Genomic Visualization and Analysis with IMAS
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Available at: http://biov.iat.sfu.ca/IMASProjectWeb, shaw@sfu.ca

IMAS helps analysis of Microbial DNA by
- Finding genes with Glimmer 3
- BLAST Aligning similar genes / proteins
- Finding Motifs with Hmmer
- Multialigning like genes / proteins with ClustalW

IMAS integrates analysis and display
- Zoomable along sequence Horizontally
- Selectable detail Vertically
- Maintains a sequence analysis data collection
- Visual display aligned to sequence
- Integration of commonly-used sequence analysis tools into single interactive zoomable framework

IMAS: Zoomed in

BLAST Local Data

Zoomed in

Zoomed out x 6

Zoomed out x 30

Plot percent identity:
- Computed via BLOSUM log-odds matrix for AA pairs.
- Computed via Codon identity for NTs.
- If Codons encode different AAs, compute AA similarity w/BLOSUM

HMMFam on local data

Syntenic visualization of related Microbes

Zoomed out x 225

Zoomed Out x 30 with Percent identity in syntenic connectors

Used at the CDC Viral & Rickettsial Zoonoses Branch to help annotate Orientia Tsutsugamushi (Greg A Dasch, Marina E. Eremeeva)

Written in C++
Rapid visualization response -- average 25ms zoom response time
Integrated common tools
Local databases

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