

Resource Summary Report

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Genezilla

RRID:SCR_014657

Type: Tool

Proper Citation

Genezilla (RRID:SCR_014657)

Resource Information

URL: <http://www.genezilla.org/>

Proper Citation: Genezilla (RRID:SCR_014657)

Description: Reconfigurable eukaryotic gene finder based on the Generalized Hidden Markov Model framework. The run time and memory requirements are linear in the sequence length. Genezilla utilizes Interpolated Markov Models (IMMs), Maximal Dependence Decomposition (MDD), and includes states for signal peptides, branch points, TATA boxes, and CAP sites.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: eukaryotic gene finder, markov, framework, c++, signal peptide, branch point, tata, cap site

Availability: Available for download

Resource Name: Genezilla

Resource ID: SCR_014657

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260912T195820+0000

Ratings and Alerts

No rating or validation information has been found for Genezilla.

No alerts have been found for Genezilla.

Data and Source Information

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Hamilton EP, et al. (2016) Structure of the germline genome of *Tetrahymena thermophila* and relationship to the massively rearranged somatic genome. *eLife*, 5.

Numa H, et al. (2014) MEGANTE: a web-based system for integrated plant genome annotation. *Plant & cell physiology*, 55(1), e2.

Zhou D, et al. (2014) Genome sequence of *Anopheles sinensis* provides insight into genetics basis of mosquito competence for malaria parasites. *BMC genomics*, 15, 42.

Cervantes MD, et al. (2013) Selecting one of several mating types through gene segment joining and deletion in *Tetrahymena thermophila*. *PLoS biology*, 11(3), e1001518.

Ehrenkaufer GM, et al. (2013) The genome and transcriptome of the enteric parasite *Entamoeba invadens*, a model for encystation. *Genome biology*, 14(7), R77.

Kappmeyer LS, et al. (2012) Comparative genomic analysis and phylogenetic position of *Theileria equi*. *BMC genomics*, 13, 603.

Goodswen SJ, et al. (2012) Evaluating high-throughput ab initio gene finders to discover proteins encoded in eukaryotic pathogen genomes missed by laboratory techniques. *PLoS one*, 7(11), e50609.

Coyne RS, et al. (2011) Comparative genomics of the pathogenic ciliate *Ichthyophthirius multifiliis*, its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. *Genome biology*, 12(10), R100.

Amano N, et al. (2010) Efficient plant gene identification based on interspecies mapping of full-length cDNAs. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 17(5), 271.

Lorenzi HA, et al. (2010) New assembly, reannotation and analysis of the *Entamoeba histolytica* genome reveal new genomic features and protein content information. *PLoS neglected tropical diseases*, 4(6), e716.

Numa H, et al. (2009) Genome-wide validation of *Magnaporthe grisea* gene structures based on transcription evidence. *FEBS letters*, 583(4), 797.

Fitzpatrick DA, et al. (2008) Evidence of recent interkingdom horizontal gene transfer between bacteria and *Candida parapsilosis*. *BMC evolutionary biology*, 8, 181.

Mondego JM, et al. (2008) A genome survey of *Moniliophthora perniciosa* gives new insights into Witches' Broom Disease of cacao. *BMC genomics*, 9, 548.

Coyne RS, et al. (2008) Refined annotation and assembly of the *Tetrahymena thermophila* genome sequence through EST analysis, comparative genomic hybridization, and targeted gap closure. *BMC genomics*, 9, 562.

Knapp K, et al. (2007) An evaluation of contemporary hidden Markov model genefinders with a predicted exon taxonomy. *Nucleic acids research*, 35(1), 317.

Stajich JE, et al. (2007) Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. *Genome biology*, 8(10), R223.

Fitzpatrick DA, et al. (2006) A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. *BMC evolutionary biology*, 6, 99.

Allen JE, et al. (2006) JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. *Genome biology*, 7 Suppl 1(Suppl 1), S9.1.

Eisen JA, et al. (2006) Macronuclear genome sequence of the ciliate *Tetrahymena thermophila*, a model eukaryote. *PLoS biology*, 4(9), e286.