Week2 Assignment

Name: Youcheng ZHANG

Course: Project in molecular Life science (KB8024/KB8025)

Project: Signal Peptide in Gram-negative bacteria

List of papers:

1   Costa, T. R. *et al.* Secretion systems in Gram-negative bacteria: structural and mechanistic insights. *Nature reviews. Microbiology* **13**, 343-359, doi:10.1038/nrmicro3456 (2015).

2   Chou, K. C. Prediction of protein signal sequences. *Current protein & peptide science* **3**, 615-622 (2002).

3   Kazemian, H. B., Yusuf, S. A. & White, K. Signal peptide discrimination and cleavage site identification using SVM and NN. *Computers in biology and medicine* **45**, 98-110, doi:10.1016/j.compbiomed.2013.11.017 (2014).

4   Reynolds, S. M., Kall, L., Riffle, M. E., Bilmes, J. A. & Noble, W. S. Transmembrane topology and signal peptide prediction using dynamic bayesian networks. *PLoS computational biology* **4**, e1000213, doi:10.1371/journal.pcbi.1000213 (2008).

5   Petersen, T. N., Brunak, S., von Heijne, G. & Nielsen, H. SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nature methods* **8**, 785-786, doi:10.1038/nmeth.1701 (2011).

Summary of papers:

The first review paper Costa, T. R. *et al.*, 2015[1], provided a brief introduction on secretion systems in Gram-negative bacteria, highlighting the members' structures, mechanism, specific pathways of six secretion systems, within which features and important roles of signal peptide sequence to the biological processes are mentioned[1]. The second paper from Chou, K. C, 2002[2] summurized the development of protein signal prediction, from discovery of signal peptides involving with their patterns and properties to development of prediction methods including weight-matrix approach, neural network approaches and sibsite coupling approahces. The third paper Kazemian, H. B. *et al.*, 2014[3] introduced a novel dual phase methodology cascading Support Vector Machine and Neural Network as the classification approach to identify signal peptides as well as cleavage sites, which performs well with high-level accuracy on SP and non-SP discrimination and cleavage sites prediction. The fourth paper by Reynolds, S. M., 2008[4] published a combined approach applying Dynamic Bayesian networks which are generalizations of both HMMs and BNs, into detecting and differentiating signal peptides and transmembrane proteins. The last paper von Heijne, G., 2011 presented SignalP 4.0 method and made comparison with other current methods of signal peptide prediction algorithm performance in different organisms[5].