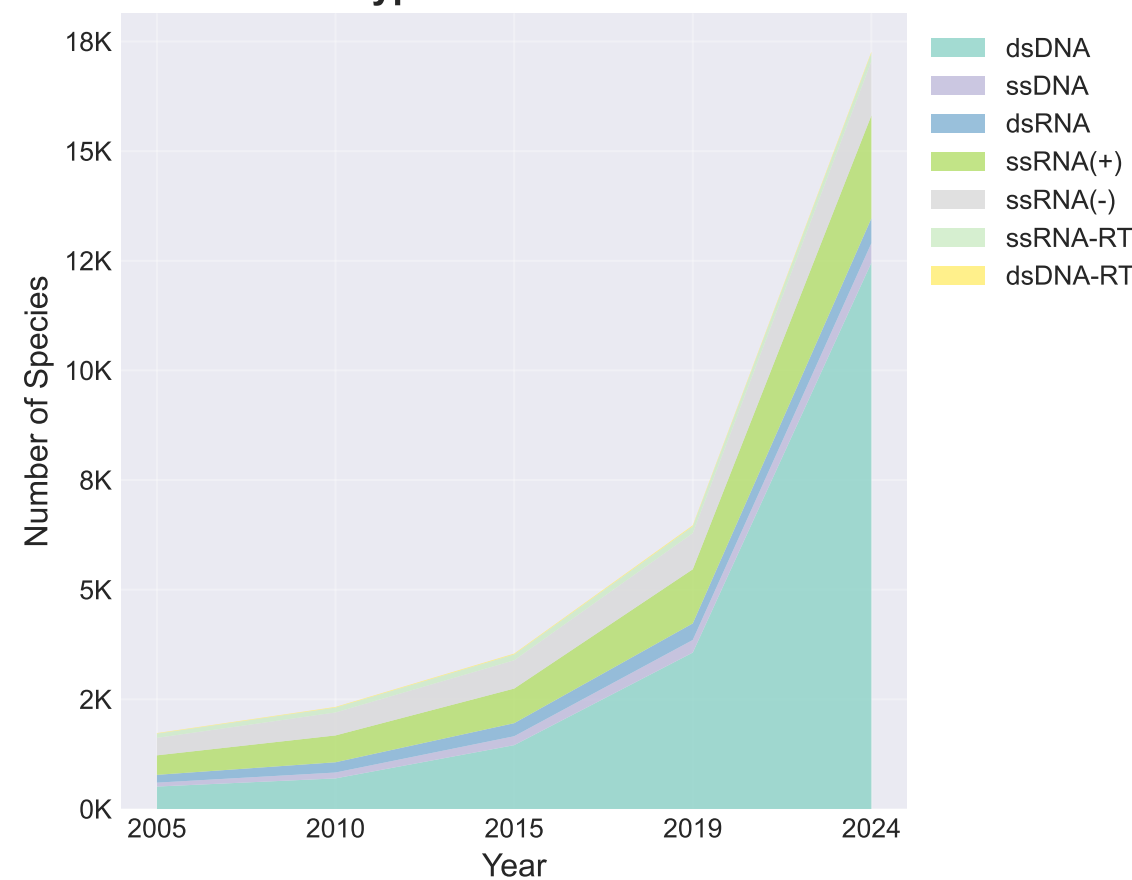
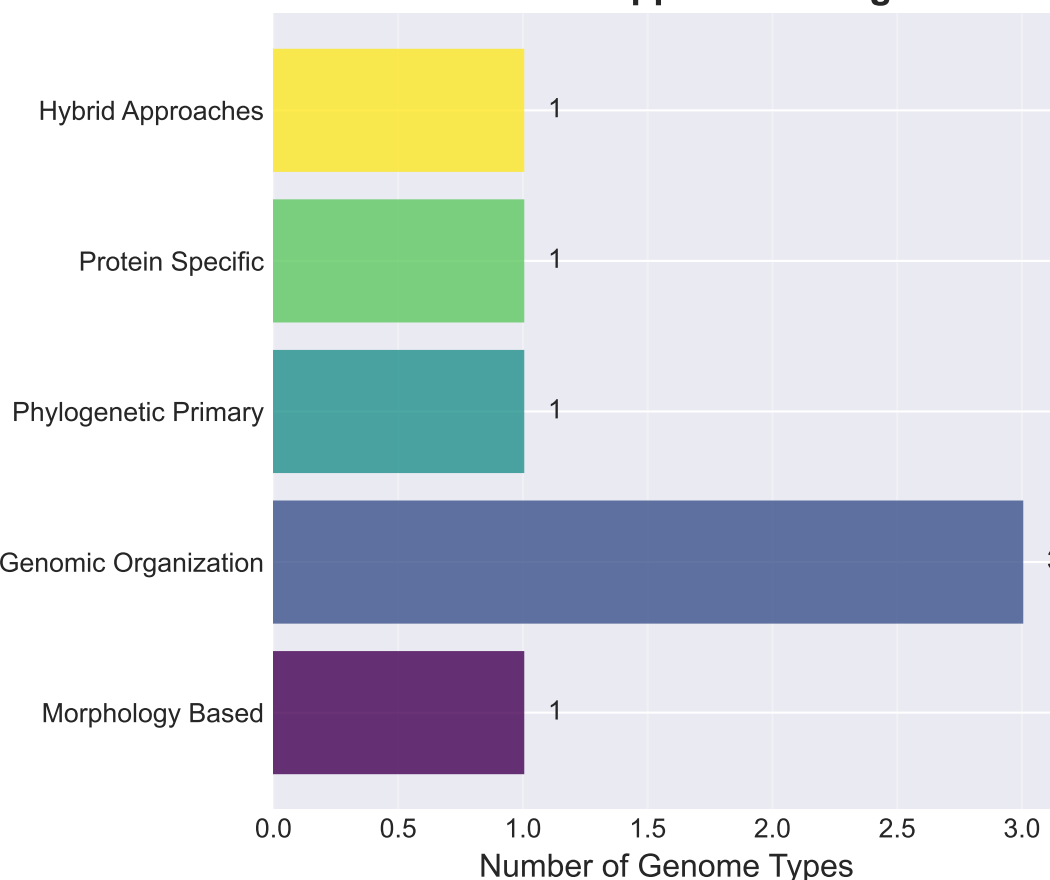


# Genome Architecture Constraints: How Structure Shapes Viral Taxonomy

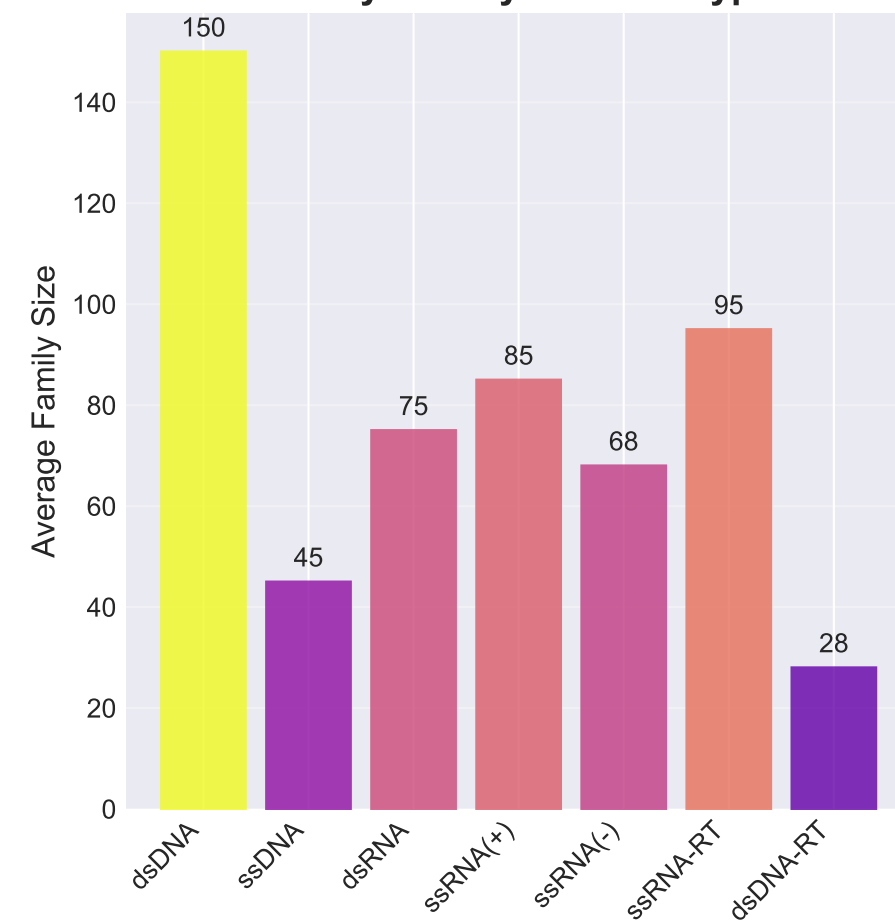
## Genome Type Distribution Evolution



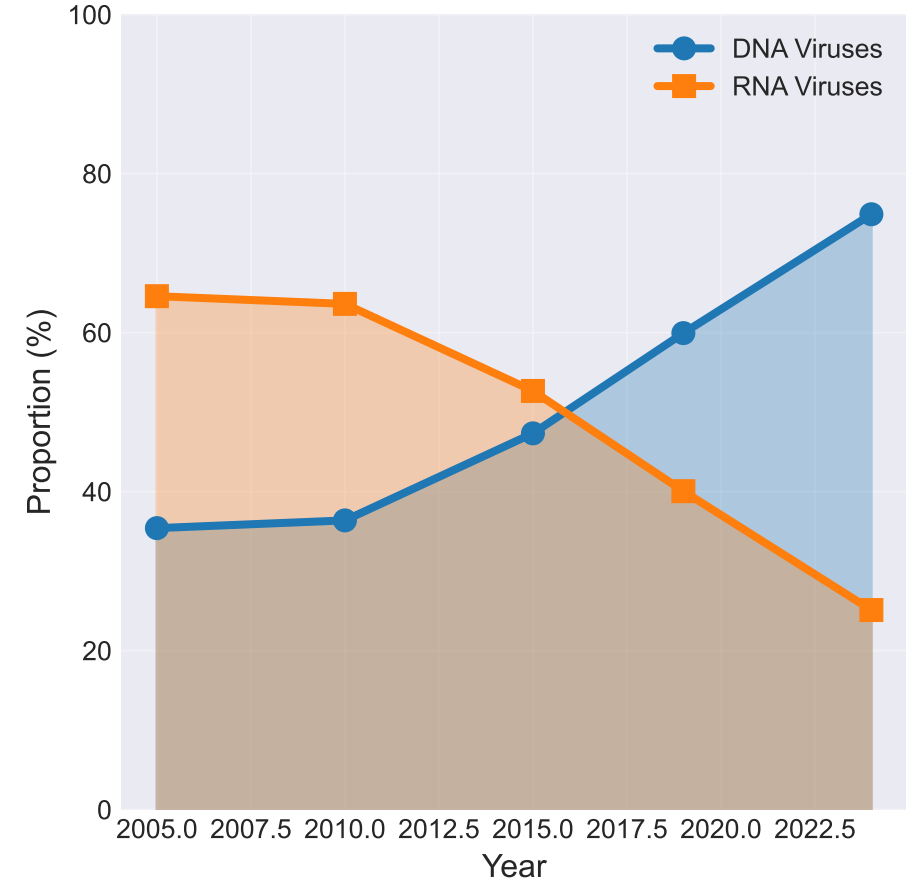
## Classification Approach Categories



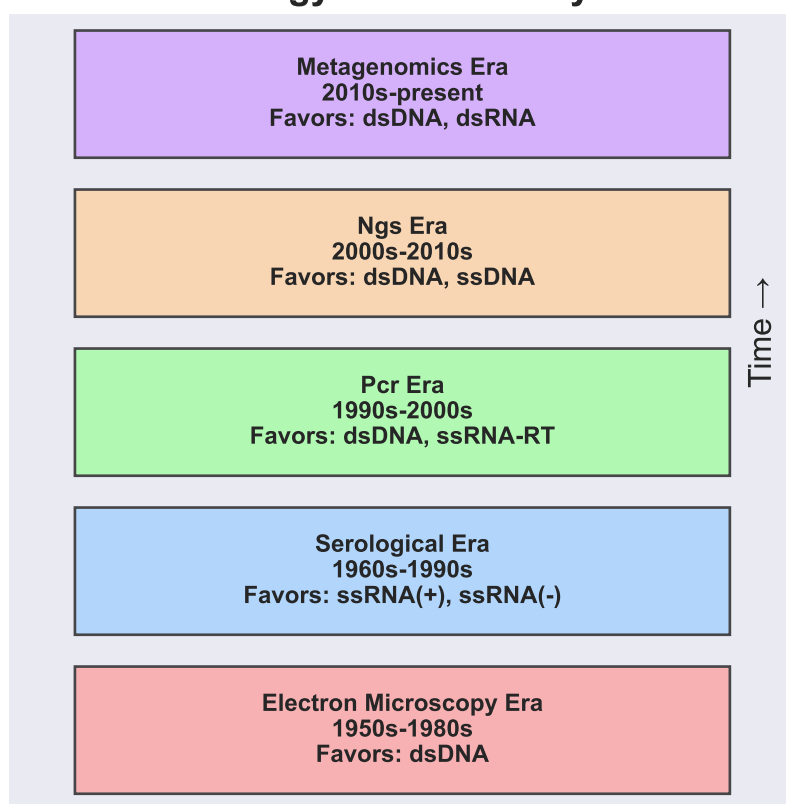
## Family Size by Genome Type



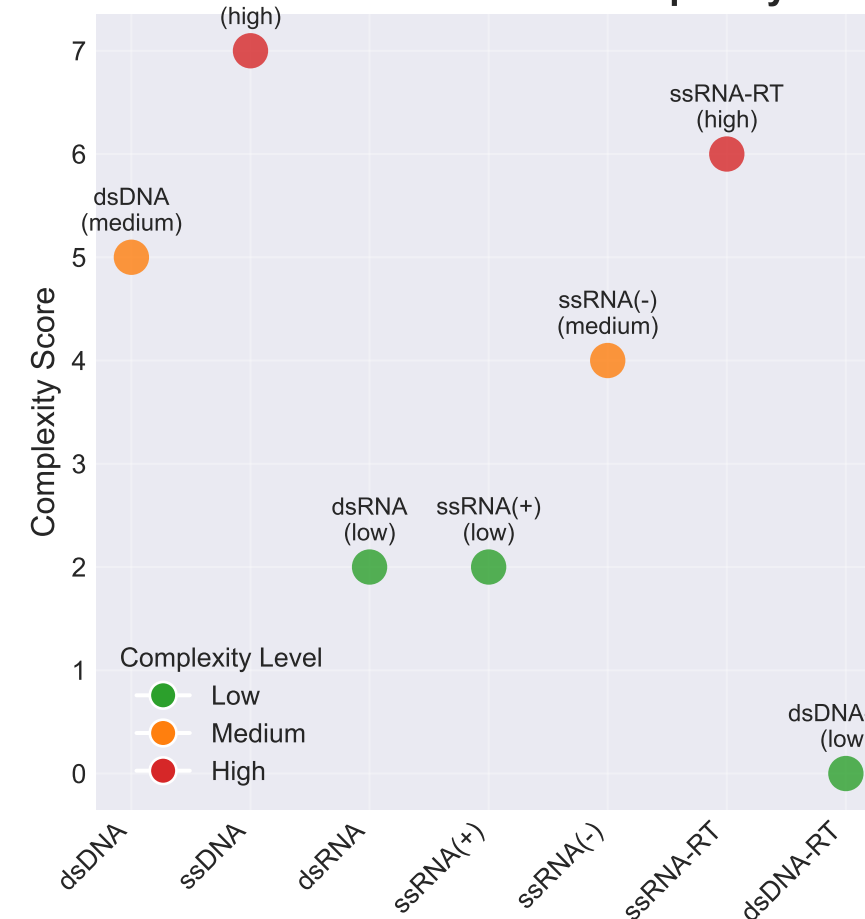
## DNA vs RNA Virus Evolution



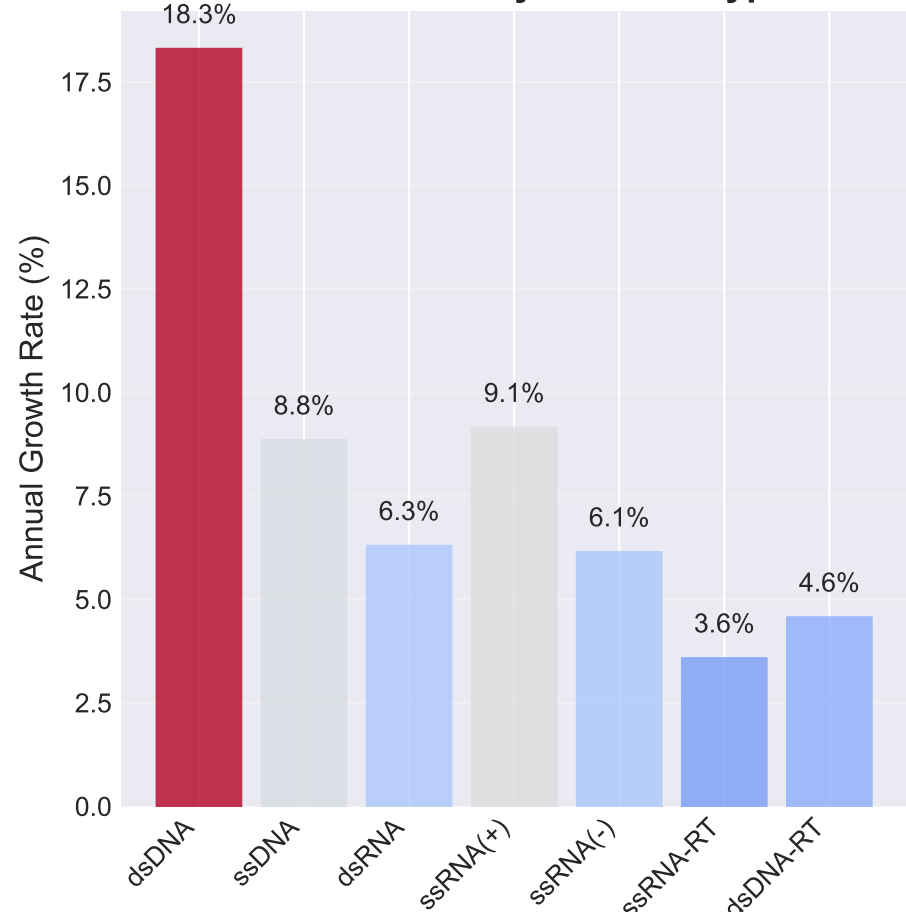
## Technology Era Discovery Bias



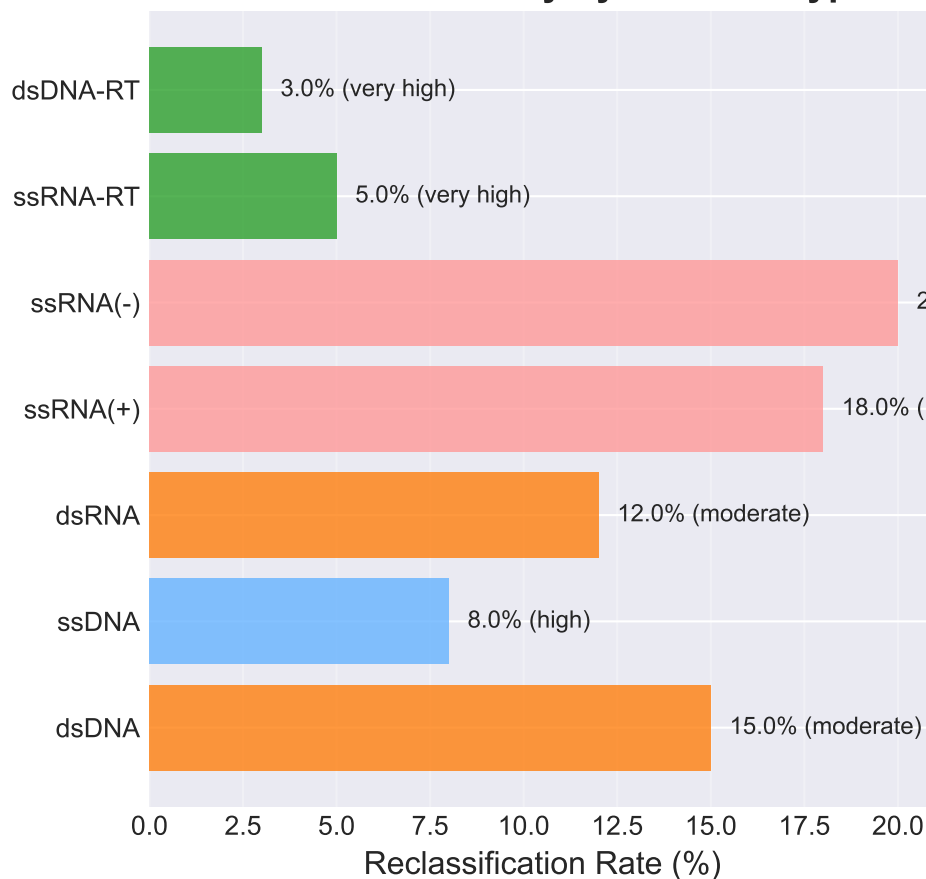
## Classification Method Complexity



## Growth Rates by Genome Type



## Taxonomic Stability by Genome Type



## Key Findings

### 1. dsDNA viruses dominate viral diversity

- 12,456 species (72.2%) driven by bacteriophage metagenomics
- Environmental sampling creates strong bias toward stable DNA genomes

### 2. Genome architecture determines classification complexity

- High complexity methods required for: ssDNA, ssRNA-RT
- Structural constraints, not just phylogeny, shape taxonomic approaches

### 3. Large genome types form larger, less stable families

- Average family sizes >100 species: dsDNA
- Complex genomes enable more species diversity but require frequent reorganization

### 4. Technology bias drives genome type discovery rates

- Fastest growing: dsDNA (18.3% annually)
- Current metagenomics revolution strongly favors DNA virus discovery