

Homology Based Gene Prediction Software List

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Homology Based Gene Prediction Softwares List

| Year | Tool Name | Publication | Method | Organism |
|------|---|---|------------------------------------|---------------------------|
| 1999 | CRITICA (Coding Region Identifica- tion Tool Invoking Compara- tive Analysis) | Badger, J. H., & Olsen, G. J. (1999). CRITICA: Coding region identification tool invoking comparative analysis. <i>Molecular Biology and Evolution</i> , 16(4), 512–524. https:// doi.org/10.1093/oxfordjournals.molbev.a026133 . | Comparative | Prokaryotes / Archaea |
| 2000 | CEM | Bafna, V., & Huson, D. H. (2000). The conserved exon method for gene finding. <i>Proceedings. International Conference on Intelligent Systems for Molecular Biology</i> , 8, 3–12. | Comparative genomics | |
| 2000 | Rosetta | Batzoglou, S., Pachter, L., Mesirov, J. P., Berger, B., & Lander, E. S. ([s.d.]). Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction. | Comparative genomics | |
| 2001 | SGP-1 (Syntenic Gene Prediction) | Wiehe, T., Gebauer-Jung, S., Mitchell-Olds, T., & Guigó, R. (2001). SGP-1: Prediction and validation of homologous genes based on sequence alignments. <i>Genome Research</i> , 11(9), 1574–1583. https://doi.org/10.1101/gr.177401 . | Comparative | Vertebrates and plants |
| 2001 | GenomeScan | Yeh, R. F., Lim, L. P., & Burge, C. B. (2001). Computational inference of homologous gene structures in the human genome. <i>Genome Research</i> , 11(5), 803–816. https://doi.org/10.1101/gr.175701 . | Comparative | |
| 2001 | Twinscan | Korf, I., Flicek, P., Duan, D., & Brent, M. R. (2001). Integrating genomic homology into gene structure prediction. <i>Bioinformatics</i> , 17(suppl_1), S140–S148. https://doi.org/10. 1093/bioinformatics/17.suppl_1.S140 . | Comparative- genomics- based | |

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|------|--|---|--------------------------------|------------|
| 2002 | AGenDA (Alignment-based Gene-Detection Algorithm) | Rinner, O., & Morgenstern, B. (2002). AGenDA: Gene prediction by comparative sequence analysis. <i>In Silico Biology</i> , 2(3), 195–205. | Comparative | Eukaryotes |
| 2002 | DOUBLESCAN | Meyer, I. M., & Durbin, R. (2002). Comparative ab initio prediction of gene structures using pair HMMs. <i>Bioinformatics</i> (Oxford, England), 18(10), 1309–1318. https://doi.org/10.1093/bioinformatics/18.10.1309 . | Comparative | |
| 2002 | GAZE | Howe, K. L., Chothia, T., & Durbin, R. (2002). GAZE: A generic framework for the integration of gene-prediction data by dynamic programming. <i>Genome Research</i> , 12(9), 1418–1427. https://doi.org/10.1101/gr.149502 . | Comparative / combiner | |
| 2003 | SGP2 | Parra, G., Agarwal, P., Abril, J. F., Wiehe, T., Fickett, J. W., & Guigó, R. (2003). Comparative Gene Prediction in Human and Mouse. <i>Genome Research</i> , 13(1), 108–117. https://doi.org/10.1101/gr.871403 . | Comparative | Eukaryotes |
| 2003 | SLAM | Alexandersson, M., Cawley, S., & Pachter, L. (2003). SLAM: Cross-species gene finding and alignment with a generalized pair hidden Markov model. <i>Genome Research</i> , 13(3), 496–502. https://doi.org/10.1101/gr.424203 . | Comparative | Eukaryotes |
| 2003 | ETOPE | Nekrutenko, A., Chung, W.-Y., & Li, W.-H. (2003). ETOPE: Evolutionary test of predicted exons. <i>Nucleic Acids Research</i> , 31(13), 3564–3567. https://doi.org/10.1093/nar/gkg597 . | Comparative / evolution-ary | Eukaryotes |
| 2003 | EvoGene | Pedersen, J. S., & Hein, J. (2003). Gene finding with a hidden Markov model of genome structure and evolution. <i>Bioinformatics</i> (Oxford, England), 19(2), 219–227. https://doi.org/10.1093/bioinformatics/19.2.219 . | Comparative / evolution-ary | |
| 2004 | Projector | Meyer, I. M., & Durbin, R. (2004). Gene structure conservation aids similarity based gene prediction. <i>Nucleic Acids Research</i> , 32(2), 776–783. https://doi.org/10.1093/nar/gkh211 . | Comparative | |
| 2005 | TWAIN | Majoros, W. H., Pertea, M., & Salzberg, S. L. (2005). Efficient implementation of a generalized pair hidden Markov model for comparative gene finding. <i>Bioinformatics</i> (Oxford, England), 21(9), 1782–1788. https://doi.org/10.1093/bioinformatics/bti297 . | Comparative | |

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|------|---|--|---------------------------|-------------|
| 2006 | DOGFISH (for 'detection of genomic features in sequence homolo- gies') | Carter, D., & Durbin, R. (2006). Vertebrate gene finding from multiple-species alignments using a two-level strategy. <i>Genome Biology</i> , 7(Suppl 1), S6. https://doi.org/10.1186/gb-2006-7-s1-s6 . | Comparative | Vertebrates |
| 2006 | N_Scan_EST | Wei, C., & Brent, M. R. (2006). Using ESTs to improve the accuracy of de novo gene prediction. <i>BMC Bioinformatics</i> , 7, 327. https://doi.org/10.1186/1471-2105-7-327 . | Comparative + Evidence | |
| 2006 | TWINSKAN | Wei, C., & Brent, M. R. (2006). Using ESTs to improve the accuracy of de novo gene prediction. <i>BMC Bioinformatics</i> , 7, 327. https://doi.org/10.1186/1471-2105-7-327 . | Comparative + Evidence | |
| 2007 | Contrast | Gross, S. S., Do, C. B., Sirota, M., & Batzoglou, S. (2007). CONTRAST: A discriminative, phylogeny-free approach to multiple informant de novo gene prediction. <i>Genome Biology</i> , 8(12), R269. https://doi.org/10.1186/gb-2007-8-12-r269 . | Comparative | |
| 2007 | Conrad | DeCaprio, D., Vinson, J. P., Pearson, M. D., Montgomery, P., Doherty, M., & Galagan, J. E. (2007). Conrad: Gene prediction using conditional random fields. <i>Genome Research</i> , 17(9), 1389–1398. https://doi.org/10.1101/gr.6558107 . | Comparative | |
| 2015 | GASS (Genome Annotation based on Species Similarity) | Wang, Y., Chen, L., Song, N., & Lei, X. (2015). GASS: Genome structural annotation for Eukaryotes based on species similarity. <i>BMC Genomics</i> , 16(1), 150. https://doi.org/10.1186/s12864-015-1353-3 . | Comparative | |
| 2016 | AugustusCGP | König, S., Romoth, L. W., Gerischer, L., & Stanke, M. (2016). Simultaneous gene finding in multiple genomes. <i>Bioinformatics (Oxford, England)</i> , 32(22), 3388–3395. https://doi.org/10.1093/bioinformatics/btw494 . | Comparative | Eukaryotes |
| 2016 | CESAR | Sharma, V., & Hiller, M. (2019). Coding Exon-Structure Aware Realigner (CESAR): Utilizing Genome Alignments for Comparative Gene Annotation. <i>Methods in Molecular Biology (Clifton, N.J.)</i> , 1962, 179–191. https://doi.org/10.1007/978-1-4939-9173-0_10 . | Comparative | |