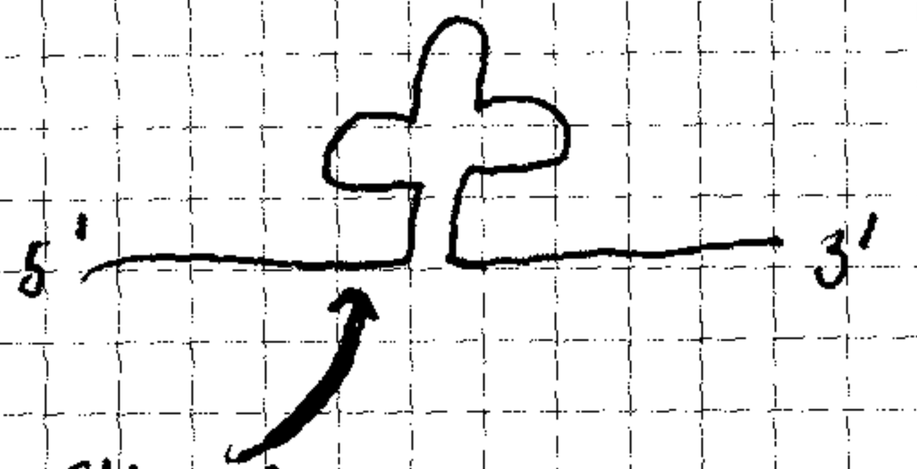
2/7/90

Norman Pace

Diversity can be invisible.

① align homologous sequences
② count differences in each pair of sequences
③ calculate the evolutionary distance between the sequences
④ define the tree that best fits ALL distances

Structural Analysis



- RNase P · cuts 5' end of tRNA
  - v. similar in E. coli & B. subtilis
  - RNA and protein
    RNA is catalytic unit

- what is structure of RNA subunit of RNase P
  2°
  3°

- difficulties
  ① short binding regions (~5 bp) but only 4 diff. bases so very many poss. solutions
  ②

3 methods of working out 2° structure

①

② minimum energy

③ phylogeny

- compare E. coli & B. subtilis since NOT v. similar can pick a closer relative (based on RNA phylogeny)

- see when similar complements occur in closely related organisms.

After get general 2° structure

① deletion experiments

- moved "gaps" across molecule and activity remained.

② see what deletions lead to damage

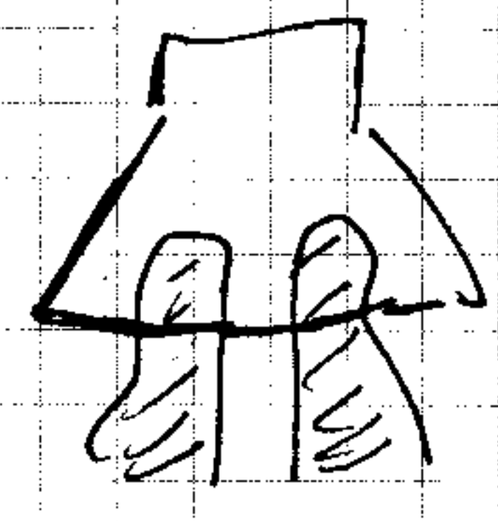
③ see what deletions do nothing

w/ conserved structure that should be the region of conserved function so can remove other sequences

Upper Temperature limits of life

① put contact slides down

② vent caps

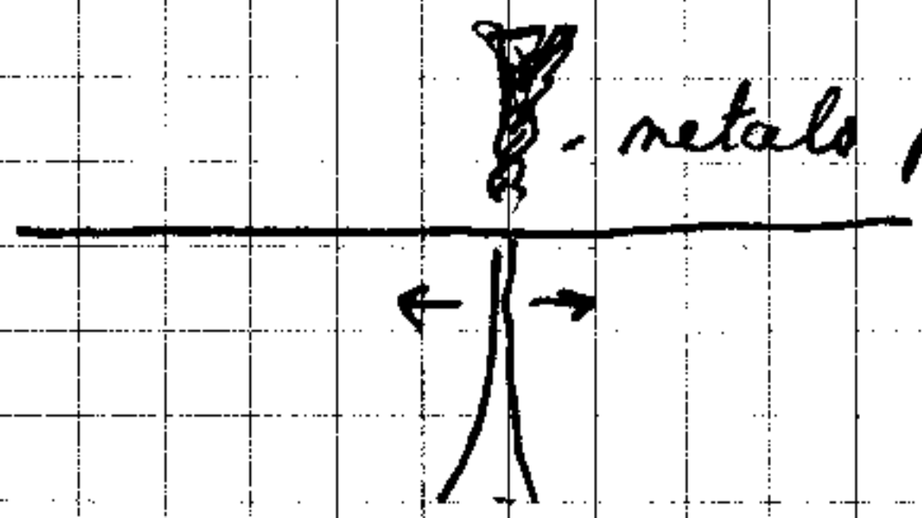


May be able to do phylogeny on
<u>living</u> cells through oligonucleotide
probes.

① probes for all life
② kingdom level probes
③ species " "

(Growth <u>rate</u> determines # of ribosome
(or is it vice versa)

Hydrothermal Vents



but

can't cultivate symbionts

- phylogeny may tell a great deal about general bioches of symbionts

Methods of Characterizing Microbial World

Problems

- Cultivation difficult

So what use --

- Phylogeny

- phylogeny can help guide future research (such as was used for RNAse P 2° structure)

DNA

↓

Library

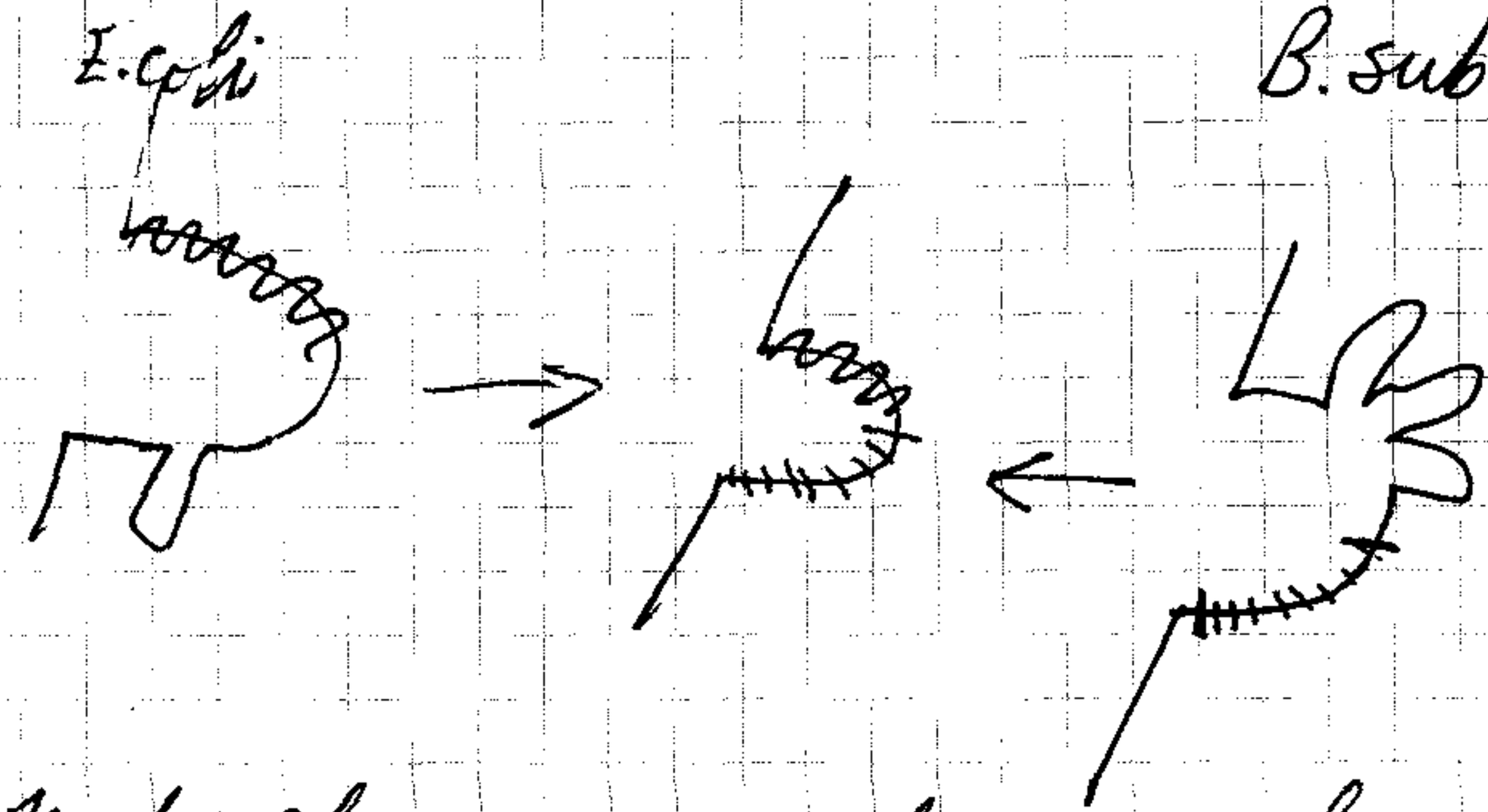
↓

165 clones

↓

Sequences

but there is a problem because you dont know what to learn



Make chimera - combine simpler regions of two molecules.