
12 Bibliografia

- [1] Genomic Proteomic Data Warehouse, <http://www.bioinformatics.dei.polimi.it/GPKB/> .
- [2] O. King, R. Foulger, S. Dwight, J. White, F. Roth, “Predicting gene function from patterns of annotation”, *Genome res.*, vol. 13, no. 5, pp. 896-904, 2003.
- [3] Y. Tao, L. Sam, J. Li, C. Friedman, and Y. A. Lussier, "Information theory applied to the sparse gene ontology annotation network to predict novel gene function", *Bioinformatics*, vol. 23, no. 13, pp. 529–538, 2007.
- [4] P. Khatri, B. Done, A. Rao, A. Done, and S. Draghici, "A semantic analysis of the annotations of the human genome", *Bioinformatics*, vol. 21, no. 16, pp. 3416–3421, 2005.
- [5] D. Chicco, M. Tagliasacchi, M. Masseroli, "Biomolecular annotation prediction through information integration", *Proceedings of CIBB2011 -8th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Gargnagno sul Garda, Italy, pp. 1-9, 2011.
- [6] R. Sarati, “Metodi e architetture software per la predizione di annotazioni genomiche funzionali e la stima di similarità semantica di geni e proteine”, 2009.
- [7] T. Hofmann, "Probabilistic Latent Semantic Indexing", *Proceedings of the Twenty-Second Annual International SIGIR Conference on Research and Development in Information Retrieval (SIGIR-99)*, pp. 50–57, 1999.
- [8] M. Masseroli, D. Chicco, P. Pinoli, “Probabilistic Latent Semantic Analysis for predicting Gene Ontology annotations”, *IEEE WCCI 2012 - the 2012 IEEE World Congress on Computational Intelligence proceedings*, pp. 1-8, 2012.
- [9] C. Ding, L. Tao, and Wei Peng, "On the equivalence between non-negative matrix factorization and probabilistic latent semantic indexing", *Computational Statistics & Data Analysis*, 52.8, pp. 3913-3927, 2008.
- [10] B. Done, P. Khatri, A. Done, S. Draghici, “Semantic analysis of genome annotations using weighting schemes”, *Proceedings of 2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, pp. 212-218, 2007.

- [11] D. Blei, A. Ng, M. Jordan, “Latent Dirichlet Allocation”, *Journal of Machine Learning Research*, pp. 993-1022, 2003.
- [12] Cullum and Willoughby, “Lanczos Algorithms for Large Symmetric Eigenvalue Computations”, Vol. 1, 2002.
- [13] A. Vinokourov, M. Girolami, “A Probabilistic Framework for the Hierarchic Organisation and Classification of Document Colletions” , *Information Processing and Management*, 2002.
- [14] R. Nallapati, W. Cohen, “Link-PLSA-LDA: a new unsupervised model for topics and influence of blogs”, 2009.
- [15] A. Bosch. A. Zisserman, X. Munoz, “Scene classification via pLSA”, *ECCV Proceedings*, 2006.
- [16] A. Dempster, N. Laird, D. Rubin, “Maximum likelihood form incomplete data via EM algorithm”, *Journal of Royal Statistical Society*, 1977.
- [17] M. Masseroli, G. Ghisalberty, S. Ceri, “Bio-Search Computing: Integration and global ranking of bioinformatics search results”, *Journal of Integrative Bioinformatics*, pp. 1-9, 2011.
- [18] Stefano Ceri, Marco Brambilla , “Search Computing challenges and directions”, 2010.
- [19] A. Nuzzo, F. Mulas , M. Gabetta , E. Arbustini , B. Zupan, C. Larizza, R. Bellazzi,, “Text Mining approaches for automated literature knowledge extraction and representation.”, *Studies Health Technol Informatics*, 2010;