

Shotgun sequencing is the method that was used by the private genome project. Shotgun sequencing requires multiple copies of the genome, which are effectively blown up into millions of small fragments. Each fragment is then sequenced. The small fragments are assembled using an immense amount of computer power to match overlapping sections. The drawback of this method comes when dealing with repeat sequences. Often there is no way of knowing how long the repeat sequence is. Or in which of the many different possible positions the fragments overlap. Even the incredibly powerful software used to shotgun sequence the human genome couldn't cope with this. So Celera, the private company which relied on this approach, had to use the public data to fill in the gaps left by the repeats.