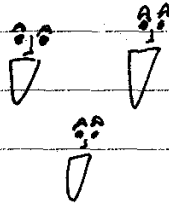


Gene Density

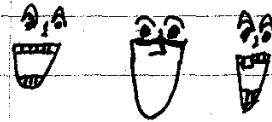
- microbes 80-90% are genes



Bacterial Genomes

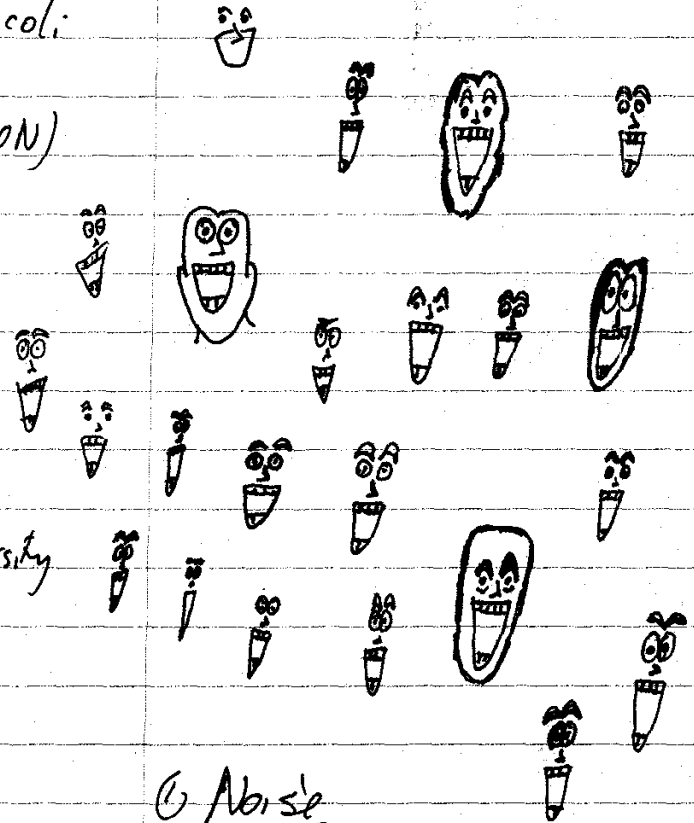
- Hamilton Smith + H. influenzae
- gaps were regions that were toxic in E. coli
- things that were found

① repeats in front of genes (MOXON)
- found in front of 100's of genes



② M. genitalium - v. small genome

- 470 genes
- strand bias
- 1/4 of genes are novel
- splice variation to generate diversity



③ M. jannaschii

- autotroph (CO₂, H₂)
- 50% of genes have no match

④ A. fulgidus

① Noise

② % Sim. comparisons between genomes not meaningful

③ why phylog. works

④ % sim still accurate for most