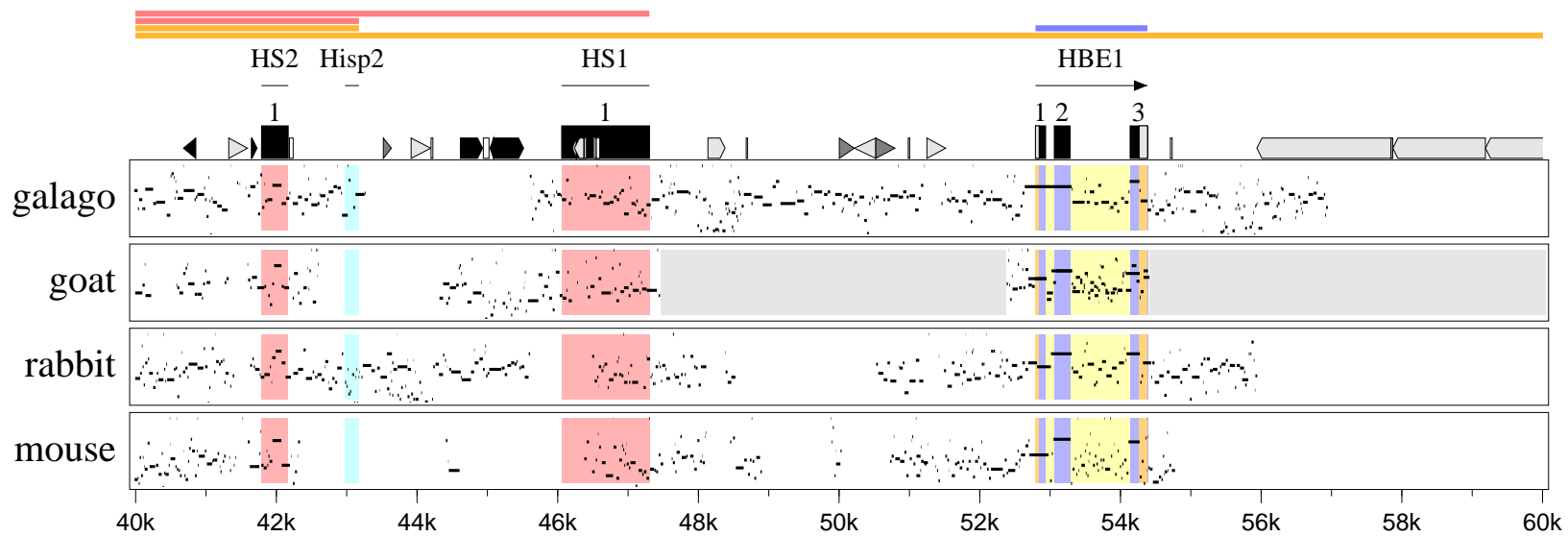


Recent Additions to PipMaker

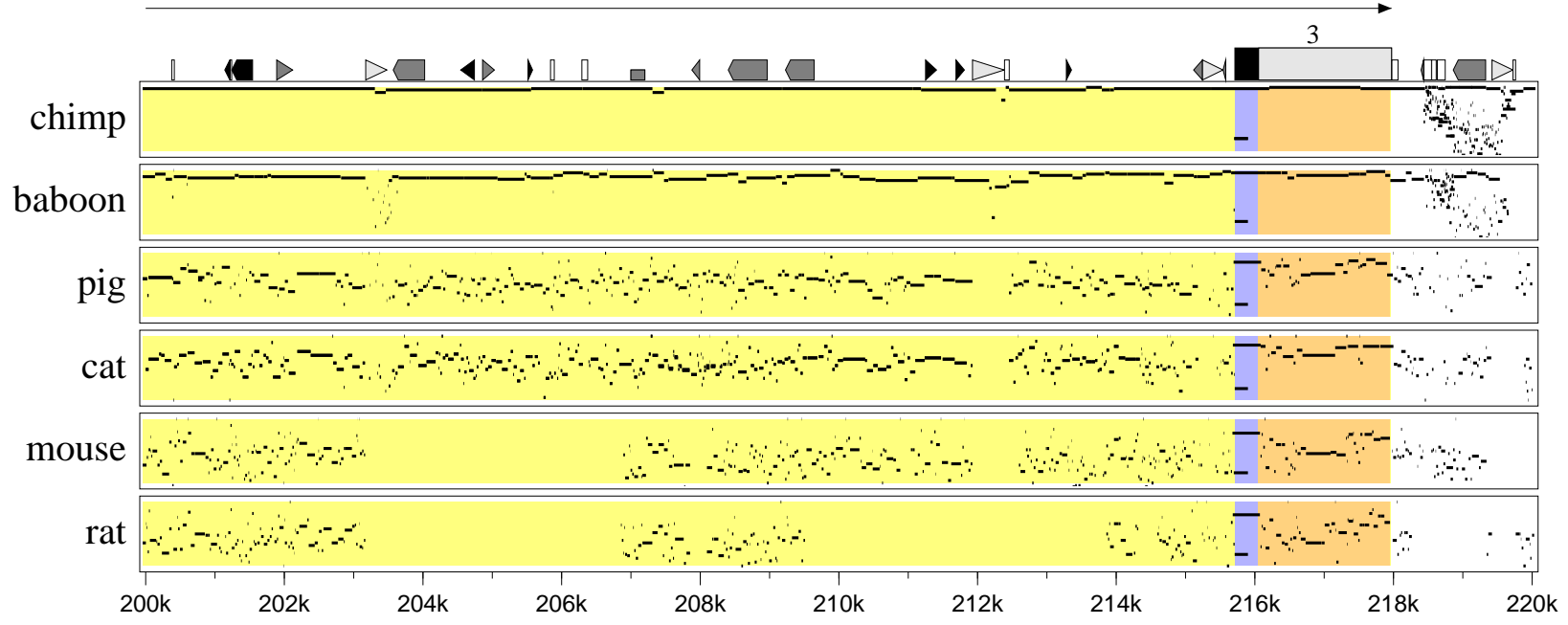
Webb Miller
Penn State

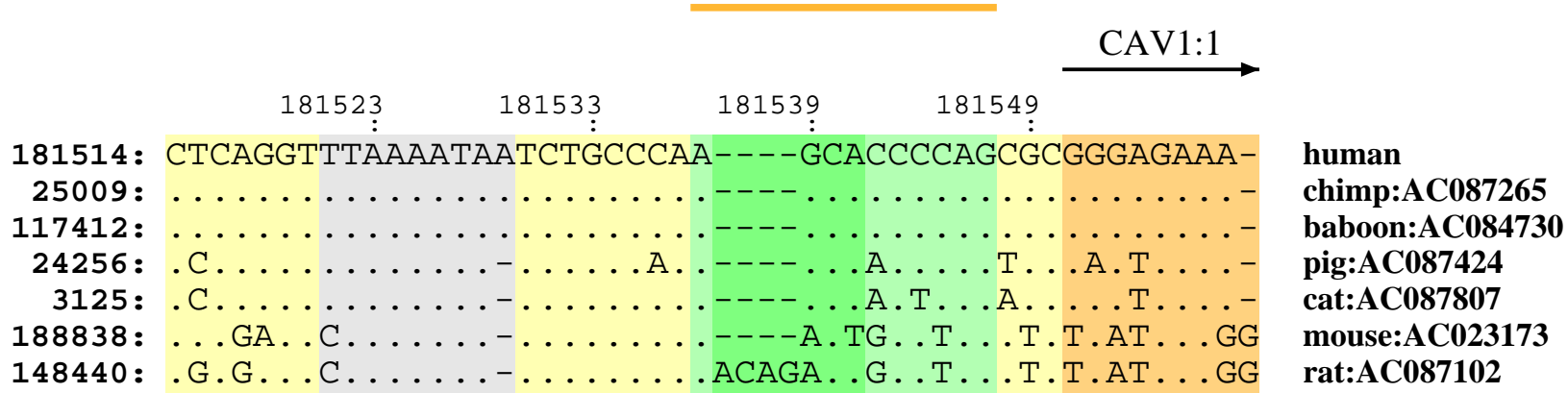
Outline

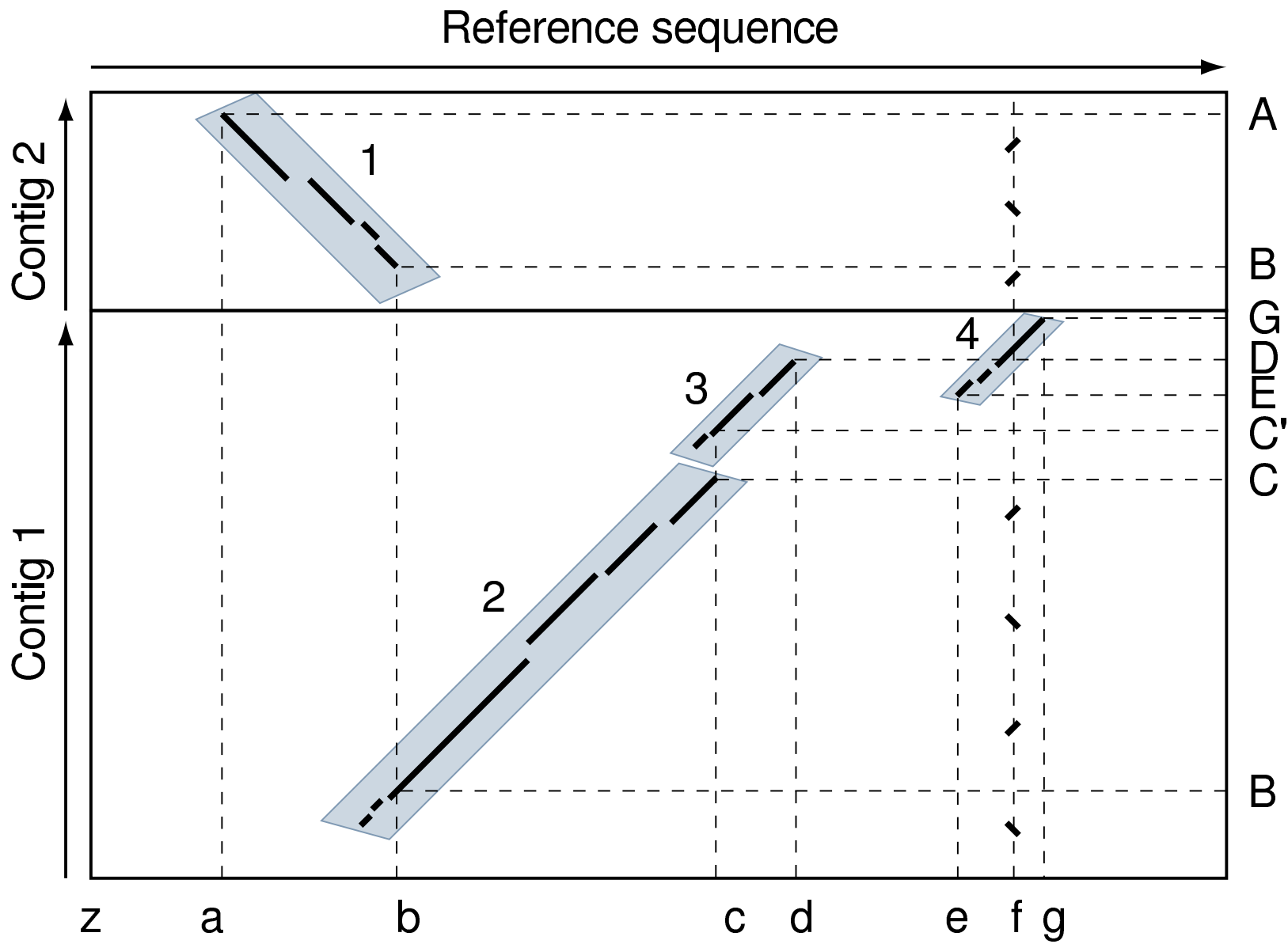
1. MultiPipMaker — simultaneous analysis of more than two sequences.
2. LAJ — locally run program for interactive viewing of PipMaker alignments
3. PipTools — locally run tools to facilitate use of PipMaker
4. Enterix — archived alignments of enteric bacterial genomes

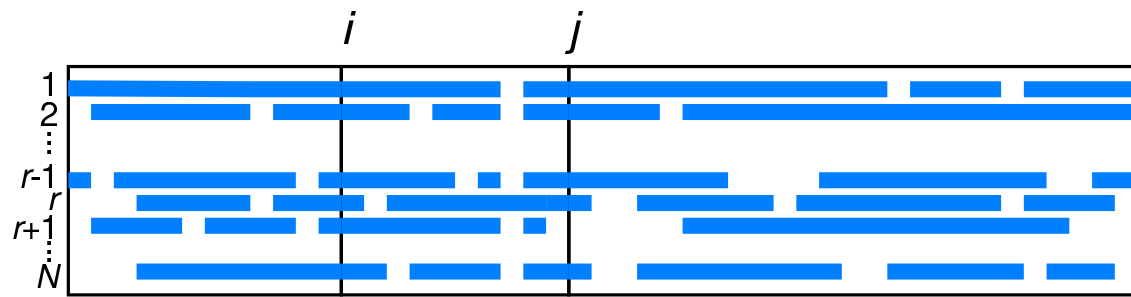


CAV1

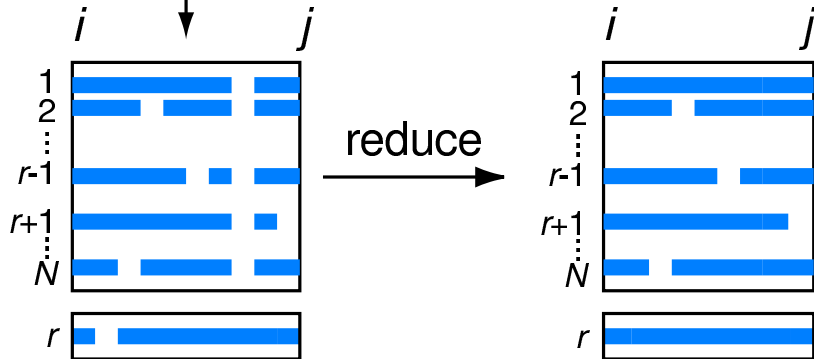




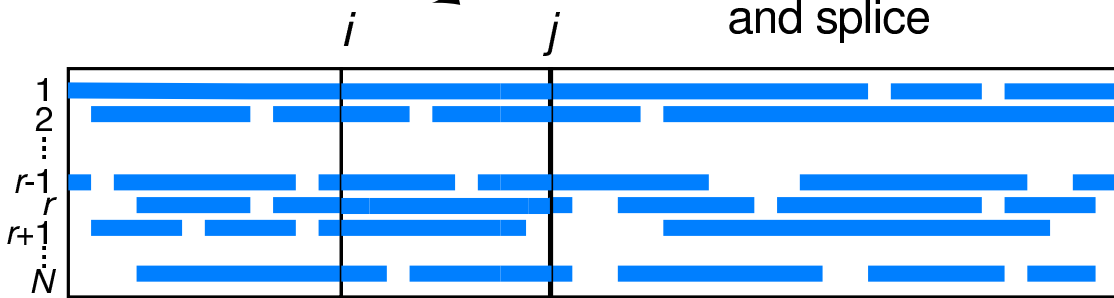




extract

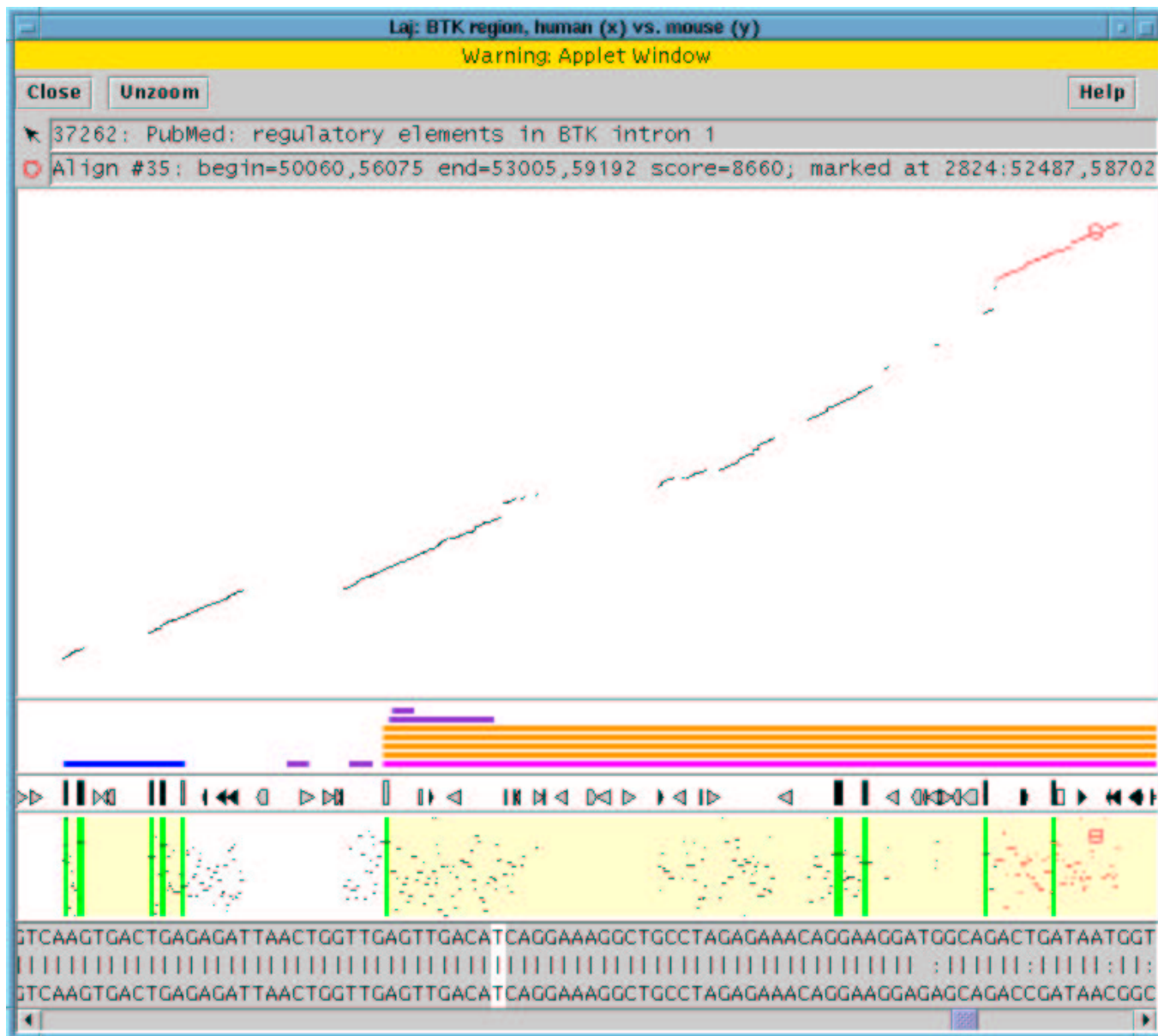


compute alignment and splice



LAJ

LAJ ("Local Alignments in Java") is an interactive viewer for alignments generated by Blastz (PipMaker's pairwise alignment program). Both dotplot and PIP views of the alignments are given. The user can zoom in, click to see a nucleotide-level view, click on hyperlinks.



LAJ for an “Electronic Supplement”

A biologist can establish a Web site as an “electronic supplement” to a sequence analysis project, where LAJ is provided as an applet that can be loaded by any Java-compliant browser. That way, other biologists can browse the electronic supplement using the full power of LAV. For instance, see:

<http://linus.ceh.uvic.ca/mdwilson/laj.html>

PipTools for Preparing Annotations

(i.e., repeats, exons and underlay files)

Program	From	To
<i>exons2underlays</i>	exons file	underlay file
<i>genbank2exons</i>	GenBank	exons file
<i>genbank2repeats</i>	GenBank	repeats file
<i>genscan2exons</i>	Genscan	exons file
<i>genscan2underlays</i>	Genscan	underlay file
<i>rmask2repeats</i>	RepeatMasker	repeats file
<i>sim4</i>	cDNA sequence	exons file

PipTools for Modifying Annotations (e.g. if the reference sequence changes)

Program	Function
<i>exons2mrna</i>	extract putative cDNA sequence
<i>shift-pos</i>	shift positions in annotations
<i>transform-pos</i>	transfer positions to other sequence

PipTools for Analyzing Alignments

Program

strong-hits

strong-hits2underlays

infocon

slice

multi-pat

Function

find strong hits in a pairwise alignment

color strong hits

find strong hits in a multiple alignment

extract part of a multiple alignment

match patterns in a multiple alignment

- yellow = E. coli sequence not found in the other species
- red = sequence in the other species whose immediate neighbor has a homolog elsewhere in E. coli
- blue = sequence in the other species whose immediate neighbor has no detectable homolog in E. coli
- gray = apparently not sequenced in the other species
- purple = overlapping colors, such as red and blue

