Understanding Microbial Diversity in an Unusual Lake: Fayetteville Green Lake, NY

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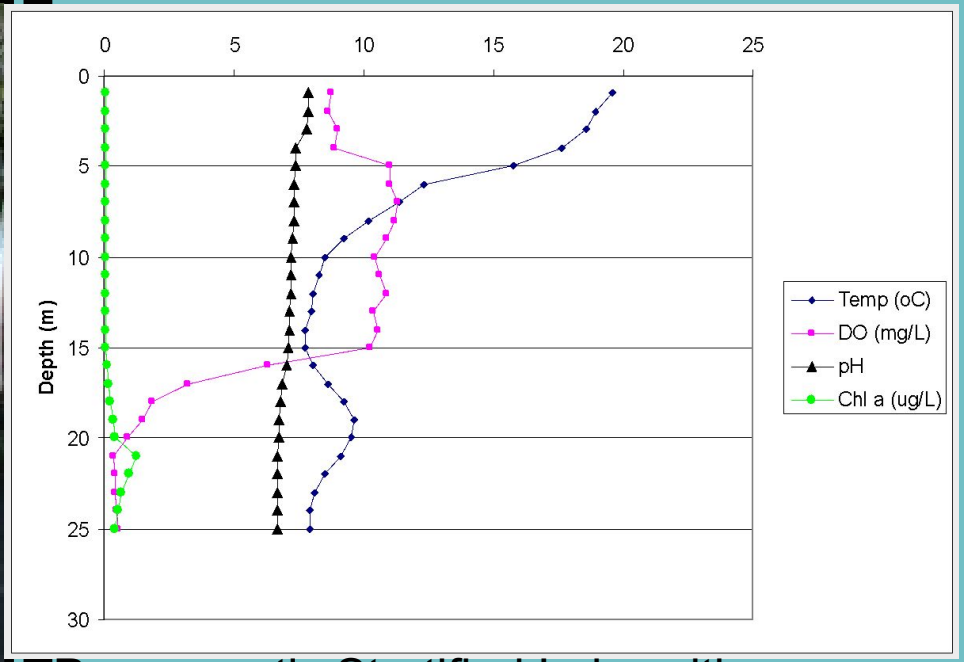
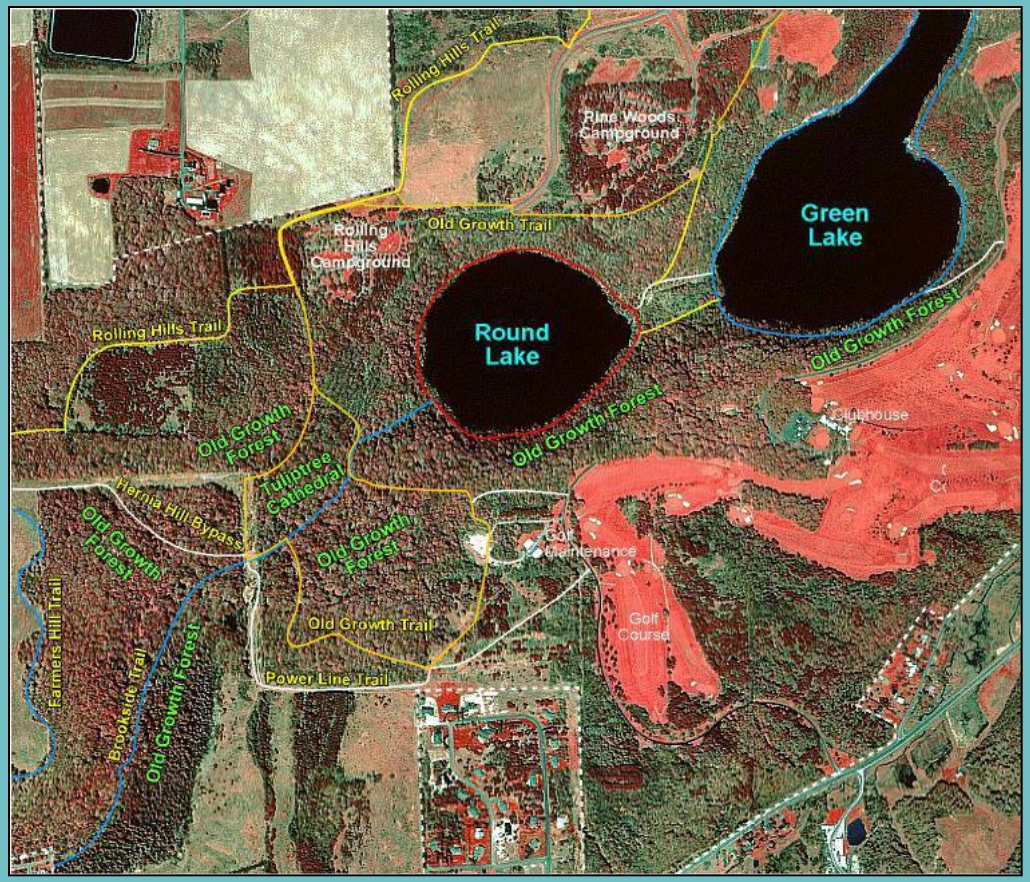
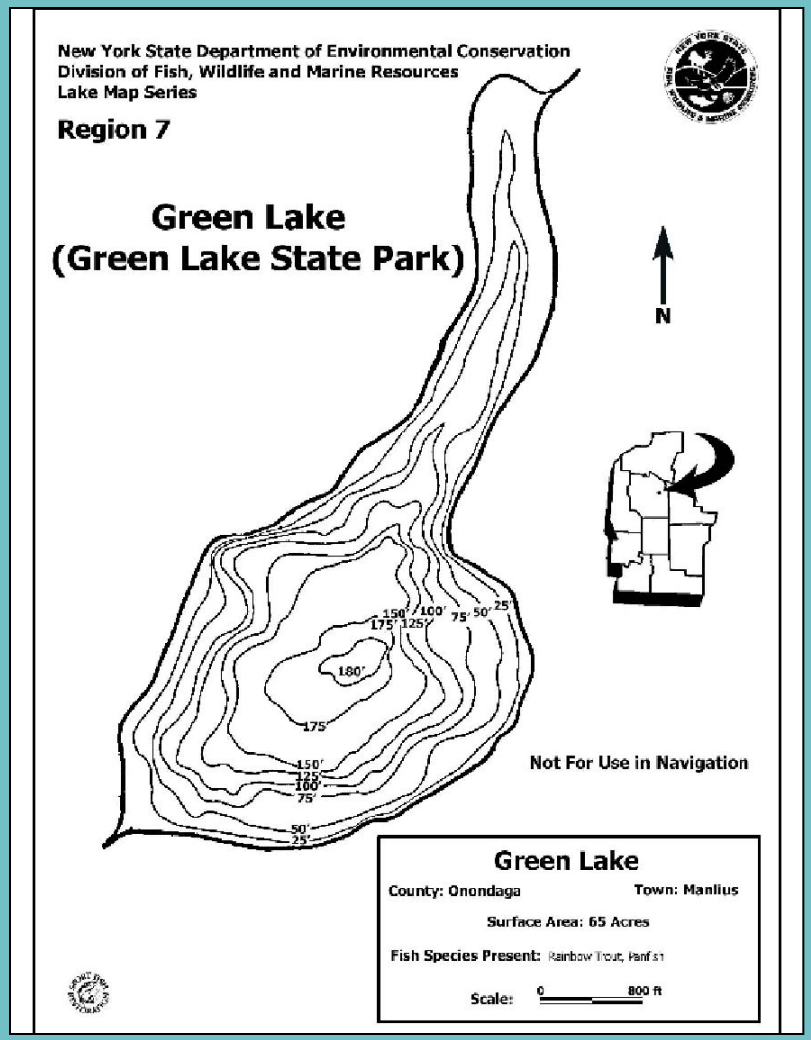
Ed Harcourt, Mathematics, Computer Science, and Statistics



Permanently Stratified Lake with upper oxygenated layer and lower anaerobic layer



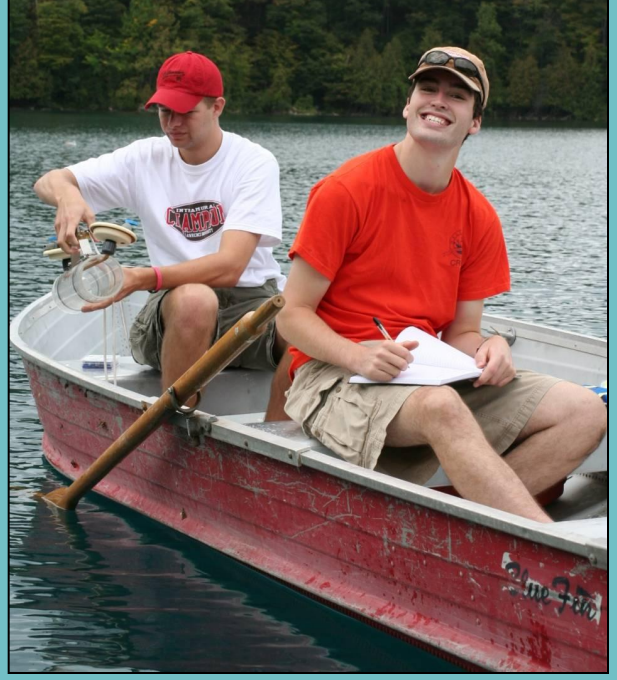


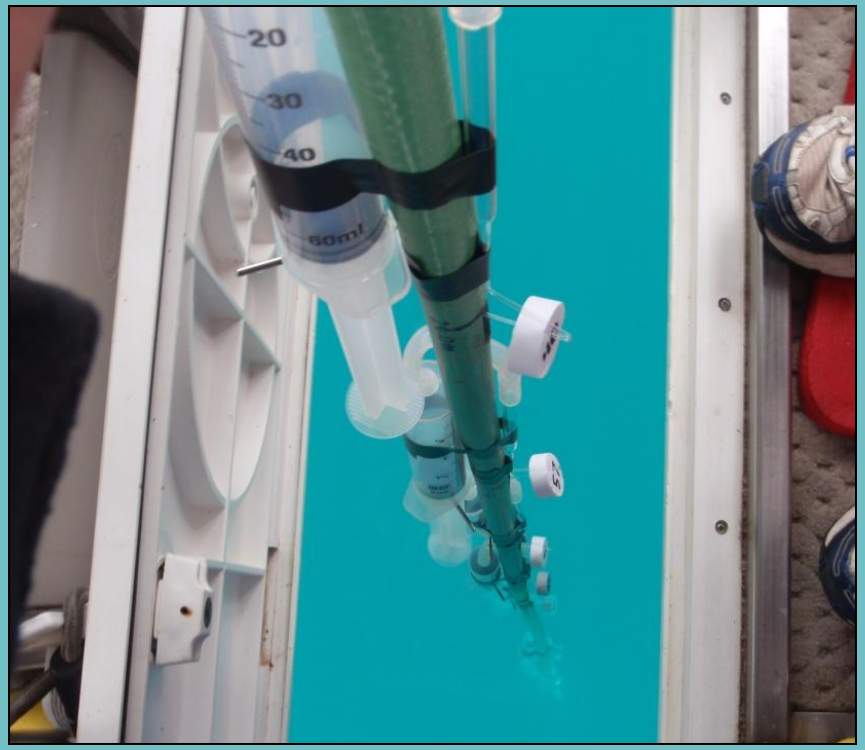
- "TERRA: The Earth Restoration and Renewal Alliance." The copyright date is 2003. Courtesy of Dr. E. A. Schiff

Microbialites and Whiting Events

Why Study Green Lake Microbial Communities?

- Analog of early ecosystems
- Model system for ancient anoxic oceans and hypoxic zones in lakes (e.g. Great Lakes)
- Spatial separation in response to different environmental gradients (O_2, $S0_4^-/H_2S$, NO_3^-/NH_4^+, CH_4)
- Good environment for teaching about microbial diversity – diverse metabolisms




20
30
40
60ml

Life at the Chemocline

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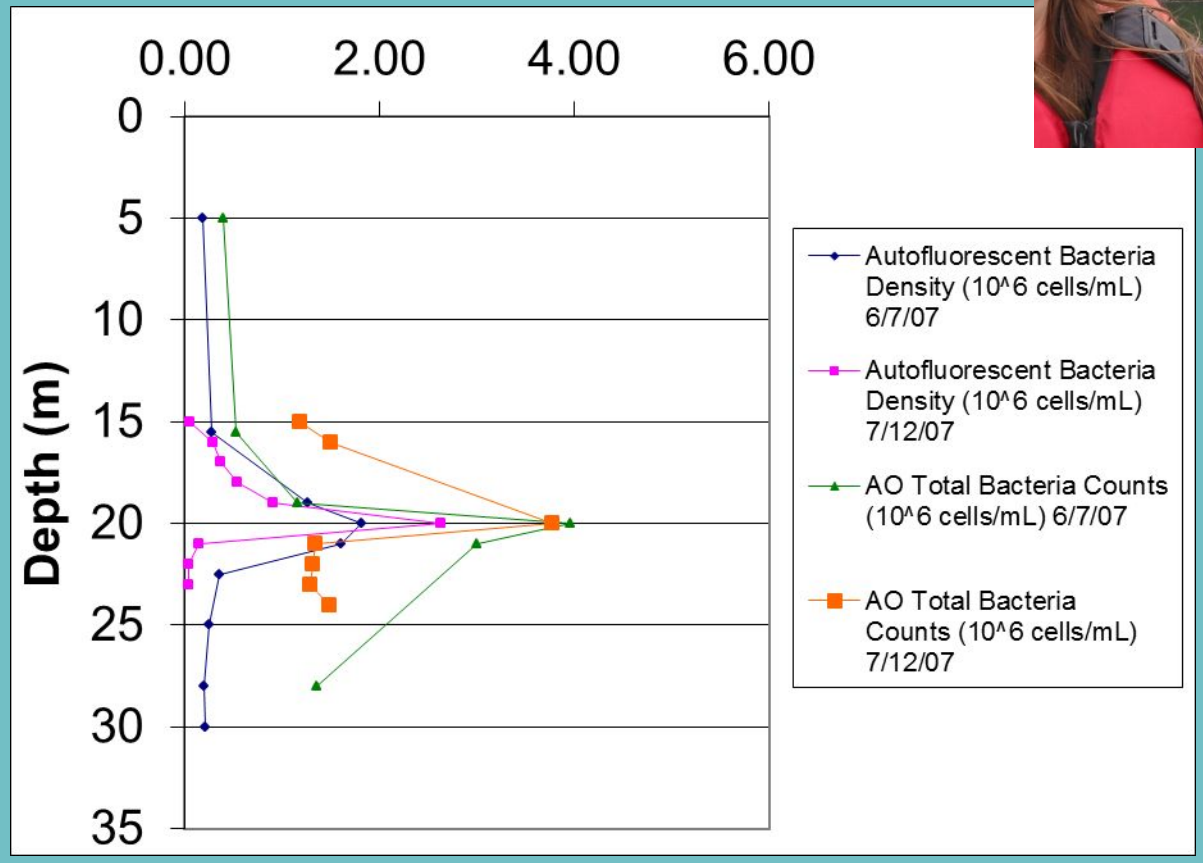
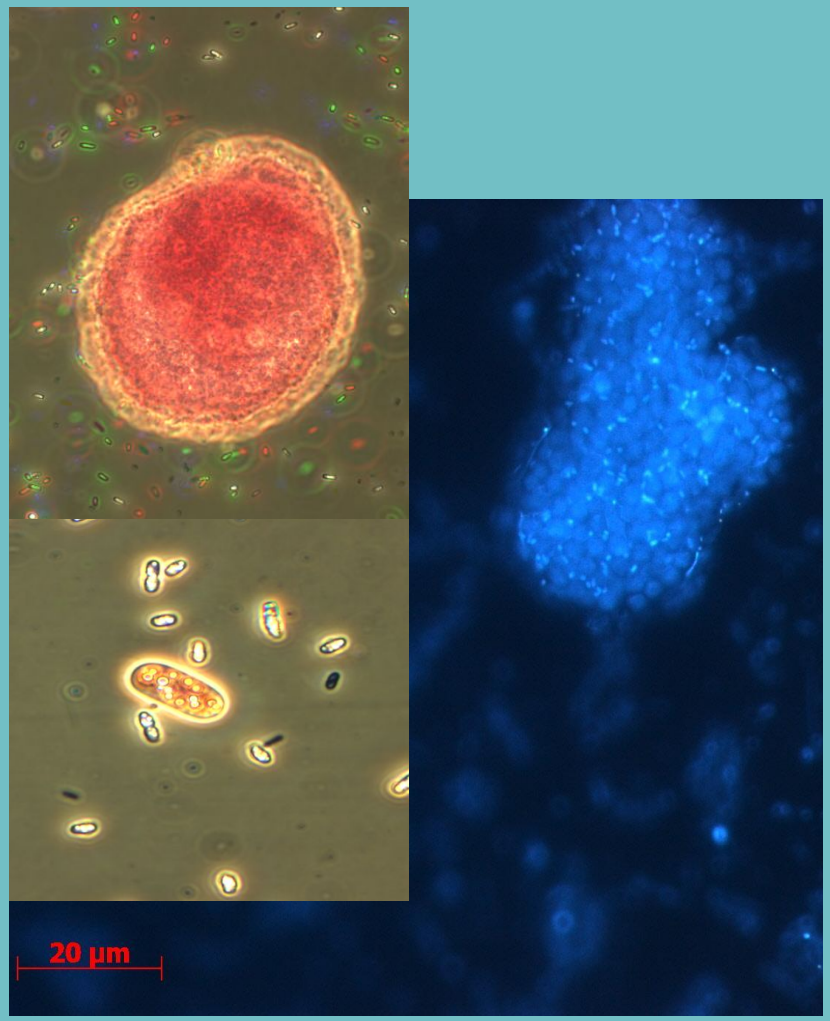


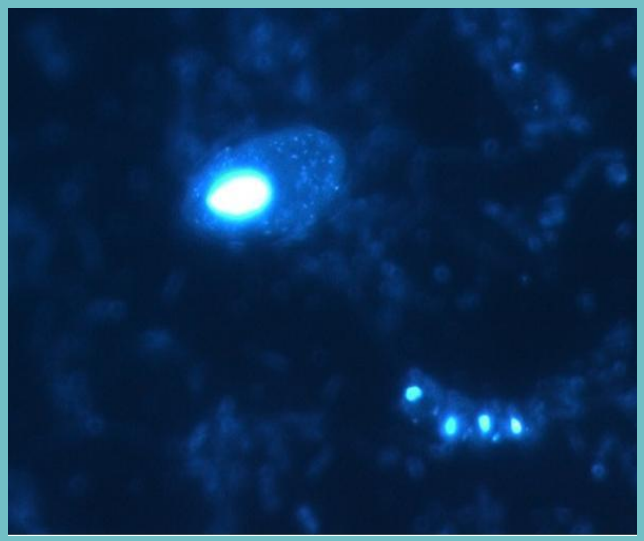
Vertical Stratification of Bacterial Types

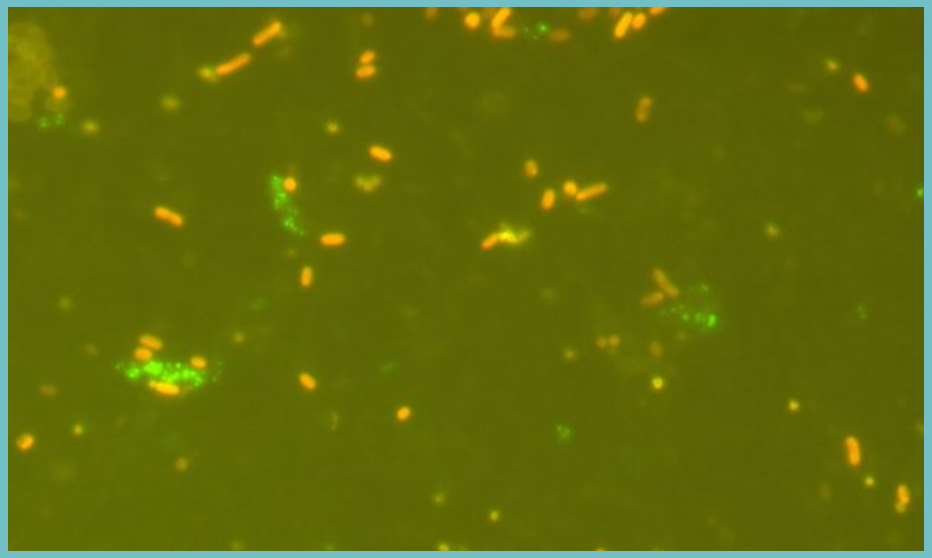
High concentration of bacteria at 20 m

Pink layer – anaerobic purple photosynthetic bacteria

Fluorescence and light microscopy
in situ hybridization using specific probes

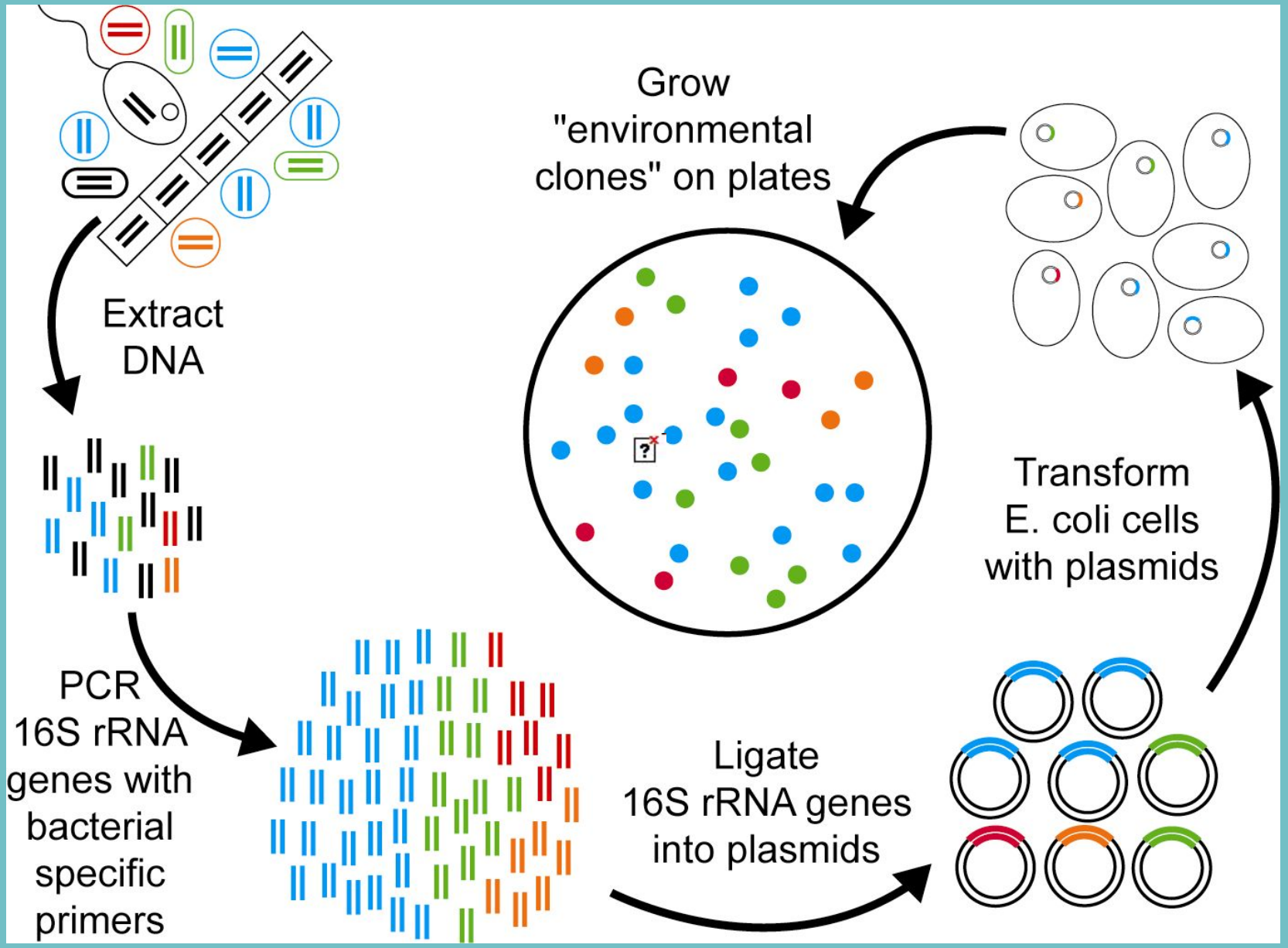




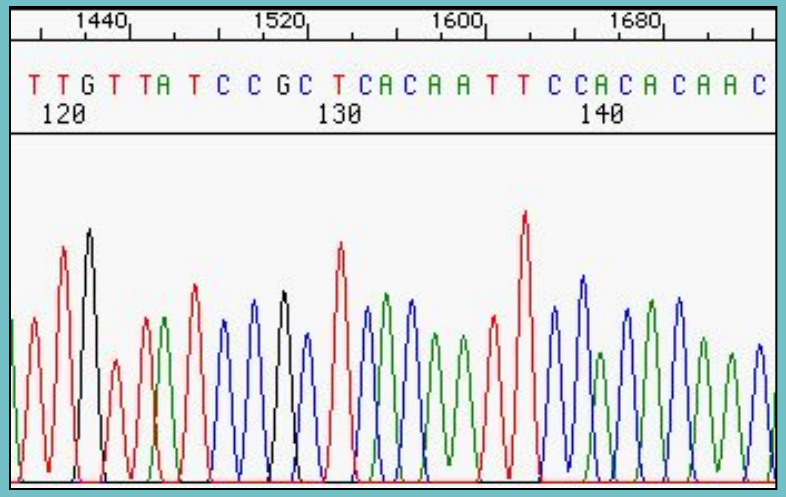


Purple sulfur bacteria

Environmental 16S rRNA Clone Library



Schematic courtesy of B. Crump



Chromatogram from ABI DNA Sequencer

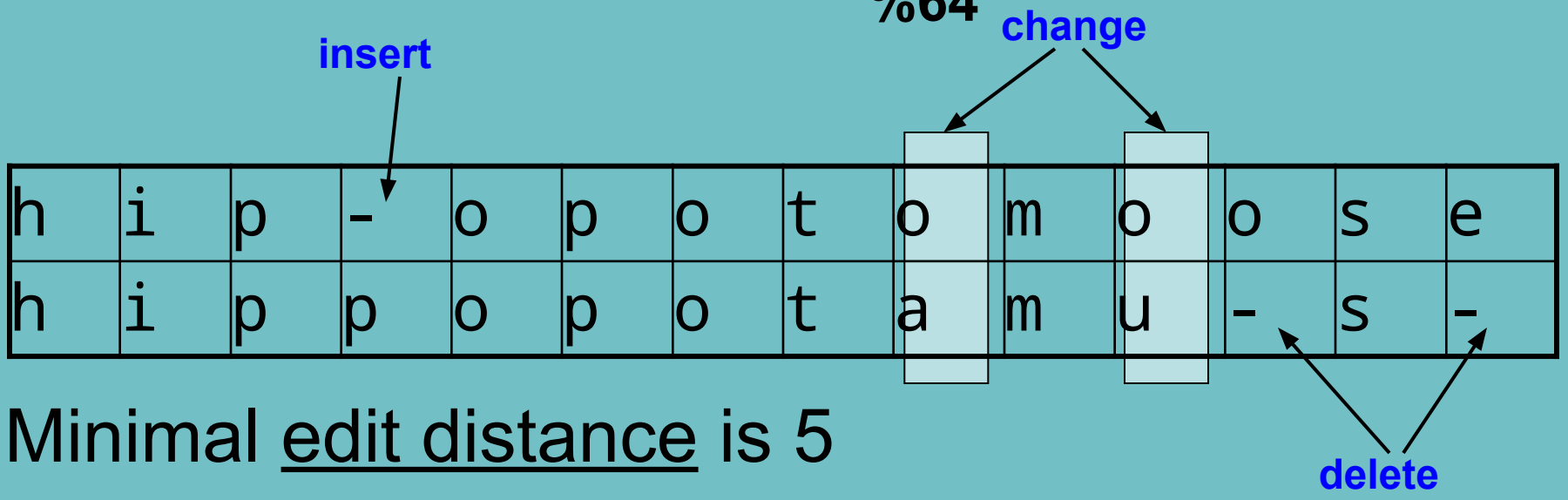
```
>16s28M6_08A01
AGAGTTTGATCCTGGCTCATTATTAACGCTAGCGGCAGGCCTAATACATGCAAGTTGAA
CGGCAGCACGGGTAGCAATACCTGGTGGCGAGTGGCGCACGGGTGCGTAACGCGTATGC
AACCTACCTTTGACTGGAGAATAGCCCCGAGAAATCGGGATTAATACTTCATAATATTA
TAGGATGGCATCATTCTATAATTAAAGCTCCGGCGGTCTTAGATGGGCATGCGTGACAT
TAGTTTGTTGGTGAGGTAACGGCTCACCAAGACTACGATGTCTAGGGGTTCTGAGAGGA
TTTTCCCCCACACTGGTACTGAGACACGGACCAGACTCCTACGGGAGGCAGCAGTAAGG
AATATTGGGCAATGGACGCAAGTCTGACCCAGCCATGCCGCGTGCAGGATGACAGCCCT
ACGGGTTGTAAACTGCTTTTGTACGGGAAAAATTCCCTGGTCGTGTACCGGGGTTGATG
GTACCGTAAGAATAAGCATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGAT
GCAAGCGTTATCCGGATTCATTGGGTTTAAAGGGTGCGCAGGCGGAATGATAAGTCAGT
GGTGAAATCCTACAGCTTAACTGTAGAACTGCCATTGATACTGTTGTTCTTGAGTACAT
```

Sequence Similarity - Edit Distance

The minimal number of *editing operations* applied to a string **S** to convert it into a string **T**

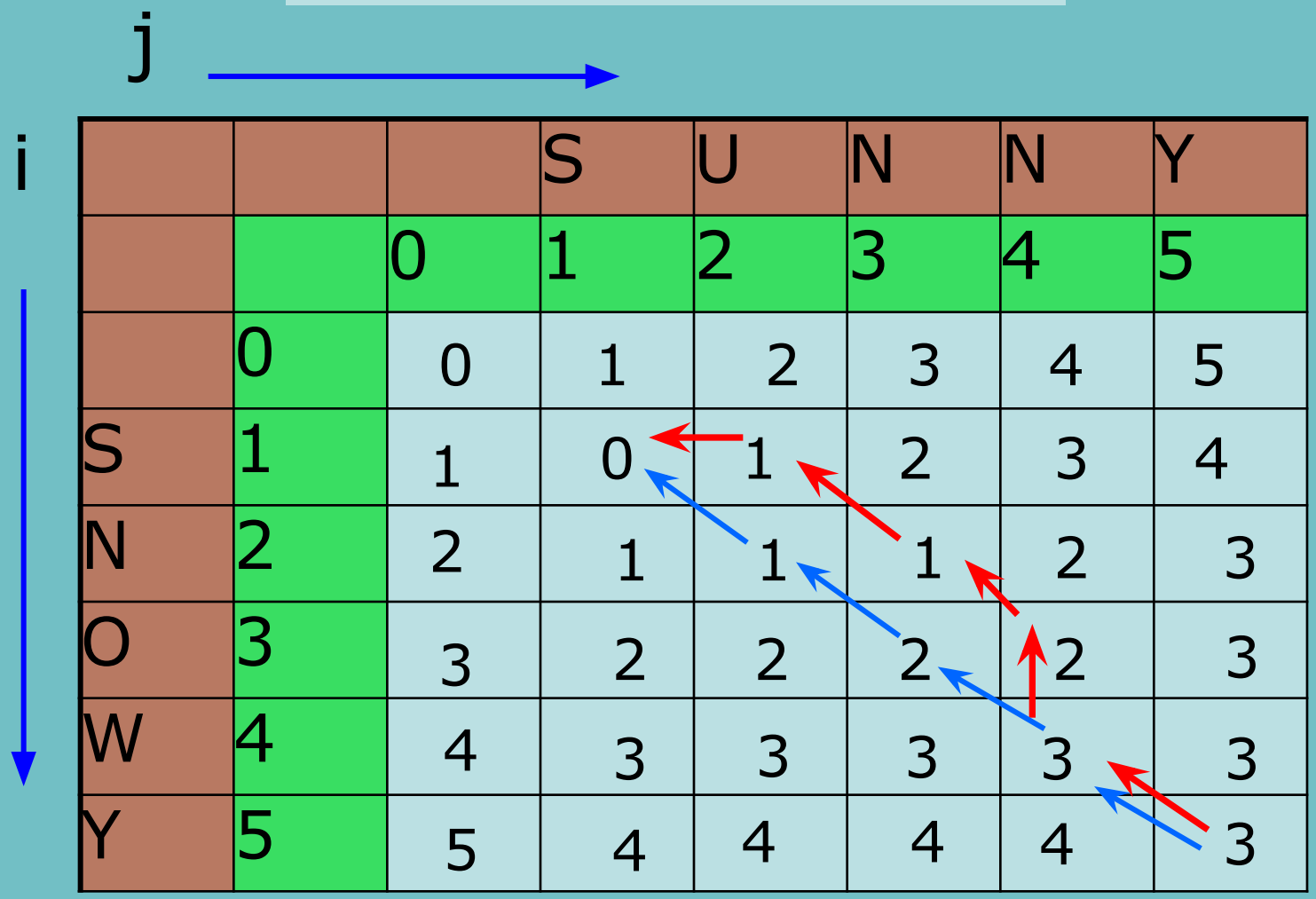
```
S = hipopotomoose
T = hippopotamus
```

Percent Identical 9/14 = %64



Minimal edit distance is 5

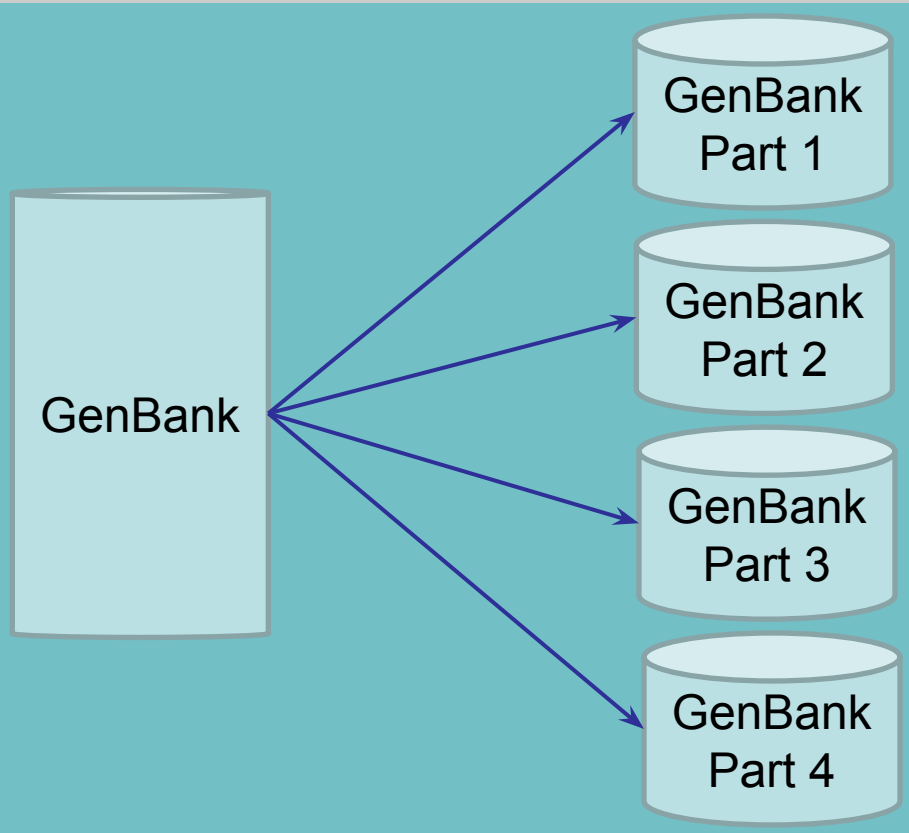
distance(i,j)

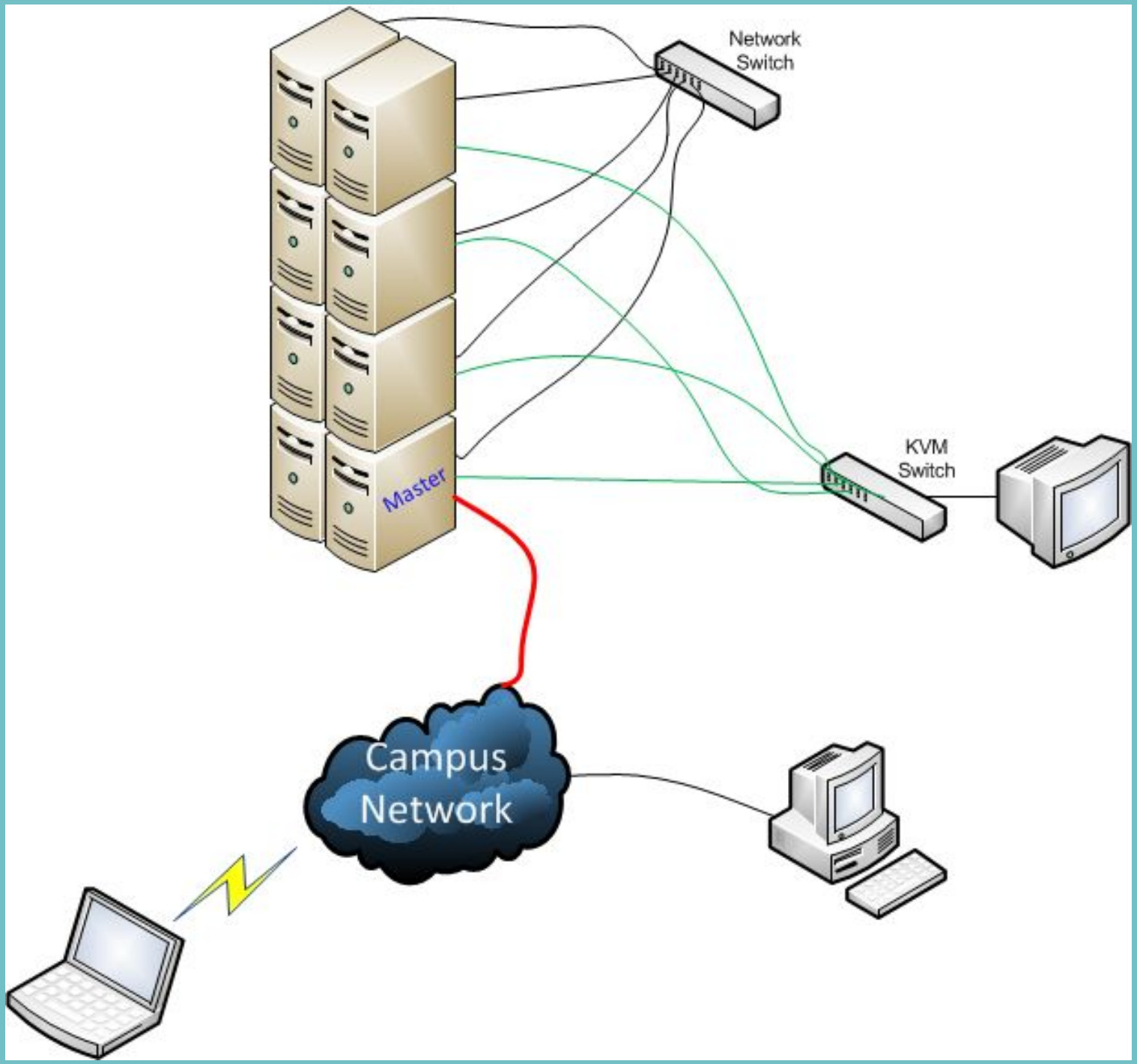


Find shortest path from (5,5) to (0,0)

GenBank > 135 million sequences

```
target = aggtacggatcaaacgtagct
for each sequence in GenBank:
  d = distance(target,sequence)
```




Network
Switch
KVM
Switch
Master
Campus
Network

High Performance Computing On the Cheap

- Eight dual-core machines
- Each/2GB RAM
- 2TB HD

CSBIOHPC

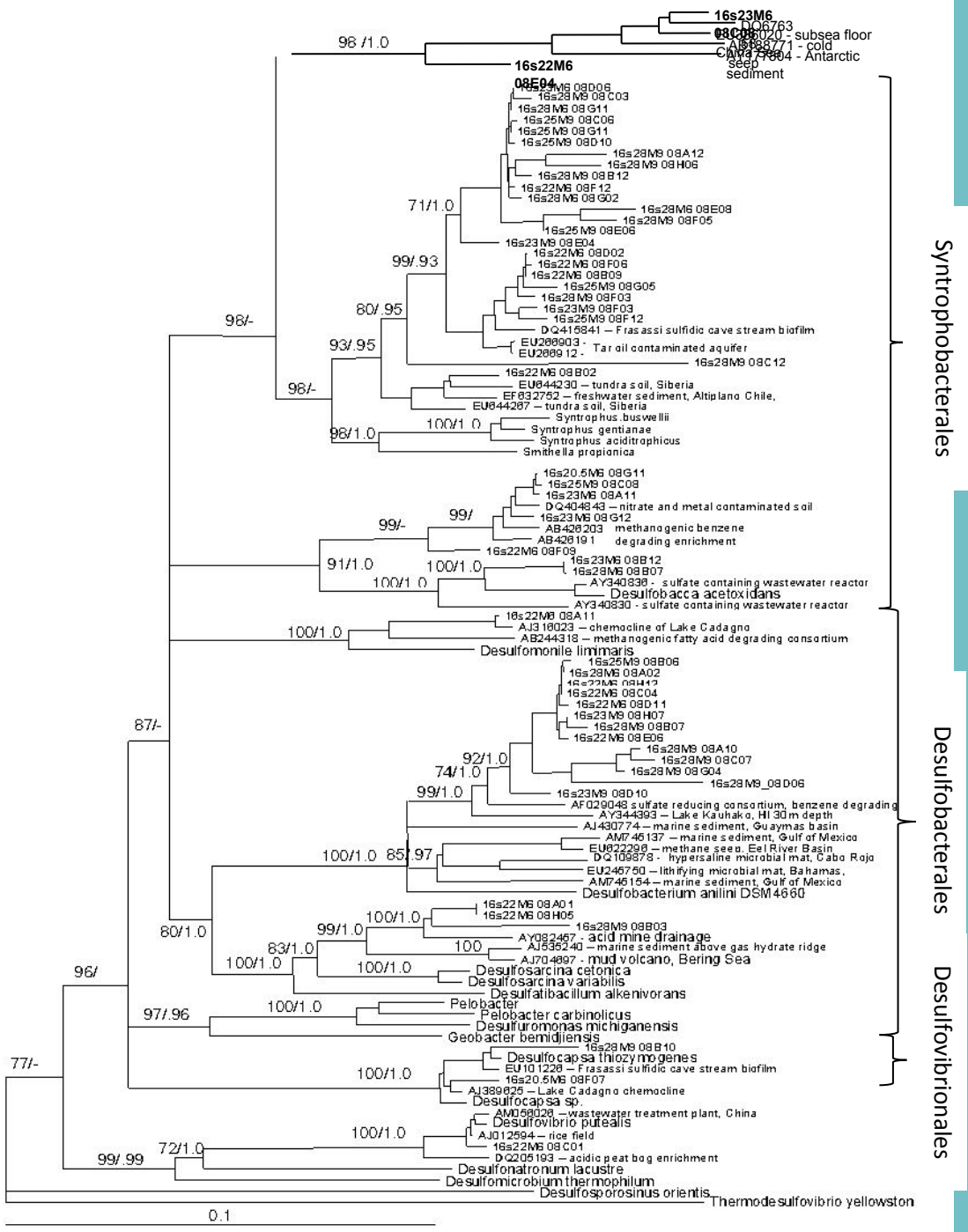
CS, Biology, High Performance Computer

- NSF Grant $179K (Ana, Ed, Emily, Lorraine, Rich)
- 128 Processors
- 1TB RAM
- 2TB HD

Phylogenetic tree of Deltaproteobacteria from FGL

Our sequences group with 5 different clades of sulfate reducers

Many sequences from lower depths fall into the Syntrophobacterales, a poorly understood group



Conclusions:

5 groups of Deltaproteobacteria dominate the sulfate reducing bacteria in FGL

Phylotypes of SRBs and other bacteria do not differ significantly between whiting and non-whiting events

One species of sulfate reducing bacterium is closely related to bacteria that perform sulfur disproportionation (uses sulfur and generates both H_2S and sulfate) and may be living in consortium with colonial purple sulfur bacteria

Currently we are:

Characterizing other components of the microbial community, including Archaea and Eukaryotes using clone libraries

Characterizing functional genes responsible for methanogenesis, and ammonia oxidation.

Developing microarray approach for surveying sulfate reducing bacteria at different depths and times.

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Adam Bleau ’09
Ryan Wolfe ‘09

Rachel Yalowich ’12
Ryan Ross ’12
Greg Wolfe ‘12

Computing Minimal Edit Distance

We don't know which will result in smallest edit distance: change, delete, or insert

Try them all and take the smallest

```
distance(i,j) =
 min (
    1 + distance(i,j-1),      // insert

    1 + distance(i-1,j),      // delete

    if s[i] ≠ s[j]
      1 + distance(i-1, j-1) // change
)
```