

Detailed versions and parameters of the gene reconstruction and prediction tools

Scenario 1

| Tool | Version | Parameters |
|-------------------------|---|--|
| Scipio v1.0 | Scipio: v1.0 Blat: v. 34 | Scipio: --min_identity=0.6 --min_score=0.3 --max_mismatch=0 Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Scipio v1.5 | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --min_identity=60 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --gap_to_close=15 --min_intron_len=22 --exhaust_align_size=15000 --max_mismatch=0 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Scipio v1.5 (1 gene) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --min_identity=60 --accepted_intron_penalty=1.0 --min_score=0.3 --gap_to_close=15 --min_intron_len=22 --exhaust_align_size=15000 --max_mismatch=0 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Prosplign | 07/09/07 | -full -two_stages |
| Prosplign (Blast) | Prosplign: 07/09/07 Blast: 2.2.20 Compart: 07/09/07 | Prosplign: -full -two_stages Compart: -add 10000 |
| Prosplign (Blat) | Prosplign: 07/09/07 Blat: v. 34 Compart: 07/09/07 | Prosplign: -full -two_stages Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 Compart: -add 10000 |
| Exonerate | 2.2.0 | --model protein2genome |
| Exonerate (1 gene) | 2.2.0 | --model protein2genome --bestn 1 |
| Wise2 | 2.2.0 | -both |
| Wise2 (global) | 2.2.0 | -both -init global |
| Augustus | 2.5 | --species=human --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on |
| Blat | v. 34 | -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Blast | 2.2.20 | |

Scenario 2

| Tool | Version | Parameters |
|----------------------------------|---|--|
| Scipio v1.0 | Scipio: v1.0 Blat: v. 34 | Scipio: --min_identity=0.6 --min_score=0.3 --max_mismatch=0 Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Scipio v1.5 | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --min_identity=60 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --gap_to_close=15 --min_intron_len=22 --exhaust_align_size=15000 --max_mismatch=0 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Scipio v1.5 (Blat tileSize 6) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --min_identity=60 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --gap_to_close=15 --min_intron_len=22 --exhaust_align_size=15000 --max_mismatch=0 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=6 -minIdentity=54 -minScore=15 -oneOff=1 |
| Scipio v1.5 (Blat tileSize 5) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --min_identity=60 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --gap_to_close=15 --min_intron_len=22 --exhaust_align_size=15000 --max_mismatch=0 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=5 -minIdentity=54 -minScore=15 -oneOff=1 |
| Prosplign | 07/09/07 | -full -two_stages |
| Prosplign (Blast) | Prosplign: 07/09/07 Blast: 2.2.20 Compart: 07/09/07 | Prosplign: -full -two_stages Compart: -add 10000 |
| Prosplign (Blat) | Prosplign: 07/09/07 Blat: v. 34 Compart: 07/09/07 | Prosplign: -full -two_stages Blat: -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 Compart: -add 10000 |
| Exonerate | 2.2.0 | --model protein2genome |
| Exonerate (1 gene) | 2.2.0 | --model protein2genome --bestn 1 |
| Prot_map | 24. Jul 2007 | Similarity: Weak; Search for one best alignment only; Maximal area covered by alignment on target: 1000000; Remove trailing X; Protein mode: Map whole protein; Join similar aminoacids: no join |
| Fgenesh+ | 24. Jul 2007 | Organism: Human |
| Wise2 | 2.2.0 | -both |
| Wise2 (global) | 2.2.0 | -both -init global |
| Augustus | 2.5 | --species=human --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on |
| Augustus (1 gene) | 2.5 | --species=human --strand=both --singlestrand=false --genemodel=exactlyone --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on |
| Fgenesh | 24. Jul 2007 | Organism: Human |
| Genscan | November, 2009 | Organism: Vertebrate; Suboptimal exon cutoff: 1.00 |
| Blat | v. 34 | -tileSize=7 -minIdentity=54 -minScore=15 -oneOff=1 |
| Blat (tilesize 6) | v. 34 | -tileSize=6 -minIdentity=54 -minScore=15 -oneOff=1 |
| Blat (tilesize 5) | v. 34 | -tileSize=5 -minIdentity=54 -minScore=15 -oneOff=1 |
| Blast | 2.2.20 | |

Scenario 3

| Tool | Version | Parameters | Organism specific parameters |
|-------------------------|--|--|---|
| Scipio v1.0 | Scipio: v1.0 Blat: v. 34 | Scipio: --min_score=0.3 Blat: -minScore=15 | Scipio: Ned, Phs: --min_identity=0.6 --max_mismatch=0 Hs, Pug, Mm, Th: --min_identity=0.9 --max_mismatch=7 Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Scipio v1.5 | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --min_intron_len=22 --exhaust_align_size=15000 --max_move_exon=6 --min_coverage=60 Blat: -minScore=15 | Scipio: Ned, Phs: --min_identity=60 --gap_to_close=15 --max_mismatch=0 Hs, Pug, Mm, Th: --gap_to_close=6 --max_mismatch=7 Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Scipio v1.5 (1 gene) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --accepted_intron_penalty=1.0 --min_score=0.3 --min_intron_len=22 --exhaust_align_size=15000 --max_move_exon=6 --min_coverage=60 Blat: -minScore=15 | Scipio: Ned, Phs: --min_identity=60 --gap_to_close=15 --max_mismatch=0 Hs, Pug, Mm, Th: --gap_to_close=6 --max_mismatch=7 Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Prospign | 07/09/07 | -full -two_stages | |
| Prospign (Blast) | Prospign: 07/09/07 Blast: 2.2.20 Compart: 07/09/07 | Prospign: -full -two_stages Compart: -add 10000 | |
| Prospign (Blat) | Prospign: 07/09/07 Blat: v. 34 Compart: 07/09/07 | Prospign: -full -two_stages Blat: -minScore=15 Compart: -add 10000 | Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Exonerate | 2.2.0 | --model protein2genome | |
| Exonerate (1 gene) | 2.2.0 | --model protein2genome --bestn 1 | |
| Wise2 | 2.2.0 | -both | |
| Wise2 (global) | 2.2.0 | -both -init global | |
| Augustus | 2.5 | --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on | Ned: --species=neurospora Phs, Pug, Th: --species=generic Hs, Mm: --species=human |
| Blat | v. 34 | -minScore=15 | Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Blast | 2.2.20 | | |

Ned: *Neurospora discreta*, Phs: *Phytophthora sojae*, Hs: *Homo sapiens*, Pug: *Puccinia graminis*, Mm: *Mus musculus*, Th: *Thielavia heterothallica*

Scenario 4

| Tool | Version | Parameters | Organism specific parameters |
|----------------------------------|---|---|---|
| Scipio v1.0 | Scipio: v1.0 Blat: v. 34 | Scipio: --min_score=0.3 Blat: -minScore=15 | Scipio: Ned, Phs: --min_identity=0.6 --max_mismatch=0 Hs, Pug, Mm, Th: --min_identity=0.9 --max_mismatch=7 Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Scipio v1.5 | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --min_intron_len=22 --exhaust_align_size=15000 --max_move_exon=6 --min_coverage=60 Blat: -minScore=15 | Scipio: Ned, Phs: --min_identity=60 --gap_to_close=15 --max_mismatch=0 Hs, Pug, Mm, Th: --gap_to_close=6 --max_mismatch=7 Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Scipio v1.5 (Blat tileSize 6) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --min_intron_len=22 --exhaust_align_size=15000 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=6 -minIdentity=81 -minScore=15 | Scipio: Hs, Pug, Mm, Th: --gap_to_close=6 --max_mismatch=7 |
| Scipio v1.5 (Blat tileSize 5) | Scipio: v1.5 Blat: v. 34 | Scipio: --exhaust_gap_size=30 --max_assemble_size=75000 --accepted_intron_penalty=1.0 --min_score=0.3 --multiple_results --min_intron_len=22 --exhaust_align_size=15000 --max_move_exon=6 --min_coverage=60 Blat: -tileSize=5 -minIdentity=81 -minScore=15 | Scipio: Hs, Pug, Mm, Th: --gap_to_close=6 --max_mismatch=7 |
| Prosplign | 07/09/07 | -full -two_stages | |
| Prosplign (Blast) | Prosplign: 07/09/07 Blast: 2.2.20 Compart: 07/09/07 | Prosplign: -full -two_stages Compart: -add 10000 | |
| Prosplign (Blat) | Prosplign: 07/09/07 Blat: v. 34 Compart: 07/09/07 | Prosplign: -full -two_stages Blat: -minScore=15 Compart: -add 10000 | Blat: Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Exonerate | 2.2.0 | --model protein2genome | |
| Exonerate (1 gene) | 2.2.0 | --model protein2genome --bestn 1 | |
| Prot_map | 24. Jul 2007 | Similarity: Weak; Search for one best alignment only; Maximal area covered by alignment on target: 1000000; Remove trailing X; Protein mode: Map whole protein; Join similar aminoacids: no join | |
| FgenesH+ | 24. Jul 2007 | | Ned, Th: Organism: Neurospora crassa Phs: Organism: Phytophthora Hs: Organism: Human Pug: Organism: Puccinia Mm: Organism: Mouse |
| Wise2 | 2.2.0 | -both | |

| | | | |
|----------------------|-------------------|---|--|
| Wise2 (global) | 2.2.0 | -both -init global | |
| Augustus | 2.5 | --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on | Ned: --species=neurospora Phs, Pug, Th: --species=generic Hs, Mm: --species=human |
| Augustus (1 gene) | 2.5 | --strand=both --singlestrand=false --genemodel=exactlyone --codingseq=on --sample=100 --keep_viterbi=true --alternatives-from-sampling=false --exonnames=on | Ned: --species=neurospora Phs, Pug, Th: --species=generic Hs, Mm: --species=human |
| Fgenesh | 24. Jul 2007 | | Ned, Th: Organism: Neurospora crassa Phs: Organism: Phytophthora Hs: Organism: Human Pug: Organism: Puccinia Mm: Organism: Mouse |
| Genscan | November, 2009 | Organism: Vertebrate; Suboptimal exon cutoff: 1.00 | |
| Blat | v. 34 | -minScore=15 | Ned, Phs: -tileSize=5 -minIdentity=54 -oneOff=1 Hs, Pug, Mm, Th: -tileSize=7 -minIdentity=81 |
| Blat (tilesize 6) | v. 34 | -tileSize=6 -minIdentity=54 -minScore=15 -oneOff=1 | |
| Blat (tilesize 5) | v. 34 | -tileSize=5 -minIdentity=54 -minScore=15 -oneOff=1 | |
| Blast | 2.2.20 | | |

Ned: *Neurospora discreta*, Phs: *Phytophthora sojae*, Hs: *Homo sapiens*, Pug: *Puccinia graminis*, Mm: *Mus musculus*, Th: *Thielavia heterothallica*