Is this Bioinformatics?

1. Invention of a new cell sorting, DNA amplification and sequencing approach that allows to sequence the genome of single cells.

2. Development of tools to assemble genomes from sequencing reads.

3. Using X-rays to determine the structure of a homing endonuclease bound to DNA.

4. Putting together a databank of known protein structures and their functions.

5. Developing and using a search tool that finds similar structures in protein data banks.

6. Developing a computational pipeline to assemble bacterial genomes from metagenome sequencing projects (i.e. you take a sample of what you are interested in – poop, mud, microbial mat, water, …), isolate the DNA that is in the sample and sequence everything.

7. Sequencing the metagenome from the gut of a vampire bat.