RNA Secondary Structure References

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Classics

Tinoco et al.: Estimation of Secondary Structure in Ribonucleic Acids   tinoco1971

I. Tinoco, O. C. Uhlenbeck, and M. D. Levine. "Estimation of Secondary Structure in Ribonucleic Acids". In: *Nature* 230 (1971), pp. 362–367.

Annotations: In this seminal paper Tinoco and Uhlenbeck propose that the free energy of hybridization of RNA single strands is base-pair additive.

File: `../tinoco1971.pdf`.

Tinoco et al.: Improved Estimation of Secondary Structure in Ribonucleic Acids   tinoco1973

I. Tinoco et al. "Improved Estimation of Secondary Structure in Ribonucleic Acids". In: *Nature New Biology* 246 (1973), pp. 40–41.

File: `../tinoco1973.pdf`.

Nussinov et al.: Algorithms for Loop Matchings   nussinov1978

Ruth Nussinov et al. "Algorithms for Loop Matchings". In: *SIAM Journal on Applied Mathematics* 35 (1978), pp. 68–82.

Annotations: Here the algorithm to find the maximum number of base-pairs is presented for the first time. The previous papers of Tinoco and Uhlenbeck did not aim at solving the dynamic programing problem but were only interested in computing a free-energy based score assuming that single base-pair energies could be additive.

File: `../nussinov1978.pdf`.

Experimental

Howard: Thermodynamics of DNA Duplex Formation
howard2000

Kathleen P. Howard. "Thermodynamics of DNA Duplex Formation". In: *Journal of Chemical Education* 77 (2000), pp. 1469–1471. DOI: `10.1021/ed077p1469`.

Annotations: This Journal of Chemical Education article shows in a practical fashion all the details to measure the enthalpy, entropy, and Gibbs free-enery for DNA melting. This experiment provides the main data allowing to score secondary structure folding algorithms. The meaning of a Van't Hoff plot is shown in a very clear manner.

File: `../howard2000.pdf`.

Reviews

Eddy: How do RNA Folding Algorithms Work?   eddy2004

Sean R. Eddy. "How do RNA Folding Algorithms Work?" In: *Nature Biotechnology* 22 (2004), pp. 1457–1458. DOI: `10.1038/nbt1104-1457`.

File: `../eddy2004.pdf`.

Software

Harmanci et al.: Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign   harmanci2007

Arif Ozgun Harmanci, Gaurav Sharma, and David H. Mathews. "Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign". In: *BMC Bioinformatics* 8 (2007), p. 130. DOI: 10.1186/1471-2105-8-130. URL: http://dx.doi.org/10.1186/1471-2105-8-130.

File: ../harmanci2007.pdf.

Inverse Folding

Avihoo et al.: RNAexinv: An Extended Inverse RNA Folding from Shape and Physical Attributes to Sequences   avihoo2011

Assaf Avihoo, Alexander Churkin, and Danny Barash. "RNAexinv: An Extended Inverse RNA Folding from Shape and Physical Attributes to Sequences". In: *BMC Bioinformatics* 12 (2011), p. 319. DOI: 10.1186/1471-2105-12-319. URL: http://dx.doi.org/10.1186/1471-2105-12-319.

File: ../avihoo2011.pdf.

lncRNA

Baker: Long Noncoding RNA's: The Search for Function
baker2011

Monya Baker. "Long Noncoding RNA's: The Search for Function". In: *Nature Methods* 8 (2011), pp. 379–383.

File: ../baker2011_lncRNA.pdf.