## Big Bio Job Board

Click on the Job ID below to apply for the job listed.

<table>
<thead>
<tr>
<th>JobID</th>
<th>PI</th>
<th>Description of Job</th>
<th>Reward</th>
</tr>
</thead>
<tbody>
<tr>
<td>GA13001</td>
<td>AE</td>
<td>Write code in Python or R to calculate descriptive statistics on a dataset. The dataset will contain between 1 and 100 million lines with each line containing 1 to 10 categorical variables and 1 to 10 continuous variables (i.e. 2 to 20 total factors).</td>
<td>To be negotiated; inquire</td>
</tr>
<tr>
<td>GA13002</td>
<td>SPHS</td>
<td>Review about five hundred Agilent BioAnalyzer data files on about 1500 samples, extracting mean and standard deviation (skewness and kurtosis also desired but optional) into a new data table. Extract similar-size data from excel files containing qPCR data and from final sequencing output. The end result will be one data table with 1500 rows and about 10 columns.</td>
<td>To be negotiated; inquire</td>
</tr>
</tbody>
</table>
| GA13003 | AE | You have an irregular object, in 2D, given to you as a silhouette on a background.  
You take the volume of the irregular object.  
You divide the irregular object via vertical lines; up to ten such lines.  
You place the lines within the irregular object such that the lines represent some fraction of the volume. That is, if 10:10:10:30:40 is input, then you drop four vertical lines, dividing the irregular object into areas of 10%, 10%, 10%, 30%, and 40%.  
As a bonus, you color the areas differently.  
In the end, your project will look something like this (but with solid colors, rather than arty stuff):                                                                 | To be negotiated; inquire                   |


And will be applied to something like this:                                                                 |                                            |
