

Genomic Visualization and Analysis with IMAS

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Available at: <http://biov.iat.sfu.ca/IMASProjectWeb>, shaw@sfu.ca

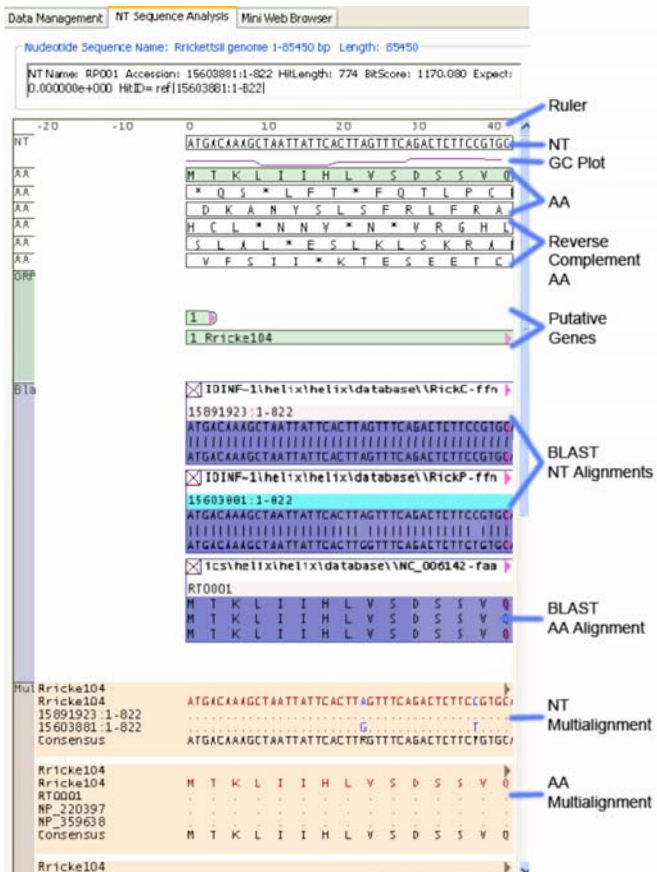
IMAS helps analysis of Microbial DNA by

- 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

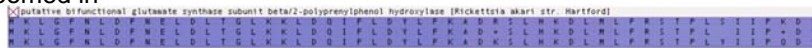
- Zoomable along sequence Horizontally
- Selectable detail Vertically
- Maintains a sequence analysis data collection
- Visual display aligned to sequence
- **Integration of commonly-used sequence analysis tools into single interactive zoomable framework**

IMAS: Zoomed in



BLAST Local Data

Zoomed in



Zoomed out x 6



Zoomed out x 30



Plot percent identity:

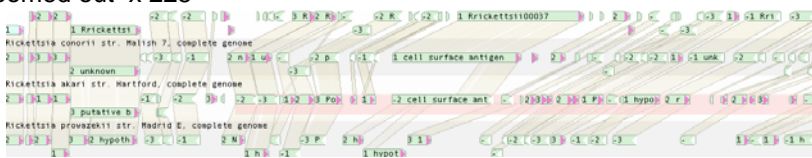
- Computed via BLOSUM log-odds matrix for AA pairs.
- Computed via Codon identity for NTs.
- If Codons encode different AAs, compute AA similarity w/BLOSUM

HMMProfam on local data

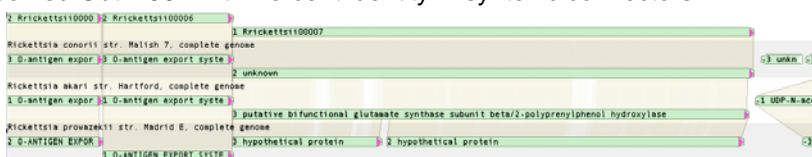


Syntenic visualization of related Microbes

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. Ereemeeva)

Written in C++

Rapid visualization response -- average 25ms zoom response time

Integrated common tools

Local databases

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