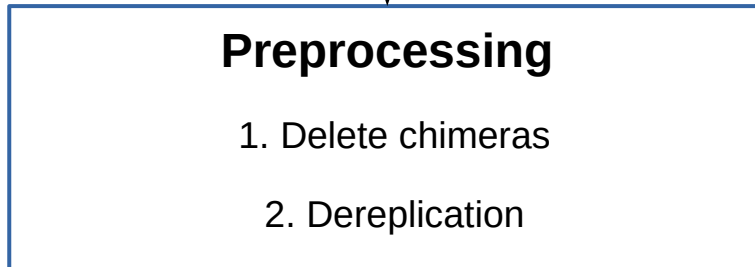


- Sequencing simulation from real 16S rRNA sequences (SILVA database)
- Simulation with 1000 species and powerlaw distribution, 100k reads per sample



- In mean, 80k reads after chimeras removal and 24k reads after dereplication

