Resource Summary Report

Generated by NIF on May 19, 2025

Segway - a way to segment the genome

RRID:SCR_004206
Type: Tool

Proper Citation

Segway - a way to segment the genome (RRID:SCR_004206)

Resource Information

URL: http://segway.hoffmanlab.org/

Proper Citation: Segway - a way to segment the genome (RRID:SCR_004206)

Description: The free Segway software package contains a novel method for analyzing multiple tracks of functional genomics data. The method uses a dynamic Bayesian network (DBN) model, which enables it to analyze the entire genome at 1-bp resolution even in the face of heterogeneous patterns of missing data. This method is the first application of DBN techniques to genome-scale data and the first genomic segmentation method designed for use with the maximum resolution data available from ChIP-seq experiments without downsampling. Segway uses the Graphical Models Toolkit (GMTK) for efficient DBN inference. The software has extensive documentation and was designed from the outset with external users in mind.

Synonyms: Segway

Resource Type: software resource, source code

Defining Citation: PMID:22426492

Keywords: genome annotation, source code, bayesian network model, bayesian, chip seq, dbn, bio.tools

Funding:

Availability: Free

Resource Name: Segway - a way to segment the genome

Resource ID: SCR_004206

Alternate IDs: nlx_22911, biotools:segway

Alternate URLs: https://www.pmgenomics.ca/hoffmanlab/proj/segway/, https://bitbucket.org/hoffmanlab/segway/, https://bio.tools/segway

Old URLs: http://noble.gs.washington.edu/proj/segway/

License: GNU General Public License version 2

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250519T205055+0000

Ratings and Alerts

No rating or validation information has been found for Segway - a way to segment the genome.

No alerts have been found for Segway - a way to segment the genome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Ankill J, et al. (2024) Integrative pan-cancer analysis reveals a common architecture of dysregulated transcriptional networks characterized by loss of enhancer methylation. PLoS computational biology, 20(11), e1012565.

Pálinkás HL, et al. (2020) Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. eLife, 9.

Chan RCW, et al. (2018) Segway 2.0: Gaussian mixture models and minibatch training. Bioinformatics (Oxford, England), 34(4), 669.

Benleulmi MS, et al. (2017) Modulation of the functional association between the HIV-1 intasome and the nucleosome by histone amino-terminal tails. Retrovirology, 14(1), 54.

Sen S, et al. (2016) Genome-wide positioning of bivalent mononucleosomes. BMC medical

genomics, 9(1), 60.

Hayes JE, et al. (2015) Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. PloS one, 10(9), e0139360.

Shihab HA, et al. (2015) An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics (Oxford, England), 31(10), 1536.

Rosse SA, et al. (2014) Functional annotation of putative regulatory elements at cancer susceptibility Loci. Cancer informatics, 13(Suppl 2), 5.