Reading material for Stora Tentan at DBB

Everything marked in yellow is mandatory but a general understanding of all topics mentioned below is needed.

1. Resources from Intro course on the web
    a. Biological Databases
        i. http://en.wikipedia.org/wiki/Biological_databases
        ii. http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.0010034
        iii. http://www.uniprot.org/help/about
        iv. http://en.wikipedia.org/wiki/List_of_biological_databases
        v. EMBD http://www.emdatabank.org
        vi. http://en.wikipedia.org/wiki/Entrez
        vii. http://metadatabase.org/wiki/Main_Page
    b. Genes, sequencing and genomes
        i. http://www.yourgenome.org/facts/what-is-a-genome
        ii. http://en.wikipedia.org/wiki/Bioinformatics
        iii. http://en.wikipedia.org/wiki/Genome
        iv. http://en.wikipedia.org/wiki/Introduction_to_genetics
        v. http://en.wikipedia.org/wiki/Human_genome
        vi. http://en.wikipedia.org/wiki/Genome_evolution
        vii. http://en.wikipedia.org/wiki/Sequencing
        viii. http://www.ploscollections.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1002173
        ix. https://www.ebi.ac.uk/training/onli
        x. ne/course/ebi-next-generation-sequencing-practical-course/what-you-will-learn/what-next-generation-dna-

    c. Sequence alignment and searches
        i. http://en.wikipedia.org/wiki/Sequence_alignment
        ii. http://en.wikipedia.org/wiki/Needleman-Wunsch_algorithm
        iii. http://en.wikipedia.org/wiki/Substitution_matrix
        iv. http://en.wikipedia.org/wiki/BLOSUM
        v. http://en.wikipedia.org/wiki/Point_accepted_mutation
        vi. http://www.avatar.se/molbioinfo2001/dynprog/dynamic.html
        vii. http://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm
        viii. http://www.ncbi.nlm.nih.gov/blast/tutorial/
        ix. http://en.wikipedia.org/wiki/BLAST
        x. http://www.youtube.com/watch?v=HXEpBnUbAMo
        xi. http://en.wikipedia.org/wiki/FASTA
        xii. http://en.wikipedia.org/wiki/Sequence_alignment_software
        xiii. http://www.ncbi.nlm.nih.gov/books/NBK1734/
        xiv. http://openwetware.org/wiki/Wikiomics:BLAST_tutorial
    d. Multiple sequence alignments
        i. https://en.wikipedia.org/wiki/Multiple_sequence_alignment
        ii. https://en.wikipedia.org/wiki/Hidden_Markov_model

e. Phylogeny and evolution
    i. http://evolution.berkeley.edu/evolibrary/article/phylogenetics_01
    ii. https://en.wikipedia.org/wiki/Phylogenetics
    iii. https://www.ted.com/talks/svante_paeaebo_dna_clues_to_our_inner_neanderthal?language=en
f. Machine learning
    i. https://en.wikipedia.org/wiki/Machine_learning
    ii. https://en.wikipedia.org/wiki/Deep_learning
    iii. http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.0030116
g. Protein structure and folding
    i. https://en.wikipedia.org/wiki/Protein_folding
    ii. https://en.wikipedia.org/wiki/Homology_modeling
    iii. https://en.wikipedia.org/wiki/Protein_structure_prediction
    iv. https://en.wikipedia.org/wiki/Membrane_topology
h. Systems biology
    i. https://en.wikipedia.org/wiki/Systems_biology
    ii. https://en.wikipedia.org/wiki/Flux_balance_analysis
    iii. https://en.wikipedia.org/wiki/Metabolic_network_modelling

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    h. Hidden Markov models in computational biology. Applications to protein modeling. Krogh A, Brown M, Mian IS, Sjölander K, Haussler D. J Mol Biol. 1994 Feb 4;235(5):1501-31. pdf
    i. A probabilistic model of local sequence alignment that simplifies statistical significance estimation. Eddy SR. PLoS Comput Biol. 2008 May 30;4(5):e1000069. PDF
    j. A tutorial on hidden Markov models and selected applications in speech recognition. Lawrence R Rabiner, PDF
    k. Söding J. **Protein homology detection by HMM-HMM comparison.**Bioinformatics. 2005 Apr 1;21(7):951-60. Epub 2004 Nov 5. Erratum in: Bioinformatics. 2005 May 1;21(9):2144. PMID: PubMed

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    b. Jones DT, Taylor WR, Thornton JM. **A new approach to protein fold recognition.** Nature. 1992 Jul 2;358(6381):86-9, PubMed
    c. Park J, Karplus K, Barret C, Hughey R, Haussler D, Hubbard T, Chothia C. **Sequence Comparisons Using Multiple Sequences Detect Three Times as Many Remote Homologues as Pairwise Methods.** J. Mol. Biol.(1998) 284, 1201-1210. PubMed
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    b. Meng, EC; SHoichet, BK; Kuntz, ID **Automated docking with grid-based energy evaluation** JOURNAL OF COMPUTATIONAL CHEMISTRY Volume: 13 Issue: 4 Pages: 505- 524 DOI: 10.1002/jcc.540130412 Published: MAY 1992
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Links to many PDFs of papers:

https://sites.google.com/a/scilifelab.se/elofsson/teaching/classical-papers