References

[1] Richa Agarwala, Leslie G. Biesecker, and Alejandro A. Schäffer. Inverse inbreeding coefficient problems with an application to linkage analysis of recessive diseases in inbred populations. *Discrete Appl. Math.*, 104(1-3):3–44, 2000.

[2] Tatsuya Akutsu. Dynamic programming algorithms for rna secondary structure prediction with pseudoknots. *Discrete Appl. Math.*, 104(1-3):45–62, 2000.

[3] Richard Arratia, Béla Bollobás, Don Coppersmith, and Gregory B. Sorkin. Euler circuits and dna sequencing by hybridization. *Discrete Appl. Math.*, 104(1-3):63–96, 2000.

[4] B. Berger, J. King, R. Schwartz, and P.W. Shor. Local rule mechanism for selecting icosahedral shell geometry. *Discrete Appl. Math.*, 104(1-3):97–111, 2000.

[5] R. Bundschuh and T. Hwa. An analytic study of the phase transition line in local sequence alignment with gaps. *Discrete Appl. Math.*, 104(1-3):113–142, 2000.

[6] John D. Kececioglu, Hans-Peter Lenhof, Kurt Mehlhorn, Petra Mutzel, Knut Reinert, and Martin Vingron. A polyhedral approach to sequence alignment problems. *Discrete Appl. Math.*, 104(1-3):143–186, 2000.

[7] Brendan Mumey. Probe locaction in the presence of errors: A problem from dna mapping. *Discrete Appl. Math.*, 104(1-3):187–201, 2000.

[8] Laxmi Parida and Bud Mishra. Partitioning single-molecule maps into multiple populations: Algorithms and probabilistic analysis. *Discrete Appl. Math.*, 104(1-3):203–227, 2000.

[9] Manuela S. Pereira, Lucio Andrade, Sameh El Difrawy, Barry L. Karger, and Elias S. Manolakos. Statistical learning formulation of the dna base-calling problem and its solution in a beyesian em framework. *Discrete Appl. Math.*, 104(1-3):229–258, 2000.

[10] Mireille Régnier. A unified approach to word occurrence probabilities. *Discrete Appl. Math.*, 104(1-3):259–280, 2000.

[11] Lusheng Wang, Bin Ma, and Ming Li. Fixed topology alignment with recombination. *Discrete Appl. Math.*, 104(1-3):281–300, 2000.