### 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>
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<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>
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<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) of the data, and comparing the samples to each other using a distance or dissimilarity function (such as Euclidean, Manhattan, or Mahalanobis).</td>
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| 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, the lines will be placed so that the first 10% of the volume is on the left, the next 10% is in the middle, the next 10% is to the right, the next 30% is divided into two equal parts, and the final 40% is divided into three equal parts.  
As a bonus, you color the areas differently.  
In the end, your project will look something like this (but with solid colors, rather thanarty stuff):  
And will be applied to something like this:  