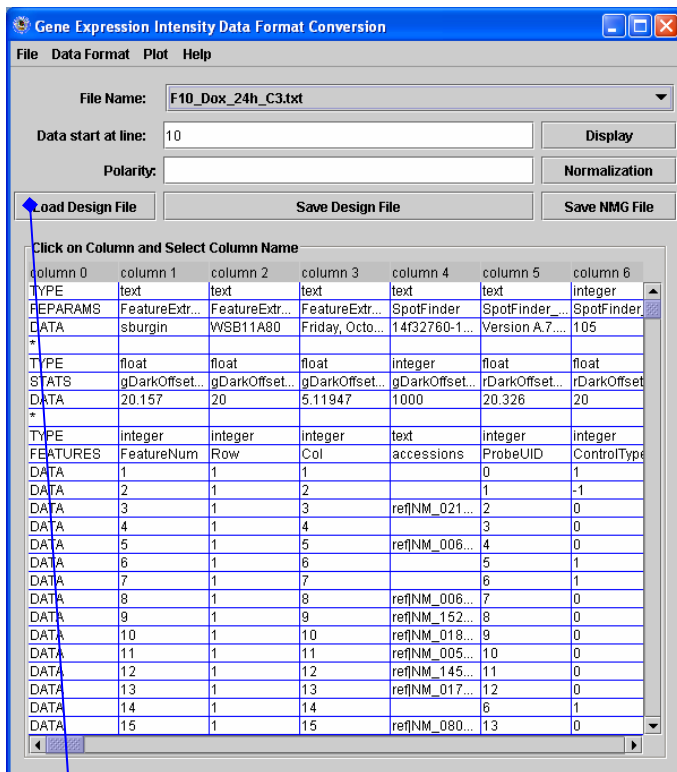


Generic Intensity Data Sets

This interface allows users to load tab-delimited text files. The loaded files have 2-D structure, where rows are gene specified data, columns are specified to the meaning of the data. Here is an example of a loaded Agilent data file. User can load a set of files, which have same data structure.



Once the files loaded, user should load an experiment design file by clicking button “**Load Design Files**”.

In the case of Agilent data files, there are two different polarities, i.e. **plus (C5)** and **minus (C3)**. Plus polarity has g as control and r as treated. Minus polarity has g as treated and r as control. The log ratio is always calculated based on r/g. Therefore, in the case of minus polarity, the log ratio values will be reversed after converted to NMG format.

User can create and edit a Design File. Here are two examples:

Plus (C5) polarity file example (tab delimited)

```
Polarity      plus
Data Start Line  10
CLONE 9
CLUST 10
TITLE 11
CAL_RATIO      14
SAMPLE_MEAN_R      22
SAMPLE_MEAN_G      21
SAMPLE_DEV_R      24
SAMPLE_DEV_G      23
SAMPLE_SIZE_R      30
SAMPLE_SIZE_G      29
BKG_MEAN_R  40
BKG_MEAN_G  39
SAMPLE_TOTAL_R      32
SAMPLE_TOTAL_G      31
```

The Agilent file has polarity plus

Data starts at line 10.

CLONE (gene id) is assigned to column 9

CLUST (an additional gene info) is assigned to column 10.

TITLE (gene description) is assigned to column 11.

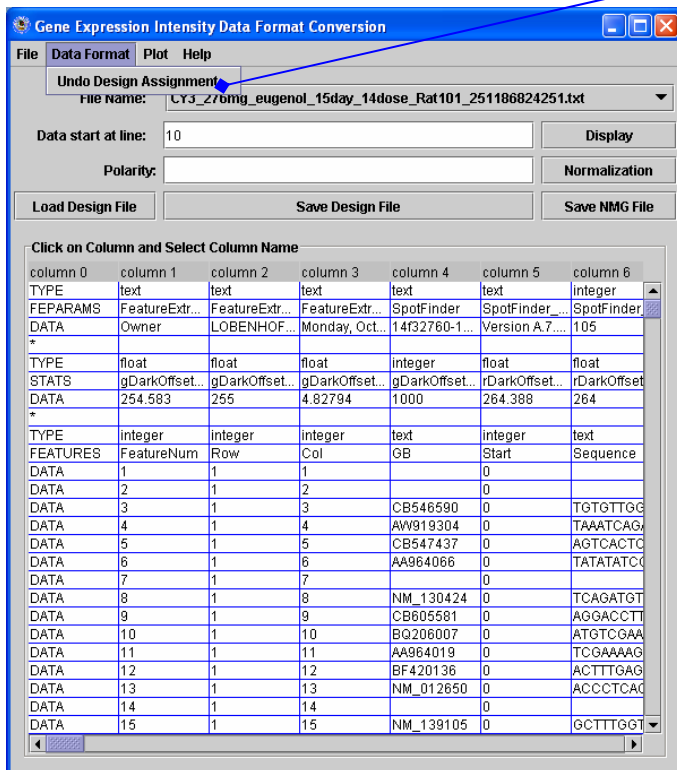
User may assign them to columns as they wish. Others can be seen as

```
CAL_RATIO (log2 ratio) column 14
SAMPLE_MEAN_R (treated mean pixel intensity) column 22
SAMPLE_MEAN_G (control mean pixel intensity) column 21
SAMPLE_DEV_R (treated pixel intensity deviation) column 24
SAMPLE_DEV_G (control pixel intensity deviation) column 23
SAMPLE_SIZE_R (treated pixel number) column 30
SAMPLE_SIZE_G (control pixel number) column 29
BKG_MEAN_R (treated background pixel intensity) column 40
BKG_MEAN_G (control background pixel intensity) column 39
SAMPLE_TOTAL_R (treated total pixel intensity) column 32
SAMPLE_TOTAL_G (control total pixel intensity) column 31
```

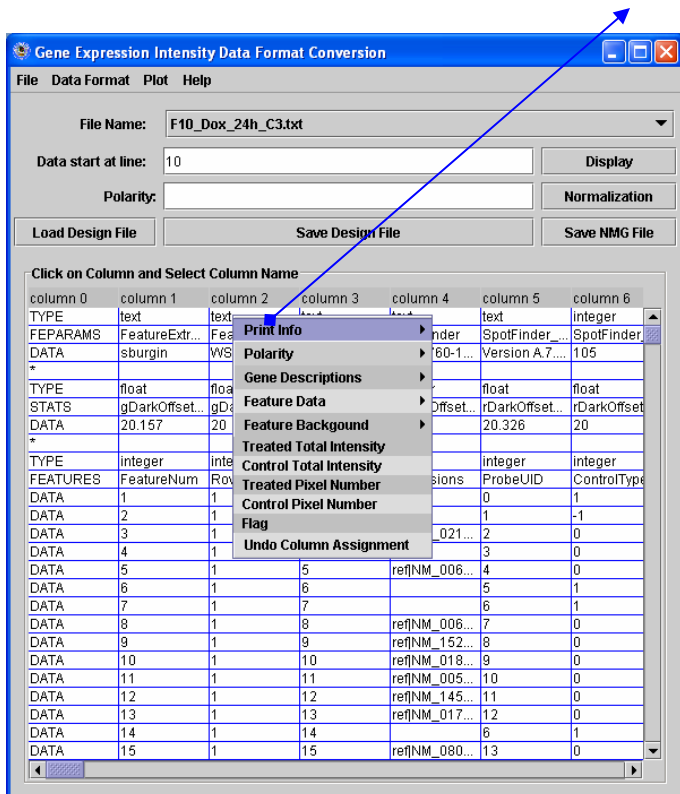
Here is an example design file of minus polarity

Polarity minus
Data Start Line 10
CLONE 9
CLUST 10
TITLE 11
CAL_RATIO 14
SAMPLE_MEAN_R 21
SAMPLE_MEAN_G 22
SAMPLE_DEV_R 23
SAMPLE_DEV_G 24
SAMPLE_SIZE_R 29
SAMPLE_SIZE_G 30
SAMPLE_TOTAL_R 31
SAMPLE_TOTAL_G 32
BKG_MEAN_R 39
BKG_MEAN_G 40

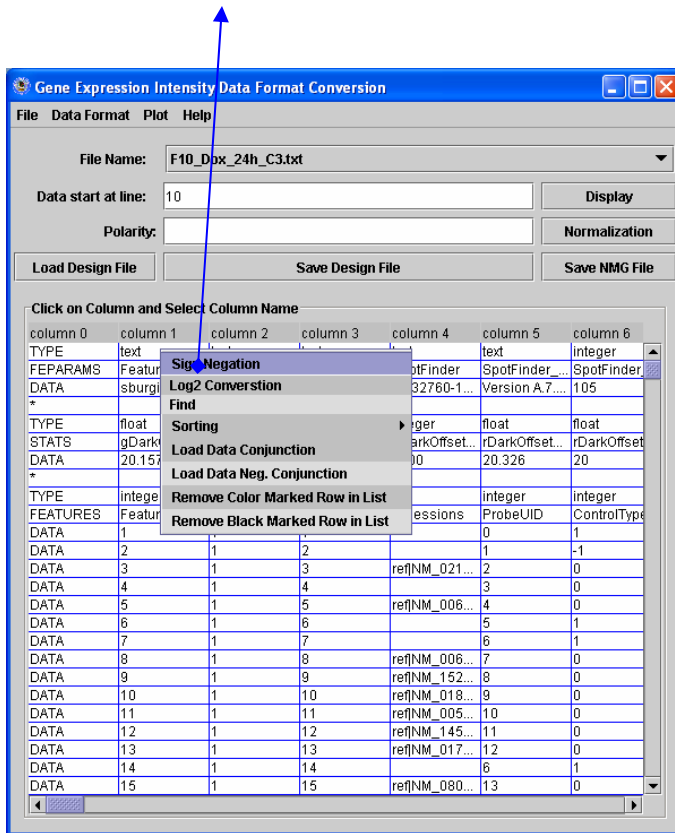
User may undo the column assignment by click “Undo Design Assignment”.



User may manually assign columns by **right clicking mouse** over a selected column



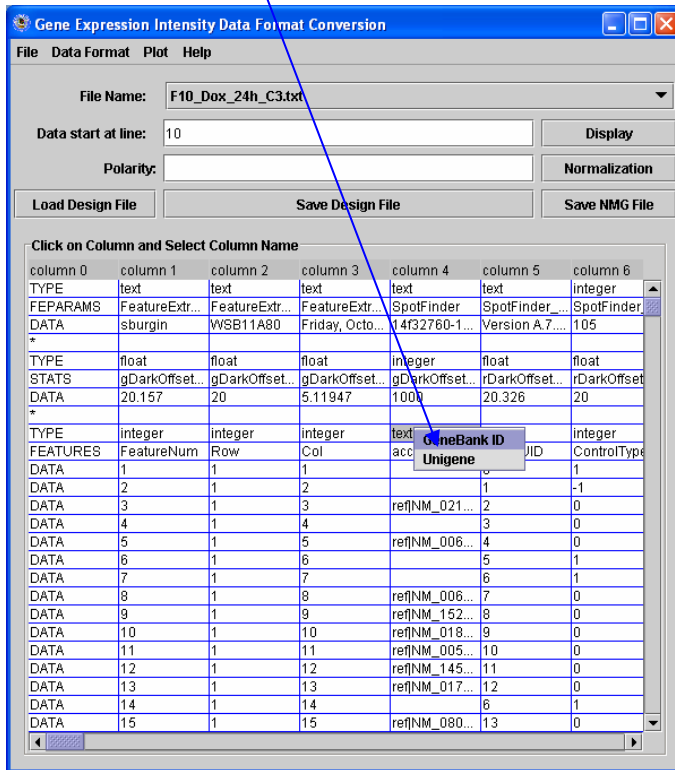
User may **left click mouse** over a selected column to perform some operation



The operations include

- (1) Sign Negation – change a value d to $-d$
- (2) Log₂ Conversion - change a value d to $\log_2(d)$
- (3) Find
- (4) Sorting – ascending or descending
- (5) Load Data Conjunction – Highlight those rows which are intersected with a loaded list.
- (6) Load Data Neg. Conjunction – Highlight those rows which are not intersected with a loaded list.
- (7) Remove Color Marked Row in List
- (8) Remove Black Marked Row in List

User may **left click mouse** over a selected cell to go to Explore with given GenBank ID or Unigene



User may **right click mouse** over a selected cell to assign data start row

