**ESTScan**

RRID:SCR_005742  
Type: Tool

**Proper Citation**

ESTScan (RRID:SCR_005742)

**Resource Information**

**URL:** [http://estscan.sourceforge.net/](http://estscan.sourceforge.net/)

**Description:** ESTScan is a program that can detect coding regions in DNA sequences, even if they are of low quality. ESTScan will also detect and correct sequencing errors that lead to frame shifts. ESTScan is not a gene prediction program, nor is it an open reading frame detector. In fact, its strength lies in the fact that it does not require an open reading frame to detect a coding region. As a result, the program may miss a few translated amino acids at either the N or the C terminus, but will detect coding regions with high selectivity and sensitivity. ESTScan takes advantage of the bias in hexanucleotide usage found in coding regions relative to non-coding regions. This bias is formalized as an inhomogeneous 3-periodic fifth-order Hidden Markov Model (HMM). Additionally, the HMM of ESTScan has been extended to allow insertions and deletions when these improve the coding region statistics.

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

**Keywords:** dna, dna sequence, coding region, perl module, c, btlib perl module

**Resource ID:** SCR_005742

**Parent Organization:** SourceForge

**References:** PMID: 10786296
Website Status: Last checked up

Alternate IDs: nlx_149202

Abbreviations: ESTScan

Mentions Count: 234

Ratings and Alerts

No rating or validation information has been found for ESTScan.

No alerts have been found for ESTScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 234 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


