Upon analyzing the sequences of both cycles of the first biochemistry, we see error rates of 3.9% and 6.5% for the two cycles, with an average error of 5.2% for biochem1.

The second biochemistry has a misconfigured dye to base pairing. Taking this into account, we find that the dyes that were matched to A, C, G and T originally should ideally map to C, G, T and A respectively. This particular dye to base map results in the most accurate base calls, as compared to other possible dye to base maps.

Taking into account this reconfiguration, we get error rates of 5.5% and 4.9% for the two cycles, with an average error of 5.2% for biochem2. Thus, we see that both the biochemistries yield the same average error, making it seem like they are equally accurate sequencing methods.

In order to measure the confidence with which the two competing methods make base calls, we define a metric to measure the extent to which the dye producing the highest signal is larger than the others. In other words, we measure the contrast between the dye intensities at each spot and then compare the two DNA sequencing methods based on this contrast value. A higher contrast implies the dye with which the base call was made produces a signal of significantly higher intensity than the other dyes, thus making a more "confident" base call.

We calculate contrast for each cycle of each DNA sequencing method as:

$$contrast = \frac{\sum_1^N {}^2\sqrt{\frac{\sum_1^m (I_{max} - I_m)^2}{m}}}{N}$$

Where m is the number of dyes (= 4) and N is the number of spots (= 1000) per cycle. This is, essentially, the root mean square (RMS) distance of the set of all dye intensities from the maximum dye intensity.

The contrast values for cycles 1 and 2 for the first biochemistry are 0.416 and 0.398 respectively, making the average contrast 0.407.

The contrast values for cycles 1 and 2 for the second biochemistry are 0.234 and 0.232 respectively, making the average contrast 0.233.

Additionally, the number of spots that were missed by the two biochemistries (no signal was received for any dye) were exactly the same (20 per cycle).

Since the first biochemistry yields a higher contrast, we conclude that this method is better able to differentiate between bases and is, overall, a better sequencing method. The biochemistry team should, hence, proceed with the first sequencing method, provided other factors, such as the time required to sequence using both methods, are acceptable.

	Biochemistry 1				Biochemistry 2			
Dye-base map	A	C	G	T	A	C	G	T
(red : dye, green : base)	A	C	G	T	C	G	T	A
Average Error	5.2%				5.2%			
Average Contrast	0.407				0.233			