

1 Metagenomics and Assembly

- [1] BENTLEY, D. Whole-genome re-sequencing. *Current Opinion in Genetics & Development* 16, 6 (2006), 545–552.
- [2] BUTLER, J., MACCALLUM, I., KLEBER, M., SHLYAKHTER, I., BELMONTE, M., LANDER, E., NUSBAUM, C., AND JAFFE, D. ALLPATHS: De novo assembly of whole-genome shotgun microreads. *Genome Research* 18, 5 (2008), 810.
- [3] CHAISSON, M., AND PEVZNER, P. Short read fragment assembly of bacterial genomes. *Genome Research* 18, 2 (2008), 324.
- [4] EPPLEY, J., TYSON, G., GETZ, W., AND BANFIELD, J. Strainer: software for analysis of population variation in community genomic datasets. *BMC Bioinformatics* 8 (2007), 398.
- [5] GOLDBERG, S., JOHNSON, J., BUSAM, D., FELDBLYUM, T., FERRIERA, S., FRIEDMAN, R., HALPERN, A., KHOURI, H., KRAVITZ, S., LAURO, F., ET AL. A sanger/pyrosequencing hybrid approach for the generation of high-quality draft assemblies of marine microbial genomes. *Proceedings of the National Academy of Sciences* 103, 30 (2006), 11240.
- [6] MARGULIES, M., EGHOLM, M., ALTMAN, W., ATTIIYA, S., BADER, J., BEMBEN, L., BERKA, J., BRAVERMAN, M., CHEN, Y., CHEN, Z., ET AL. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437 (2005), 376–380.
- [7] MILLER, J. R., DELCHER, A. L., KOREN, S., VENTER, E., WALENZ, B. P., BROWNLEY, A., JOHNSON, J., LI, K., MOBARRY, C., AND SUTTON, G. Aggressive assembly of pyrosequencing reads with mates. *Bioinformatics Advance Access originally published on October 24, 2008. This version published October 28.* (2008).
- [8] MYERS, E., SUTTON, G., DELCHER, A., DEW, I., FASULO, D., FLANIGAN, M., KRAVITZ, S., MOBARRY, C., REINERT, K., REMINGTON, K., ET AL. A Whole-Genome Assembly of Drosophila. *Science* 287, 5461 (2000), 2196.
- [9] NAGARAJAN, N., READ, T., AND POP, M. Scaffolding and validation of bacterial genome assemblies using optical restriction maps. *Bioinformatics* (2008).
- [10] PEVZNER, P., TANG, H., AND WATERMAN, M. An Eulerian path approach to DNA fragment assembly. *Proceedings of the National Academy of Sciences* 98, 17 (2001), 9748.
- [11] POP, M., KOSACK, D., AND SALZBERG, S. Hierarchical Scaffolding With Bambus, 2004.
- [12] RUSCH, D., HALPERN, A., SUTTON, G., HEIDELBERG, K., WILLIAMSON, S., YOOSEPH, S., WU, D., EISEN, J., HOFFMAN, J., REMINGTON, K., ET AL. The sorcerer ii global ocean sampling expedition: Northwest atlantic through eastern tropical pacific. *PLoS Biol* 5, 3 (2007), e77.
- [13] SIMMONS, S., DiBARTOLO, G., DENEY, V., GOLTSMAN, D., THELEN, M., ET AL. Population Genomic Analysis of Strain Variation in Leptospirillum Group II Bacteria Involved in Acid Mine Drainage Formation. *PLoS Biol* 6, 7 (2008), e177.

[14] VENTER, J., REMINGTON, K., HEIDELBERG, J., HALPERN, A., RUSCH, D., EISEN, J., WU, D., PAULSEN, I., NELSON, K., NELSON, W., ET AL. Environmental genome shotgun sequencing of the sargasso sea. *Science* 304, 5667 (2004), 66–74.

[15] ZERBINO, D., AND BIRNEY, E. Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. *Genome Research* 18, 5 (2008), 821.

2 Graph Theory and Visualization

[16] ANDREAS, D., DAVID, W., TOBIAS, R., AND KNUT, R. SeqAn An efficient, generic C++ library for sequence analysis. *BMC Bioinformatics* 9.

[17] BERGER, B., AND SHOR, P. Approximation algorithms for the maximum acyclic subgraph problem. In *Proceedings of the first annual ACM-SIAM symposium on Discrete algorithms* (1990), Society for Industrial and Applied Mathematics Philadelphia, PA, USA, pp. 236–243.

[18] EDMONDS, J., AND JOHNSON, E. Matching: A Well-Solved Class of Integer Linear Programs. *LECTURE NOTES IN COMPUTER SCIENCE* (2002), 27–30.

[19] EVEN, G. Approximating Minimum Feedback Sets and Multicuts in Directed Graphs. *Algorithmica* 20, 2 (1998), 151–174.

[20] FASULO, D., HALPERN, A., DEW, I., AND MOBARRY, C. Efficiently detecting polymorphisms during the fragment assembly process. *Bioinformatics* 18, 1 (2002), 294–302.

[21] GROCHOW, J., AND KELLIS, M. Network Motif Discovery Using Subgraph Enumeration and Symmetry-Breaking. *LECTURE NOTES IN COMPUTER SCIENCE* 4453 (2007), 92.

[22] HERMAN, I., MELANÇON, G., AND MARSHALL, M. Graph Visualization and Navigation in Information Visualization: A Survey. *IEEE TRANSACTIONS ON VISUALIZATION AND COMPUTER GRAPHICS* (2000), 24–43.

[23] LEE, C. Generating consensus sequences from partial order multiple sequence alignment graphs, 2003.

[24] LI, W., AND KURATA, H. A grid layout algorithm for automatic drawing of biochemical networks. *Bioinformatics* 21, 9 (2005), 2036–2042.

[25] MILO, R., SHEN-ORR, S., ITZKOVITZ, S., KASHTAN, N., CHKLOVSKII, D., AND ALON, U. Network Motifs: Simple Building Blocks of Complex Networks, 2002.

[26] NEWMAN, M. Modularity and community structure in networks. *Proceedings of the National Academy of Sciences* 103, 23 (2006), 8577–8582.

[27] SHANNON, P., MARKIEL, A., OZIER, O., BALIGA, N., WANG, J., RAMAGE, D., AMIN, N., SCHWIKOWSKI, B., AND IDEKER, T. Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks, 2003.

3 High Performance Computing

- [28] DAGUM, L., AND MENON, R. OpenMP: An Industry-Standard API for Shared-Memory Programming. *IEEE COMPUTATIONAL SCIENCE & ENGINEERING* (1998), 46–55.
- [29] DEAN, J. Experiences with MapReduce, an abstraction for large-scale computation. In *PACT: Proceedings of the 15 th international conference on Parallel architectures and compilation techniques* (2006), vol. 16, pp. 1–1.
- [30] DEAN, J., AND GHEMAWAT, S. Mapreduce: simplified data processing on large clusters. *Commun. ACM* 51, 1 (2008), 107–113.
- [31] DONGARRA, J., OTTO, S., SNIR, M., AND WALKER, D. A message passing standard for MPP and workstations. *Communications of the ACM* 39, 7 (1996), 84–90.
- [32] VISHKIN, U. Structural parallel algorithmics. In *18th International Colloquium on Automata, Languages and Programming, LNCS Vol. 510, Springer-Verlag* (1991), Springer, pp. 363–380.
- [33] WAN, P., ALZOUBI, K., AND FRIEDER, O. Distributed Construction of Connected Dominating Set in Wireless Ad Hoc Networks. *Mobile Networks and Applications* 9, 2 (2004), 141–149.