Scipio Documentation

Contents

Example searches

Expert searches

Gene containing a mismatch and a frameshift

Organism	Fusarium oxysporum f. sp. lycopersici 4287
Genome file	supercontigs v 1.0.0
	Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MALVIPYTYIQCPCSDQSPPDLPQARQSQSSDERTFDPRDPRSNYSLYPLEYLLYCEDCQ QIRCPRCVNEEVVTYYCPNCLFEVPSSNLRSDGNRCTRSCYQCPVCIGPLQVMETPIEKD QSHLGADIPGPQYALYCQYCNWTSTEIGIKFDKPNGIHSQLSKINNGGDLKLTAKELKER RKENPDEPPLADSDVDTDLQYANLKSFYQSQLADTNAASSGISPLNDTTGYGSPAASLSR IMAMYTGHGHARKRNGPSEVMREALSAEEGLKLADLDESAQIKKLHQEGWDATATIQQNL EQAEVQRFQDGLRPIPHLLRTKRSKRCSVCRHIISKPENKVTSTRFKIRLVAKSYIPTIT IKPLNPTAGTVPTTQRPQILEERPLKPLTPHHYIITFKNPLFDGIKVTLATPNSTPGRFS SKVTILCPQFDIDANTDMWDDALKDDDRDKKRKGEESSGQPEAGKIWERGRNWVSIILEV VPASLRLDGQKDKSPLKEDEDILEIPMFVRMEWEPDSQQDVGAASAKEKDAQERRELAYW CVLGVGRISHD
Search parameters	standard parameters
Result	
Resultfile	ScipioResult_Fusarium_oxysporum.yaml

Gene spread on several contigs and containing a gap

Query sequence derived from cDNA.

|	
Organism	Bombyx mori str. Dazao
Genome file	⊗ supercontigs v 1.0.0
	⬇ Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MEHSLQHRERVGVQDFVLLEDYRSEAAFIDNLKKRFHENIIYTYIGNVLISVNPYKNLPI YTEEKTKLYFKKAFFEAPPHVFAIADNAYRSLVYEHREQCILISGESGSGKTEASKKVLE YIAARTNHLRNVENVKDKLLQSNPLLEAFGNAKTHRNDNSSRFGKYMDIQFNYEGGPEGG HILNYLLEKSRVVSQMHGERNFHIFYQLLASSDQSLMTHLKLQGRPEAYKYTSDSTSHMS QRANDQEQFRVVQEAMKVIEIGESEQREIFEIVASVLHLGNVKFVQNDKGYAEILSHDAN SGNAADLLKVNATALREALTNRTIEARGDVVSTPLDVEQAQYARDALAKAIYDKHFSWLV SRLNSSLAPIEKDAKSSVIGILDIYGFEIFPKNSFEQFCINFCNEKLQQLFIQLTLRQEQ EEYLREGIEWEPVEYFNNIIICDLIEARHKGIISILDDECLRPGDATDASFLDKLNQHLD GHQHYKSHRKSDTKTQKLMGRDEFCLVHYAGEVTYNVNTFLEKNNDLLFRDIQSLMASSD NTIVGCCFKVTFSNREPSYIRCIKPNDFKAPMQFDDKLVSHQVKYLGLMENLRVRRAGFA YRRTYEAFLERYKCLSAETWPNYRGAARDGVQRLVEALQYEKEEYRMGNTKIFVRFPKTL FATEDAFQIKKNDIATIIQSRWRGYYLRKRYLRMRNAAIVIQKWVRRFLAQRLRERRRKA ADVIRAFIKGFITRNGPETPENRRFLGVAKVHWLKRLSAQLPTKLLDLSWPPCPSTCREA SEELHRLHRAHLARKYRLALSPDDKKQFELKVLAEKIFKYSCEAVKYDRRGYKARARGLL ASRAALYVLDAGGRRTFRLKHRLPLDRLTVVVTNESDSLLLVKVPRDLKKDKGDLIISVT HLIEALTIVTDYTKKPELIEIVDTRTIAHSLVNGKQGGTIEVTKGTQPAIQRAKSGNLLV VATP
Search parameters	standard parameters
Result	
Resultfile	⬇ ScipioResult_Bombyx_mori.yaml

4000 bps

1 gi|56194950|gb|CH383895.1| (8299bp)

2 gi|56185721|gb|CH393055.1| (5647bp)

3 gi|56196943|gb|CH381902.1| (18279bp)

Gene with a 5' exon just encoding a methionine

Organism	Magnaporthe grisea 70-15
Genome file	⬛ supercontigs v 6.0.0
	⬇ Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MGITRRGKDKAAAGQAVAGGASGGRARPKKATFETSKKKDVGVSDLTLLSKVSNEAINEN LQKRFEGREIYTYIGHVLVSVNPFRDLGIYTDQVLDSYKGKNRLEMPPHVFAIAESAYYN MKAYKDNQCVIISGESGAGKTEAAKRIMQYIASVSGGDSTDIQQIKDMVLATNPLLESFG NAKTLRNNNSSRFGKYLQIHFNSVGEPVGADITNYLLEKSRVVGQITNERNFHIFYQFTK GASEHYRQMFGIQKPETYIYTSRSKCLDVDGIDDLAEFQDTLNAMKVIGLSQEEQDSVFR ILAAILWTGNLVFREDDEGYAAVTDQSVVEFLAYLLEVDPQQLIKAITIRILTPRSGEVI ESPANVAQAMATRDALAKSLYNNLFDWIVERINQSLKARQPTSNSVGILDIYGFEIFEKN SFEQLCINYVNEKLQQIFIQLTLKAEQDEYAREQIKWTPIKYFDNKIVCDLIESVRPPGV FSALKDATKTAHADPAACDRTFMQSVNGMSNAHLIPRQGSFIIKHYAGDVAYTVDGITDK NKDQLLKGLLGMFQVSQNPFLHTLFPNQVDQDNRKQPPTAGDRIRTSANALVETLMKCQP SYIRTIKPNENKSPTEYNVPNVLHQIKYLGLQENVRIRRAGFAYRQSFEKFVDRFFLLSP ATSYAGEYTWQGSYEAAVKQILKDTSIPQEEWQMGVTKAFIKSPETLFALEHMRDRYWHN MATRIQRMWRAYLAYRAESATRIQTFWRKKRTGAEYLQLRDHGHRVLQGRKERRRMSILG SRRFIGDYLGINASSGPGAHIRNAIGIGSNEKTVFSCRGEILEAKFGRSSKASPRILIVT NSKFYVVAQMLVNGQVQITAEKAIPLGAIKFIGASSSRDDWFSLGVGSPQEADPLLNCVL KTEMFTQMERVMPGGFNLKIGDSIEYAKKPGKMQVVKVLKDSPNPVDFYKSGAVHTQQGE PPNSVSRPTPKGKPVPPRPITRGKLIRPGGPNGRPARGTTNRTPQPRPGGASASAVASRP VPQAQPQAQAQVAASIPVRTQQQSQTSSASVRAPPPPPPAAPPAKAKIMAKVLYDFAGQK ENEMSIKEGDLIEIVQKENNGWWLAKSGNQQAWVPAAYVEEQKQAPPPVAASRPPPPAPP AANGKNKPLPPAKRPAAGKKPASLQPRDSGMSLNGSDGSRSNTPTPSLGNSLADALLARK QAMAKKDDDDDW
Search parameters	standard parameters
Result
500 bps

1 supercontig_6.21 (3793bp) |
| **Resultfile** | ⬇ ScipioResult_Magnaporthe_grisea.yaml |

Parameters to account for additional/missing bases in predicted exons

Organism	Phytophthora sojae P6497
Genome file	⑤ supercontigs v 2.0.0
	⬇ Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MTSEGDVVDDVCVRYACKCGHLAPVSSLFYSETCEKLVCRLPGCSVEEFESYYCGNLLVNLPSKEASM YQNRSSRCFSCPTCENALSTAFHENEQRFFFLCAHCRWESLSVGLADDDPDALVMTAITRERQAAHED IFQALHSHYSTLSSSPANGGAAGVLSASSGAPFGRSSSLQLLADSMKELQREHQMKKFRLQRMAEMGG WKYDQALAKVEEKERWLMEQRREHQWPELSMQLAALSKQGTSYGEESPEKTREVLRNLSQKCDMGEVS TLHQRLLNPLDQAREADQLFPSRPLLRVKRTWRCVESIERGTAGILVKPQISPMSGDSSLPVSASWFK KANLAAQYVPVVTFQRLPYRVGEGGGVECILLVENPLDDAIRITFHSTPTASEDSNENGYVDFQDLTP IIVGPYEDPNLADAFIDDEPPFGANGDEHNTMLLQATRNLIKIKLPLSVNAATTIPISTLSARFIMDT EKFDEDANEVIENSLLSVPVVITAPIIKIGD
Search parameters	Min. Score = 0.2; Min. Identity = 60%; Max. Mismatch = "∞"; Gap to Close = 15 aa; Min. Intron Length = 34 na
Result	200 bps

1 scaffold_1 (1645bp)
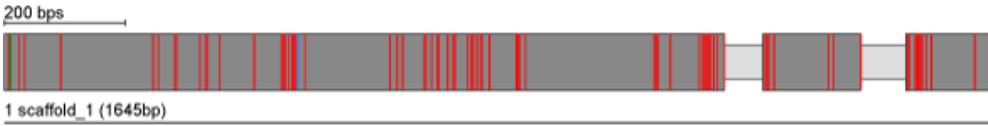
Resultfile	⬇ ScipioResult_Phytophthora_sojae.yaml

Parameters to identify divergent exons and very short exons

Organism	Homo sapiens
Genome file	⟩ chromosome_assembly1 v 1.0.0
	⬇ Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MADPKYADLPGIARNEPDVYETSDLPEDDQAEFDAFAQELEELTSTSVEHIIVNPNAAYD KFKDKRVGTKGLDFSDRIGKTKRTGYESGEYEMLGEGLGVKETPQQKYQRLLHEVQELTT EVEKIKTTVKESATEEKLTPVLLAKQLAALKQQLVASHLEKLLGPDAAINLTDPDGALAK RLLLQLEATKNSKGGSGGKTTGTPPDSSLVTYELHSRPEQDKFSQAAKVAELEKRLTELE TAVRCDQDAQNPLSAGLQGACLMETVELLQAKVSALDLAVLDQVEARLQSVLGKVNEIAK HKASVEDADTQSKVHQLYETIQRWSPIASTLPELVQRLVTIKQLHEQAMQFGQLLTHLDT TQQMIANSLKDNTTLLTQVQTTMRENLATVEGNFASIDERMKKLGK
Search parameters	Exhaust Align Size = 15000 bp
Result	
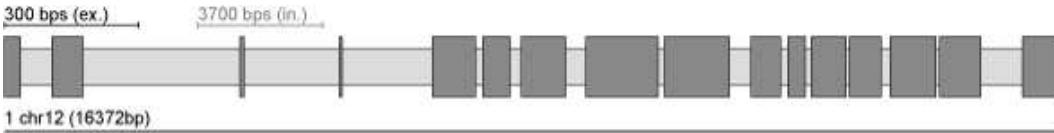
For clarity introns have been scaled down by a factor of 13.27

Resultfile	⬇ ScipioResult_Homo_sapiens.yaml

Parameters to account for low homology at intron borders

Organism	Thielavia heterothallica ATCC 42464
Genome file	supercontigs v 1.0.0
	Genomic DNA subsequence (useful for command-line tests of Scipio)
Query sequence	MSSHKAIVSSFVEGAPPGELSDVVADIKALTISSPGLVNELGPAFQKYNEEQFTTVKLPG GSQPVIISSHSALGNGRYYDLESSCSFAFDHITQKASAVESYVPEGDGVDLAKSILKGLS TYVNEHFTNAAYGAYPIENGSKIAIIIVANKYSPNNFWNGRWRSLYIFNPASSALEGSIK VDVHYYEDGNVRLLTNKSATATVPSGTGAAIAKEISAGERKYQEELNRSFTSLSEGAFKA LRRQLPVTRQKIEWDKVASYRLGQDIGGGSSRR
Search parameters	Max. Move Exon = 6 aa
Result	
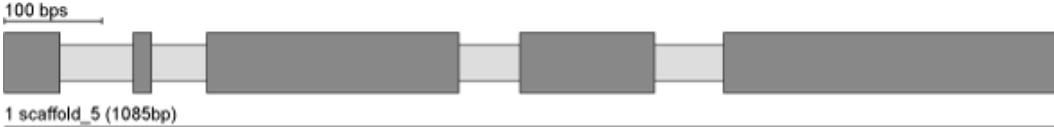
 ScipioResult_Thielavia_heterothallica.yaml

Resultfile