Using Bacterial Division Rates to Estimate Genome Size

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By doing quick measurements of the growth of simple Prokaryote bacteria, it should be possible to estimate the relative genome size. This is possible by a simple estimation of the growth rates of the bacteria in question. By measuring this for a short period of time in an ideal growth environment, we will have the information needed to make our genome size estimation. We applied this method to five different bacteria to measure the accuracy of this method. The link between genome size and divisionary rates can be attributed to the necessity of the bacteria to replicate its genome before dividing. In a perfect growth environment, with ample nutrients, the life cycle of Prokaryote bacteria will respond to the environment by shifting its cycle away from the gap phase, meaning an average bacterial life cycle will be mostly dominated by the replication phase. Using this information that we will derive experimentally and a combination of other easily obtainable information regarding the bacteria in question, we can successfully estimate the size of the bacterial genome in base pairs. After testing this method on five different Prokaryote bacterial specimens, we were able to derive a value for the base pair count accurate with a degree of error less than 14% in every case. Given time and further exploration we are confident that this process could be implemented as a cost effective and fast way for identifying unknown bacterial specimens.

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