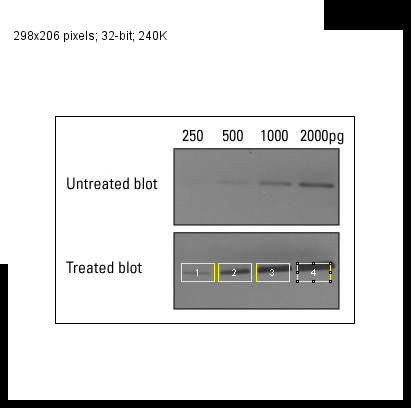
Practice manual of free-software in bioinformatics

1. Please install Bioedit v-7.1.3 form <http://www.mbio.ncsu.edu/bioedit/bioedit.html> or e-learning homepage of Bioinformatics http://e-learning.kku.ac.th
2. Please install ImageJ from https://imagej.net/Downloads, select the version compatible with your system

Exercise after lecture

1. Bioedit: Please perform the following process:
   1. Convert DNA sequence 5’-AACCTTGG-3’ to its complementary strand (correct answer is 5’-CCAAGGTT-3’)
      1. Command: Sequence 🡪nucleic acid 🡪reverse complement
   2. Translate sequence: ATGGATTTCTGAATCCAATGCTATGTGGGCAACATGA to amino acid sequence, which frame is readable? (WISESNAMWAT ☺)
      1. Command: Sequence 🡪nucleic acid 🡪Sort or unsort translation 🡪change minimum aa length from 20 to 10 aa
   3. Translate sequence: “sequence1.txt” to amino acid sequence in all 6 possible frame
      1. Command: Sequence 🡪nucleic acid 🡪Sort or unsort translation
   4. Analyze restriction enzymes site in sequence1 [learn by yourself]
   5. Draw plasmid map of sequence1 [learn by yourself]
      1. Click “Sequence🡪Nucleic Acid🡪Create plasmid form sequence
      2. Click “Vector🡪add feature
      3. Add Restriction sites of Eco\*, PstI, SmaI, ect.
      4. Create TetR gene (arrow) in position 300-100 in red color.
      5. Create promoter box at position 450-550
      6. try drawing by tool at <http://www.bioinformatics.org/savvy/>
   6. Please perform multiple alignment by using seq2,3 and 4.
      1. Create new window, Sequence 🡪New alignment
      2. File 🡪open seq3
      3. File🡪import 🡪sequence alignment file🡪seq4 and 5
      4. Select all sequences
      5. Accessory Applications🡪 ClustalW multiple alignment
   7. Try other function of the program. [learn by yourself]
2. Try web-based free software in Expasy.org by analyze DNA and amino acid sequences.
3. ImageJ:
   1. Open file
   2. Image: modify type 8, 16 32 bit or RGB
   3. Use “rectangle ” to draw cover band in lane 1,   
      make it as wide as possible to prevent over layer of next frame
   4. Analyze 🡪 gel 🡪Select first lane(Ctrl 1)
   5. Use pointer (**Arrow pointer**, not hand or plus sign) drag rectangle to lane 2, drop at the align position near the previous regtangle
   6. Analyze 🡪 gel 🡪Select next lane (Ctrl 2)
   7. Repeat 3.5 and 3.6
   8. Analyze 🡪 gel 🡪plot lane
   9. At graph windows: use straight line to close base of each peak
   10. Use worn tool to measure area of each peak
   11. The pixel amount number appear in new windows, copy and paste in excel and then analyze.
   12. This protocol follows this clip <https://www.youtube.com/watch?v=JlR5v-DsTds>
   13. 