NSF

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MiGA
Microbial Genomes Atlas

www.microbial-genomes.org

**"The genome-equivalent of RDP"**

NAR 2018

The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of *Archaea* and *Bacteria* at the whole genome level

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Key underlying data is AAI values among Type Genomes*

*Or another genome collection. Type Genomes is based on NCBI's Type Material database and includes named isolates & some *Candidatus*.

So, it is very easy to incorporate new Taxonomies
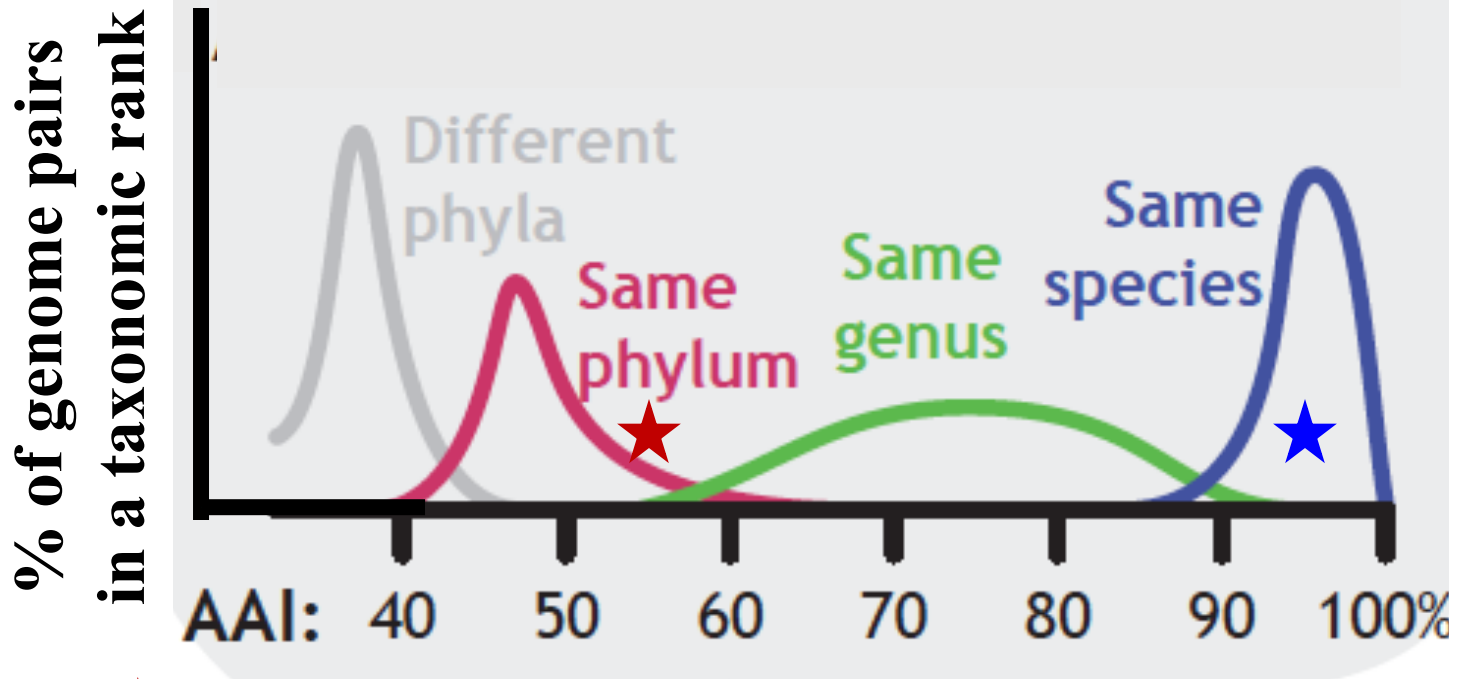
★ Query is novel genus   ★ Query is member of existing species

Protologues with key metadata will be highly useful!

Novel taxa can be identified at species, genus & phylum levels

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Novel species <95% AAI
Novel genus <65% AAI
Novel phylum <45% AAI

MAGs and SAGs in MiGA

- **Not yet available as a single large searchable database (this is coming soon…~20% more MAGs/SAGs than found in NCBI based on manual hunting)**

- **Many MAGs/SAGs available as separate databases by habitat (e.g., TARA Oceans, Oil spills) or project (e.g., Chattahoochee River, Bio-Gas microbiome).**

- **Taxonomy of MAGs/SAGs is (currently) based on AAI values against Type Genomes. Taxonomy of Type Genomes is based on NCBI (no corrections applied).**

- **MAG/SAG quality is check by completeness and contamination using universal protein HMMs, and (optionally) by MyTaxa_Scan** (Luo et al., NAR 2014).

- **Low quality MAGs flagged by <u>not</u> removed.**