

DAFTAR PUSTAKA

- [1] Ching, W.K. dan Michael K. Ng. 2006. *Markov chains models, algorithms and applications*. Springer, USA: xiv + 205 hlm.
- [2] Doron-Faigenboim, Adi. *Jukes and Cantor method*.
<http://tau.ac.il/~doronadi/jc.pdf>, 27 Maret 2008, pk. 11:50.
- [3] Graur, Dan dan Wen-Hsiung Li. 1991. *Fundamentals of molecular evolution*. Sinauer Associates: 284 hlm.
- [4] Harville, David A. 1997. *Matrix algebra from a statistician's perspective*. Springer, New York: xvii + 630 hlm.
- [5] Isaev, Alexander. 2004. *Introduction to mathematical methods in Bioinformatics*. Springer, Berlin Heidelberg: xiii + 294 hlm.
- [6] Kimura, Motoo. 1980. *A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences*. Springer, J. Mol. Evol. 16: 111-120.
- [7] Peng, Chuang. 2007. *Distance based methods in phylogenetic tree construction*. Morehouse College. Atlanta, 11 hlm.
- [8] Penn, Osnat. *Kimura two parameters model*.
<http://tau.ac.il/~zomerosn/K2P.doc>, 7 Juni 2008, pk. 14:25.
- [9] Ponidi dan Arie Wibowo. 2002. *Persamaan diferensial biasa: pendahuluan sistem dinamika & aplikasinya*. Jurusan Matematika Universitas Indonesia: iii + 14-13 hlm.

- [10] Shen, Shiyi dan Jack A. Tuszynski. 2008. *Theory and mathematical methods for bioinformatics*. Springer, Berlin Heidelberg: xvi + 445 hlm.

