Resource Summary Report

Generated by NIF on Apr 29, 2025

HMMSeg

RRID:SCR_010670
Type: Tool

Proper Citation

HMMSeg (RRID:SCR_010670)

Resource Information

URL: http://noble.gs.washington.edu/proj/hmmseg/

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Description: HMMSeg is a program for the scale-specific segmention of continuous genomic data using hidden Markov models (HMMs). It can segment multiple datasets simultaneously. Scale-specificity is achieved via an optional smoothing step using wavelets. HMMSeg is written in Java and may be downloaded for unrestricted use. It has been tested on Windows and several Unix-type operating systems.

Resource Type: software resource

Defining Citation: PMID:17384021

Funding:

Resource Name: HMMSeg

Resource ID: SCR_010670

Alternate IDs: nlx_75182

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014506+0000

Ratings and Alerts

No rating or validation information has been found for HMMSeg.

No alerts have been found for HMMSeg.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Roberts BS, et al. (2021) Genome-wide strand asymmetry in massively parallel reporter activity favors genic strands. Genome research, 31(5), 866.

Ji Z, et al. (2021) The forkhead transcription factor FOXK2 premarks lineage-specific genes in human embryonic stem cells for activation during differentiation. Nucleic acids research, 49(3), 1345.

Yang Y, et al. (2018) Continuous-Trait Probabilistic Model for Comparing Multi-species Functional Genomic Data. Cell systems, 7(2), 208.

Ing N, et al. (2017) A novel machine learning approach reveals latent vascular phenotypes predictive of renal cancer outcome. Scientific reports, 7(1), 13190.

Wei K, et al. (2016) Choosing panels of genomics assays using submodular optimization. Genome biology, 17(1), 229.

Walker LC, et al. (2015) The Role of Constitutional Copy Number Variants in Breast Cancer. Microarrays (Basel, Switzerland), 4(3), 407.

Glusman G, et al. (2015) Identification of copy number variants in whole-genome data using Reference Coverage Profiles. Frontiers in genetics, 6, 45.