A branch point consensus from Arabidopsis found by non-circular analysis allows for better prediction of acceptor sites - DTU Orbit (24/12/2018)

A branch point consensus from Arabidopsis found by non-circular analysis allows for better prediction of acceptor sites

Little knowledge exists about branch points in plants; it has even been claimed that plant introns lack conserved branch point sequences similar to those found in vertebrate introns. A putative branch point consensus sequence for Arabidopsis thaliana resembling the well known metazoan consensus sequence has been proposed, but this is based on search of sequences similar to those in yeast and metazoa. Here we present a novel consensus sequence found by a non-circular approach. A hidden Markov model with a fixed A nucleotide was trained on sequences upstream of the acceptor site. The consensus found by the Markov model shares features with the metazoan consensus, but differs in its details from the consensus proposed earlier. Despite the fact that branch point consensus sequences in plants are weak, we show that a prediction scheme incorporating them leads to a substantial improvement in the recognition of true acceptor sites; the false positive rate being reduced by a factor of 2. We take this as an indication that the consensus found here is the genuine one and that the branch point does play a role in the proper recognition of the acceptor site in plants.

General information
State: Published
Organisations: Department of Chemistry, Ghent University
Contributors: Tolstrup, N., Rouzé, P., Brunak, S.
Pages: 3159-3163
Publication date: 1997
Peer-reviewed: Yes

Publication information
Journal: Nucleic Acids Research
Volume: 25
Issue number: 15
ISSN (Print): 0305-1048
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 10.84 SJR 9.025 SNIP 3.028
Web of Science (2017): Impact factor 11.561
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 9.28 SJR 7.883 SNIP 2.744
Web of Science (2016): Impact factor 10.162
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 9.48 SJR 7.358 SNIP 2.631
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 8.74 SJR 6.64 SNIP 2.552
Web of Science (2014): Impact factor 9.112
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 8.46 SJR 6.801 SNIP 2.284
Web of Science (2013): Impact factor 8.808
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Web of Science (2012): Impact factor 8.278
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 7.86 SJR 5.976 SNIP 2.19
Web of Science (2011): Impact factor 8.026
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 5.381 SNIP 2.034
Web of Science (2010): Impact factor 7.836
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 5.669 SNIP 1.874
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 4.912 SNIP 1.578
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 5.1 SNIP 1.807
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 4.776 SNIP 2.051
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 5.092 SNIP 2.147
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 4.912 SNIP 1.971
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.895 SNIP 1.529
Scopus rating (2001): SJR 3.852 SNIP 1.393
Scopus rating (2000): SJR 4.936 SNIP 1.661
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 4.69 SNIP 1.548
Original language: English
Source: orbit
Source-ID: 168858
Research output: Research - peer-review › Journal article – Annual report year: 1997