

DAFTAR PUSTAKA

- [1] Isaev, Alexander. 2004. *Introduction to mathematical methods in Bioinformatics*. Springer, Canberra: XIII + 294 hlm.
- [2] Peng, Chuang. 2007. *Distance based methods in Phylogenetic Tree construction*. Morehouse College. Atlanta, 11 hlm.
- [3] Shamir, Ron & Itsik Pe'er. 1999. *Algorithm for molecular biology*. Lecture 9.
- [4] Terribilini. 2002. *Phylogenetic-Distance-Based Methods*. Lecture 30.
- [5] M. Abdushomad E, D. Astuti A. *Bioinformatika : Perkembangan, Disiplin Ilmu, dan Penerapannya di Indonesia*. 2004.
- [6] Rodrigue, Jean-Paul. 2008. *Graph Theory : Definition and Properties*. <http://people.hofstra.edu/geotrans/eng/ch2en/ch2m1en.html>, 24 Januari 2008, pk 13:24.
- [7] Wikipedia .2008. *Tree (Graph Theory)*. [http://en.wikipedia.org/wiki/Tree_\(graph_theory\).html](http://en.wikipedia.org/wiki/Tree_(graph_theory).html), 24 Januari 2008, pk 13:42.
- [8] Tizag. 2008. *PHP Tutorial*. <http://www.tizag.com>, 14 Pebruari 2008, pk 11:34.
- [9] Sidik, Betha. 2004. *Pemrograman WEB Dengan PHP*. Informatika, Bandung.
- [10] Imansyah, Muhammad. 2003. *PHP & MySql Untuk Orang Awam*. Maxikom, Palembang.
- [11] Understanding Evolution: your one-stop source for information on evolution. http://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_02, 3 Juni 2008, pk 10:30.
- [12] Thompson,J.D., Gibson,T.J., Plewniak,F., Jeanmougin,F. and Higgins,D.G. 1997. *The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools*. *Nucleic Acids Research*, 25:4876-4882.