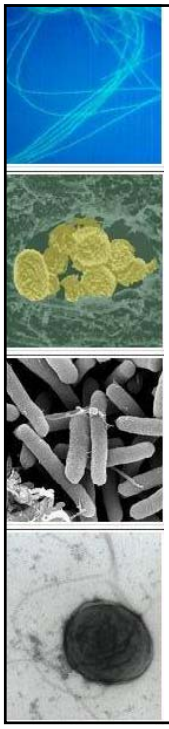

Microbial Genome & Metagenome Analysis: Computational Challenges

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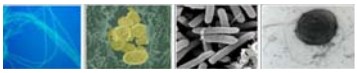
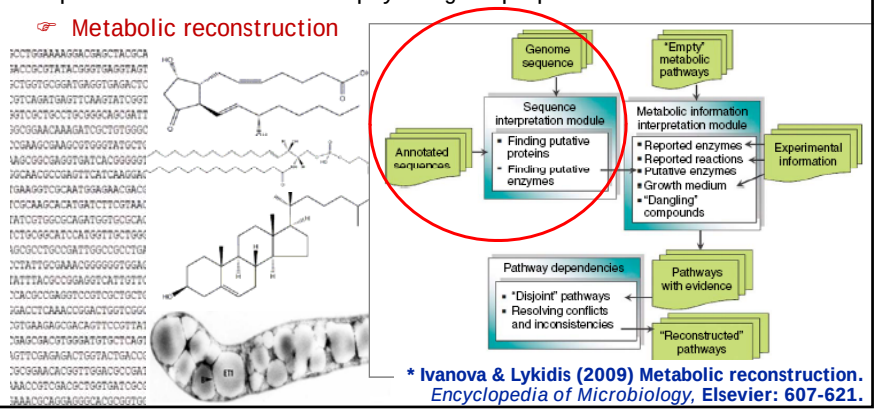
Microbial genome & metagenome analysis



- **General aims**
  - Understand microbial life
  - Apply to agriculture, bioremediation, biofuels, human health
- **Specific aims include**
  - Predict biochemistry & physiology of organisms based on genome sequence
  - Explain known biochemical & physiological properties
    - ☞ Metabolic reconstruction



*** Ivanova & Lykidis (2009) Metabolic reconstruction.** *Encyclopedia of Microbiology,* **Elsevier: 607-621.**

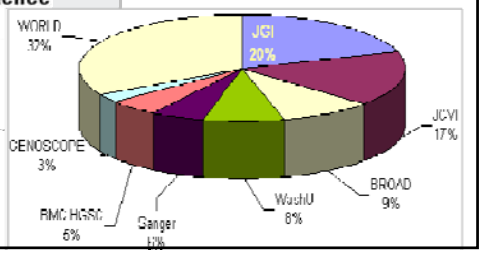
Genome sequence data size

Now

- ~1,400 microbial genomes = 5.5 mil genes
- ~ 100 metagenomes samples = 2.5 mil genes

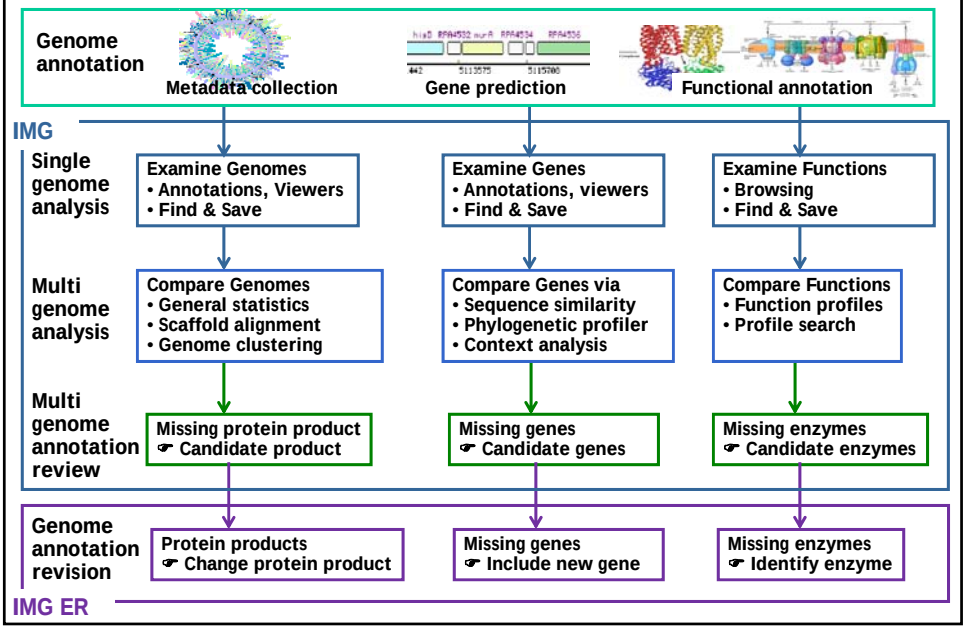
Next 3 Years

- ~10,000 microbial genomes = 40 mil genes (4K genes/genome)
- ~ 400 fungal genomes = 4 mil genes (10K genes/genome)
- ~ 200 plant genomes = 6 mil genes (30K genes/genome)
- ~ 500 metagenome samples = 50 mil genes (100K genes/sample)

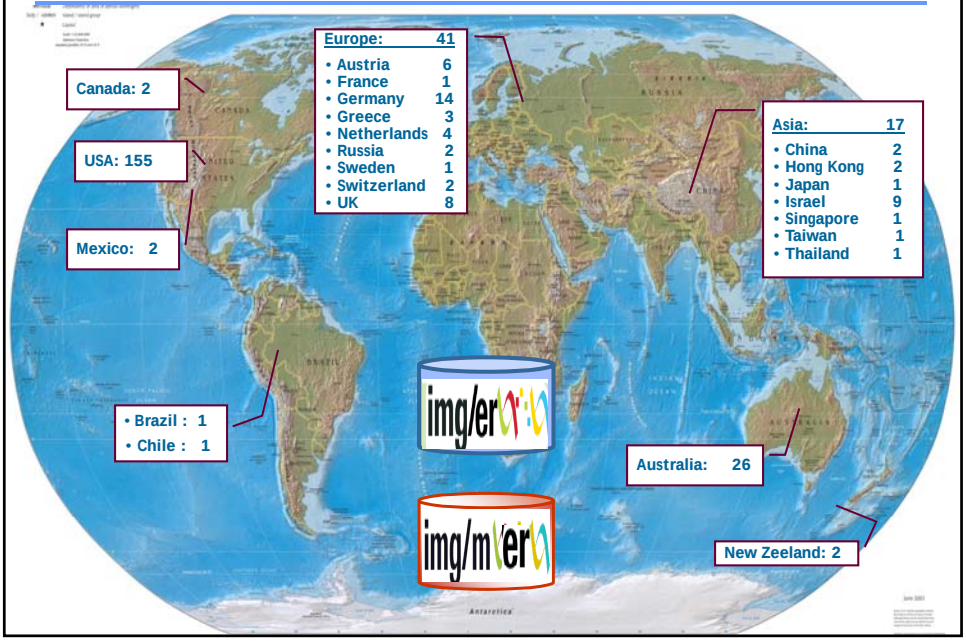


Major Sequencing Centers
(Jan 2009: 4,370 projects)

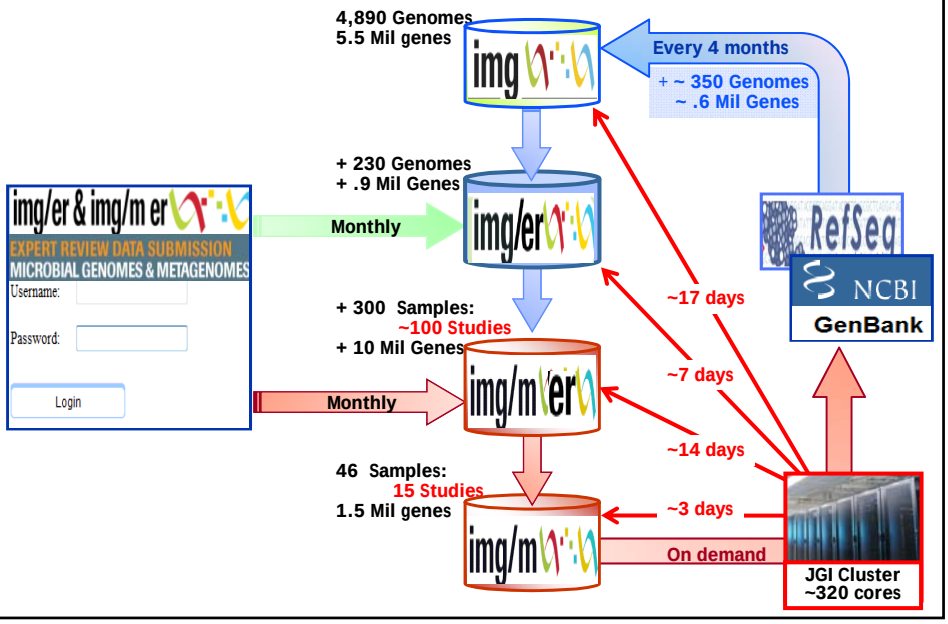
Genome sequence data processing & analysis



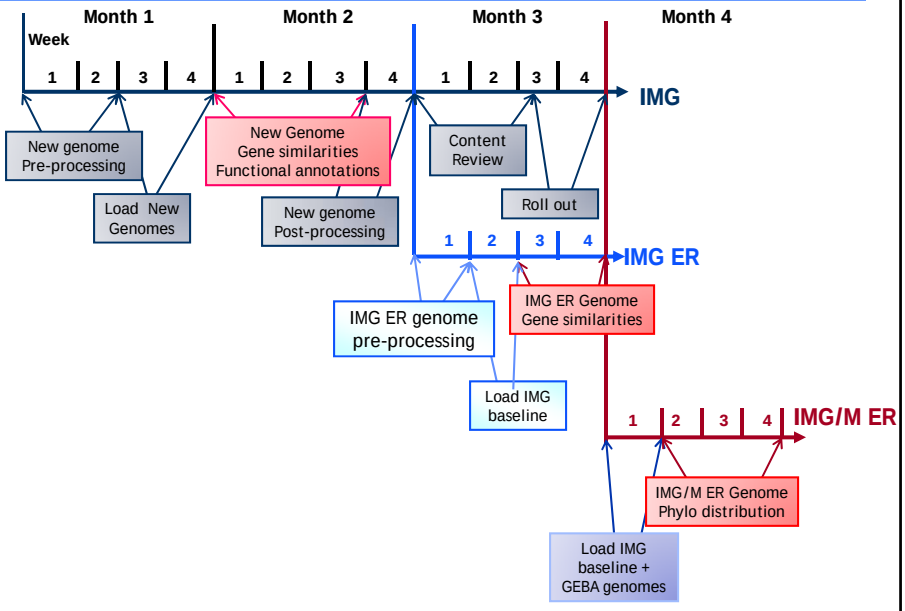
IMG ER systems: community users



IMG systems: genome/metagenome data flow



IMG systems: maintenance process



Current requirements

- **Architectures:** Linux cluster
- **Typical production run:**
  - 232 cores, 4 GB/core, 500 GB data read/written
  - 20 TB on-line storage
- **Data read/written: ~ 1 GB**
- **Current primary codes and their methods or algorithms**
  - Various flavors of BLAST
  - HMM protein searches
- **Known limitations/obstacles/bottleneck**
  - Managing, reformatting, reordering computation results