Elkin P (2003). Primer on medical genomics. Part V: Bioinformatics. *Mayo Clin Proc*, 78: 57

1. What is phenomics? Is it the same as genetic association analysis?
2. What is the difference between bioinformatics and biomedical informatics?
3. What is the difference between bioinformatics and molecular biology?
4. How does systems biology fit in the picture?
5. Can BLAST handle protein sequences?
6. What is an intron?
7. What is a false positive rate?
8. Can BLAST control for false positives?
9. What is the difference between sensitivity and specificity?
10. Can PSI-BLAST increase the specificity of a BLAST search?
11. What are the key differences between PSI-BLAST and BLAST?
12. What is the purpose of motif searching?
13. Can you name an annotated database that contains protein motifs?

14. What is the meaning of annotated?
15. Why is the identification of analogous proteins important?
16. What is Cn3D?
17. What is the purpose of gene expression analysis?
18. What is the difference between cDNA and oligonucleotide arrays in terms of array construction?
19. What is the difference between cDNA and oligonucleotide arrays in terms of interpretation of the analysis results?
20. With “messy” data, would you prefer to use hierarchical clustering or SOMs? Why?
21. What is gene filtering?
22. What are the 3 major data bases of publicly available information on nucleotide sequences?
23. Why is it difficult to identify coding regions of the human genome?
24. What are hidden Markov models? How can they be useful in bioinformatics?
25. What is homology?

26. What is a Z-score?
27. What type of information can be found in a signaling pathways database?
28. Based on this article, do you think that bioinformatics is all about data basing and data storage?
29. How can bioinformatics be useful in drug development?
30. What is the difference between genetics and genomics?
31. What is the Gene Ontology Project?