GTDB is an initiative to establish a complete, rank normalized, and phylogenetically consistent genome-based taxonomy for Bacteria and Archaea

GTDB methodology in brief:
- species delineated using average nucleotide identity (ANI)
- higher taxa circumscribe lineages in reference phylogeny
- higher taxa normalized to have similar divergence times
- all genomes have species to domain assignments
- “uncultivated” majority given placeholder names

GTDB data dependencies:
- covers all genomes deposited in the NCBI Assembly Database
  - 194,600 genomes as of GTDB R05-RS95
- type material established by consulting LPSN
- SILVA used to classify 16S rRNA sequences
**GTDB MEETS SeqCode**

**Potential advantages:**
- type material will be genomes, the entity used by many biologists and bioinformatic resources and tools
- provide stable and less burdensome avenue to naming species
  - ~70% of GTDB species have placeholder names
  - validated species allow for validated higher taxon names
- provide nomenclatural information in format suitable for easy database integration (i.e. machine friendly)
  - LPSN must be manually consulted though efforts are underway to make this data more accessible

**Potential challenges:**
- requires consulting multiple nomenclatural resources to establish priority and type material
  - unless SeqCode resources cover names validated under the ICNP
- SeqCode resources will diverge from ICNP resources on application of nomenclature in addition to taxonomic opinion